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We would appreciate any comments on this publication.

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magellan Intended Use
See 1.2 Intended Use of magellan

About this Manual
magellan is a universal data reduction package used to analyze data generated
from microplate assays. It is designed for professional use only.

This manual instructs how to:
- Install the software
- Operate the software

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- **Note**
  *Gives helpful information.*

- **Caution**
  *Indicates a possibility of instrument damage or data loss if instructions are not followed.*

- **WARNING**
  *INDICATES THE POSSIBILITY OF SEVERE PERSONAL INJURY, LOSS OF LIFE OR EQUIPMENT DAMAGE IF THE INSTRUCTIONS ARE NOT FOLLOWED.*
1. Introduction ........................................................................................................... 13
  1.1 Area of Application .................................................................................. 13
  1.2 Intended Use of magellan ....................................................................... 14
  1.3 User Profile .............................................................................................. 14
    1.3.1 Professional User – Administrator Level .................................. 14
    1.3.2 End User or Routine User .......................................................... 14
  1.4 Specifications ............................................................................................ 15
    1.4.1 General .......................................................................................... 15
    1.4.2 System Requirements .................................................................. 15
    1.4.3 Reader Compatibility ..................................................................... 17
  1.5 Software Installation Procedure .............................................................. 18
    1.5.1 Automatic Software Setup Program ........................................... 18
    1.5.2 Installation Qualification – IQ ...................................................... 19
    1.5.3 Operation Qualification – OQ ...................................................... 19
    1.5.4 System Recovery ........................................................................... 20
    1.5.5 Automatic Software Removal ..................................................... 22

2. Start Working with magellan .............................................................................. 23
  2.1 User Interface ............................................................................................. 23
    2.1.1 Folder Handling ........................................................................... 23
  2.2 Components & Terms – Basic Logic of magellan ...................................... 25
    2.2.1 Method (.mth) ............................................................................ 25
    2.2.2 Sample ID List (.smp) .................................................................. 26
    2.2.3 Workspace (.wsp) ......................................................................... 26
    2.2.4 Standard Curve (.std) ................................................................. 26
    2.2.5 File Types Used with magellan .................................................... 26
  2.3 User Interface – Wizard List ....................................................................... 27
    2.3.1 Start Measurement Wizard ......................................................... 27
    2.3.2 Evaluate Results Wizard ............................................................. 28
    2.3.3 Attach Signature Wizard ............................................................. 28
    2.3.4 Create/Edit a Sample ID List Wizard ........................................... 28
    2.3.5 Create/Edit a Method Wizard ..................................................... 28
    2.3.6 Icons ............................................................................................ 28
    2.3.7 Standard Elements ......................................................................... 30
    2.3.8 The Help Button ........................................................................... 31
    2.3.9 The Welcome Dialog Box ............................................................ 31
    2.3.10 Shortcuts List .............................................................................. 31
  2.4 Starting magellan ......................................................................................... 32
    2.4.1 Starting Standard Version .............................................................. 32
    2.4.2 Starting Tracker Version ............................................................... 32
  2.5 Connecting an Instrument ......................................................................... 35
2.5.1 Instrument Connected .......................................................... 35
2.5.2 Demo Mode .......................................................................... 36
2.5.3 Connecting an Instrument of the Infinite Series .................. 36
2.5.4 Connecting a Stacker .......................................................... 36

2.6 Licensing magellan .................................................................. 37
  2.6.1 Registration Wizard .......................................................... 37

3. Instrument Control & Settings .................................................... 41
  3.1 Instrument Options .................................................................. 41
    3.1.1 Movements ...................................................................... 41
    3.1.2 Temperature Control ....................................................... 41
    3.1.3 Heating Dialog (Temp Control for Infinite Series Readers) ................................................................. 42
    3.1.4 Lamp/Laser Control ........................................................ 43
    3.1.5 Injector Control ............................................................... 43
    3.1.6 Dispense Only ................................................................. 43
  3.2 Setup & Service Options ............................................................. 43
    3.2.1 Change Instrument ......................................................... 43
    3.2.2 Define Filter Slides .......................................................... 43
    3.2.3 Insert Transport Lock ...................................................... 43
    3.2.4 Optimize Z-Position ........................................................ 44
    3.2.5 Plate Geometry Editor ..................................................... 44
  3.3 Log Files .................................................................................. 50

4. Create/Edit a Method Wizard ....................................................... 51
  4.1 Introduction ............................................................................. 51
  4.2 Define the Measurement Parameters .......................................... 52
    4.2.1 Measurement Types ....................................................... 53
    4.2.2 Measurement Parameters ................................................. 54
  4.3 Define Evaluation ..................................................................... 56
    4.3.1 The Create/Edit Method Overview Window ....................... 56
    4.3.2 Method Layout: How to Define a Plate Layout .................. 60
    4.3.3 Method Layout: Conc., Dil. and Ref. Values ....................... 65
    4.3.4 Precalculation: Polarization Data Reduction .................... 68
    4.3.5 Precalculation: Spectra Data Reduction ............................ 69
    4.3.6 Precalculation: Cuvette Data Reduction ........................... 73
    4.3.7 Transformed Data: Add New Transformation .................... 73
    4.3.8 Kinetic: Kinetic Data Reduction ........................................ 76
    4.3.9 Kinetics Transformations:
      Add New Kinetics Transformations ..................................... 80
    4.3.10 Concentrations: Standard Curve ..................................... 81
    4.3.11 Concentrations Transformations:
      Add New Concentration Transformations ............................ 85
    4.3.12 Evaluate Data: Cutoff Definition ..................................... 86
    4.3.13 Evaluate Data: QC Validation .......................................... 87
    4.3.14 Data Handling: Data Export ......................................... 89
    4.3.15 Data Handling: Printed Report ....................................... 93
4.3.16 Data Handling: Automated Data Handling ........................................ 98
4.3.17 Miscellaneous: User Prompts .................................................... 102
4.3.18 Miscellaneous: Number Format ............................................. 102
4.3.19 Miscellaneous: Method Notes ............................................. 103
4.4 Saving the Method ..................................................................... 103
4.4.1 Password Protection of Methods ........................................ 104
4.5 Multiplate Methods .................................................................. 105
5. Create/Edit a Sample ID List Wizard ........................................... 109
5.1 Introduction ............................................................................. 109
5.2 Create/Edit a Sample ID List ................................................... 109
  5.2.1 Create New Sample ID List ............................................... 110
  5.2.2 Import/Edit a Sample ID List ............................................ 112
  5.2.3 Import a Sample ID List .................................................. 117
  5.2.4 Saving the Sample ID List ............................................... 126
6. Start Measurement Wizard ...................................................... 129
  6.1 Introduction ........................................................................... 129
  6.2 Obtain Raw Data .................................................................... 130
    6.2.1 Obtain Raw Data with the Infinite Instrument ................ 131
  6.3 Run Strip Layout .................................................................... 132
  6.4 Use Predefined Method ......................................................... 133
  6.5 Start Favorite ......................................................................... 134
  6.6 Start Measurement with a Predefined or Favorite Method ...... 136
  6.7 Measurement Status ............................................................. 141
7. Evaluate Results Wizard .......................................................... 143
  7.1 Introduction ........................................................................... 143
  7.2 Select a File ........................................................................... 143
    7.2.1 File Selection Criteria .................................................. 144
  7.3 The Workspace Overview Window ........................................ 145
  7.4 Evaluate Results Tab ............................................................ 147
    7.4.1 Menus .......................................................................... 147
    7.4.2 Toolbar Menu: File ...................................................... 148
    7.4.3 Toolbar Menu: Edit ...................................................... 153
    7.4.4 Toolbar Menu: Instrument ............................................ 154
    7.4.5 Plate Layout Window .................................................... 154
    7.4.6 Special Characters ....................................................... 155
    7.4.7 Control Bar: Instrument Data ........................................ 156
    7.4.8 Control Bar: Reduced Data .......................................... 156
    7.4.9 Control Bar: Transformed Data .................................... 156
    7.4.10 Control Bar: Kinetic Parameters .................................. 157
    7.4.11 Control Bar: Concentrations ....................................... 159
    7.4.12 Control Bar: Qualitative Results .................................. 162
    7.4.13 Control Bar: Sample IDs ............................................ 163
    7.4.14 Control Bar: Method Layout ....................................... 163
    7.4.15 Control Bar: QC Validation ......................................... 163
<table>
<thead>
<tr>
<th>Section</th>
<th>Title</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>7.4.16</td>
<td>Control Bar: Miscellaneous</td>
<td>163</td>
</tr>
<tr>
<td>7.4.17</td>
<td>Color Scale Dialog Box</td>
<td>164</td>
</tr>
<tr>
<td>7.4.18</td>
<td>Context-Sensitive Menu of a Well</td>
<td>164</td>
</tr>
<tr>
<td>7.5</td>
<td>Edit Method Tab</td>
<td>170</td>
</tr>
<tr>
<td>7.6</td>
<td>Saving the Evaluated Results</td>
<td>171</td>
</tr>
<tr>
<td>8.</td>
<td>Attach Signature Wizard</td>
<td>173</td>
</tr>
<tr>
<td>8.1</td>
<td>Introduction</td>
<td>173</td>
</tr>
<tr>
<td>8.2</td>
<td>Sign a File</td>
<td>173</td>
</tr>
<tr>
<td>9.</td>
<td>Batch Processing</td>
<td>175</td>
</tr>
<tr>
<td>9.1</td>
<td>Introduction</td>
<td>175</td>
</tr>
<tr>
<td>9.2</td>
<td>Microplate Requirements for Batch Processing</td>
<td>175</td>
</tr>
<tr>
<td>9.3</td>
<td>Hardware Connections</td>
<td>175</td>
</tr>
<tr>
<td>9.4</td>
<td>Working with Tecan Readers</td>
<td>176</td>
</tr>
<tr>
<td>9.4.1</td>
<td>Software Connections</td>
<td>176</td>
</tr>
<tr>
<td>9.4.2</td>
<td>Prepare for Batch Processing</td>
<td>176</td>
</tr>
<tr>
<td>9.4.3</td>
<td>Start Batch Processing</td>
<td>178</td>
</tr>
<tr>
<td>9.4.4</td>
<td>Control Stacker Movements</td>
<td>178</td>
</tr>
<tr>
<td>9.5</td>
<td>Working with Infinite Series Readers</td>
<td>179</td>
</tr>
<tr>
<td>9.5.1</td>
<td>Connecting Infinite Series Readers</td>
<td>179</td>
</tr>
<tr>
<td>9.5.2</td>
<td>Prepare for Batch Processing for Infinite Series Readers</td>
<td>180</td>
</tr>
<tr>
<td>9.5.3</td>
<td>Start Batch Processing for Infinite Series Readers</td>
<td>181</td>
</tr>
<tr>
<td>9.5.4</td>
<td>Control Stacker Movements for Infinite Series Readers</td>
<td>183</td>
</tr>
<tr>
<td>10.</td>
<td>Gas Control Module (GCM) Enhanced Support</td>
<td>185</td>
</tr>
<tr>
<td>10.1</td>
<td>Introduction</td>
<td>185</td>
</tr>
<tr>
<td>10.2</td>
<td>Prerequisites</td>
<td>185</td>
</tr>
<tr>
<td>10.3</td>
<td>Connecting to GCM Enhanced</td>
<td>186</td>
</tr>
<tr>
<td>10.4</td>
<td>Data Logging</td>
<td>186</td>
</tr>
<tr>
<td>10.4.1</td>
<td>Importing Logged Data Into Microsoft Excel</td>
<td>188</td>
</tr>
<tr>
<td>10.5</td>
<td>GCM Enhanced Data Displayed in Status Bar</td>
<td>188</td>
</tr>
<tr>
<td>10.6</td>
<td>GCM Enhanced Data Displayed in Measurement Status Dialog</td>
<td>189</td>
</tr>
<tr>
<td>10.7</td>
<td>Precautions before Starting a Measurement</td>
<td>189</td>
</tr>
<tr>
<td>11.</td>
<td>Miscellaneous Icon</td>
<td>191</td>
</tr>
<tr>
<td>11.1</td>
<td>Instrument Control</td>
<td>191</td>
</tr>
<tr>
<td>11.2</td>
<td>File Handling</td>
<td>191</td>
</tr>
<tr>
<td>11.2.1</td>
<td>Archive Files</td>
<td>191</td>
</tr>
<tr>
<td>11.2.2</td>
<td>Automatic Archiving</td>
<td>193</td>
</tr>
<tr>
<td>11.2.3</td>
<td>Import Raw Data</td>
<td>194</td>
</tr>
<tr>
<td>11.2.4</td>
<td>Convert To</td>
<td>195</td>
</tr>
<tr>
<td>11.2.5</td>
<td>Convert From</td>
<td>196</td>
</tr>
<tr>
<td>11.2.6</td>
<td>Save LogFiles</td>
<td>197</td>
</tr>
<tr>
<td>11.3</td>
<td>Options</td>
<td>198</td>
</tr>
</tbody>
</table>
11.3.1 Default Data Paths ........................................................... 199
11.3.2 Copy/Export Options ...................................................... 200
11.3.3 Plate View Settings ......................................................... 202
11.3.4 Miscellaneous ............................................................... 203

11.4 User Administration (magellan Tracker) .................................. 205
   11.4.1 Add/Modify User (magellan Tracker) .......................... 206
   11.4.2 Add/Modify Role ......................................................... 208
   11.4.3 User Administration Audit Trail .................................. 209
   11.4.4 User Rights (magellan Tracker) ................................... 209
   11.4.5 User Administration Options ..................................... 213
   11.4.6 User Administration Summary .................................... 216

11.5 User Administration (magellan Standard) ................................. 217
   11.5.1 Add/Modify User (magellan Standard) ......................... 218
   11.5.2 Login ........................................................................... 219
   11.5.3 Change User ............................................................... 219
   11.5.4 User Rights (magellan Standard) ................................. 219

11.6 About magellan ................................................................. 221

12. Additional Features for magellan Tracker ................................. 223
   12.1 User Administration ......................................................... 223
      12.1.1 Audit Trail ............................................................... 223
   12.2 File Handling ................................................................. 224
      12.2.1 Saving a File ............................................................ 224
      12.2.2 Changing a Method or Workspace File ..................... 224
      12.2.3 Opening a File .......................................................... 224
      12.2.4 Opening a File Created on Another PC – Add HUIDs .... 225
   12.3 System Audit Trail ............................................................ 226

13. Calculations .......................................................................... 229
   13.1 Evaluate Results – Calculation Procedure ........................... 229
      13.1.1 Statistics ................................................................. 230
   13.2 Polarization Data Reduction .............................................. 230
      13.2.1 Introduction ............................................................. 230
      13.2.2 Determination of the G-Factor .................................. 230
      13.2.3 Blank Correction ...................................................... 231
      13.2.4 Intensity Calculation ................................................. 231
      13.2.5 Calculation of the Polarization / Anisotropy / Total Intensity .................................................. 231
   13.3 Spectra Data Reduction ..................................................... 232
      13.3.1 Mathematical Description .......................................... 232
   13.4 How to Write a Formula .................................................... 233
      13.4.1 Introduction ............................................................. 233
      13.4.2 Formula Variables ..................................................... 233
      13.4.3 Formula Functions .................................................... 235
      13.4.4 Basic Functions ....................................................... 236
      13.4.5 Statistical Functions ................................................. 237
      13.4.6 Elimination Functions ............................................... 239
<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>13.4.7 Other Functions</td>
<td>242</td>
</tr>
<tr>
<td>13.4.8 Spectra Functions</td>
<td>243</td>
</tr>
<tr>
<td>13.4.9 Examples</td>
<td>244</td>
</tr>
<tr>
<td>13.5 Standard Curve Analysis Types</td>
<td>246</td>
</tr>
<tr>
<td>13.5.1 Definitions</td>
<td>246</td>
</tr>
<tr>
<td>13.5.2 Analysis Type Parameters</td>
<td>246</td>
</tr>
<tr>
<td>13.5.3 Error Messages</td>
<td>246</td>
</tr>
<tr>
<td>13.5.4 Point to Point</td>
<td>246</td>
</tr>
<tr>
<td>13.5.5 Linear Regression</td>
<td>247</td>
</tr>
<tr>
<td>13.5.6 Non-Linear Regression</td>
<td>247</td>
</tr>
<tr>
<td>13.5.7 Polynomial</td>
<td>248</td>
</tr>
<tr>
<td>13.5.8 Cubic Spline</td>
<td>249</td>
</tr>
<tr>
<td>13.5.9 Akima</td>
<td>249</td>
</tr>
<tr>
<td>13.5.10 LogitLog</td>
<td>250</td>
</tr>
<tr>
<td>13.5.11 Four Parameters</td>
<td>252</td>
</tr>
<tr>
<td>13.5.12 Four Parameters – Marquardt</td>
<td>253</td>
</tr>
<tr>
<td>13.5.13 Five Parameters – Marquardt</td>
<td>254</td>
</tr>
<tr>
<td>13.5.14 Weighting for Four / Five Parameter Fit – Marquardt / Polynomial Fit</td>
<td>255</td>
</tr>
<tr>
<td>13.6 Calculation of Dilution Series</td>
<td>256</td>
</tr>
<tr>
<td>13.6.1 Detection of Dilution Series</td>
<td>256</td>
</tr>
<tr>
<td>13.6.2 Curve Parameter Calculation</td>
<td>256</td>
</tr>
<tr>
<td>13.6.3 Calculation of IC Values</td>
<td>256</td>
</tr>
<tr>
<td>14. Application Example</td>
<td>257</td>
</tr>
<tr>
<td>14.1 Introduction</td>
<td>257</td>
</tr>
<tr>
<td>14.2 Step-by-Step Example: Quantitative ELISA</td>
<td>257</td>
</tr>
<tr>
<td>14.2.1 Test Kit Description</td>
<td>257</td>
</tr>
<tr>
<td>14.2.2 Create a Method</td>
<td>259</td>
</tr>
<tr>
<td>14.2.3 Run the Method</td>
<td>273</td>
</tr>
<tr>
<td>14.2.4 Evaluate the Result</td>
<td>274</td>
</tr>
<tr>
<td>14.2.5 Summary of Definition of Quantitative ELISA in magellan</td>
<td>276</td>
</tr>
<tr>
<td>15. Glossary of Terms</td>
<td>277</td>
</tr>
<tr>
<td>Index</td>
<td>283</td>
</tr>
</tbody>
</table>
1. Introduction

1.1 Area of Application

magellan is a universal reader control and data reduction software for analyzing data generated from microplate tests using Tecan measuring devices. magellan is available in two versions:

- **magellan Tracker** and
- **magellan Standard**.

magellan Standard software is intended for endpoint, kinetic and multilabel assays in pharmaceutical, biotechnological and life science industry, for research use, for food analysis and veterinary applications.

magellan Tracker offers all functionality to become compliant with the FDA Regulation 21 CFR part 11 and with the European in vitro diagnostic directive 98/79/EC.

**Note**

It is important to note that the proper installation of the instrument and the magellan software alone will not ensure compliance with laws and requirements. Corresponding policies concerning processes and standard operating procedures, including validation and quality control, must also be established.

When using magellan Tracker, the user administration system must be customized by a designated administrator, who is responsible for the setup of user accounts and for the assignment of user rights.

**Note**

Training dates, their duration and frequency are available at your customer support. Address and telephone number can be found in these Instructions for Use and in the web: http://www.tecan.com/customersupport

Three default levels of user rights can be selected: Administrator, Application Specialist and Operator. The Administrator must always be trained by Tecan or a Tecan authorized organization.

1. The Administrator is responsible for procedural and technical laboratory issues and for compliance with federal regulations. It is recommended this individual be a Laboratory Supervisor.

   For detailed description of the Rights of an Administrator refer to chapter 11.4.4 User Rights (magellan Tracker) and 11.5.4 User Rights (magellan Standard).

2. The Application Specialist is responsible for performance of routine tests and examinations and assistance in the setup of experiments. magellan allows the Application Specialist to define specifications containing measurement parameters and evaluation settings and carry out measurements accordingly. The Application Specialist must be trained by the Administrator. It is recommended this individual meet the minimum requirements necessary to be a Laboratory Technician.

   For a detailed description of the rights of an Application Specialist refer to chapter 11.4.4 User Rights (magellan Tracker), respectively to chapter 11.5.4 User Rights (magellan Standard).
1. Introduction

3. The Operator performs routine analysis under immediate supervision. It is recommended this individual meet the minimum requirements necessary to be a Laboratory Assistant. magellan allows the Operator to carry out measurements according to the specifications given by the Application Specialist or Administrator. The Operator cannot change those specifications. The Operator must be trained by the Administrator. For a detailed description of the user rights of an Operator refer to chapter 11.4.4 User Rights (magellan Tracker) respectively to chapter 11.5.4 User Rights (magellan Standard).

magellan Tracker is designed for use with the operating systems and Microsoft Office versions specified in chapter 1.4.2 System Requirements. If additional programs are installed, functionality in accordance with IVD for Europe and FDA Regulations cannot be guaranteed.

**Note**
magellan is designed to be used with one computer; it is not intended to be integrated into a network.

1.2 Intended Use of magellan

magellan Standard software is a reader control and data reduction software for analyzing data generated from microplates using a Tecan absorbance, fluorescence, luminescence and/ or AlphaScreen/ AlphaLISA microplate reader. The software is intended for endpoint, kinetic, multilabel, fluorescence lifetime, and spectral scanning assays.

magellan software is intended for professional use according to the software specifications described in the manual (Instructions for Use for magellan).

magellan Tracker software offers all functionality for compliance with the FDA regulation 21 CFR part 11 for electronic records and signatures in addition to the functionality of magellan Standard. magellan Tracker software is also intended for in vitro diagnostic use in Europe according to the In vitro diagnostic directive 98/79/EC as an accessory together with a Tecan SUNRISE or INFINITE F50 absorbance reader. magellan cannot be used for agglutination assays.

1.3 User Profile

1.3.1 Professional User – Administrator Level

The administrator is a person who has suitable technical training and corresponding skills and experiences. If the product is used as intended, the person is able to recognize and avoid dangers.

The administrator has extensive skills and is able to instruct the end user or the routine user in assay protocols in connection with a Tecan product within the bounds of the intended use.

Computer application skills and good English skills are required.

1.3.2 End User or Routine User

The end user or routine user is a person who has suitable technical training and corresponding skills and experiences. If the product is used as intended, the person is able to recognize and avoid dangers.

Computer application skills and good language skills for the respective national language at the installation site and English are required.
1.4 Specifications

1.4.1 General

magellan software is available in two different versions:

- **magellan Standard** software is intended for endpoint, kinetic and multilabel assays in pharmaceutical, biotechnological and life science industry, for research use, for food analysis and veterinary applications. It supports a basic user administration.

- **magellan Tracker** software is designed to support FDA 21 CFR part 11 regulated environments. It offers all functionality to become compliant with the FDA Regulation 21 CFR part 11 and with the European In Vitro diagnostic directive 98/79/EC.

1.4.2 System Requirements

<table>
<thead>
<tr>
<th></th>
<th>Minimum</th>
<th>Recommended</th>
</tr>
</thead>
<tbody>
<tr>
<td>PC</td>
<td>Windows XP (32-bit):</td>
<td>2 GHz (Dual Core)</td>
</tr>
<tr>
<td></td>
<td>Windows compatible PC with a</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Pentium compatible processor</td>
<td></td>
</tr>
<tr>
<td></td>
<td>running at 1 GHz</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Windows Vista (32 bit):</td>
<td>2 GHz (Dual Core)</td>
</tr>
<tr>
<td></td>
<td>Windows compatible PC with a</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Pentium compatible processor</td>
<td></td>
</tr>
<tr>
<td></td>
<td>running at 1,5 GHz</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Windows 7 (32- or 64-bit):</td>
<td>2 GHz (Dual Core)</td>
</tr>
<tr>
<td></td>
<td>Windows compatible PC with a</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Pentium compatible processor</td>
<td></td>
</tr>
<tr>
<td></td>
<td>running at 1 GHz</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Windows 8 (32- or 64-bit):</td>
<td>2 GHz (Dual Core)</td>
</tr>
<tr>
<td></td>
<td>Windows compatible PC with a</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Pentium compatible processor</td>
<td></td>
</tr>
<tr>
<td></td>
<td>running at 1 GHz</td>
<td></td>
</tr>
<tr>
<td>Operating System</td>
<td>Windows XP (32-bit) – SP3</td>
<td>Windows 7 (64-bit) – SP1</td>
</tr>
<tr>
<td></td>
<td>Edition: Professional</td>
<td>Edition: Professional</td>
</tr>
<tr>
<td></td>
<td>Windows Vista (32-bit) – SP2</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Editions: Business, Enterprise, Ultimate</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Windows 7 (32-bit) – SP1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Windows 7 (64-bit) – SP1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Editions: Professional, Ultimate, Enterprise</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Windows8 (32-bit)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Windows8 (64-bit)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Editions: Pro, Enterprise</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>RT NOT supported!</strong></td>
<td></td>
</tr>
</tbody>
</table>
## 1. Introduction

<table>
<thead>
<tr>
<th>Minimum</th>
<th>Recommended</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Memory</strong></td>
<td></td>
</tr>
<tr>
<td>Windows XP:</td>
<td></td>
</tr>
<tr>
<td>512 MB RAM</td>
<td>1 GB RAM</td>
</tr>
<tr>
<td>Windows Vista (32-bit):</td>
<td>2 GB RAM</td>
</tr>
<tr>
<td>1 GB RAM</td>
<td></td>
</tr>
<tr>
<td>Windows 7 (32-bit):</td>
<td>2 GB RAM</td>
</tr>
<tr>
<td>1 GB RAM</td>
<td></td>
</tr>
<tr>
<td>Windows 7 (64-bit):</td>
<td>4 GB RAM</td>
</tr>
<tr>
<td>2 GB RAM</td>
<td></td>
</tr>
<tr>
<td>Windows 8 (32-bit):</td>
<td>2 GB RAM</td>
</tr>
<tr>
<td>1 GB RAM</td>
<td></td>
</tr>
<tr>
<td>Windows 8 (64-bit):</td>
<td>4 GB RAM</td>
</tr>
<tr>
<td>2 GB RAM</td>
<td></td>
</tr>
<tr>
<td><strong>Space Requirements</strong></td>
<td>1 GB</td>
</tr>
<tr>
<td></td>
<td>2 GB</td>
</tr>
<tr>
<td><strong>Monitor</strong></td>
<td>Super VGA Graphics</td>
</tr>
<tr>
<td><strong>Resolution</strong></td>
<td>1024 x 600</td>
</tr>
<tr>
<td></td>
<td>1280 x 1024</td>
</tr>
<tr>
<td><strong>Color Depth</strong></td>
<td>256</td>
</tr>
<tr>
<td><strong>Mouse</strong></td>
<td>Microsoft mouse or compatible pointing device</td>
</tr>
<tr>
<td><strong>Communication</strong></td>
<td>1 x USB 2.0</td>
</tr>
<tr>
<td></td>
<td>2 x USB 2.0</td>
</tr>
<tr>
<td></td>
<td>1 x RS232 (Serial)</td>
</tr>
<tr>
<td><strong>Devices</strong></td>
<td>1 x CD-ROM drive</td>
</tr>
<tr>
<td>Windows Vista:</td>
<td>DirectX 9 graphics and 128 MB of graphics memory plus WDDM support</td>
</tr>
<tr>
<td>Windows 7:</td>
<td>DirectX 9 graphics device with WDDM 1.0 or higher driver</td>
</tr>
<tr>
<td>Windows 8:</td>
<td>DirectX 9 graphics device with WDDM driver</td>
</tr>
<tr>
<td><strong>.NET</strong></td>
<td>Microsoft .NET Framework 3.5</td>
</tr>
<tr>
<td></td>
<td>If this version is not present, the install/upgrade program will install it side-by-side with any existing installations of the .NET Framework.</td>
</tr>
<tr>
<td><strong>Windows Installer</strong></td>
<td>3.1</td>
</tr>
<tr>
<td></td>
<td>If this version is not present, the install/upgrade program will install it.</td>
</tr>
</tbody>
</table>
1. Introduction

<table>
<thead>
<tr>
<th>Minimum</th>
<th>Recommended</th>
</tr>
</thead>
<tbody>
<tr>
<td>Microsoft Excel</td>
<td>2002 2003 2007 2010</td>
</tr>
</tbody>
</table>

Only 32-bit editions supported! Starter editions NOT supported!

1.4.3 Reader Compatibility

The following Tecan readers can be used with **magellan**:

<table>
<thead>
<tr>
<th>Instrument Types</th>
<th>Measurement Mode</th>
</tr>
</thead>
<tbody>
<tr>
<td>DNA Expert</td>
<td>Fluorescence / Absorbance / Luminescence</td>
</tr>
<tr>
<td>GENios</td>
<td>Fluorescence / Absorbance / Luminescence</td>
</tr>
<tr>
<td>GENios FL</td>
<td>Fluorescence</td>
</tr>
<tr>
<td>GENios Plus</td>
<td>Fluorescence / Absorbance / Luminescence</td>
</tr>
<tr>
<td>GENios Pro</td>
<td>Fluorescence / Absorbance / Luminescence / Fluorescence Polarization</td>
</tr>
<tr>
<td>SPECTRAFluor</td>
<td>Fluorescence / Absorbance</td>
</tr>
<tr>
<td>SPECTRAFluor Plus</td>
<td>Fluorescence / Absorbance / Luminescence</td>
</tr>
<tr>
<td>SAFIRE</td>
<td>Fluorescence / Absorbance</td>
</tr>
<tr>
<td>SAFIRE²</td>
<td>Fluorescence / Absorbance / Luminescence / Fluorescence Polarization</td>
</tr>
<tr>
<td>SUNRISE</td>
<td>Absorbance</td>
</tr>
<tr>
<td>ULTRA Evolution</td>
<td>Fluorescence / Absorbance / Luminescence / Fluorescence Polarization / FLT</td>
</tr>
<tr>
<td>ULTRA</td>
<td>Fluorescence / Absorbance / Luminescence / Fluorescence Polarization</td>
</tr>
<tr>
<td>ULTRA 384</td>
<td>Fluorescence / Absorbance / Luminescence / Fluorescence Polarization</td>
</tr>
<tr>
<td>Infinite M200</td>
<td>Fluorescence / Absorbance / Luminescence</td>
</tr>
<tr>
<td>Infinite M200 PRO</td>
<td>Fluorescence / Absorbance / Luminescence / Fluorescence Polarization</td>
</tr>
<tr>
<td>Infinite F200</td>
<td>Fluorescence / Absorbance / Luminescence / Fluorescence Polarization</td>
</tr>
<tr>
<td>Infinite F200 PRO</td>
<td>Fluorescence / Absorbance / Luminescence / Fluorescence Polarization / AlphaScreen/AlphaLISA</td>
</tr>
<tr>
<td>Infinite F500</td>
<td>Fluorescence / Absorbance / Luminescence / Fluorescence Polarization</td>
</tr>
<tr>
<td>Infinite M1000</td>
<td>Fluorescence / Absorbance / Luminescence / Fluorescence Polarization</td>
</tr>
<tr>
<td>Infinite M1000 PRO</td>
<td>Fluorescence / Absorbance / Luminescence / Fluorescence Polarization / AlphaScreen/AlphaLISA</td>
</tr>
<tr>
<td>Infinite F50</td>
<td>Absorbance</td>
</tr>
</tbody>
</table>
1. Introduction

**Note**
The Connect stacker can be used together with Tecan instruments in order to measure batches of plates. Please refer to the Instruction for Use for Connect for more information.

1.5 Software Installation Procedure

1.5.1 Automatic Software Setup Program

*magellan* is installed by an automatic software setup program. All necessary components are installed automatically.

Start *Setup.exe* to begin the installation procedure:

- In the first InstallShield Wizard window the components, which are required prior to installing Magellan are shown. Click **Install** to continue.
- A **Welcome Window** appears with information about the software and the installation process. Click **Next** to continue.
- The next window displays the **License Agreement**. Read the **License Agreement** and click **I agree** to accept it and continue.
- The **Customer Information** window appears next. If you have already purchased the software, enter now your serial number and click **Next**. If you do not yet have a serial number, click **Next** as well to continue the setup. You can register later (see chapter 2.6 Licensing *magellan*).
- The **Destination Folder** window appears next. The default installation path is displayed. Click **Browse** to change the default destination path, if desired. Click **Next** to continue.
- The **Language Selection** window appears next. Choose your preferred language.
- In the **Use For Regulated Environments** window, select *magellan Standard* or *magellan Tracker*, depending on which version you have ordered, to install the software. Click **Next** to continue.
- The setup program is now ready for installation. Click **Next** to start installation.
- Click **Finish** to end installation and to close the setup program.

The software can be started via the Windows **Start** menu by selecting Magellan.

The setup program automatically detects a previous installation of *magellan*. The old version has to be de-installed before being able to install a new Magellan version. The de-installation can be performed automatically by using the installation wizard (see also chapter 1.5.5 Automatic Software Removal).

**Note**
It is very important that the person who installs the software has administrator rights on the computer.
1. Introduction

1.5.2 Installation Qualification – IQ

It is recommended to use the automatic installation qualification program to check that the installation of magellan was successful.

Start Magellan IQ.exe from the Windows Start menu: Start > Programs > Tecan > Magellan IQ or directly from the file system in the default installation path specified in the setup program (typically, C:\Program Files\Tecan\Magellan).

The installation qualification program automatically detects the installed version of magellan. Click Check to start the installation qualification.

The IQ tool shows the state of all installed components. There are three possible states: Successful, Warning and Failed (=Error). If any errors are reported please contact your local dealer for support.

After the check is finished, it is possible to generate a report containing the information displayed by the IQ tool. In addition to the information of the IQ tool, the report contains a signature field, so that the report can be saved and printed for auditing purposes. Click the Report button in: File > Report to generate a report. The report can be saved as a PDF file as well as other file types.

Click Cancel or Exit to close the Installation Qualification program.

1.5.3 Operation Qualification – OQ

In addition to the installation qualification check, Tecan also recommends that the calculation abilities of magellan are tested. For this purpose, the installation medium of magellan contains a workspace and report file.

Open the OQ workspace file for the installed magellan version and print the report. The newly printed report has to be identical to the corresponding OQ pdf report (except, of course, for the time and date information).

If the two reports differ, please contact your local dealer for support.
1.5.4 System Recovery

In order to repair a damaged magellan installation after a hardware failure, it is important to start the data backup ahead of time.

System Recovery with Data Backup Software

The data backup is usually performed with data backup software. This makes it possible to save the entire system, including all data, so it can be restored whenever needed.

A detailed description and precise user instructions can be found in Windows Help (for Windows backup software packages) or in the provided documentation.

The magellan license is tied to the computer’s hardware, which means it can become invalid after a hardware change. You should therefore check to make sure your license is still valid after a system restoration. This can be done in the About Magellan dialog box by starting the registration wizard and checking whether the registered serial number and license number are still valid. In case of an error message, please contact Tecan’s customer support to get a new license number.

Manual System Recovery

In those cases where a complete system restoration is not possible with the backup software (e.g. because the hardware changes are too extensive, or because a different version of the Windows operating system was installed on the new computer), magellan has to be re-installed and several files have to be copied from a backup archive.

In that case, the system restoration process consists of these steps:

1. Install magellan
2. Start magellan and define the magellan Administrator
3. Re-enter the user and user rights.
4. Copy magellan.ini file from the backup archive.
5. Copy magellan methods from the backup archive.
6. Copy sample ID lists from the backup archive.
7. Copy workspaces from the backup archive.
8. Copy exported data from the backup archive.

After the hardware changes and a relicensing of magellan Tracker have been completed, the user, when opening method and workspace files generated under the old license, is informed that the files originate from a different computer. To solve this problem, please follow the detailed description in chapter 12.2.4 Opening a File Created on Another PC – Add HUIDs.

Data Security

To make sure that the steps of the system restoration process listed above can be completed quickly, a backup archive should be set up in time. The backup archive should include magellan methods, workspaces, sample ID lists, exported data, audit trail files, system audit trail files and the magellan.ini file. The contents of the backup archive should always be up to date. Tecan recommends using the Auto Archiving option for the backup of the methods, workspaces and sample ID lists. You can find details about Auto Archiving in chapter 11.2.2 Automatic Archiving.
### Magellan Paths – Windows XP

<table>
<thead>
<tr>
<th>Category</th>
<th>Path Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Magellan.ini</td>
<td>C:\Documents and Settings\All Users\Documents\Tecan\Magellan</td>
</tr>
<tr>
<td>Methods</td>
<td>C:\Documents and Settings\All Users\Documents\Tecan\Magellan\mth or as set in the Options dialog box</td>
</tr>
<tr>
<td>Workspaces</td>
<td>C:\Documents and Settings\All Users\Documents\Tecan\Magellan\wsp or as set in the Options dialog box</td>
</tr>
<tr>
<td>Sample ID lists</td>
<td>C:\Documents and Settings\All Users\Documents\Tecan\Magellan\smp or as set in the Options dialog box</td>
</tr>
<tr>
<td>Exported data</td>
<td>C:\Documents and Settings\All Users\Documents\Tecan\Magellan\asc or as set in the Options dialog box</td>
</tr>
<tr>
<td>Audit Trail files</td>
<td>Path as shown in the Audit Trail dialogue box (under user administration)</td>
</tr>
<tr>
<td>System Audit Trail</td>
<td>Path as specified in chapter 12.2.4 Opening a File Created on Another PC – Add HUIDs</td>
</tr>
<tr>
<td>GCM Logfile</td>
<td>C:\Documents and Settings\All Users\Documents\Tecan\Logfiles\Magellan\Version\Instrument Serial Number</td>
</tr>
</tbody>
</table>

### Magellan Paths – Windows Vista, Windows 7, Windows 8

<table>
<thead>
<tr>
<th>Category</th>
<th>Path Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Magellan.ini</td>
<td>C:\Users\Public\Documents\Tecan\Magellan</td>
</tr>
<tr>
<td>Methods</td>
<td>Standard path: C:\Users\Public\Documents\Tecan\Magellan\mth or as set in the Options dialog box</td>
</tr>
<tr>
<td>Workspaces</td>
<td>C:\Users\Public\Documents\Tecan\Magellan\wsp or as set in the Options dialog box</td>
</tr>
<tr>
<td>Sample ID lists</td>
<td>C:\Users\Public\Documents\Tecan\Magellan\smp or as set in the Options dialog box</td>
</tr>
<tr>
<td>Exported data</td>
<td>C:\Users\Public\Documents\Tecan\Magellan\asc or as set in the Options dialog box</td>
</tr>
<tr>
<td>Audit Trail files</td>
<td>Path as shown in the Audit Trail dialogue box (under user administration)</td>
</tr>
<tr>
<td>System Audit Trail</td>
<td>Path as specified in 12.3 System Audit Trail</td>
</tr>
<tr>
<td>GCM Logfile</td>
<td>C:\Users\Public\Documents\Tecan\Logfiles\Magellan\Version\Instrument Serial Number</td>
</tr>
</tbody>
</table>
1.5.5  Automatic Software Removal

The magellan software can be removed using the standard Windows uninstall routine:

magellan must be closed.
Select Add/Remove Programs from the Settings - Control Panel in the Windows Start menu.
Select the magellan icon and click Remove.
The Uninstall wizard is started. Select the preferred uninstall method (Automatic or Custom) and click Next to continue.
In the next window, click Finish to uninstall magellan.
In the next window, decide whether or not shared components should be removed. If Yes is selected, magellan will be completely uninstalled and other Tecan programs such as XFluor, HS Control Manager or Gemini will no longer work. Leaving these components installed will not harm your system. If you are not sure what to do, we suggest to not remove the shared components. After clicking Yes or No, the magellan software is uninstalled.

Note
When removing all shared components, the user administration data is also removed. Some Tecan programs, for example EVOware, will not work any more and must be re-installed.
2. Start Working with magellan

2.1 User Interface

The main type of the user interface in magellan is the wizard. Standard magellan wizards represent workflow modules, which are step-by-step guides for performing complex procedures. Occasionally, menus are available in the heading bar. The Menu offers a conventional way of using the software: the relevant menu item is selected from the main menus. All subsequent actions are started instantly, or a dialog box is displayed where further selections or entries can be made.

2.1.1 Folder Handling

In magellan, it is possible to create a user-specific folder structure for saving files (methods, workspaces, standard curves and sample ID lists) in any folder of the Windows Explorer.

New folders can be created by right-clicking and selecting New folder from the context sensitive menu. Files and folders can be moved easily from one folder to another by drag and drop or cut/copy/paste respectively, in the same manner as in Windows Explorer.
2. Start Working with magellan

File Type Symbols

magellan uses the following symbols for methods, workspaces, standard curves and sample ID lists in the file view window:

- Method
- Standard curve
- Workspace
- Password protected method
- Sample ID list

**magellan Standard**

Default paths for saving newly created files can be set via: Wizard list main page → Miscellaneous button → Options button → Paths tab. If the user administration is activated, users can define individual default paths.

When the Create/edit a method, Create/edit a sample ID list, Evaluate results wizards, or Use predefined method of Start measurement wizard are started, the specified default path is opened automatically. Users can create new folders in any folder of the Windows Explorer during the saving process.

In the Save window, the folder, specified by the default path of the method, workspace, standard curve or sample ID list, is opened automatically, whenever a new file is created. If an already existing file is modified, the path to the current location of the file will be opened. However, it is possible to save files in any folder of the Windows Explorer or in a newly created folder.

**magellan Tracker**

magellan users with administration rights can set the default paths for saving newly created files via: Wizard list main page → Miscellaneous button → Options button → Paths. These default paths are valid for all users.

When the Create/edit a method, Create/edit a sample ID list, Evaluate results wizards, or Use predefined method of Start measurement wizard are started, the specified default path is opened automatically. Users can also create new subfolders in the folder specified by the default path during the saving process.
In the **Save** window, the folder, specified by the default path of the method, workspace, standard curve or sample ID list, is opened automatically, whenever a new file is created. If an already existing file is modified, the path to the current location of the file will be opened. However, it is only possible to save files in the default folder, or in an existing or newly created subfolder within this folder.

### 2.2 Components & Terms – Basic Logic of magellan

**magellan** supports four file types:

- Methods (.mth)
- Sample ID Lists (.smp)
- Workspaces (.wsp)
- Standard curves (.std)

**Note**

The menus and toolbars available vary depending on the type of file currently opened.

The **magellan** main window contains the **window area** and a **status bar** at the bottom of the page. Depending on the data selected, a **toolbar** (e.g. plate view, graph) and a **menu bar** (plate view – evaluate results) in the header are displayed.

#### 2.2.1 Method (.mth)

With the Create/edit a method wizard **methods** are created which combine all of the necessary parameters for the measurement, evaluation and data handling of an assay: measurement parameters, evaluation settings, a printed report setup, data export setup, number format, and automated data handling settings. They do not, however, contain any measurement data (refer to chapter 4 Create/Edit a Method Wizard).

Methods accelerate data evaluation and can be customized for assays which are processed regularly.

When a new method is created, at first all wells of the plate layout will be empty. When defining the layout, transformations etc., the identifiers, formulas etc. are displayed in the corresponding wells.

Data can be analyzed with different methods.
2. Start Working with magellan

2.2.2 Sample ID List (.smp)

With the Create/edit a sample ID list wizard sample ID lists are created which contain the alphanumeric IDs of each sample in the microplate. magellan supports the import of various sample ID list formats (see chapter 5.2.3 Import a Sample ID List generated by pipetting software applications. It is also possible to generate sample ID lists for the corresponding analysis plates by allocating names to the individual wells. Up to three sample IDs per well can be defined. Barcodes can be read or well numbers can be generated automatically.

2.2.3 Workspace (.wsp)

A Workspace is created whenever a measurement is performed (Run a Method or Obtain raw data without method) and contains measured and calculated data as well as all method settings.

The Workspace stores all of the information gathered during a measurement run: the used method with measurement parameters, raw data, evaluation settings, printed report setup, automated data handling, etc. A Sample ID List can also be included.

Data display settings (numbers, graphs, colors, etc.) can be defined in the workspace.

In the control bar pane of an open wsp-file on the left hand side, all available data is listed. The selected data is displayed in the plate layout, in the information window or in a separate graph window, according to the type of selected data.

In the Edit method tab of a workspace method, settings can be changed for the currently opened workspace which results in a re-calculation of data but has no influence on the saved method file itself.

2.2.4 Standard Curve (.std)

A measured standard (calibration) curve can be saved as a .std file and used for subsequent evaluations of other measurements (refer to chapter 4.3 Define Evaluation / Control Bar of Create/Edit Method Tab).

2.2.5 File Types Used with magellan

The following file types are used with magellan.

By default, all file types associated with magellan are stored in subdirectories in the appropriate directory:

\All Users\Documents\Tecan\Magellan

The subdirectories are displayed in the table below:

<table>
<thead>
<tr>
<th>Type of File</th>
<th>File Extension</th>
<th>Directory</th>
</tr>
</thead>
<tbody>
<tr>
<td>Workspace</td>
<td>.wsp</td>
<td>\magellan\wsp</td>
</tr>
<tr>
<td>Method</td>
<td>.mth</td>
<td>\magellan\mth</td>
</tr>
<tr>
<td>Sample ID List</td>
<td>.smp</td>
<td>\magellan\smp</td>
</tr>
<tr>
<td>Export Files</td>
<td>.asc</td>
<td>\magellan\asc</td>
</tr>
<tr>
<td>Standard Curve</td>
<td>.std</td>
<td>\magellan\wsp</td>
</tr>
<tr>
<td>Plate Definition</td>
<td>.pdf / pdfx</td>
<td>\Reader\pdf  \Reader\pdfx</td>
</tr>
</tbody>
</table>
2. Start Working with magellan

Note
The difference between plate definition files with .pdf extension and .pdfx extension is that Infinite Series instruments use the .pdfx format files, whereas all other Tecan instruments use .pdf files.

2.3 User Interface – Wizard List

After launching magellan, the Wizard List appears:

The displayed screenshot shows the wizard list page when magellan Tracker is installed. With magellan Standard the Attach signature wizard is not available.

Each wizard can be started either by double-clicking or by selecting it and clicking the Next button.

2.3.1 Start Measurement Wizard

For a detailed description, refer to chapter 6 Start Measurement Wizard.

The following choices are available:

- **Obtain Raw Data** is used to generate raw data quickly and easily by setting the required measurement parameters and starting a measurement. The Obtain raw data wizard creates a new workspace in which the obtained values are presented and stored.

- **Run Strip Layout** is used to collect strips from different methods, combine the strips to one method and run this method.

- **Use Predefined Method** is used to perform measurements based on previously defined methods. The wizard creates a new workspace containing the selected method (which consists of all measurement parameters and evaluation definitions) and enables you to insert a sample ID list. After the measurement, the workspace is completed with the obtained raw data that will be evaluated.

- **Start Favorite** is used to select one of the most frequently used methods from the list of numbered icons.
2. Start Working with magellan

After the measurement is finished a workspace file is created (.wsp; refer to chapter 2.2 Components & Terms – Basic Logic of magellan).

2.3.2 Evaluate Results Wizard

For a detailed description, refer to chapter 7 Evaluate Results Wizard. The Evaluate Results wizard is used to view the raw data and to evaluate the results. The evaluation parameters can be viewed and data can be re-evaluated. All this information is stored in workspace file (.wsp; refer to chapter 2.2 Components & Terms – Basic Logic of magellan).

2.3.3 Attach Signature Wizard

For a detailed description, refer to chapter 8 Attach Signature Wizard. The Attach Signature wizard is used to sign method and workspace files. This feature is only available with magellan Tracker. Signatures are always included in the printed report. Signed records can only be modified by users with the appropriate rights. It is possible to fully control the use of methods by allowing users to run only signed methods. The Attach signature wizard is only available with magellan Tracker.

2.3.4 Create/Edit a Sample ID List Wizard

For a detailed description, refer to chapter 5 Create/Edit a Sample ID List Wizard. The Create/Edit a Sample ID list wizard is used to create new and to edit existing sample ID lists. Up to three sample IDs per well can be entered or imported. The sample ID lists are saved as .smp files (refer to chapter 2.2 Components & Terms – Basic Logic of magellan).

2.3.5 Create/Edit a Method Wizard

For detailed description, refer to chapter 4 Create/Edit a Method Wizard. The Create/edit a method wizard is used to define or edit methods. Methods contain all necessary parameters for measurement, evaluation and data handling according to the performed assay. Methods are saved as .mth files (refer to chapter 2.2 Components & Terms – Basic Logic of magellan).

2.3.6 Icons

Icon: Change Current User

If the user administration is active (refer to chapter 11.4 User Administration (magellan Tracker) and to chapter 11.5 User Administration (magellan Standard)) click this icon to log out the current user and to login a new user.

With magellan Standard, user administration is optional. With magellan Tracker user administration is obligatory.
2. Start Working with magellan

Icon: Miscellaneous

click on the Miscellaneous icon to select the following options:

<table>
<thead>
<tr>
<th>Instrument control</th>
<th>Options</th>
</tr>
</thead>
<tbody>
<tr>
<td>File handling</td>
<td>User administration</td>
</tr>
<tr>
<td>About magellan</td>
<td></td>
</tr>
</tbody>
</table>

- **Instrument control** provides quick access to several instrument functions, to service and setup options. See chapter 3 Instrument Control & Settings.
- **File handling** is used to move files to an archive location, to convert files from or to another magellan version and to import raw data from an ASCII-file. See chapter 11.2 File Handling.
- **Options** is used to customize certain default settings as path of generated files, clipboard and Excel copy options, the plate view and miscellaneous wizard, startup, language and password settings. See chapter 11.3 Options.
- **User administration** is used to add or disable users and to set or modify user rights. See chapter 11.4 User Administration (magellan Tracker), respectively chapter 11.5 User Administration (magellan Standard).
- **About magellan** provides license information and details on the currently installed version and components. Registration can be requested starting the Register wizard (see chapter 2.6 Licensing magellan).

Close the Miscellaneous window to go back to the wizard list.

Icon: Temperature control

For detailed description, refer to chapter 3.1.2 Temperature Control...

Use this icon to set the target temperature for the connected instrument.

Icon: Move plate

Use this icon to move the plate carrier in or out of the instrument.
2. Start Working with magellan

2.3.7 Standard Elements

Each wizard displays sequentially a number of windows, in which all necessary information, settings and data entry possibilities are provided.

Standard Elements of a magellan Wizard

For navigation from one window to another there are several buttons at the bottom of the wizard page. The following buttons are used in the individual windows of a wizard:

**Back button**

The Back button is used to navigate back to the previous window within a wizard.

When the window is the active area click **Back** or press **SHIFT+B** to navigate back to the previous window.

**Next button**

The Next button is the large green arrow in the bottom right corner and is used to navigate forward to the next window within a wizard.

When the window is the active area click **Next** or press **SHIFT+N** or **ENTER** to navigate forward to the next window.

**Finish button**

The Finish button is the large green arrow in the bottom right corner and is used to navigate forward to the save window of the wizard.

When the window is the active area click **Next** or press **SHIFT+N** or **ENTER** to navigate forward to the next window.

**Save button**

The Save button is only found in the last window of a wizard and replaces the Next button. The Save button is a large green arrow in the bottom right corner. It is used to close the wizard and save all changes or to start a process.

When the window is the active area click **Save** or press **ENTER** to close a wizard and to save all changes.

**Cancel button**

The Cancel button is used to close a wizard without saving any changes to settings or documents.

When the window is the active area click **Cancel** or press **ESC** to close a wizard without saving any changes.

**Help button**

The Help button opens the help window.

When the window is the active area click **Help** or press **F1** to open the help window.

Standard Elements of Microsoft Windows

**OK button**

This button confirms settings, applies and saves changes accordingly and closes the dialog box.

**Cancel button**

This button closes the dialog box without saving any changes to settings or documents.

**Help button**

Click the Help button to open the magellan online help.
Status Bar Information

The status bar displays the following information:

- Current command info
- User name of the currently logged in user.
- Name of connected instrument. For example: Sunrise
- Method: measurement mode and unit. For example: Absorbance [OD]
- Workspace: date and time of measurement. For example: 27.11.2002
  14:13:03
- Number of selected wells. For example: 3 well(s) selected
- Keyboard status information: activity of the keyboard toggles: CAP (caps lock), NUM (Numeric block lock), SCRL (Scroll lock)
- Instrument connection state icon

2.3.8 The Help Button

Click the Help button or press ‘F1’ to open the magellan online help. The tabs Contents, Index and Search are available. For further details on using the Windows Help function refer to your Windows instructions of use.

2.3.9 The Welcome Dialog Box

Each wizard starts with a Welcome dialog box, which gives a short introductory description of the procedure to be performed.

Clear the Show welcome page check box to suppress welcome pages when starting wizards in the future.

2.3.10 Shortcuts List

<table>
<thead>
<tr>
<th>Key Combination</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>SHIFT+B</td>
<td>Back button</td>
</tr>
<tr>
<td>SHIFT+N</td>
<td>Next button</td>
</tr>
<tr>
<td>ESC</td>
<td>Cancel button</td>
</tr>
<tr>
<td>ENTER</td>
<td>Next or Finish button, if active window</td>
</tr>
<tr>
<td>F1</td>
<td>Help menu</td>
</tr>
<tr>
<td>CTRL+C or CTRL+INSERT</td>
<td>Copy</td>
</tr>
<tr>
<td>CTRL+V or SHIFT+INSERT</td>
<td>Paste</td>
</tr>
<tr>
<td>CTRL+X</td>
<td>Cut</td>
</tr>
<tr>
<td>CTRL+Y</td>
<td>Redo</td>
</tr>
<tr>
<td>CTRL+Z</td>
<td>Undo</td>
</tr>
<tr>
<td>DEL</td>
<td>Delete content of active well (edit sample ID, edit formula)</td>
</tr>
<tr>
<td>CTRL+SHIFT</td>
<td>Show formula of selected well when transformation result is viewed (Evaluate Results wizard)</td>
</tr>
</tbody>
</table>
2. Start Working with magellan

2.4 Starting magellan

Note
magellan can be run with an instrument connected or in a demo mode, simulating an instrument. If you want to connect to an instrument (see chapter 2.5 Connecting an Instrument), switch the instrument on before starting magellan.

2.4.1 Starting Standard Version

Perform the following steps to start magellan:
1. Make sure that an instrument is connected or that Demo mode is allowed.
2. In the Windows Start menu, select the Tecan program group and click the magellan icon.
3. magellan starts.

2.4.2 Starting Tracker Version

Logging in for the First Time with magellan Tracker

When magellan Tracker is started for the first time, a dialog box appears, informing the user that a User Administrator must be created first. Click OK and the Create Administrator dialog box appears.

Complete the text fields and click OK to save the settings. At least one user administrator must be created.

Caution
If the User Administrator password is forgotten, User Administration settings cannot be changed and magellan must be completely reinstalled.

Note
We recommend to create at least two User Administrators.
2. Start Working with magellan

After clicking OK, the **User Administration** dialog box appears:

Users and groups can be added, edited or disabled and user rights can be defined. Options for login, password, and email can be edited. See chapter 11.4 User Administration (magellan Tracker) and chapter 11.5 User Administration (magellan Standard).

**Change Password**

**Initial Password (magellan Tracker only)**

When a user logs in for the first time, the password assigned by the administrator has to be changed.

After entering the **User name** and **Password** and clicking OK, the message “Your initial password is only valid once. You have to change the password!” appears. Click OK; the **Change Password** window forces the user to enter a new password.

**Password Expiration (magellan Tracker only)**

When the password expires, the user will be prompted to enter a new password. The old password has to be entered. The new password must comply with the defined password rules and has to be entered twice to prevent typing errors. Old passwords cannot be reused. The new password will expire after a defined period of time. See chapter 11.4.5 User Administration Options.
2. Start Working with magellan

Login

Once user administration has been activated, the Login dialog box will appear each time magellan starts.

The Login dialog box contains the following elements:

- **Username** text box | Enter your UserID
- **Password** text box | Enter your Password

Click the GO button to close the dialog box and the user is logged in. Only those user actions can be performed, that correspond to the user’s rights.

Click the Cancel button to close the dialog box and magellan is terminated.

The user account will be disabled after the maximum number of consecutive unsuccessful logins has been reached (see chapter 11.4.5 User Administration Options/ Login Options).

Application Locked

If the application has not been in use for the specified maximum of time (user defined only in magellan Tracker) it will be locked. The password must be entered to unlock the application.
2.5 Connecting an Instrument

*magellan* can be run either with an instrument connected or in a demo mode, simulating an instrument connected.

### 2.5.1 Instrument Connected

Connect the instrument to your computer as described in the instructions for use for the instrument and switch on the instrument before starting *magellan*.

**First Start of magellan**

The first time *magellan* is started, the Setup Port dialog box appears:

In the *Instrument* group box, select the connected instrument from the drop down list or select *Find any*.

Select the appropriate *COM port* from the drop down list or select *Find any* and Click OK. If the connection was successful a Dialog is displayed with Information, which instrument is connected to which port. The instrument is now connected and ready for operation using the *magellan* software.

**Stacker Port**

If a Tecan *Connect* stacker is used together with the instrument, select the connecting port from the drop down list or select *Find any*. If no stacker is used select *None* for the stacker port.

**Change Instrument**

Click the *miscellaneous* icon in the wizard list and *instrument control* in the miscellaneous list. The instrument control window is displayed showing two group boxes: *Instrument* and *Setup & Service*. Select *Change instrument* from Setup & Service to connect an instrument or to change the currently connected instrument.
2. Start Working with magellan

2.5.2 Demo Mode

If no instrument is connected, select the instrument to be simulated from the drop down list in the Instrument group box and select Demo mode in the Port group box and Click OK. magellan is now in demo mode.

Demo mode allowed (in the Options dialog) is selected by default (see chapter 11.3.4 Miscellaneous to change this default setting).

In demo mode it is possible to perform all functions except running actual measurements.

2.5.3 Connecting an Instrument of the Infinite Series

Select Infinite Series in the Instrument group box in the Setup Port dialog box. Click OK to display the Connect to Instrument dialog box, select the instrument and click OK. For demo mode select the Show simulated instruments checkbox and the preferred instrument from the drop down list and click OK.

2.5.4 Connecting a Stacker

The Tecan Connect stacker can be used additionally. See chapter 9 Batch Processing for further details.
2.6 Licensing magellan

Note

magellan can be used unregistered for 30 single days of work. If magellan is not registered after this period, the save and print options will be disabled.

For licensing magellan there are two possibilities:

1. The software has been purchased. Together with the software the serial number is delivered.
2. The software was delivered as a demo version together with the instrument. A registration is possible afterwards (No serial number is delivered).

Note

It is very important that the person who registers the software has administrator rights on the computer with operating system Win XP.

The licensing of magellan is performed with the Register magellan wizard. If magellan has not been registered, this wizard will launch automatically each time the program is started.

The Register magellan wizard can also be opened over the miscellaneous icon in the wizard list starting page. (miscellaneous → About magellan → Register).

In order to register magellan, a serial number, the hardware (PC) unit identification number (HUID) and a license number are required.

After the serial number has been entered in the register magellan dialog box, fill out the registration form to start the license number request. The completed registration form is sent together with the individual HUID to Tecan Austria. The HUID number is generated by the software and is inserted into the registration form automatically. It is related to Windows given system drive number.

After receiving the serial number and the license number you have to start the registration wizard again and enter both numbers. The Register magellan wizard confirms the license number and summarizes the user information. Click the Finish button to complete the registration procedure. magellan’s functions will then remain fully available to the user.

2.6.1 Registration Wizard

The registration wizard starts with the Welcome dialog box, which contains a short description of the wizard. Click Next and the Serial Number dialog box appears.
2. Start Working with magellan

Serial and License Number

Order a Serial Number for magellan

To purchase magellan and to receive a serial number, select the option **Order magellan to obtain a valid license**. The **Registration Form** window will then appear (see chapter Registration Form below).

magellan Has Already Been Purchased

Select **Enter your magellan serial number**. Enter the serial number, which is found in the magellan package.
2. Start Working with magellan

After having entered the serial number, click **Next** and the **License Number** dialog box appears.

Users installing the software for the first time will not yet have a license number and must select **Request a magellan license number because you did not receive one**. Click **Next** and the **Registration Form** window appears.

**Registration Form**

Complete the registration form. Fields marked with an asterisk are mandatory.

Click **Next** and the license agreement window appears. Read it carefully and click the **I agree** button.
2. Start Working with magellan

Click **Next** and the registration information is displayed.

Click **E-Mail Form**... to send the information using the default e-mail program on your computer or click **Print Form**... to print out the registration form for faxing or mailing it to Tecan. Click **View Form**... to view the registration form using WordPad or Notepad. Within 24 hours you will receive the license number.

Click **Next** and the Registration requested window appears:

**Registration requested**

You successfully created and sent a Magellan registration form.
When you have received your license number start the Registration wizard again and register Magellan on your computer.

Click **Finish**; the Register magellan wizard will close and magellan’s functions will remain fully available to the user.

Finishing Licensing magellan

After having received the license number of Tecan, repeat the steps above and insert the license number. Click **Next**. The registration wizard then confirms the license number and summarizes the user information.
3. Instrument Control & Settings

Click the Instrument Control button in the Wizard List dialog box and the Instrument Control dialog box appears.

Depending on the instrument connected, different instrument and setup & service options are enabled or disabled.

3.1 Instrument Options

3.1.1 Movements...

This opens the Movements dialog box, in which it is possible to control the movements of the plate carrier and the filter slides.

In the Movements dialog box, specific In and Out buttons can be used to move the plate carrier or filter slides into the reader or out of it.

3.1.2 Temperature Control...

Only available for instruments equipped with temperature control.

In the Instrument Control dialog box, click the Temperature Control button.

This option allows the user to establish the temperature inside the reader.

This dialog is also accessible via the Start Measurement dialog box before starting a measurement. (See chapter 6.6 Start Measurement with a Predefined or Favorite Method).
3. Instrument Control & Settings

### 3.1.3 Heating Dialog (Temp Control for Infinite Series Readers)

**Target temperature**

This command is used to set the target temperature of the instrument manually. Select or enter the **Target temperature** and click **Set**. Click **On/Off** to start/stop instrument heating.

**Current temperature**

Click the **Read** button to display the current temperature of the instrument or click the **Auto** check box to have it read automatically. Click **Off** to stop heating.

Click the down button, "", to display the heating graph and click the up button, "", to collapse. Click the close button, "", to exit the **Heating** dialog box.

---

**Current temperature**
The current temperature is displayed in the corresponding field. Click the **Refresh** button to update the current temperature.

**Target temperature**

To start or stop the temperature control, select or clear the check box and enter the target temperature.

To set the temperature of the instrument, click the **Apply** button. The temperature is sent to the instrument, but the dialog box is still displayed. Click **OK**, the target temperature is sent to the instrument and the dialog box disappears.
3. Instrument Control & Settings

3.1.4 Lamp/Laser Control...

Instrument feature (see the corresponding Instructions for Use of the instrument connected for more information).

3.1.5 Injector Control...

This option is only applicable for instruments equipped with injectors. See the respective Instructions for Use of the instrument for further details.

3.1.6 Dispense Only...

This option is only applicable for instruments equipped with Injectors. See the respective Instructions for Use of the instrument for further details.
Instrument features – baud rate, power down. See the corresponding Instructions for Use of the instrument for further details.

3.2 Setup & Service Options

3.2.1 Change Instrument...

In the Setup & Service box, click Change instrument… to open the Setup Port dialog box. This option allows connecting magellan to an instrument. See chapter 2.5 Connecting an Instrument for further details. Click the Change instrument… menu option and the currently connected instrument will be disconnected. In the Setup Port dialog box, the desired instrument and the communication port can be selected and thus be connected to magellan. When connected to an Infinite instrument, refer to the Instructions for Use for i-control.

3.2.2 Define Filter Slides...

Standard and custom filter slides can be defined.

3.2.3 Insert Transport Lock...

Instrument feature (see the corresponding Instructions for Use for more information).
3. Instrument Control & Settings

3.2.4 **Optimize Z-Position**

*Only applicable for instruments with z-positioning option.*

In the Instrument Control dialog box, click **Optimize Z-Position**...

This option can be used to find the optimum Z-position of the plate transport in relation to the measuring head for specific instruments. Therefore, the **Optimize Z-Position** dialog box is displayed.

3.2.5 **Plate Geometry Editor...**

Click the **Miscellaneous** icon from the wizard list.

Select **Instrument Control** and connect to an instrument (button **Change instrument**). Then click the button **Plate geometry editor** in the Instrument Control dialog box and **Continue** (green arrow) on the wizard welcome page.

**magellan** offers a wide selection of predefined plate geometry files for standard plate formats to choose from. Use the **Plate geometry editor** to create plate geometry files for not listed plates in order to use them with **magellan** or to validate existing plate geometry files.

The **Plate geometry editor** is a software application accessible via **magellan**. The following commands and options are available.

<table>
<thead>
<tr>
<th>Command/Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Create/ edit plate geometry</td>
<td>A new plate definition file can be created or an existing plate definition file can be edited or verified.</td>
</tr>
<tr>
<td>Basic dimensions</td>
<td>Basic dimensions of the plate and the wells can be set (e.g. number of rows and columns, well shape, well diameter, well depth).</td>
</tr>
<tr>
<td>Scan plate / Enter well position</td>
<td>Select between 2, 4 or whole plate scan or enter the corresponding distance of top left well and bottom right well.</td>
</tr>
<tr>
<td>Measurement parameters</td>
<td>When <strong>Scan plate</strong> is selected, the measurement parameters can be inserted, clicking the corresponding button.</td>
</tr>
<tr>
<td>Save</td>
<td>The newly created or modified plate geometry can be saved entering a name (and remarks).</td>
</tr>
</tbody>
</table>
Create New Plate Definition File or Validate an Existing Plate Definition File

Select Create new in the Create/edit plate geometry dialog box and click on the green arrow Make Your Selection to open the editor.

### Plate Definition

Insert the **Basic dimensions:**

<table>
<thead>
<tr>
<th>Basic dimension</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of rows</td>
<td></td>
</tr>
<tr>
<td>Number of columns</td>
<td></td>
</tr>
<tr>
<td>Plate height</td>
<td></td>
</tr>
<tr>
<td>Plate height with cover</td>
<td></td>
</tr>
</tbody>
</table>

*Note: Be careful with settings of µm and µl values!*

Measure with a caliper ruler or better use values from the plate design drawings, given by the plate manufacturer. Be aware, that when you manually measure the plate height, any plate tolerances caused by the production process of the plate will not be covered!
Select **Define Positions** by clicking on the green arrow button (example when connected to an Infinite F500 instrument).

**magellan** allows scanning of plates on 2 or 4 corners, depending on the instrument connected. With an instrument of the Infinite Series connected, also a whole plate can be scanned.

**Note**

*Usually a scan of 2 corners is sufficient. In case of a strip plate we recommend to use 4 corners. Select the number of corners and continue with the measurement parameters.*
Click the button **Measurement parameters** to setup the measurement (example when connected to an Infinite F500).

**Scanning a Black Plate**

If you scan a black plate you have to fill in an appropriate reagent into the upper left well (in this case A1) and the lower right well (here H12) (in case of 2 corners) and in case of 4 corners into the upper left well, upper right well (here A12); lower left well (here H1) and lower right well (here H12).

Click **OK** to close the measurement parameter dialog.

Put the microplate on the plate transport and start the scanning by clicking on the green arrow button **Scan / View Summary**.

Next adjust the position of 2 of the 4 scanned wells starting with the upper left position (example when connected to an Infinite F500).

Click on the cursor and adjust the grid to the scanned image:
Continue with the remaining well (lower right position) by clicking on the green arrow button **Lower Right Position** and also adjust the grid.

Click on the cursor and adjust the grid to the scanned image:
In case the picture does not show an acceptable result, go back to Measurement Parameters and enter different gain settings.

**Note**

*When using a fluorescent reagent for performing this plate definition scan, it is recommended to measure this sample first in a comparable but known microplate using a typical filling volume to determine the gain and z-position for the measurement in the unknown plate.*

Continue by clicking on the green arrow button **View Summary** to see the summary.
3. Instrument Control & Settings

Finish and Save

In the summary dialog you can finally check the grid for the new microplate. A zoom function allows a more detailed view of the plate. In case you are not fully satisfied you can use the Back button to do further optimizations (example when connected to an Infinite F500).

3.3 Log Files

During working with magellan log files are created. The communication between the software and the instrument and the communication between components of the software are stored in these log files.

They can be found in the following paths:

- magellan Log files (communication between single components of magellan):
  C:\documents and settings\allusers\documents\tecan\logfiles

- Infinite Series Log files (communication between magellan and Infinite series instrument):
  C:\documents and settings\allusers\documents\tecan\logfiles\magellan\v x.y

- Rdr.OLE Log files (communication between magellan and Rdr.ole Instrument) by default:
  C:\documents and settings\currentuser\local settings\temp

- Collection of necessary Log files

Log files can be saved as zip archive by selecting the Save Logfiles... button in the File handling dialog (Miscellaneous → File Handling). The zip archive can now be named and saved in a defined directory. In case of any magellan measurement or status error(s), this archive contains all well data, status (e.g. overflow, lamp low) or calculation error(s) and can be easily sent to Expertline-at@tecan.com for support request. For further information please refer to chapter 11.2 File Handling – Save Log Files.
4. Create/Edit a Method Wizard

4.1 Introduction

The Create/Edit a Method wizard is used to
• Create or edit methods,
• Set measurement and evaluation parameters,
• Define the plate layout,
• Select the format of the printed report and
• Set the automated data handling parameters.

Workflow Summary

Click Continue on the welcome page of the Create/Edit a Method wizard. In the
next window, select
• Create new if you want to define a new method or
• Edit if you want to modify an existing method.

In the Define Measurement Parameters window, measurement parameters can
be set. Click Define Evaluation to define the plate layout, evaluation parameters,
print out and automated data handling parameters. At the end of the wizard the
new or modified method is saved as .mth file.

Note

For a step-by-step description of how to create a method, refer to the
Quantitative Elisa example in chapter
14.2 Step-by-Step Example: Quantitative ELISA.

File Selection Page

In the wizard list, click Create/Edit a method button. Click Next on the welcome
page of the Create/Edit a Method and the File Selection page appears.

The File Selection window contains the following elements:

<table>
<thead>
<tr>
<th>Element</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Create new button</td>
<td>The Create New button must be selected to create a new method.</td>
</tr>
<tr>
<td>Edit button</td>
<td>The Edit button must be selected to edit an existing method.</td>
</tr>
<tr>
<td>Show combo box</td>
<td>In the Show combo box a file filter can be defined in order to get only those methods in the list, which fulfill the selected criteria: • All files • Files from this instrument • My files: This option is available if the user administration is enabled (always enabled in magellan Tracker). • Signed files: only available for magellan Tracker • Example files: only available if they have been installed.</td>
</tr>
<tr>
<td>Filename list</td>
<td>Select the method to be edited from the Filename list. A Remarks field next to every file name contains - if entered - a short description of the method. All methods available in the standard method directory will be displayed (see chapter 11.3.1 Default Data Paths).</td>
</tr>
</tbody>
</table>
4. Create/Edit a Method Wizard

Click the Print Preview... button to open the Print Preview dialog box, where a preview of the settings of the selected method is displayed and a printout can be started.

Note
If the proper instrument for the selected file is not connected, the Instrument Mismatch dialog box appears. The dialog offers two options:

- Connect to the proper instrument
- Convert the measurement parameters to those compatible with the connected instrument.

This option is not available if the measurement mode is not supported by the connected instrument, for example, a Sunrise does not support Fluorescence measurements.

It is highly recommended to review the measurement parameters.

4.2 Define the Measurement Parameters

In the Measurement Parameters window it is possible to set all required parameters for the measurement, including measurement mode, wavelengths, read mode, temperature, etc. depending on the type of instrument connected.

When connected to an Infinite instrument, refer to the Instructions for Use for i-control for further details on defining measurement parameters.

Note
The available parameters to be defined depend on the instrument connected.

Note
After the magellan 30-day demo license has expired, printing and saving will not be possible.
4. Create/Edit a Method Wizard

4.2.1 Measurement Types

Click Make your selection and the Measurement type dialog box appears:

The measurement type is to be selected from an option button list. The Measurement type window contains the following elements (depending on the instrument connected):

Measurement type group box
- Select Endpoint measurement to perform a single measurement.
- Select Kinetic measurement to perform kinetic measurements per plate with a specified interval time.
- Select Well kinetic (injector) measurement to perform kinetic measurements per well with a specified interval time and injector control.
- Select Multilabel measurement to perform multilabel measurements with different measurement parameters.

Plates group box
- Select a number of plates in the edit box for Multiplate measurements (only available with Safire II instrument).

Click Measurement parameters... to open the Measurement Parameter dialog box.
4. Create/Edit a Method Wizard

4.2.2 Measurement Parameters

Select the required *Measurement type* and click *Measurement parameters...* to open the Measurement Parameter dialog box for adjustment of:

- General measurement parameters,
- Plate format,
- Stacker,
- Wavelength,
- Measurement parameters (gain, integration time, number of reads, Z-position),
- Temperature and
- Shaking.

Click the **OK** button to save the changes and the **Cancel** button to reject them.

Depending on the instrument connected and on the measurement type selected, the *Measurement Parameters* dialog box and the respective tabs available vary. When connected to an Infinite instrument refer to the Instructions for Use for i-control.

Multilabel Measurement

If the measurement type multilabel measurement was selected, the *Multilabel Measurement* dialog box is displayed.

To create a list of parameter windows the **New** button must be clicked. The *Measurement Parameters* dialog box will appear where a new set of measurement parameters can be defined. At least two sets of measurement parameters must be created in the multilabel dialog box.

```
Note
If Move plate out after measurement is selected when running the method, magellan displays a message box where liquids in the plate can be modified and the measurement continued. Otherwise the measurement is performed without a break.
```

The measurement parameter *Comments* can be used to label the set of measurement parameters in the list.
The **Multilabel** dialog box contains the following elements:

### Label list
In the **Multilabel** list the existing measurement parameter definitions are listed line by line. In the **No.** column a guide number counts up the existing measurement parameter definitions and a small icon is presented. The **Label** column displays a customizable name (in Measurement Parameters – General Tab – Comment to this measurement). The **Measurement parameters** column lists a summary of the selected measurement parameters.

### New button
Click the **New** button and the measurement parameters of each new measurement can be defined. The **Measurement Parameters** dialog box will appear. Define names for each label. In the **Measurement Parameters** dialog box the name written in the comment field of the **General** tab is used as label. All parameters must be entered to define a new measurement.

### Properties... button
Click the **Properties** button and all **measurement parameters** of the highlighted label in the measurement parameters list are displayed and can be edited.

### Delete button
Click **Delete** or press **DEL** to delete the highlighted measurement parameter(s) from the multilabel field.

### Number of cycles
Defines the number of kinetic cycles for a multilabel kinetic measurement.

### Interval
Defines the kinetic interval or the pause between labels (if only one cycle is defined).

---

**Note**

Defining multilabel measurements with Safire2:

*It is not allowed to define absorbance dual wavelength labels. On closing the measurement parameter dialog any defined reference wavelength will be set to 0. A message box will inform the user about this change.*
4. Create/Edit a Method Wizard

4.3 Define Evaluation

4.3.1 The Create/Edit Method Overview Window

In the Define Evaluation window the user defines the plate layout, he inserts transformations and calculations, selects the format of the printed report and sets the automated date handling parameters.

Toolbar

On top of the window a Toolbar is displayed with the most common functions depending on the currently selected options.

In the central area of the window the Plate Layout window displays a schematically layout of a microplate. Rows are marked alphabetically, columns numerically.

If a new method has been generated, all wells are empty. A mouse click selects an individual well.

Wells that will not be measured, as given by the part of the plate settings, are displayed in grey color.

When defining the layout, transformations etc., the identifiers, formulas etc. are displayed in the corresponding wells.
4. Create/Edit a Method Wizard

Toolbar Buttons

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Undo button</td>
<td>Performs an undo of the last action. Click <strong>Undo</strong> or press <strong>CTRL-Z</strong> to undo a previous action.</td>
</tr>
<tr>
<td>Redo button</td>
<td>Repeats the action, which was performed before the undo step. Click <strong>Redo</strong> or press <strong>CTRL+Y</strong> to redo an action that was undone.</td>
</tr>
<tr>
<td>Select all unused button</td>
<td>Plate Layout mode only: All unused wells of the plate are marked.</td>
</tr>
<tr>
<td>Zoom to 10% button</td>
<td>This will set the plate layout view to 10%.</td>
</tr>
<tr>
<td>Zoom to 100% button</td>
<td>This will set the plate layout view to 100%.</td>
</tr>
<tr>
<td>Zoom mode button</td>
<td>In case the well plate consists of a large number of wells, the individual well assignments cannot be displayed in the 100% zoom mode. Use the <strong>Zoom mode</strong> button to zoom into the marked area. If activated, the user can select an area to zoom in by clicking and dragging a frame over the desired layout area. Click the right mouse button to zoom out to 100% display.</td>
</tr>
</tbody>
</table>

Plate Layout Window

The **Plate Layout** window shows the defined parameters and/or procedures depending on the selection in the control bar (see chapter below Control Bar of Create/Edit Method Tab).

Parameters and procedures are:

- **Method Layout**: plate layout; concentration-, dilution- and reference values
- **Precalculation**: polarization, FLT, spectra and cuvette data reduction
- **Transformed Data**: add new transformation…
- **Kinetic**: kinetic data reduction
- **Kinetics Transformation**: add new kinetic transformation…
- **Concentrations**: standard curve
- **Conc. Transformation**: add new concentration transformation…
- **Evaluate data**: cutoff definition, QC validation
- **Data Handling**: data export, printed report, automated data handling
- **Miscellaneous**: user prompts, number format, method notes.

Each of these inputs is invoked with a separate option, preferably in this sequence.

Plate Layout: Context-Sensitive Menu

By right-clicking on a well on the plate layout, a context-sensitive menu for the marked wells is displayed. The following commands are available:

<table>
<thead>
<tr>
<th>Menu</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Summary…</td>
<td><em>Any plate view.</em> The <strong>Summary</strong> dialog box is displayed. Refer to chapter 7.4.18 Context-Sensitive Menu of a Well/Summary Dialog for further information on the <strong>Summary…</strong> dialog box. This option is available if a layout has been assigned to the selected well.</td>
</tr>
</tbody>
</table>
### 4. Create/Edit a Method Wizard

<table>
<thead>
<tr>
<th>Menu</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Fill Selection</strong></td>
<td><em>Plate Layout mode only.</em> If a well or an area of the plate has been marked, it can be filled with the respective identifiers. The IDs and the color identifiers will be displayed on the plate layout.</td>
</tr>
<tr>
<td><strong>Delete Selection</strong></td>
<td><em>Plate Layout mode only:</em> This command will delete the IDs and color identifiers of the selected wells and leave them blank.</td>
</tr>
<tr>
<td><strong>Select all Unused</strong></td>
<td><em>Plate Layout mode only:</em> All unused wells of the plate are marked.</td>
</tr>
<tr>
<td><strong>Set / Remove Alias…</strong></td>
<td><em>Plate Layout mode only:</em> Sets or removes alias designations for the well names. See chapter 4.3.2 Method Layout: How to Define a Plate Layout/ Assign Alias to the Required Well.</td>
</tr>
</tbody>
</table>

### Control Bar of Create/Edit Method Tab

The Control Bar on the left of the screen provides a number of options, which should be executed in the suggested sequence. Depending on the kind of measurement and the connected reader type, some of the options may not be available and therefore are hidden.

When selecting an item in the control bar the corresponding dialog or plate view is displayed in the Plate Layout window pane on the right side of the screen.

All available options will be marked with a checkmark, once they have been defined. For any kind of transformation the transformation name is displayed.

The Control bar - Create/edit method tab contains the following elements:

#### Method layout group

- **Plate layout** item
  - The Plate layout window is opened, displaying the plate layout and the Well assignment dialog box.

- **Conc., Dil., and Ref.-values** item
  - The Concentration/Dilution/Reference definition dialog box is opened, displaying the dilution, concentration or reference value of each well. The standard concentrations can be established as well as the dilution factors and the reference values. An Autofill function provides easy assignment of concentrations in case of distinctive mathematical relations of the concentrations between the individual wells.

#### Precalculation

- **Polarization data reduction** for fluorescence polarization measurements
- **Spectra data reduction** for wavelength scans
- **Cuvette data reduction** for combined plate and cuvette measurements

#### Transformed data group

- **Add new transformation** ... item
  - The Plate layout window is opened, displaying the plate layout and the Transformations dialog input field.

#### Kinetic group

- **Kinetic data reduction** item
  - The Kinetics Calculation Parameters window is opened. The evaluation of the kinetics measurement data can be defined.
4. Create/Edit a Method Wizard

<table>
<thead>
<tr>
<th>Kinetics transformation</th>
<th>Add new kinetic transformation ... item</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>The Plate layout window is opened, displaying the plate layout and the Transformations dialog input field (only kinetic input data can be selected).</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Concentrations group</th>
<th>Standard curve item</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>The Standard Curve window is opened to set the parameters for the calculation of concentrations and the graphical display of the standard curve of the evaluated data.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Concentration transformation data group</th>
<th>Add new concentration transformation ... item</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>The Plate layout window is opened, displaying the plate layout and the Concentration Transformations dialog input field (only concentrations can be selected as input data).</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Evaluate data group</th>
<th>Cutoff definition item</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>QC validation item</td>
</tr>
<tr>
<td></td>
<td>The Define Cutoff window is opened. In this dialog box the limits for a qualitative evaluation (screening) can be defined.</td>
</tr>
<tr>
<td></td>
<td>The Define QC Validation window is opened. It is used to verify the validity of a test.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Data handling group</th>
<th>Data export item</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Printed report item</td>
</tr>
<tr>
<td></td>
<td>Automated data handling item</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Miscellaneous group</th>
<th>User prompts item</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Number format item</td>
</tr>
<tr>
<td></td>
<td>Method notes item</td>
</tr>
<tr>
<td></td>
<td>The Define User Prompts window enables the assignment of data (keywords, comments or prompts) to each measurement, which can then be incorporated into a printout.</td>
</tr>
<tr>
<td></td>
<td>The Number format window allows the user to define the number format for the displayed raw data or transformed data.</td>
</tr>
<tr>
<td></td>
<td>In the Method notes it is possible to enter a description of the method.</td>
</tr>
</tbody>
</table>

Control Bar – Create/Edit Method Tab: Context-Sensitive Menu

By right-clicking on any transformation, kinetic transformation and concentration transformation on the control bar, a context-sensitive menu for the marked transformation is displayed. The following commands are available:

<table>
<thead>
<tr>
<th>Menu</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rename transformation</td>
<td>A different name can be assigned to the selected transformation.</td>
</tr>
<tr>
<td>Insert transformation</td>
<td>Used to define a new transformation.</td>
</tr>
<tr>
<td>Remove transformation</td>
<td>Used to delete a transformation.</td>
</tr>
</tbody>
</table>
4. Create/Edit a Method Wizard

4.3.2 Method Layout: How to Define a Plate Layout

In the Control bar expand Method layout and select Plate layout. The Plate view and the Well Assignment dialog box are displayed.

To each well in the analysis plate an identifier can be assigned. On this basis the plate layout should be defined, (i.e. a well that is to be viewed as being a positive control, would be allocated a different identifier from that of a well that is to be viewed as being a negative control).

Assign an Identifier to the Required Well

In the Well Assignment dialog box, well identification and layout definition can be carried out. This box provides also a number of automated ID assignment capabilities, which is an essential tool for high density plates.

The desired settings have to be made in the Well Assignment dialog box. There are several ways to select the wells:

- Clicking the individual well.
- Dragging the mouse over the required wells.
- Click one of the letters (A – H) or numbers (1 – 12) to select a row or column.
- Click the O symbol in the upper left corner of the microplate to select the whole plate.
- Add wells in a certain area: After selecting a single well, hold the Shift-key and click and drag the previously selected well to the currently selected well.
- Toggle selection state of a well: When holding the Ctrl-key, the selection state of the selected well is toggled. For example: a click on an already selected well removes the well from the current selection.

Following ways are possible to assign the selected identifier to the wells:

- Double-click when making the selection of the well
- Select the wells on the microplate and then click the Fill selection button (or click the right mouse button and select Fill selection in the context-sensitive menu) on the Well Assignment dialog box
- Select the wells on the microplate and then double click the identifier in the identifier list box of the well assignment dialog.
After assigning the definitions the display in the modified wells will change.

**Example of a labeled well:**

<table>
<thead>
<tr>
<th>Identifier</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>SM1_4</td>
<td>1st line: sample, experimental group number of 1, sample ID number of 4.</td>
</tr>
<tr>
<td>1/14</td>
<td>2nd line: number of replicate is 1, total number of replicates is 14.</td>
</tr>
<tr>
<td>x-BL1</td>
<td>3rd line: primary empty – filled with the transformation formula after Transformations are defined and selected: reduce the value of this well (x) by the mean of the blanks (refer to chapter 13.4 How to Write a Formula).</td>
</tr>
<tr>
<td>1.000</td>
<td>or 3rd line: Concentration, dilution or reference value if Conc.-Dil.-Ref.-values is selected in the control bar: dilution factor value of 1.0.</td>
</tr>
</tbody>
</table>

The **Well assignment** dialog box contains the following elements:

- **Identifiers** group box
  - In this group box, corresponding identifiers for the marked wells have to be selected.
  - All available identifiers are listed in a drop down list.
  - Click the Define Identif... button to define additional identifiers. The Define Identifiers dialog box appears, see below for further details.

- **Exp. group** selection field
  - If the plate is made up of more than one test, then there needs to be more than one experiment group. In the Experiment group selection field, define which experiment the wells belong to.

- **ID-Num.** group box
  - The ID Number is used to assign the same ID to replicates that belong together. The ID Number is only available for samples and standards.
  - **ID-Num.** selection field
    - The ID-Num option allows the user to mark those replicates that are associated with the same ID. This can be used if the replicates have been assigned to different areas of the plate.
  - **Arrow buttons**
    - The ID will be calculated automatically. If a number of wells is marked, the direction in which the IDs are assigned to the wells (vertically, horizontally) can be established using the arrow buttons.
4. Create/Edit a Method Wizard

<table>
<thead>
<tr>
<th>Replicates group box</th>
<th>Determines the number of replicates for the selected identifier type. Two option buttons allow the decision whether multiple or individual values are to be defined:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>• <strong>Fix number</strong> option button&lt;br&gt;Only enabled for standards and samples where IDs can be used.&lt;br&gt;If this option button is active a number can be entered in the corresponding text field. This number defines how many replicates are intended for this identifier. The selected wells are then filled with the entered number of replicates. Therefore the number of selected wells must be a multiple of the entered number of replicates.</td>
</tr>
<tr>
<td></td>
<td>• <strong>All</strong> option button&lt;br&gt;All selected wells are defined as replicates of one identifier. If an existing ID number for the samples and standards is chosen, the selected wells are then added as replicates to the existing replicates. With all other identifier types the selected wells are added as replicates to the existing replicates.</td>
</tr>
<tr>
<td></td>
<td>Two <strong>Arrow buttons</strong> define the direction of counting up the replicate number.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Fill section button</th>
<th>If an area of the plate has been marked, it can be filled with the respective identifiers. The IDs and the color of the identifiers will be displayed on the plate layout.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Delete section button</td>
<td>Click <strong>Delete</strong> or press <strong>DEL</strong> to delete the IDs and color identifiers of the selected wells and leave them blank.</td>
</tr>
<tr>
<td>Define identifier button</td>
<td>Click <strong>Def. identif.</strong> if a new identifier is to be defined or if an existing identifier is to be edited (see Expert's Know How, Define a New Identifier)</td>
</tr>
</tbody>
</table>

**Assign Alias to the Required Well**

To assign alias designations for defined well names, click the right mouse button in the required well, select **Set/Remove Alias...** and choose an alternative identifier name in the drop down list. The alias is marked with an asterisk * and has same experimental group, ID number and replicate number as the primarily defined well. This feature is used, if e.g. the 0-Standard is also used as Negative control.
4. Create/Edit a Method Wizard

**EXPERT’S KNOW HOW**

**DEFINE A NEW IDENTIFIER**

In the **Well Assignment** dialog box, click **Def. Identif. to define** a new identifier or edit an existing one.

![Define Identifiers dialog box](image)

The identifiers are listed in groups (see table below). Highlighting an identifier, its properties are displayed in the right window.

Standard identifiers are:

<table>
<thead>
<tr>
<th>Group</th>
<th>Identifiers</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sample</td>
<td>SM (Sample)</td>
</tr>
<tr>
<td>Blank</td>
<td>BL (Blank)</td>
</tr>
<tr>
<td></td>
<td>BF (Polarization reference buffer)</td>
</tr>
<tr>
<td>Reference</td>
<td>RF (Polarization reference)</td>
</tr>
<tr>
<td>Standard</td>
<td>ST (Standard)</td>
</tr>
<tr>
<td>Control</td>
<td>PC (Positive control)</td>
</tr>
<tr>
<td></td>
<td>NC (Negative control)</td>
</tr>
<tr>
<td></td>
<td>LPC (Low positive control)</td>
</tr>
<tr>
<td></td>
<td>HPC (High positive control)</td>
</tr>
<tr>
<td></td>
<td>CL (Calibrator)</td>
</tr>
</tbody>
</table>

The **Define Identifiers** dialog box contains the following elements:

- **Identifier tree structure**: A structured view of all existing identifiers, their colors and abbreviations is offered in a small window. The identifiers are listed under the groups **Sample, Blank, Reference, Standard** and **Control**.

- **Identifier group box**: The criteria held by the various identifiers used in the program will be displayed. If new identifiers are required, they can be inserted here.

In the **Identifier group box** the type, abbreviation, well color and description of the identifier selected in the tree structure is displayed.
4. Create/Edit a Method Wizard

The Identifier group box is only activated for entering data, when
- one of the identifier groups in the tree structure is selected and the Insert button has been clicked or
- one of the identifiers in the tree structure is selected and the Edit button has been clicked.

Then, in this group box, the type, abbreviation, well color and description of the new identifier need to be defined.

| **Type** text field: The type of identifier is displayed. No changes are possible. |
| **Abbreviation** text field: The identifier’s abbreviation will be used in the analysis plate display. |
| **Color** drop down list: The color of the identifier on the plate layout has to be selected here. |
| **Description** text field: A text description can be entered for each identifier. |

Use one of these two buttons to save changes of newly entered data or to discard any changes:

| **Save** button: The Save button saves the entered color, abbreviation and description of the relevant identifier. |
| **Discard** button: The Discard button will cancel any changes. |

**Insert** button
Click the Insert button to create a new identifier. This new identifier will be associated with the currently selected identifier group in the tree structure.

**Edit** button
A selected identifier can be modified.

**Delete** button
Click Delete or press DEL to delete any selected identifier.

**Set as default** button
Using this option, the settings can be defined as default for future use.

**Restore default** button
Using this option, the settings can be reset to the previously defined default.
4.3.3 **Method Layout: Conc., Dil. and Ref. Values**

In the **Control bar** expand **Method layout** and select **Conc./Dil./Ref.-values**. The **Plate View** and the **Select Identifier** dialog box are displayed.

The concentrations for the standards, the reference values for the Reference (used with Fluorescence Polarization measurements) and the dilution factors for all other identifiers can be entered or edited in the table next to the **Plate View** window. The values can be defined for each well individually. By default the dilution factors are set to 1, the concentrations are set to 0 and the reference value is set to 22. Entering a dilution factor of 2 means that the sample has been diluted by half. The calculated concentration will therefore be multiplied by 2.

The **Concentration/Dilution/Reference** window contains the following elements:

- **Select Identifier** drop down list
  - The values are co-related within the individual well types; this field provides all wells currently included in the measurement. Select an identifier to edit the corresponding dilution or concentration factors. All wells, which match the selected well type identifier, are listed.

- **Exp. group** selection field
  - Select the respective experimental group. If there is only one experimental group, the field cannot be edited.

- **Table with Identifier and Concentration/Dilution columns**
  - This table displays all wells in the **Identifier** column, which match the selected identifier (as from the **Select Identifier** list). The corresponding dilutions, concentrations or reference values are listed in the **Dilution/Concentration/Reference** column, where they can be edited individually.

- **Unit** text field
  - The displayed concentration unit can be determined.
4. Create/Edit a Method Wizard

**Autofill check box**
The **Autofill** function provides the calculation of the corresponding concentrations or dilution factors according to available types of series. This is useful when the dilution series is quite large and the concentrations are in a clear mathematical relationship to each other.

**Option buttons for the mathematical concentration calculation**
If the **Autofill** check box has been selected, the following options are available:
- Arithmetic series: \( a(n+1) = a(n) + \ldots \)
- Geometric series: \( a(n+1) = a(n) \times \ldots \)
- User defined series \( a(n+1) = \ldots \)

  Example 1: Each subsequent concentration should contain twice + 0.5 of the previous concentration:
  Formula 1: \( a(n+1) = 2 \times n + 0.5 \)

  Example 2: Each subsequent concentration should contain one third of the previous concentration:
  Formula 2: \( a(n+1) = n/3 \)

**Apply button**
The **Apply** button applies the selected mathematical concentration calculation to the wells as displayed in the table with **Identifier** and **Concentration/Dilution** columns.

**Dilution series group box**

**Calculate ICx check box**
Displays a dilution graph of the sample and automatically calculates the ICx values. This requires samples with at least 4 replicates and at least 4 different dilutions defined (see chapter Expert's Know How below for further details).

**Input Data drop down list**
Select from the drop down list the input data.

**Calculation Condition text field**
The intercept will be calculated with the entered percentage of the maximum value respectively maximum value minus minimum value (see chapter Expert's Know How below for further details).

**ICx name text field**
Data can be selected for ICx calculation. The name is filled in automatically based on the calculation condition.

**Set 0% value to**
Intensity 0: (see chapter Expert's Know How below for further details).
Min. intensity of dilution series: (see chapter Expert's Know How below for further details).

Dilution can be edited directly in the plate layout window by right mouse clicking in one or more selected wells. In this way, it is possible to assign different dilution values to replicates.
EXPERT’S KNOW HOW

ICx CALCULATION

The mathematical calculation of the fit for the dilution series is identical to the calculation of the standard curve with the Marquardt 4 parameter algorithm.

This requires at least four replicates with different dilutions.

In addition, the specified intercept(s), e.g., IC 50 is calculated.

It is possible to define more than one intercept for the dilution series.

It is possible to define the 0% value for the calculation by selecting:

- **Intensity 0**
  
  Using 0 OD/RFU

  The largest value of the dilution series is considered 100%, the value of 0 is considered 0%. The ICx (e.g., IC 50) is then defined as the dilution where the response reaches x% (e.g., 50%). It is only calculated, if the value is within the available data (no extrapolation is used).

  or

- **Minimum intensity of the dilution series**

  Using the minimal intensity of the dilution series

  *Note*

  The IC 50 is often calculated with the mean value of dilution=1:1 and dilution=1:infinity. To achieve this, the dilution series must be baseline corrected before ICx calculation.

  The largest value of the dilution series is considered 100%, the minimum intensity of the dilution series is considered 0%.
4.3.4 Precalculation: Polarization Data Reduction

Expand Precalculation in the control bar and select Polarization Data Reduction.

This option is only available for Fluorescence Polarization (FP) measurements. FP measurements consist of two fluorescence intensity measurements, one with polarizers in parallel and one with polarizers in perpendicular position. The G-factor compensates for differences in optical components between parallel and perpendicular measurement. The G-factor can be established by a calibration measurement using a reference solution with known polarization value and a corresponding reference blank solution.

The appropriate entries for fluorescence polarization measurements must be made under the G-factor and Sample blank reduction group boxes of the Polarization Settings dialog box. Under Reference the appropriate reference value has to be typed in mP units. It is recommended to use a reference blank for the G-factor calibration. The reference blank check box has to be activated and the appropriate identifier (which has been defined in the plate layout) has to be selected from the list box.

In the Sample blank reduction group box it has to be determined if the blank reduction is applied to the samples measurement values or not. If the blank reduction is selected, a blank reduction is performed before the calculation of the polarization values.

The option Automatically precalculate polarization data can be disabled for further custom evaluation of parallel and perpendicular raw data.

The Polarization Settings dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Automatically precalculate polarization data check box</th>
<th>Select this option in order to use automatic precalculation of polarization data. This option cannot be enabled for multilabel measurements.</th>
</tr>
</thead>
<tbody>
<tr>
<td>G-factor group box</td>
<td>A G-factor must be established when measuring with polarization.</td>
</tr>
<tr>
<td>• Use option button and text field:</td>
<td>If the G-factor is known, it can be directly entered in the text field attached to the option button.</td>
</tr>
<tr>
<td>• Confirm at runtime check box:</td>
<td>If this box is selected, the user is prompted to confirm or modify the G-factor.</td>
</tr>
<tr>
<td>• Request from instrument check box:</td>
<td>If this box is selected, the G-factor is read directly from the reader and cannot be entered manually.</td>
</tr>
<tr>
<td>• Calibrate option button:</td>
<td>The G-factor is determined by calibration measurement. Select under Reference the appropriate reference identifier and enter the polarization value.</td>
</tr>
<tr>
<td>• Reference blank check box and drop down list:</td>
<td>If blanks are to be used in the calculation, the Reference blank check box has to be selected and the correct identifier has to be chosen from the list.</td>
</tr>
<tr>
<td>Blank reduction group box</td>
<td>• Exp. group list: If the method contains a number of individual experimental groups, the desired group can be selected using this option.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Automatically precalculate polarization data check box</th>
<th>Select this option in order to use automatic precalculation of polarization data. This option cannot be enabled for multilabel measurements.</th>
</tr>
</thead>
<tbody>
<tr>
<td>G-factor group box</td>
<td>A G-factor must be established when measuring with polarization.</td>
</tr>
<tr>
<td>• Use option button and text field:</td>
<td>If the G-factor is known, it can be directly entered in the text field attached to the option button.</td>
</tr>
<tr>
<td>• Confirm at runtime check box:</td>
<td>If this box is selected, the user is prompted to confirm or modify the G-factor.</td>
</tr>
<tr>
<td>• Request from instrument check box:</td>
<td>If this box is selected, the G-factor is read directly from the reader and cannot be entered manually.</td>
</tr>
<tr>
<td>• Calibrate option button:</td>
<td>The G-factor is determined by calibration measurement. Select under Reference the appropriate reference identifier and enter the polarization value.</td>
</tr>
<tr>
<td>• Reference blank check box and drop down list:</td>
<td>If blanks are to be used in the calculation, the Reference blank check box has to be selected and the correct identifier has to be chosen from the list.</td>
</tr>
<tr>
<td>Blank reduction group box</td>
<td>• Exp. group list: If the method contains a number of individual experimental groups, the desired group can be selected using this option.</td>
</tr>
</tbody>
</table>
4. Create/Edit a Method Wizard

- **No blank reduction** option button: This option button has to be selected if blank reduction is not to be applied at the measurement.

- **Reduce** option button: Before calculating the polarization values a blank reduction is used.

- **All by** check box and **Identifier** drop down list: If all by is checked, all measurement values will be reduced by the value of the well as defined by its identifier in the drop down list.

- **Except .... by** check box: The except by check box defines, whose value (identifier) is to be deducted from the first selected identifier (drop down list). This setting is used for individual Sample blanking. Create a new identifier (e.g.: SMB: Sample Blank) under the identifier group samples in the **Identifiers Definition** dialog box to use this function.

**Note**

*It is recommended to use always a reference on the plate to calculate the G-factor.*

For more information on calculation refer to chapter 13 Calculations.

4.3.5 **Precalculation: Spectra Data Reduction**

Expand **Precalculation** in the control bar and select **Spectra Data Reduction**. This option is only available for measurements containing a two-dimensional scan (absorbance scan, excitation scan, emission scan).

Spectra data reduction allows to perform a spectra blank reduction and to extract specific data, e.g. intensities, from the scan.

The **Spectra data reduction** window contains the following elements:
### Blank reduction check box
This option is only available if blanks are defined on the layout. The blank reduced spectra is calculated by subtracting the spectrum of the blank well from all other wells. When more blanks are defined on the plate, e.g. when multiple experimental groups are defined, an additional options button appears. This allows to define the blank to be used.

- **Input data** text box: shows the input data to be processed.
- **Blank reduction** option button: select, if a blank reduction should be performed on the selected experimental group.
- **Reduce all by** dropdown list: select to define the identifier to be used for blank reduction.

### Smooth check box
A spectrum containing a lot of noise can be smoothed. A smooth factor can be set in the options part. This factor defines the degree of smoothing.

- **Input data** text box: shows the input data to be processed.
- **Smooth factor**: to define the smooth factor.

### Wavelength pick check box
**Wavelength pick** is used to extract intensities at specific wavelengths and calculate results like ratios. It is mandatory to set the options.

The **Wavelength pick** parameters dialog box contains the following elements:

- Intensities at a specific wavelength can be extracted, ratios and areas can be calculated and customized formulas can be entered.
- **Input data** text box: shows the input data to be processed.
- **Pick Wavelengths** option button: an intensity at a specific wavelength can be added to the list of calculated results.
### 4. Create/Edit a Method Wizard

<table>
<thead>
<tr>
<th><strong>Calculate Ratio</strong> option button: two wavelengths can be specified. The ratio of the intensities at those wavelengths is calculated and available as result.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Area</strong>: to calculate the area below the spectra curve between two defined wavelengths.</td>
</tr>
<tr>
<td><strong>Custom</strong> option button: a user defined formula can be entered. Intensities at specified wavelengths can be used in formulas.</td>
</tr>
<tr>
<td><strong>Results</strong> list box: summarizes all defined formulas</td>
</tr>
<tr>
<td><strong>Add</strong> button: the current selection is added to the list of results.</td>
</tr>
<tr>
<td><strong>Delete</strong> button: the selected result is removed from the list.</td>
</tr>
<tr>
<td><strong>Edit</strong> button: the data name of the selected result can be defined.</td>
</tr>
</tbody>
</table>

**Normalize check box**  
The **Normalize parameters** dialog box contains the following elements:

| **Input data** text box: shows the input data to be processed. |
| **Normalize to**: select between maximum intensity or insert customized intensity. |

**Peak check box**  
A peak is defined as the position of the maximum value of the spectrum. Overflows and maxima at the left or right border of the spectrum are not treated as peaks. It is very important to sufficiently smooth the spectrum before finding a peak.
4. Create/Edit a Method Wizard

The **Peak parameters** dialog box contains the following elements:

<table>
<thead>
<tr>
<th><strong>Input data:</strong> Normalized spectrum</th>
<th><strong>OK</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Wavelength range:</strong> from 400 nm to 600 nm</td>
<td><strong>Cancel</strong></td>
</tr>
<tr>
<td><strong>Ignore peaks below 0 OD/RFU</strong></td>
<td><strong>Help</strong></td>
</tr>
<tr>
<td><strong>Calculate width and area at 50 % of max intensity</strong></td>
<td></td>
</tr>
</tbody>
</table>

Use this option to find the peak with the highest intensity within a defined wavelength.

The threshold (OD/RFU value) and the calculation criteria for calculation of width and area can be defined as well.

The following data will be calculated for the found path:

- peak intensity
- wavelength of the peak
- peak width
- peak area

| **Custom formulas check box** | Select this check box to enter formulas to calculate the spectrum using given functions; e.g. smooth. Refer to chapter 13.3 Spectra Data Reduction for further information. Transformation must either return a spectrum or a single data for all wells; it is not possible to mix both. Using this option, functions can be defined which are not available in the standard selection. E.g. to find more peaks within a spectrum or to create a derivation of a spectrum. |

| **Calibration check box** | Use this check box to calibrate the curve at a certain wavelength using a calibration factor. |

| **Available results** | Available results of all data are listed. S is a spectrum V is a value. |

See Note below when connected to a Safire instrument.
4. Create/Edit a Method Wizard

4.3.6 Precalculation: Cuvette Data Reduction

If you are using an Infinite M200 with Cuvette option you can define methods with a combination of plate and cuvette measurements. For the cuvette Absorbance ratio, Absorbance scans and Absorbance kinetic measurements can be defined. Using the Precalculation - cuvette data reduction dialog it is possible to define formulas to get single values from a scan or a kinetic measurement.

**Examples:**

For scan:
Formula $x[698]/x[600]$ gives you as result the ratio between the value at 698 nm and the value at 600 nm.

For kinetic:
Formula $x[5]-x[0]$ means that the value of the 6th kinetic cycle is reduced by the value of the 1st kinetic cycle.

4.3.7 Transformed Data: Add New Transformation

In the control bar expand Transformed data. All defined transformations are displayed in the control bar.

To define a new transformation click Add new transformation... . The new transformation with a default name will be inserted.

The default name should be changed immediately in the edit box. The name can be inserted or changed also later, clicking Rename Transformation from the context-sensitive menu.

**Note**

The name of a transformation is used to represent the result of the calculations and will also be used when the values are displayed in the specific data output menus. Calculated values of the transformations are also available as input data for further evaluations.

**Note**

The transformation name has to be in Latin characters in order to make the transformation available as additional input data for further transformations with multiple input data.

A number of transformation calculations can be defined when setting up the method. A typical example of this is the deduction of the empty value (blank) from all wells. Refer to chapter 13.4 How to Write a Formula for more details.
4. Create/Edit a Method Wizard

The formula text box above the plate view is used to define these various transformation calculations, using raw data and previous transformations as input data.

On the microplate, the wells for which the transformation is to be applied must be selected.

The transformations edit field contains the following elements:

**Input data** drop down list

The list contains the measurement values, the results from precalculations and all already defined transformations, as well as the averages. If Mean data is selected as Input data for Transformations, then transformations will be assigned to the first replicate of an identifier only.

**Formula text box fx**

Formulas can be entered by typing or by selecting the needed function from the Functions&Constants list box.

**Formula drop down list**

This list contains some standard formulas (see Notes below) and all formulas which have been incorporated into the current method. A formula may therefore be selected from this list or a new formula can be added. Formulas for transformations can be entered using the appropriate variables, operators and multiple functions.

**Confirm button**

*Formula edit mode only.* Green hook

Assigns the transformations to the selected well.

Click Confirm button or press ENTER key to assign the formula definition to the well and change to Select mode.

**Cancel button**

*Formula edit mode only.* Red cross

Click the Cancel button or press the CANCEL key to leave the Edit mode without assigning the formula definition to the well.

**Available data** drop down list

Select from this list the appropriate data, if more than one set of input data shall be used for calculations. The data set will appear in the formula text box within apostrophes followed by an exclamation sign. To complete the definition, enter the identifier’s name or refer to the corresponding value within the well. E. g. ‘Raw data’ ! BL1

The list contains the measurement values, the results from precalculations and all, up to this moment defined transformations.

**Functions drop down list**

Lists all mathematical and Boolean functions for the definition of formulas.

**Options button**

Use this button to customize the behavior when selecting wells in the edit mode. It is possible to select between the following options:

- Identifier average name
- Identifier replicate name
- Plate well name

**Constants button**

Click this button to open the Define Constants dialog box where constants for calculation can be defined.
4. Create/Edit a Method Wizard

**Note**

If a blank is set in the Plate Layout, the formula to calculate the blank reduction is offered in the combo box: \( x - BL1 \).

The symbol \( x \) refers to the current value within a well. \( BL1 \) is the average value of the blank well(s).

**Note**

If a multilabel measurement with two labels is defined, different formulas to reduce the multilabel data are offered in the combo box.

- ‘Label1’!x/’Label2’!x … predefined ratio calculation
- ‘Label2’!x/’Label1’!x … predefined ratio calculation
- ‘Label1’!x-’Label2’!x … predefined difference calculation
- ‘Label2’!x-’Label1’!x … predefined difference calculation
- (‘Label1’!x-’Label1’!BL1)/(‘Label2’!x-’Label2’!BL1) … predefined ratio calculation with blank reduction
- (‘Label2’!x-’Label2’!BL1)/(‘Label1’!x-’Label1’!BL1) … predefined ratio calculation with blank reduction

**Note**

If the read mode is set to absorbance, the formula to calculate the transmission is offered in the combo box: \( 1/10^x \).

The transformation definition has two modes:

| **Select mode** | When clicking on a well, the corresponding formula is displayed in the text box. The currently active well is displayed with a red border. |
| **Edit mode** | When entering a formula or pressing the ‘=’ key, the active well is displayed with a blue border. Selecting other wells adds the corresponding identifier to the current formula. When selecting the currently active well an ‘x’ is added to the formula. The symbol ‘x’ refers to the current value within a well. |

Once the formula is created, it will be assigned to the selected well with pressing enter or clicking the confirm button (green hook). After assigning the formula the select mode is reached. An integrated formula checker verifies the plausibility of the formula. A warning appears in case the created formula is not executable. Select CANCEL to discard the defined formula and to reach the select mode. It is also possible to use the corresponding buttons on the left of the formula text box.

When in **Select mode** click the red square in the right lower edge of the well and drag the red selection frame over those wells for which the formula should be set.

It is also possible to select the desired wells and use the functions **Set Formula** and **Remove Formula(s)** which are available from the context-sensitive menu.

These actions have to be performed for all wells, which shall contain transformations.
4. Create/Edit a Method Wizard

**EXPERT’S KNOW HOW**

**DEFINE CONSTANTS**

Use the Define Constants dialog box to define the constant values of a method. These constants can be used wherever a formula can be entered.

Click the OK button to save the edited parameters.

The Define Constants dialog box contains the following elements:

- **Constants list**
  - In each row, a constant can be defined. The rows are divided into 4 columns:
    - **Name**
      - In the Name text field an appropriate identifier name for the constant, for example: a code or an abbreviation, must be entered. Only letters can be used.
    - **Value**
      - In the Value text field a numerical value must be allocated to the constant.
    - **Comment**
      - Enter a short comment to the constant.
    - **Req.** (*required*)
      - The Req. check box indicates, that a measurement can only be launched on receipt or confirmation of the value for the constant.

4.3.8 **Kinetic: Kinetic Data Reduction**

In the control bar expand Kinetic and select Kinetic data reduction.

The dialog box is structured in tabs: Slopes, Onsets, Min./Max./Area, Available output data, Enzyme kinetics. The unit of the values is displayed according to the selected measurement mode (for example: OD for absorbance).

Use the Slopes tab to establish the evaluation of the kinetic curve’s slope behavior.

The Onsets tab defines calculation of the time by which a certain OD/RFU value is reached.

Use the Min./Max./Area tab to define the evaluation of the minimum and maximum values contained in the curve and to define the calculation of the area under the kinetic curve.

Use the Enzyme kinetics tab to define the evaluation of enzyme kinetics.

Use the Available output data tab to display the data, calculated using the kinetics evaluation.

**Note**

Unusable data (e.g. overflow values) are ignored for kinetic data calculation.
## Slopes Tab

This tab allows the user to establish the evaluation of the kinetic curve’s slope. The *Slopes* tab contains the following elements:

<table>
<thead>
<tr>
<th>Input data drop down list</th>
<th>Select the input data to be processed.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Calculation drop down list</td>
<td>Select the calculation method, linear or quadratic (refer to chapter 13 Calculations).</td>
</tr>
<tr>
<td>Mean slope check box</td>
<td>The start and end time can be typed into the provided text fields, otherwise the whole kinetic is analyzed.</td>
</tr>
</tbody>
</table>

- **Time/Points** option buttons:
  - If *Time* is selected the start and end time is entered in hours, minutes and seconds. If *Points* is selected the start and end point for the analysis is given through the entered kinetic cycle number.

- **Start** field:
  - The start time (in hours, minutes and seconds) or cycle number must be entered here.

- **End** field:
  - The end time (in hours, minutes and seconds) or cycle number must be entered here.

<table>
<thead>
<tr>
<th>Maximum slope check box</th>
<th>The start and end time can be typed into the provided text fields, otherwise the whole kinetic is analyzed.</th>
</tr>
</thead>
</table>

- **Time/Points** option buttons:
  - If *Time* is selected the start and end time is entered in hours, minutes and seconds. If *Points* is selected the start and end point for the analysis is given through the entered kinetic cycle number.

- **Start** field:
  - The start time (in hours, minutes and seconds) or cycle number has to be entered here.

- **End** field:
  - The end time (in hours, minutes and seconds) or cycle number has to be entered here.

- **Points** text field:
  - Select for how many points the maximum slope calculation is performed.

The *mean slope* option determines the mean slope (mean increase/decrease) throughout the defined interval. A start and an end time must first be entered. All measurement points that fall within the interval of the slope will be determined and then, from these details, the mean slope will be formed. The mean slope is defined as the arithmetical mean of the slopes that are calculated from the center points of two adjacent measurement points. The kinetics data made available through this method, includes the mean slope per second, per minute and per hour, as well as the correlation coefficient and the goodness of fit.
4. Create/Edit a Method Wizard

Using the **maximum slope** option, the maximum slope (maximum increase/decrease) achieved in the selected interval will be determined. Under the **Points** option, the number of combined points has to be entered. At the beginning the slope will be calculated from the center point of the 1st and the n\textsuperscript{th} point from the first n points. Then the interval will be moved one point further and the process is repeated. This process will continue over all points within the selected interval. The result will be determined as the largest absolute value of these individual slopes. The kinetics data made available through this method includes the maximum slope per second, per minute and per hour, as well as the time span from the first measurement to the maximum slope in seconds.

**Onsets Tab**

Use the **Onsets** tab to determine the time to reach a certain point (OD/RFU/Polarization value).

The **Onsets** tab contains the following elements:

<table>
<thead>
<tr>
<th>Input data drop down list</th>
<th>Select the input data to be processed.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Time to onset</strong> check box</td>
<td>If the <strong>Time to onset</strong> check box is selected, an absolute value for the onset can be entered in the following text field.</td>
</tr>
<tr>
<td>• Text field: An <strong>absolute</strong> value for the onset must be entered.</td>
<td></td>
</tr>
<tr>
<td>• <strong>Basis mean of the first n points</strong> option button and text field: If the option button is selected, the points text field is active and the desired number of points can be entered here.</td>
<td></td>
</tr>
<tr>
<td>• <strong>Basis</strong> option button and text field: If the <strong>Basis</strong> option button is selected, an absolute value for the basis must be entered in the adjacent text field.</td>
<td></td>
</tr>
<tr>
<td><strong>Time to onset %</strong> check box</td>
<td>If the <strong>Time to onset %</strong> check box is selected, a percentage value for the onset can be entered in the following text field.</td>
</tr>
<tr>
<td>• Text field: A <strong>percentage</strong> value for the onset must be entered.</td>
<td></td>
</tr>
<tr>
<td>• <strong>Basis mean of the first n points</strong> option button and text field: If the option button is clicked, the points text field is active and the desired number of points can be entered here.</td>
<td></td>
</tr>
<tr>
<td>• <strong>Basis</strong> option button and text field: If the <strong>Basis</strong> option button is selected, an absolute value for the basis must be entered in the adjacent text field.</td>
<td></td>
</tr>
</tbody>
</table>

The result data made available through this method includes the basis value, the time taken to reach the basis value, the time taken to reach the sum of basis and onset value, and the difference of these two time spans (Time Basis to Onset). With increasing kinetic measurement values the onset value is to be defined as a positive number, with decreasing values the onset value is to be defined as a negative number.
Min./Max./Area Tab

Use this tab to define the evaluation of the minimum and maximum values contained in the curve and to define the calculation of the area under the kinetic curve.

The Min./Max./Area tab contains the following elements:

<table>
<thead>
<tr>
<th>Input data drop down list</th>
<th>Select the input data to be processed.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean minimum value check box</td>
<td>Select to open the Points text field where the fixed number of points has to be entered for the minimum value. An even curve will then be generated using these points and the lowest value contained in the curve determined.</td>
</tr>
<tr>
<td>Mean maximum value check box</td>
<td>Select to open the Points text field where the fixed number of points must be entered for the maximum value. An even curve will then be generated using these points and the highest value contained in the curve determined.</td>
</tr>
<tr>
<td>Area check box</td>
<td>The start and end time can be typed into the provided text fields, otherwise the whole kinetic is analyzed.</td>
</tr>
</tbody>
</table>

- **Time/Points** option buttons:
  - If **Time** is selected the start and end time is entered in hours, minutes and seconds. If **Points** is selected the start and end point for the analysis is given through the entered kinetic cycle number.

- **Start** field:
  - The start time (in hours, minutes and seconds) or cycle number has to be entered here.

- **End** field:
  - The end time (in hours, minutes and seconds) or cycle number has to be entered here.

Averages are taken from the number of points starting from the first kinetic measurement value and stepping through one by one until the last kinetic measurement point is included in the average calculation. The minimum/maximum value is determined from these averages.

The result data made available through this method includes minimum/maximum value, and the time span from the first measurement to the minimum/maximum value in seconds.

**Example:**

With a kinetic of 5 cycles and a fixed number of 3 points, following averages are taken:

- average of 1\textsuperscript{st}, 2\textsuperscript{nd}, and 3\textsuperscript{rd} kinetic value
- average of 2\textsuperscript{nd}, 3\textsuperscript{rd}, and 4\textsuperscript{th} kinetic value
- average of 3\textsuperscript{rd}, 4\textsuperscript{th}, and 5\textsuperscript{th} kinetic value

The minimum/maximum value is determined from these 3 averages.

The area under the curve is calculated using the formula given below:

\[
A = \sum_{i=1}^{n-1} y_i \cdot (x_{i+1} - x_i) + \frac{(y_{i+1} - y_i) \cdot (x_{i+1} - x_i)}{2}
\]
Available Data Tab

A list of the results is displayed in the Available output data tab. This gives an overview of the results of the selected calculations.

The Available output data tab contains the following elements:

| Data field | The data field lists values as selected in the previous tabs of the Kinetic Calculation Parameters dialog box. This data field is for pure display of the listed output data only and provides no edit functions. |

Enzyme Kinetics Tab

Use this tab to establish the evaluation of enzyme kinetics according to the model of Michaelis and Menten.

This tab is only available if standards are on the plate and either transformations or slope calculations are defined.

The Enzyme kinetics tab contains the following elements:

<table>
<thead>
<tr>
<th>Input data drop down list</th>
<th>Select the input data to be processed.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Calculate Km and Vmax check box</td>
<td>Decide whether to calculate Km and Vmax selecting the corresponding check box.</td>
</tr>
</tbody>
</table>
| Calculation type group box | The calculation type can be selected from:
  - Hanes
  - Eadie-Hofstee
  - Lineweaver-Burk
  The calculation type can be selected as Hanes (concentration versus concentration/input data), Eadie-Hofstee (input data/concentration versus input data) and Lineweaver-Burk (1/input data versus 1/concentration). |

The result data made available through this method includes Km and Vmax for Enzyme kinetic graph of each experimental group.

Unlike the results of the other kinetic calculations, these results are displayed in the Graph: Enzyme Kinetics dialog box.

4.3.9 Kinetics Transformations: Add New Kinetics Transformations

Select Add new kin. transform... from the control bar.

In the Kinetic transformations dialog box a transformation formula can be defined, which is used for transforming kinetic input data individually for every well.

In the Kinetic transformations dialog box further calculations can be performed on kinetic input data.

The window elements are similar to the Transformation input. Refer to chapter 4.3.7 Transformed Data: Add New Transformation for further information.
4.3.10 Concentrations: Standard Curve

In the control bar expand Concentrations and click Standard Curve. Use this option to set up standard curves for quantitative tests. The standard curve dialog box contains various settings concerning the analysis type, the axes and the display of the standard curve. The editable fields and elements are grouped in 5 different tabs.

Data Tab

This tab stipulates some basic settings like the input data source.

**Exp. group** spin control
- If several tests are to be performed on one plate the **Experiment group** must be selected. If the plate contains only one test, then the spin control will not be displayed.
- For each experiment group the input data can be defined individually.

**Input data drop down list**
- Select the **Input data** to be used for the standard curve. Select measurement data or any available transformation results.

**Standards from layout option button**
- Calculate the standard curve from the standards on the layout.

**Standards from ext. file option button**
- If the selected experimental group contains no standards, a standard curve can be loaded from a .std file. This option can save time by allowing the user to evaluate a number of plates on the basis of one saved standard curve. The **Select** button must be clicked to select the file.

**Standards from exp. group option button**
- If the selected experimental group contains no standards, a standard curve from another experimental group can be used.

**No standard curve option button**
- If the selected experimental group contains no standards, it can be decided to calculate no concentrations for this experimental group (is set per default in this case).

**Additional Concentrations button**
- Click the **Additional Concentrations** button to open the **Calculate Additional Concentration** dialog box. Select additional sets of input data, which are to be used to calculate concentrations based on the current standard curve.
### 4. Create/Edit a Method Wizard

The **Calculate Additional Concentrations** dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Element</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Input data drop down list</strong></td>
<td>Select the input data for calculation of additional concentrations.</td>
</tr>
<tr>
<td><strong>Selected data list</strong></td>
<td>The list contains the input data names for calculation of additional concentrations.</td>
</tr>
<tr>
<td><strong>Add button</strong></td>
<td>Click the <strong>Add</strong> button to add the currently selected input data in the <strong>Input data</strong> drop down list to the <strong>Selected data</strong> list.</td>
</tr>
<tr>
<td><strong>Remove button</strong></td>
<td>Click the <strong>Remove</strong> button to remove the currently selected data from the <strong>Selected data</strong> list.</td>
</tr>
</tbody>
</table>

### Analysis Type Tab

Use this tab to select the analysis type. Please refer to chapter 13.5 Standard Curve Analysis Types for a detailed description of the analysis types.

<table>
<thead>
<tr>
<th>Analysis type option buttons</th>
<th>Select which interpolation algorithm is to be employed when calculating the standard curve:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>All offered analysis types are listed and can be selected:</td>
</tr>
<tr>
<td></td>
<td>1. Point to point</td>
</tr>
<tr>
<td></td>
<td>2. Linear Regression</td>
</tr>
<tr>
<td></td>
<td>3. Non-linear Regression</td>
</tr>
<tr>
<td></td>
<td>4. Cubic spline</td>
</tr>
<tr>
<td></td>
<td>5. Akima</td>
</tr>
<tr>
<td></td>
<td>6. Polynomial (including the field for selection of the polynomial order and including weight options)</td>
</tr>
<tr>
<td></td>
<td>7. Four Parameters (including the more button for minimum and maximum determination)</td>
</tr>
<tr>
<td></td>
<td>8. Four Parameters Marquardt (including the more button for definition of the weighting options)</td>
</tr>
<tr>
<td></td>
<td>9. Five parameters (including the more button for definition of the weighting options)</td>
</tr>
<tr>
<td></td>
<td>10. LogitLog (including the more button for minimum and maximum determination)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Data scaling drop down list</th>
<th>The analysis type is applied to scaled values. Following scaling modes can be selected:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>• Lin(x)Lin(y): x and y axis are scaled linear</td>
</tr>
<tr>
<td></td>
<td>• Lin(x)Log(y): x axis is scaled linear, y axis is scaled logarithmically</td>
</tr>
<tr>
<td></td>
<td>• Log(x)Lin(y): x axis is scaled logarithmically, y axis is scaled linear</td>
</tr>
<tr>
<td></td>
<td>• Log(x)Log(y): x and y axis are scaled logarithmically</td>
</tr>
</tbody>
</table>

**Note**

*Please note, that, if one selects log-scaling for the x-axis, it is not possible to have a concentration value of 0 since it is mathematically not possible to calculate a logarithm of 0. But it is possible to use a value of for example 0.0000001.*
4. Create/Edit a Method Wizard

Click the **More** button to view the following options:

- **Standard curve** numeric selection field
  
  If there is more than one experimental group, for **LogitLog** and **Four Parameters** the **Min.** and **Max.** value can be selected for each curve individually.

- **Weighting**
  
  Select **Use weights** to use one of the following weighting methods:
  
  - Automatic using variance
  - Automatic using relative weight
  - Manual
  
  See chapter 13.5.14 Weighting for Four / Five Parameter Fit – Marquardt / Polynomial Fit

- **Weighting dialog** – select More button if “Automatic using variance” is selected => Error handling dialog is displayed – Define the weighting factors, which should be used if one of the two error cases (All replicates are equal or only one replicate is left) occurs, which give a variance of 0 and therefore would lead to a calculation error.

- **Min/Max** text fields
  
  **Min/Max** allows the user to define the minimum or the maximum limit of the standard curve for **LogItLog** and **Four Parameters**.

<table>
<thead>
<tr>
<th>Include (0,0) check box</th>
<th>If the <strong>Include</strong> option is selected, (0,0) will be added as standard point. This is only available if <strong>Linear</strong> has been selected as the axis division for both axes.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Extrapolation check box</td>
<td>Extrapolation applies the concentration calculations to those base points which lie outside of the permitted range as well as to those which lie within the range, for example: an extrapolation factor of 3 forces a concentration calculation of values between min-2*(max-min) and max+2*(max-min), where min and max correspond to the minimum and maximum concentration value of the standard curve.</td>
</tr>
<tr>
<td>Extrapolation factor numeric field</td>
<td>The factor data field is only active, if the <strong>Extrapolation</strong> check box has been selected. It defines the new limits for the concentration calculation.</td>
</tr>
</tbody>
</table>
4. Create/Edit a Method Wizard

**Intercepts Tab**

Use this tab to calculate concentrations for selected Y values based on the standard curve.

<table>
<thead>
<tr>
<th><strong>Exp. group spin control</strong></th>
<th>If a number of experimental groups is available, the appropriate group can be chosen.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Input data drop down list</strong></td>
<td>All data available for calculation is displayed in this list.</td>
</tr>
<tr>
<td><strong>Intercept name and formula list field</strong></td>
<td>A name for the intercept must be created first. Then, the intercept formula must be defined. A numerical value or a formula can be entered.</td>
</tr>
<tr>
<td><strong>Formula input operators</strong></td>
<td>The selection boxes allow for the easy input of formulas by providing a variety of functions, operators and variables.</td>
</tr>
<tr>
<td></td>
<td><strong>Variables</strong>&lt;br&gt;All variables accepted by the software are available using in the list box.</td>
</tr>
<tr>
<td></td>
<td><strong>... button</strong>&lt;br&gt;Click this button to open the Define constants dialog box.</td>
</tr>
<tr>
<td></td>
<td><strong>Operators</strong>&lt;br&gt;All operators accepted by the software are displayed here.</td>
</tr>
<tr>
<td></td>
<td><strong>Functions</strong>&lt;br&gt;All functions accepted by the software are displayed here.</td>
</tr>
</tbody>
</table>

**Example**

IC50 for standard curve:<br>Formula: (ST1_1+ST1_8)/2<br>value of the smallest standard plus the value of the highest standard, divided by 2

**Axis Tab**

Use this tab to define the appearance of the axes.

<table>
<thead>
<tr>
<th><strong>X-axis group box</strong></th>
<th>Following elements are available in each group:</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Label</strong> text field: Enter an axis label</td>
<td></td>
</tr>
<tr>
<td><strong>Color</strong> button: Select a color for all elements of the axis</td>
<td></td>
</tr>
<tr>
<td><strong>Log-scaling</strong> check box: Select this check box to display the axes of the graph logarithmically (does not affect the calculation).</td>
<td></td>
</tr>
<tr>
<td><strong>Auto select range</strong> option button: The software will automatically determine minimum and maximum value of the axis</td>
<td></td>
</tr>
<tr>
<td><strong>Range</strong> option button: The Min and Max numeric fields are enabled. The minimum and maximum value of the axis can be specified.</td>
<td></td>
</tr>
<tr>
<td><strong>Grid check box</strong>: If selected, the grid will be displayed on the axis. The Color button and the Line style drop down list can be used to customize the grid.</td>
<td></td>
</tr>
</tbody>
</table>
Graph Tab

Use this tab to define the appearance of the graph.

<table>
<thead>
<tr>
<th>Title group box</th>
<th>Following elements are available:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>• <strong>Label</strong> text field: Enter a label for the graph.</td>
</tr>
<tr>
<td></td>
<td>• <strong>Color</strong> button: Select a color for the label of the graph.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Curves group box</th>
<th>Following elements are available:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>• <strong>Experimental group</strong> spin control: Select the experimental group to be customized (only available if more than one experimental group defined).</td>
</tr>
<tr>
<td></td>
<td>• <strong>Color</strong> button: Select a color for the curve of the selected experimental group.</td>
</tr>
<tr>
<td></td>
<td>• <strong>Symbol</strong> drop down list: Select a symbol for the base points of the selected experimental group.</td>
</tr>
<tr>
<td></td>
<td>• <strong>Label</strong> text field: Enter a label for the curve of the selected experimental group.</td>
</tr>
<tr>
<td></td>
<td>• <strong>Hide curve</strong> check box: If selected, the curve is not displayed.</td>
</tr>
<tr>
<td></td>
<td>• <strong>Line Width</strong> spin control: Select the line width for the selected experimental group.</td>
</tr>
</tbody>
</table>

| Font group box | Select **Small**, **Medium**, or **Large** font size. |

<table>
<thead>
<tr>
<th>Display... group box</th>
<th>Following elements can be selected to be viewed:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td><strong>Legend</strong>: The curve color, base point style, and label are viewed together with additional information (analysis type parameters, correlation coefficient, and so on).</td>
</tr>
<tr>
<td></td>
<td><strong>Base points</strong></td>
</tr>
<tr>
<td></td>
<td><strong>Intercepts</strong>: If intercepts are specified, the intercepts can be displayed and labeled in the graph.</td>
</tr>
<tr>
<td></td>
<td><strong>Error bars</strong>: If standards are defined as replicates, a bar showing the range plus/minus standard deviation is displayed for each base point.</td>
</tr>
</tbody>
</table>

### 4.3.11 Concentrations Transformations: Add New Concentration Transformations

Select **Add new conc. transform...** from the control bar.

In the **Concentration transformations** dialog box a concentration formula can be defined, which is used for transforming concentration input data individually for every well.

In the **Concentration transformations** dialog box further calculations can be performed on concentration input data.

The window elements are similar to the **Transformation** input. Refer to chapter 4.3.7 Transformed Data: Add New Transformation for further information.
4. Create/Edit a Method Wizard

4.3.12 Evaluate Data: Cutoff Definition

In the control bar expand Evaluate data and select Cutoff definition. Use this option to categorize either raw data or calculated data on threshold limits. Threshold limits can be defined as fixed numeric values or formulas. Use the Cutoff Definition window to define the cutoff ranges and to assign colors and names to cutoff results. The results will be generated on the basis of these settings and displayed in the corresponding color.

The Cutoff Definition window contains the following elements:

<table>
<thead>
<tr>
<th>Input data drop down list</th>
<th>Select the input data which is to be used in the evaluation.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Exp. group selection list</td>
<td>In case the plate contains more than one test, the relevant experimental group to which the cutoff should apply must be selected. If the plate contains only one test, then only one group will be available and the field is not visible.</td>
</tr>
<tr>
<td>Cutoff list</td>
<td>In the Cutoff list, up to ten cutoff ranges can be defined. The limits for each range can be entered. The highest limit value must be entered on top of the list. The next lower will be placed beyond and so on. A displayed Low-High arrow shows the level. The limit values itself belong to the upper ranges (greater and equal condition).</td>
</tr>
<tr>
<td>Colors buttons</td>
<td>A color can be allocated to the individual result levels. When displaying the results these colors will be incorporated, representing the qualitative results.</td>
</tr>
<tr>
<td>Labels text fields</td>
<td>The result indicators for every value range must be named, for example: positive (pos), negative (neg), intermediate (?), ...</td>
</tr>
<tr>
<td>Limits text fields</td>
<td>The limits can be entered as a constant value or as a formula. Formulas can be entered directly into a field or via the Formula input fields. A maximum of up to nine limits may be defined.</td>
</tr>
<tr>
<td>Formula input group box</td>
<td>Formulas to be entered into the Limits field can be composed by using the variables, operators and functions below. Refer to chapter 13.4 How to Write a Formula for further details.</td>
</tr>
<tr>
<td>Competitive Test check box</td>
<td>Competitive tests allocate a positive result to low values and a negative result to high values. In the evaluation, the limits will run from top to bottom and the corresponding results symbol will be allocated when a value is found to be equal to or less than the limit. In view of this, the Low-High arrow will be reversed.</td>
</tr>
<tr>
<td>Cutoff results selection... button</td>
<td>Click the Cutoff results selection... button to open the Cutoff Results Selection dialog box.</td>
</tr>
</tbody>
</table>
4. Create/Edit a Method Wizard

Cutoff Results Selection

Use this window to select whether a qualitative result for a certain identifier type is shown or not.

The Cutoff Results Selection contains the following elements:

| Cutoff display selection tree structure | All defined identifier names are shown in a tree structure, grouped by identifier types. Each identifier is associated with a check box. Selecting or clearing the check box of an identifier name indicates, whether the qualitative results of the according wells will be shown or not. After evaluation, only cutoff results for the selected identifier types are displayed. |

4.3.13 Evaluate Data: QC Validation

In the control bar expand Evaluate data and select QC Validation. Validations are used to check the validity of a test. If the defined criteria are not met, an error message will be displayed after the measurement run and no cutoff results will be displayed. (Except the user has the right to continue evaluation when error – see chapters 11.4.4 User Rights (magellan Tracker and 11.5.4 User Rights (magellan Standard).

Upon selecting the correct input data, the desired formulas are to be entered in the Validation Conditions list field. A formula editor supports the user in the creation of the corresponding mathematical formulas.

Example:
If the validation criteria are defined as follows:
NC1>0 and NC1<0.1
the evaluation will check whether the negative control can be found within the given range. If this is not the case an error message will appear.

The Define QC Validations dialog box contains the following elements:

| Input data drop down list | Select the relevant data, to which the validation must apply. For example: Raw data, Mean concentration and so on. |
| Exp group selection field | If the plate contains more than one test, the relevant experimental group to which the validation should apply must be selected. If the plate contains only one test, then only one group will be available. |
| Validation group selection field | Use Validation groups to define validation criteria for the same experimental group with different input data. |
| Validation Conditions list field | This one-dimensional list will be filled with the formulas and logical equations, which define the Validation Conditions. These logical equations will generate a logical result. The program will examine the input data using this equation and, if the validation criteria are met, will return a result of TRUE. If the criteria did not meet, a result of FALSE and an error message will be displayed. |
4. Create/Edit a Method Wizard

**Formula input group box**

Parts of the formulas to be entered into the **Validation Conditions** field can be selected from the following drop down lists:

- **Variables** drop down list
  All available variables displayed.

- **... button**
  Click this button to open the **Define constants** dialog box.

- **Operators** drop down list
  All available operators are displayed.

- **Functions** drop down list
  Using the given palette, available functions can be chosen.

Refer to chapter 13.4 How to Write a Formula for further details.

**Plate to Plate QC**

Use this option to define a long-term QC validation. For different controls a mean value and a standard deviation can be entered. Every measured workspace using this method will be correspondingly evaluated (refer to chapter 7.4.2 Toolbar Menu: File/ Plate to Plate QC).

The **Plate to Plate QC** dialog box contains the following elements:

<table>
<thead>
<tr>
<th><strong>Input data drop down list</strong></th>
<th>Select the relevant data, to which the validation must be applied, from the drop down list.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Control check boxes</strong></td>
<td>Select the type of control from the drop down list, then enter the expected mean and standard deviation. A scroll bar appears next to the dialog controls to define more than 4 QC controls.</td>
</tr>
<tr>
<td><strong>Workspaces to be evaluated options</strong></td>
<td>Select the appropriate filter to define which workspaces should be evaluated.</td>
</tr>
</tbody>
</table>
4. Create/Edit a Method Wizard

4.3.14 Data Handling: Data Export

This dialog box provides options for organizing data export.
In the control bar expand Data handling and select Data export.
Data to be exported into an ASCII or Excel file can be selected using this dialog box.
A list of all available data, according to the method definition is displayed.
The actual exporting of data only occurs using automated data handling (see 4.3.16 Data Handling: Automated Data Handling).
The Data export dialog box contains the following elements:

Available data list
Data for exporting can be selected simply with drag and drop or by clicking the data in the Available data window and then the arrow pointing towards the Selected data window. Data can be deselected by operating the reverse procedure.

← and → buttons
The order of the selected data can be changed by selecting an item and pressing the button Up to move it up or Down to move it down.

Selected data list
This list shows all selected data, which has been transferred from the Available data field list.

Export options...
Click this button to open the Export Options dialog box.

Export Options

The Export Options dialog box contains the following elements

Direction group box
The user can define whether the plate data is extracted horizontally line by line or vertically column by column and written in this order to the file.

• Horizontal option button
  The data is collected in rows.

• Vertical option button
  The data is collected in columns.

Result group box
Select how to export the data in the form of a matrix or of a continuous list:

• Matrix (nested) option button
  Data of all selected data sets is arranged in a single matrix. This matrix contains the first columns of all data sets followed by the second columns of all data sets.

• Matrix (separated) option button
  Data of each selected data set is arranged in a separate matrix.

• Matrix (XFluor style) option button
  Data of each selected data set is arranged in a separate matrix together with column and well description similar to XFluor.

• Table (well data in rows) option button
  All data of one well is arranged in horizontal direction starting with data of the well position A1.
4. Create/Edit a Method Wizard

- **Table (well data in columns)** option button
  All data of one well is arranged in vertical direction starting with data of the well position A1.

- If the **Add kinetic timestamps** check box is selected, the time stamps of the measurements are added.
- If the **Add Temperatures** check box is selected, the temperatures of the measurements are added.
- If the **Insert Data names** check box is selected, a list with the names of the exported data is displayed on top of the ASCII-file respectively the EXCEL worksheet.

**Add data** group box

- Provides selectable data options.
- The selected information will be attached to the end of the data and then exported with the selected data.
- Select the respective check boxes:
  - Date/time of measurement check box
  - Method filename check box
  - Method pathname check box
  - Workspace filename check box
  - Workspace pathname check box
  - Filter wavelength value(s) check box
  - User prompts check box
  - Current user name check box
  - Measurement parameters check box
  - Multiplate plate information check box
  - Workspace audit trail check box
    *(magellan Tracker only)*
  - Workspace signatures check box
    *(magellan Tracker only)*

**Set as default button**

- Settings can be logged as a default for future use.

**Restore default button**

- Settings can be reset to the previously defined default.
4. Create/Edit a Method Wizard

Example
Raw data, kinetic cycle 1, timestamp 0 s
11 12 13
21 22 23
Raw data, kinetic cycle 2, timestamp 33 s
81 82 83
91 92 93

Matrix (nested), horizontal:
11 81 12 82 13 83
21 91 22 92 23 93

Matrix (separated), horizontal, with timestamps:
0 s
11 12 13
21 22 23
33 s
81 82 83
91 92 93

Matrix (XFluor style):
<> 1    2    3
A   11 12 13
B   21 22 23
<> 1    2    3
A   81 82 83
B   81 82 83

Table (well data in rows), horizontal, with timestamps:
0 s 33 s
11 81
12 82
13 83
21 91
22 92
23 93

Table (well data in columns), horizontal:
11 12 13 21 22 23
81 82 83 91 92 93

Table (well data in columns), vertical:
11 12 13 21 22 23
81 82 83 91 92 93

Export of Multiple Reads per Well Data

Note
When multiple reads per well data are available, it is possible to export the single values of such a measurement beside the averages by selecting the Data name – Multiple Reads per Well in the export data list. A separate data block in fix format is generated. Multiple reads per well is exported in the following format only:
Well name followed by a block of Value separator Value separator and so on.
### Export to ASCII File

The Export to ASCII File dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Group Box</th>
<th>Description</th>
</tr>
</thead>
</table>
| **Decimal character group box** | The decimal character may be a point or a comma:  
  - **Point (x.xx)** option button  
  - **Comma (x,xx)** option button |
| **Delimiter group box** | This option sets a delimiter to separate the individual values within the data in the lines of an ASCII file. TAB is the default delimiter. A different symbol can be used:  
  - **Tabulator** option button  
    - This check box is selected by default, and specifies, that tabulators are used as delimiters.  
  - **Other symbol** text field  
    - This text field is only active, if the Other symbol option button is selected. Then, a user-defined delimiter character can be entered. |
| **Path group box** | This option sets the path where the ASCII file will be stored:  
  - **Export default path** option button  
  - **Use path** option button: Select any path where the ASCII file shall be stored |
| **Encoding group box** | Select the export code:  
  - **ANSI**: For ANSI compatible characters.  
  - **Unicode**: For characters that cannot be exported with ANSI code (e.g. Chinese, Cyrillic). |

**Caution**

A suitable export delimiter must be selected. The export delimiter and decimal character should not be the same. TAB is set as the default delimiter, but another symbol can be selected.
4. Create/Edit a Method Wizard

Export to Excel

The Export to Excel dialog box contains the following elements:

**Target** group box

The option buttons define where to position the transferred data within Excel. This option is also valid for automatic Excel export.

- **New workbook** option button
  Transferred data will be stored in the first worksheet of a new workbook. A new file will always be created, no matter if Excel is started or not.

- **New worksheet** option button
  Transferred data will be put into a new worksheet within an open, active Excel workbook.
  If Excel is not open, when selecting this option, it will be started and a new workbook created, including the requested data into the first worksheet.

- **Insert into worksheet at cell** option button and cell coordinates text field
  The first value of the transferred data will be placed into the cell indicated (default is cell A1) of an open, active Excel worksheet.
  If Excel is not open when selecting this option, it will be started and a new workbook will be created, inserting the requested data into the first worksheet at the defined cell.

- **Append to current worksheet** option button
  This option will append the data to the current worksheet.
  If Excel is not open when selecting this option, it will be started and a new workbook will be created, inserting the requested data into the first worksheet.

- **Use Insert into Template** to export data into a predefined Excel template. Path and name of the Excel template must be entered, clicking the …-button. The corresponding cell position must be indicated.

**Set as default** button
Using this option, the settings can be logged as a default for future use.

**Restore default** button
Using this option, the settings can be reset to the previously defined default.

4.3.15 Data Handling: Printed Report

In the control bar expand Data handling and select Printed report.

This dialog box provides options for defining the printed report.

The Printed report dialog box provides formatting features for hardcopy printouts to customize the contents and the appearance of the printout. Output for reporting or presentation needs can be created.

The settings for the reports are grouped in four tabs, which represent certain formatting areas:

1. Data Selection tab
2. Page Setup tab
3. Header tab
4. Footer tab
## 4. Create/Edit a Method Wizard

### Data Selection Tab

The **Data Selection** tab provides a list of data available for printing.

**Print as** group box

Select whether the data is to be printed in the form of a matrix or in the form of a list:

- **List**
  The individual list format (horizontal, vertical, sorted and alternating) must be configured in the properties dialog (see below).

- **Matrix**
  The matrix selection prints the data in a 2 dimensional list (matrix).

**Data source and destination lists**

Two lists are used to define the printed data:

- **Available data** list:
  List of all available data, which can be printed. Page breaks and dividing lines can be added in order to achieve the preferred layout. Elements to be printed can be selected by double-clicking; they are listed in the selected data list.

- **Selected data** list:
  List of all selected data, which will be printed. Informative notes also help to give an awareness as to how the data will be printed, for example: whether the data will be displayed in form of a matrix, a list, as data collection or as a graph. Entries that appear under a heading will be incorporated into the corresponding list or matrix format, providing possibilities to compare different sets of values, for example, measurement values and results.

**Append** button

Click this button to transfer data highlighted in the **Available** data window to the **Selected** data window. You can also use *drag and drop*.

**Insert** button

Use this option to display two pieces of similarly formatted data within the same area. First, data from the **Available data** list must be selected, then data from the **Selected data** list. When clicking the **Insert** button, the former will be included within the latter and will then occupy the same area in the print-out as its parent element. For example, if the standard deviation values are included in the measurement value element, both will be displayed within the corresponding cell of a matrix. The measurement values will, in this case, serve as the parent element and will therefore be displayed first.

**Import...** button

This button provides the possibility to import the selected data list from another method. If this button is clicked, the **Open a file** (method) window appears and another method can be selected.

**Remove** button

Selected elements within the **Selected data** list can be deleted.

**Up and Down** buttons

Use these buttons to reorganize the sequence of lists, graphs, matrices… on the printout or to reorganize items within a matrix or a list.

**Properties** button

Is enabled when a list is selected. Style and content of the list can be selected.
4. Create/Edit a Method Wizard

**Style group box**

**Vertical list option button**
Prints the data in form of a vertical list (order A1, B1, and so on).

**Vertical list alternating option button**
The order of the data is alternating for each row or column (order A1, B1, ... H1, H2, G2, ... A2).

**Horizontal list option button**
Prints the data in form of a horizontal list (order A1, A2, and so on).

**Horizontal list alternating option button**
The order of the data is alternating for each row or column (order A1, A2, ... A12, B12, B11, ... B1).

**Sorted list option button**
This option will sort the entries of all columns according to the entries of the first column. The alphanumerical entries in the first column are split into two parts, the first containing only letters, the second numbers. The entries are sorted first alphabetically. Entries with the same name are then sorted numerically.

Example: You can use this option with sample IDs or with the layout, restricted to one experimental group. A sorting of numerical values will work only if all entries are integer values.

**Sample oriented list(s) button**
Allows the printout of individual lists per sample. The separation for the single tables is done either by the sample IDs (if available) or by the identifier names on the plate layout. Sample IDs are needed if the layout contains different experimental groups representing different parameters for the same samples. It is possible to combine the list style Sample oriented list(s) with other parameters like Identifiers, Exp. Groups and Cutoff results.
4. Create/Edit a Method Wizard

Limitations group box
Select between the following options:
- **Identifiers**: select or unselect which identifiers should be displayed in the list.
- **Exp. Group**: select between all experimental groups or enter the Experimental group number you want to displayed in the list.
- **Cutoff results**: select between all cutoff results or select from the list which results should be displayed in the list.

Page Setup Tab
In the **Page Setup** tab, general settings are defined:

**Display Header/Footer group boxes**
- **Print Header** check box
  - If selected, the header will be printed
- **Print Footer** check box
  - If selected, the footer will be printed
- **Header** option buttons
  - **Every page** (prints the header on every page)
  - **First page only** (prints the header only on the first page)
  - **Except first page** (prints the header on all pages except the first one)
- **Footer** option buttons
  - **Every page** (prints the footer on every page)
  - **First page only** (prints the footer only on the first page)
  - **Except first page** (prints the footer on all pages except the first one)

**Print/Page group**
- **Color** option button
  - The printout is in colors, if supported by the printer.
  - The well specific data is printed in the color of the layout (for example: sample raw data is printed blue).
  - The cutoff results are printed in the color of the range (for example: “pos” wells are printed red).
  - The graph is printed as displayed.
- **Black and white** option button
  - The printout is black and white.

**Margins group box**
In the **Unit** drop down list cm or inch can be selected.

- **Left** text field: enter the value of the left margin.
- **Right** text field: enter the value of the right margin.
- **Above text** field: enter the value of the top margin.
- **Below text** field: enter the value of the bottom margin.
4. Create/Edit a Method Wizard

**Header Tab**

In the **Header** tab, the content of the document header is defined:

<table>
<thead>
<tr>
<th>Option</th>
<th>Adjustment</th>
<th>Row number</th>
</tr>
</thead>
<tbody>
<tr>
<td>Page number</td>
<td>left</td>
<td>3</td>
</tr>
<tr>
<td>Date</td>
<td>centered</td>
<td>2</td>
</tr>
<tr>
<td>Time</td>
<td>centered</td>
<td>3</td>
</tr>
<tr>
<td>File name</td>
<td>left</td>
<td>1</td>
</tr>
<tr>
<td>Program name</td>
<td>centered</td>
<td>1</td>
</tr>
<tr>
<td>Comment</td>
<td>centered</td>
<td>1</td>
</tr>
</tbody>
</table>

The **Comment** text field is active, supposed the **Comment** check box has been selected.

**Adjustment option buttons**

- Left
- Centered
- Right

**Row number list**

**Row number** is a numeric field, where the row for each option can be adjusted.

**Separators check boxes**

- **Above** check box: Separator line appears above the header.
- **Below** check box: Separator line appears below the header.

**Footer Tab**

In the **Footer** tab, the content of the document footer is defined. The **Footer** tab contains the same elements as the **Header** tab. For a description of the footer tab refer to the header tab.

The footer tab will disappear if **Print Footer** is not selected in the **Page setup** tab.
4. Create/Edit a Method Wizard

4.3.16 Data Handling: Automated Data Handling

In the control bar expand Data handling and select Automated data handling. After a measurement some actions can be started automatically. Select these actions and they are executed chronologically in the following order:

- If the load sample ID list check box is selected, when running the method a sample ID list is automatically loaded.
- If the save workspace check box is selected (always selected in magellan Tracker), after running the method the created workspace is automatically saved.
- If the export to ASCII file check box is selected, after running the method the data selected for export is automatically exported to an ASCII file.
- If the export to ASTM file check box is selected, after running the method, the data selected for export is automatically exported in ASTM format and can be further used in compatible Laboratory Information Systems (LIS).
- If the export to Sample Tracking check box is selected, after running the method, the data selected for export is automatically exported to the Sample Tracking system. For more information please refer to the corresponding manual for Sample Tracking.
- If the export to Excel check box is selected, after running the method the data selected for export is automatically exported to Excel.
- If the print check box is selected, after running the method the data selected for the printed report is automatically printed on the default printer.
- If the view results after measurement check box is selected, after running the method, the measurement data and the calculated data are displayed for reviewing.

More – Load Sample ID List

Click on the More button next to the check box load sample ID list. The More (Load Sample ID List) dialog box contains the following elements:

**Filename group box**
- Select the filename of the sample ID list to be loaded:
  - Same filename as workspace option button
  - Filename option button: Enter a filename in the text field.

**Path group box**
- Select the path where the sample ID list is stored:
  - Sample ID list default path option button
  - Use path option button: Select any path.

**Format group box**
- Select the format of the sample ID list to be loaded (see chapter 5.2.3 Import a Sample ID List for details):
  - Autodetect from the list of supported formats option button
  - Custom file format option button: Click the File format... button to open the Custom Format dialog box.

**Note**

*If an only partly filled sample ID list is loaded automatically, all unused samples are automatically deleted from the layout. If a final control (e.g. in well H12) has been defined within the layout, this control is automatically moved to the well after the last used sample well.*
4. Create/Edit a Method Wizard

More – Workspace Name

Selecting Save workspace – More the Workspace Name dialog box appears. It contains the following elements:

| Format group box | One of the offered option buttons has to be selected for defining the default workspace name. The name can consist of the date, counter or a certain set of letters. Another possibility is to combine the date with a choice of letters. Counters used together with the date are reset daily otherwise the counter is incremented with each measurement:
| Date (DDMMYYYY) + Counter option button
| Date (YYYYMMDD) + Counter option button
| Total Counter option button
| Use available barcode option button

| Prefix text field | The entered text is added at the beginning of the workspace name as defined above.

| Example text field | The Example text field shows an example of the current selection.

| Set as default button | Using this option, the settings can be logged as a default for future use.

| Restore default button | Using this option, the settings can be reset to the previously defined default.

More – Export to LIS

The More (Export to LIS) dialog box contains the following elements:

| ASTM delimiter definition group box | Define the ASTM delimiters:
| Field delimiter: Enter a sign for separating fields (| by default)
| Repeat delimiter: Enter a sign for repeat (\ by default)
| Component delimiter: Enter a sign for separating components (^ by default).
| Escape character: Enter a sign for escape (& by default).

| Sender ID group box | Define the Sender ID settings that are to be displayed in the header of an ASTM file:
| Sender ID text field: Empty by default. If defined, e.g. Infinite 200, the name is displayed in the header of the ASTM file (e.g. H||\&||Infinite 200^Magellan V6.55^Standard).
| Append app. name: If selected, application name, i.e. magellan, is exported in the header of the ASTM file (e.g. magellan V6.55).
| Append app. version: If selected, the magellan version number is exported in the header of the ASTM file (e.g. Standard or Tracker).
### 4. Create/Edit a Method Wizard

#### LIS assay name group box
Select the LIS assay name to be displayed in the test order record and result record of the ASTM file:
- **Use method name**: name of the method used for the measurement.
- **Use name** text field: define a new name to be displayed.

**Example**: ELISA
Test order record: O|1|Sample ID||^^^ELISA||Date and time of measurement
Result record: R|1|^^^ ELISA^results

#### Encoding group box
Select the export code:
- **ANSI**: For ANSI compatible characters.
- **Unicode**: For characters that cannot be exported with ANSI code (e.g. Chinese, Cyrillic).

#### Path group box
Define the path for the ASTM export:
- **Export default path**: the export is performed to the folder defined in Miscellaneous.
- **Use path** text field: define a new export path.

#### Set as default button
Using this option, the settings can be logged as a default for future use.

#### Restore default button
Using this option, the settings can be reset to the previously defined default.

💡 **EXPERT’S KNOW HOW**

**ASTM EXPORT – EXAMPLE FILE**

Each ASTM export file (.txt) consists out of the following components:

- **Message Header Record**:
  ```plaintext```
  |\^&|||Infinite 200^Magellan V6.55^Standard
- **Patient Information Record (P)**:
  ```plaintext```
P|1||Sample ID 1 for patient 1
P|2||Sample ID 2 for patient 2
P|3||Sample ID 3 for patient 3.
- **Test Order Record (O)**:
  ```plaintext```
  O|1|Sample ID||^^^method name||Date and time of measurement
  O|2|Sample ID||^^^method name||Date and time of measurement
  O|3|Sample ID||^^^method name||Date and time of measurement
- **Result Record (R)**:
  ```plaintext```
  R|1|^^^ method name^results
  R|2|^^^ method name^results
  R|3|^^^ method name^results
- **Message Terminator Record**:  
  ```plaintext```
  L|1|N
Example:

ASTM Export Settings:

![Image of export settings dialog]

The corresponding ASTM file:

```
%^&|||Infinite 200^Magellan V6.55^Standard
P|1||a0
O|1|a0||^^^Absorbance1||20090114124953
R|1|^^^Absorbance1^Raw data^A1|0.1015~|OD|
P|2||a1
O|1|a1||^^^Absorbance1||20090114124953
R|1|^^^Absorbance1^Raw data^B1|0.1015~|OD|
P|3||a2
O|1|a2||^^^Absorbance1||20090114124953
R|1|^^^Absorbance1^Raw data^C1|0.1015~|OD|
P|4||a3
O|1|a3||^^^Absorbance1||20090114124953
R|1|^^^Absorbance1^Raw data^D1|0.1015~|OD|
P|5||a4
O|1|a4||^^^Absorbance1||20090114124953
R|1|^^^Absorbance1^Raw data^E1|0.1015~|OD|
P|6||a5
O|1|a5||^^^Absorbance1||20090114124953
R|1|^^^Absorbance1^Raw data^F1|0.1015~|OD|
L|1|N
```
4. Create/Edit a Method Wizard

More – View Results

The **More (View Results)** dialog box contains the following elements:

<table>
<thead>
<tr>
<th><strong>Plate view</strong> group box</th>
<th>Select the data to be displayed in the plate view:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>• <strong>1st line in well (fixed)</strong> drop down list: Select a name from the available data names.</td>
</tr>
<tr>
<td></td>
<td>• <strong>2nd line in well (fixed)</strong> drop down list: Select a name from the available data names.</td>
</tr>
<tr>
<td></td>
<td>• <strong>3rd line in well (first selection)</strong> drop down list: Select a name from the available data names. In contrast to the first two lines this selection is only applied for the first time. Whenever another data to be viewed in the plate view is selected in the control bar, this data is displayed in the 3rd line. The first two lines remain unchanged.</td>
</tr>
<tr>
<td></td>
<td>The 1st and 2nd line can be omitted by selecting <strong>not used</strong>, which makes the plate view more easily readable.</td>
</tr>
</tbody>
</table>

| **Text box** group box | Select a name from the available data names. This selection is only applied for the first time. Whenever another data to be viewed in the text box is selected in the control bar, this data is displayed in the text box. |

### 4.3.17 Miscellaneous: User Prompts

In the control bar expand **Miscellaneous** and select **User prompts**.

In every **Prompt** field of the list, a keyword can be entered. This keyword will then be displayed before measuring. Text can be entered, for example: lot number or the analyst’s full name.

By selecting **Req.** (required), a measurement can only be launched on receipt of an input (a text information must be added in the **Prompt answer** field).

Prompts will also appear in the list of available data for printing.

### 4.3.18 Miscellaneous: Number Format

In the control bar expand **Miscellaneous** and select **Number format**.

The **Number format** dialog box is used to set up the numeric format of the display of values. Additionally, the scientific number format for values out of range can be selected.

The default setting is 5 significant digits. Selecting **User defined**, a number format of 1 - 10 integer places and 0 - 7 decimal places can be set.

If the user defined number format is selected, the two numeric data fields have to be set.

Additionally the scientific (with exponent) or the non-scientific description can be used. An example of the format of current selection is displayed.

Click **Set as default** or **Restore default** accordingly to save the entered definition.
4. Create/Edit a Method Wizard

4.3.19 Miscellaneous: Method Notes

In the control bar, expand Miscellaneous and select Method notes.
The Method notes field allows the user to add some comments to the file name, which will be displayed on the method printout.
Simple formatting like bold, italic, underlined and colored text is possible. Formatting may be omitted during printout.

4.4 Saving the Method

Once all the data relevant to a method is set as desired, click Finish and the Save as window appears, in which the created or modified method can be saved.
The Save as window contains the following elements:

<table>
<thead>
<tr>
<th>Field</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Filename</td>
<td>Enter or modify the method’s file name.</td>
</tr>
<tr>
<td>File remarks</td>
<td>Add some comments to the file name, which will be displayed for example in the Open file dialog boxes.</td>
</tr>
<tr>
<td>Audit trail comment</td>
<td>Add some comment, which will be stored in the audit trail (only available for magellan Tracker).</td>
</tr>
<tr>
<td>Organize favorites... button</td>
<td>Click this button to open the Organize favorites dialog box. See 6.5 Start Favorite for further information.</td>
</tr>
<tr>
<td>Run this method now check box</td>
<td>When this check box is selected the method run will be started immediately after finishing this wizard.</td>
</tr>
</tbody>
</table>

The modified document can be saved under its current file name or under a different name.
Click Save&Finish to save the method and close the Create/Edit a Method wizard.

Additional buttons in magellan Tracker:

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Audit trail... button</td>
<td>Click this button to open the Audit trail dialog box where the user, the date, the executed action and a comment are displayed.</td>
</tr>
<tr>
<td></td>
<td>A print preview of the workspace, the method and the sample ID list of the current and all previous versions can be displayed clicking the appropriate buttons.</td>
</tr>
<tr>
<td></td>
<td>Additionally it is possible to save a previous version of the method under another name.</td>
</tr>
</tbody>
</table>
4. Create/Edit a Method Wizard

<table>
<thead>
<tr>
<th>Signature... button</th>
<th>Click this button to open the Signature dialog box, where user, date, action and comment are displayed.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td><img src="image" alt="Signature dialog box" /></td>
</tr>
<tr>
<td></td>
<td>This button is only available when the file has been signed using the Attach Signature wizard. See chapter 8 Attach Signature Wizard for further details.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Method password field</th>
<th>When entering a password for a method, this method will be password protected and cannot be modified until the correct password is entered. See detailed description below!</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td><img src="image" alt="Method password dialog box" /></td>
</tr>
</tbody>
</table>

### 4.4.1 Password Protection of Methods

#### Protect Method with a Password

Users who have the right to create and to edit methods can protect methods by assigning them a password.

Per default, Administrators and Application Specialists possess the required rights.

When a new method is created, the password protection can be set in the **Save as tab** of the Create/edit a method wizard. Enter the name of the method, type the password in the **Method password edit field** (right bottom corner of the dialog) and click **Finish**.

Confirm the password in the displayed **Method password dialog box** and click **OK**. The method is saved with the password protection.

Already saved, but not password protected methods can be protected by opening the method and setting the password in the **Save as tab** as described above.

#### Edit Password Protected Methods

When you open a password protected method, a dialog box is displayed, asking for the method password.

Enter the correct method password and the method is opened in **Edit mode**. It is possible to edit and save the method. No additional password entry is needed. If **Read only** is selected, the method is opened in read only mode. It is still possible to edit the method, but it is not possible to save the changes.

#### Change the Password of a Password Protected Method

In order to change the password of a password protected method, open the method in **Edit mode** (password entry required) and enter a new password in the **Method password edit field** of the **Save as tab**. Click **Finish**.

Confirm the password in the successive **Method password dialog box** and click **OK**. The password has been changed.
4.5 Multiplate Methods

When connected to a Tecan instrument from the Infinite series or to a Safire\textsuperscript{2} instrument, multiplate methods can be defined using magellan, version 6.0 or higher.

When connected to an instrument from the Infinite series, the number of plates to be measured can be set in the measurement parameters editor, during method definition (see the Instructions for Use for i-control):

When connected to a Safire\textsuperscript{2} instrument, the option can be selected from the Create/Edit a Method wizard page:
4. Create/Edit a Method Wizard

When two or more plates are to be measured, a counter for switching between the plates is available in the Define Evaluation window as well.

All further parameters can be defined as is done for single plate methods.

At starting a multiple plate method the following dialog box appears:

<table>
<thead>
<tr>
<th>Sample IDs list</th>
<th>For each single plate a sample ID list can be selected.</th>
</tr>
</thead>
<tbody>
<tr>
<td>STOP button</td>
<td>Measurement is stopped. The data of the already measured plates are displayed in the created workspace and it is not possible to add measurements of additional plates.</td>
</tr>
<tr>
<td>PAUSE button</td>
<td>Measurement is paused. The data of the already measured plates are displayed in the created workspace, but it is possible to add measurements of additional plates.</td>
</tr>
<tr>
<td>RUN button</td>
<td>Measurement of the next plate is started.</td>
</tr>
<tr>
<td>Plate in/ Plate out</td>
<td>The plate is moved into or out of the instrument.</td>
</tr>
</tbody>
</table>
Running a multiplate method allows to pause the measurement between two plates, saving the achieved results, and continuing the measurement for the remaining plates at a later date.

If **Automatic save workspace** is selected, the workspace is stored after each single measurement.
5. Create/Edit a Sample ID List Wizard

5.1 Introduction

The Create/edit a sample ID list wizard is used to create new sample lists or to edit existing sample lists. Up to three sample IDs can be entered or imported per well.

Workflow Summary

Start the Create/edit a sample ID list wizard. After a welcome page, the File selection page appears. Select one of the options: Create new sample ID list or Edit an existing sample ID list.

When Create new sample ID list is selected, the Select plate type page appears, in which the plate type and sample IDs per well or the import settings can be set.

Then the Import/edit a sample ID list page appears where the sample ID for the wells can be entered individually or automatically using the Autofill... function.

Finally, in the Save as page the created or modified sample ID list is saved.

5.2 Create/Edit a Sample ID List

In the wizard list, click Create/edit a sample ID list. After the welcome page, select Create new to create a new sample ID list or select Edit to edit an existing sample ID list from the file selection window.

The File Selection window contains the following elements:

a) Create new option button
When the Create new option was selected, a new sample ID list can be created. The user will be guided to the Select plate type window where plate type and number of sample IDs per well are defined.

b) Edit option button
When the Edit option was selected the Import/edit a sample ID list window is displayed where an existing sample ID list can be modified. Sample IDs can be inserted in the wells.

Show combo box
In the Show combo box the displayed list of files can be modified according to the selection:
- All files
- My files: This option is available if the user administration is enabled (always enabled in magellan Tracker)

Filename list
In the Filename list, the sample ID list to be edited has to be selected. A Remarks field next to every file name contains - if entered - a short description of the sample ID list.

All sample ID lists available in the standard sample ID list directory, which fulfill the filter criteria selected in the show combo box, will be displayed.

Print Preview... button
A preview of the selected sample ID list is displayed and a printout can be started.
5. Create/Edit a Sample ID List Wizard

5.2.1 Create New Sample ID List

In the Select Plate Type window the number of sample IDs per well and the used plate type can be selected. The Import from external sample ID list option allows to browse for different types of sample ID files and to import them into magellan.

Note
Some sample ID lists may contain additional information such as concentrations and dilutions which may affect evaluation of the measurement data.

The Select plate type dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Settings</th>
<th>Description</th>
</tr>
</thead>
</table>
| Sample IDs per well option buttons | Enter the number of sample IDs required per well (a maximum of three can be entered):  
  - One
  - Two
  - Three |
| Printout option buttons | Define the layout for printing the sample ID list:  
  - horiz. Table
  - vert. Table
  - Matrix |
Plate type option buttons

<table>
<thead>
<tr>
<th>Four option buttons define the plate type to be selected:</th>
</tr>
</thead>
<tbody>
<tr>
<td>• <strong>Plate type from method</strong></td>
</tr>
<tr>
<td>Select a method to load the plate layout.</td>
</tr>
<tr>
<td>Click <strong>Load</strong> to browse for existing method files.</td>
</tr>
<tr>
<td>The Windows™ <strong>Open</strong> dialog box appears. Select the</td>
</tr>
<tr>
<td>desired file and click <strong>Open</strong>.</td>
</tr>
<tr>
<td>• <strong>Standard plate type</strong></td>
</tr>
<tr>
<td>Standard geometry plate types can be selected to</td>
</tr>
<tr>
<td>define the plate format.</td>
</tr>
<tr>
<td>When activated, a standard geometry plate type can</td>
</tr>
<tr>
<td>be chosen from an associated drop down list.</td>
</tr>
<tr>
<td>• <strong>Plate type from pdf-file</strong></td>
</tr>
<tr>
<td>A predefined .pdf file (or .pdfx file for infinite</td>
</tr>
<tr>
<td>series instruments) can be used to define the plate</td>
</tr>
<tr>
<td>format. <strong>magellan</strong> offers a wide selection of</td>
</tr>
<tr>
<td>predefined plate formats to choose from. Plates that</td>
</tr>
<tr>
<td>are not listed can be created using the **Plate</td>
</tr>
<tr>
<td>geometry editor** option,</td>
</tr>
<tr>
<td>which is a software application accessible via</td>
</tr>
<tr>
<td><strong>magellan</strong>. For more information refer to chapter</td>
</tr>
<tr>
<td>3.2.5 Plate Geometry Editor... .</td>
</tr>
<tr>
<td>When activated, a predefined .pdf file can be chosen</td>
</tr>
<tr>
<td>from an associated drop down list.</td>
</tr>
<tr>
<td>• <strong>Import from external Sample ID list</strong></td>
</tr>
<tr>
<td>An external file type can be selected for import as</td>
</tr>
<tr>
<td>sample ID list. See chapter 5.2.3 Import a Sample ID</td>
</tr>
<tr>
<td>List.</td>
</tr>
</tbody>
</table>

The **Enter sample IDs** button is only enabled if the required settings (method has been loaded, standard plate type or pdf-file has been selected.) have been defined.
5. Create/Edit a Sample ID List Wizard

5.2.2 Import/Edit a Sample ID List

After the selection of the plate type, the Import/edit a sample ID list plate window is displayed. It contains the following elements:

- Toolbar
- Plate view
- Sample ID list (when Plate type from method has been selected)

- Dialog to insert sample IDs (when Standard plate type has been selected)
On top of the window a **Toolbar** is displayed: Settings, Edit, Autofill, Delete, Undo/Redo, Print format, Print preview and Zooming can be accessed clicking the corresponding button (see below for details).

In the main area of the window the **Plate View** displays a schematically layout of a microplate. Rows are marked alphabetically, columns numerically.

If a new sample ID list is to be created no sample IDs are assigned to the wells. A well can be selected by clicking in the well.

All required sample IDs have to be entered either manually or using the buttons in the tool bar or can be read by the handheld barcode scanner for sample IDs. The sample IDs can be defined and edited in the defined microplate type. Up to three sample IDs can be entered in each well. Sample IDs can be moved or copied.

When a method has been selected, on the left side a *List of all Samples from the plate layout* is displayed. Only samples without replicates are shown in the list. The sample IDs can be entered either in the list or on the plate. All changes are shown immediately.

### Toolbar Buttons

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Settings...</td>
<td>The button opens the <strong>Sample ID List Settings</strong> dialog box, where the number of sample IDs per well can be selected.</td>
</tr>
<tr>
<td>Edit...</td>
<td>The <strong>Edit</strong> button opens the <strong>Edit Well</strong> dialog box. The sample IDs of the marked well can be edited. See below for further information.</td>
</tr>
<tr>
<td>Autofill...</td>
<td>The whole plate or a part of the plate can be selected to be automatically filled with sample IDs. After selecting the corresponding wells, click <strong>Autofill</strong> to open the <strong>Autofill Selection</strong> dialog box. See below for further information.</td>
</tr>
<tr>
<td>Delete</td>
<td>The whole plate or part of the plate can be selected. This function deletes the sample IDs of the selected wells immediately. No dialog box asks for confirmation. Click <strong>Delete</strong> or press the <strong>DEL</strong> key to delete the sample IDs in the selected wells.</td>
</tr>
<tr>
<td>Undo</td>
<td>Performs an undo of the last action. Click <strong>Undo</strong> or press <strong>CTRL-Z</strong> to undo a previous action.</td>
</tr>
<tr>
<td>Redo</td>
<td>Repeats the action, which was performed before the undo step. Click <strong>Redo</strong> or press <strong>CTRL+Y</strong> to redo an action that was undone.</td>
</tr>
</tbody>
</table>
| Print format   | Select the layout for printing the sample ID list:  
|                | • horiz. Table  
|                | • vert. Table  
|                | • Matrix  
| Print preview  | Opens the print preview of the printed sample ID list. |
| 10% button     | This will set the plate layout view to 10%. |
| 100% button    | This will set the plate layout view to 100%. |
5. Create/Edit a Sample ID List Wizard

**Zoom check box**

In case the well plate consists of a large number of wells, the individual well assignments cannot be displayed in the 100% zoom mode. In such a case the **Zoom mode** button allows a zoom into the marked area. If activated, the user can select an area to zoom in by clicking and dragging a frame over the desired layout area. Click the right mouse button to zoom out to 100% display.

**Context-Sensitive Menu of the Plate Layout**

By right-clicking on a well on the plate layout, a context-sensitive menu for the marked wells is displayed. The following commands are available:

<table>
<thead>
<tr>
<th>Menu</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Summary...</strong></td>
<td>The <strong>Summary</strong> dialog box is displayed. See below for further information.</td>
</tr>
<tr>
<td><strong>Cut</strong></td>
<td>The sample IDs of the marked wells are deleted from the wells and copied to the clipboard.</td>
</tr>
<tr>
<td><strong>Copy</strong></td>
<td>The sample IDs of the marked wells are copied to the clipboard.</td>
</tr>
<tr>
<td><strong>Paste</strong></td>
<td>The sample IDs copied to the clipboard are pasted into the marked wells.</td>
</tr>
<tr>
<td><strong>Delete</strong></td>
<td>Click <strong>Delete</strong> or press <strong>DEL</strong> to delete the sample IDs of the marked wells.</td>
</tr>
<tr>
<td><strong>Copy in ASCII-Format</strong></td>
<td>The sample IDs of the marked wells are copied to the clipboard in ASCII file format. This way, they can easily be pasted into other applications (e.g. Excel, Notepad).</td>
</tr>
<tr>
<td><strong>Paste in ASCII-Format</strong></td>
<td>Sample IDs can be pasted from the clipboard in ASCII file format from other applications. See below for further information.</td>
</tr>
<tr>
<td><strong>Edit...</strong></td>
<td>The <strong>Edit</strong> option opens the <strong>Edit Well</strong> dialog box. The sample ID of the marked well can be edited. See below for further information.</td>
</tr>
<tr>
<td><strong>Autofill Selection...</strong></td>
<td>The whole plate or a part of the plate can be selected to be automatically filled with sample IDs. After selecting the corresponding wells, selecting the <strong>Autofill</strong> option displays the <strong>Autofill Selection</strong> dialog box. See below for further information.</td>
</tr>
</tbody>
</table>

**Note**

*When editing a Sample ID list it is possible to use Drag&Drop. Use the left mouse button to select and drag items.*
5. Create/Edit a Sample ID List Wizard

Edit well...

The **Edit Well** dialog box can be accessed via the context-sensitive menu or the tool bar button.

Sample IDs for all wells on a microplate can be defined. A maximum of three sample IDs per well is possible.

The desired sample IDs for the marked well have to be entered in the **Edit Well** dialog box. This has to be repeated for every well that shall be filled with sample IDs. The navigation functions of the **Edit Well** dialog box can be used for comfortable working. Click **OK** to close the dialog box and the sample IDs for the latest marked well are saved.

The **Edit Well** dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Element</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Left, Right, Up and Down buttons</strong></td>
<td>The direction buttons can be used to select another well on the plate while leaving the dialog box open and saving the changes of the current well. The <strong>Arrow keys</strong> can also be used for this kind of navigation.</td>
</tr>
<tr>
<td><strong>On Enter move in vertical direction check box</strong></td>
<td>On clicking <strong>Enter</strong> or <strong>Tab</strong>, the entry field is moved to the next well. Use the check box to specify the direction of movement, vertically or horizontally across the plate.</td>
</tr>
<tr>
<td><strong>Edit sample IDs text fields</strong></td>
<td>In each well up to 3 sample IDs can be entered. Therefore, the list contains three <strong>Sample ID</strong> text fields and an <strong>Autoincrement</strong> check box associated to each of them. A sample ID for the marked well can be entered in the text fields. The sample ID can contain letters, numbers or a combination of both. For example: Smp 1. Up to 100 alphanumeric characters can be entered. The entire plate can be filled with sample IDs.</td>
</tr>
<tr>
<td><strong>Autoincrement check box</strong></td>
<td>The <strong>Autoincrement</strong> check box can be selected, if the wells for the sample IDs are to be automatically numbered. For example: if the starter value is Smp1 then the next well is automatically named Smp2, using the <strong>Enter / Tab</strong> key or the arrow buttons. Using <strong>Autoincrement</strong>, the sample IDs can be allocated to the wells in a numerically consecutive manner. Simply enter the initial value into the first well. The entered ID may also be alphanumeric, although it must end in a number to enable for the consecutive numbering of further wells, for example: If John1 is entered into the first well, John2 will automatically be displayed when moving to the second well.</td>
</tr>
</tbody>
</table>
5. Create/Edit a Sample ID List Wizard

Autofill Selection

The Autofill Selection dialog box can be accessed via the context-sensitive menu or the tool bar button.

This dialog box allows the user to fill the selected wells with sample IDs automatically.

First the whole plate or parts of the plate must be selected. The desired sample IDs and increment settings for the marked wells must be entered in the Autofill Selection dialog box. Click OK to close the dialog box and to fill the selected wells with the defined sample IDs. In each well up to 3 sample IDs can be entered. Therefore, the list contains three Sample ID text fields and an Autoincrement check box, a Start index text field and a Vertical check box associated to each of them.

The Autofill Selection dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Use ID check box</th>
<th>The Use ID check box can only be accessed, if the identical number of sample ID were selected. The checkmark determines if the autoincrement function is applied to the selected sample ID.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sample ID text fields</td>
<td>Sample IDs for the marked well can be entered in the Sample ID text fields. The sample IDs can contain letters, numbers or a combination of letters and numbers.</td>
</tr>
<tr>
<td>Autoincrement check box</td>
<td>The Autoincrement check box must be selected, if the sample IDs for the wells are to be numbered automatically (incremented by 1).</td>
</tr>
<tr>
<td>Start index text field</td>
<td>The Start index text field is only editable, if the Autoincrement check box is selected. The starter value for the automated incrementing of the sample ID has to be entered.</td>
</tr>
<tr>
<td>Vertical check box</td>
<td>The Vertical check box can only be accessed, if the Autoincrement check box is selected. If this check box is selected, the sample IDs will be entered and numbered in vertical direction. If it is cleared, the sample IDs will be entered and numbered in horizontal direction.</td>
</tr>
</tbody>
</table>

Well Summary

The Well Summary dialog box can be accessed via the context-sensitive menu.

This dialog box delivers an overview of all defined Sample IDs and the Sample ID list related settings of a selected well.

The Summary dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Information tree</th>
<th>The information tree gives an overview of all defined well-based parameters of the selected well. The tree is filled according to the available information. For sample ID lists the sample IDs, the pipetting status, etc. are displayed.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Left, Right, Up and Down buttons</td>
<td>The direction buttons can be used to select another well on the plate while leaving the dialog box open.</td>
</tr>
<tr>
<td>Expand All / Shrink All</td>
<td>This button displays the information tree expanded to the highest level or shrunk to the first level.</td>
</tr>
</tbody>
</table>
5. Create/Edit a Sample ID List Wizard

### Paste in ASCII-Format

The **Paste in ASCII-Format** function can be accessed via the context-sensitive menu. This function pastes the contents of selected data in ASCII format from the clipboard into magellan. The function allows transferring data from other software applications (for example: Excel, Notepad) into the magellan plate layout. First, the relevant data must be selected in the other software application and copied to the clipboard. The rows must be separated by linefeed, the columns by tab stops. This is automatically done in Excel when selecting multiple cells. The **Paste in ASCII-Format** function pastes the copied data in ASCII format from the clipboard into the wells. Data is always inserted starting at position A1.

#### 5.2.3 Import a Sample ID List

Sample ID lists that have been created using other programs, or sample ID lists that have been defined using other forms of analytical equipment have to be imported into magellan before being used.

**Important**

Some sample ID lists may contain additional information such as concentrations and dilutions which may affect evaluation of the measurement data.

Click **Import** button in the Sample ID list settings dialog box to browse for existing external sample ID files. The Windows™ Open dialog box appears. The window offers a list of File names that match the selected File type. The File type can be chosen from an associated drop down list. The following external file types are supported:

- Easy-Files .esy
- Tecan-files .tpl
- DD1-Files .dd1
- Hamilton-Files .pro
- APL-Files .apl
- Gemini-Files .csv
- Custom Format Files .txt

Select the requested file to be imported and click the Open button. The Windows™ Open dialog box is closed and the file is loaded. Confirming the Sample ID List Setting dialog box with Next will open the Import/Edit a Sample ID List plate window with the sample IDs displayed. The Import button can also be accessed via the Insert Sample ID List dialog box, which is available in the Start Measurement window (Insert button) and Evaluate Results plate view (Edit toolbar menu).
5. Create/Edit a Sample ID List Wizard

**Caution**

Make sure that the correct ID list has been selected, otherwise the results will be assigned to another list.

**Note**

When importing .tpl, .dd1, or custom format sample ID lists, additional information that modifies the evaluation definitions can be included.

**Note**

When importing sample ID lists with dilutions, the dilution must not be more than 1:1e+12 (magellan Standard and magellan Tracker).

---

**Easy-Files .esy**

These files consist of lines which contain the sample ID and the well name.

<table>
<thead>
<tr>
<th>well name:</th>
<th>alpha numeric, max. 3 characters</th>
</tr>
</thead>
<tbody>
<tr>
<td>sample-ID:</td>
<td>alpha numeric, max. 20 characters</td>
</tr>
</tbody>
</table>

The lines are separated by CR + LF.

**Example**

C01
B01
A01 0001
H02 0002
G02 0003
F02 0004
E02 0005

**Interpretation**

When magellan is processing an .esy-file

- Number of sample IDs is set to 1
- Sample ID is set as sample-ID in well
5. Create/Edit a Sample ID List Wizard

**Tecan-files .tpl**

These files (<PLATEID>.TPL) consist of lines, which contain parameters separated by semicolons. The format is:

- **H**: date; time
- **D**: testno; sample-ID + control-name; position; pre-dilution; errors
- **L**:

The file starts with an H and ends with an L. The fields are defined as follows:

<table>
<thead>
<tr>
<th>Field</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>date; time; testno; sample-ID</td>
<td>the same as in the job list (BES3)</td>
</tr>
<tr>
<td>control name</td>
<td>alpha numerical, max 8 characters</td>
</tr>
<tr>
<td></td>
<td>Note! This entry contains sample-ID or the name of a control</td>
</tr>
<tr>
<td>position</td>
<td>alpha numerical, max. 3 characters</td>
</tr>
<tr>
<td>pre-dilution</td>
<td>numerical, max. 8 characters plus 1 decimal (separated by a '.')</td>
</tr>
<tr>
<td>errors</td>
<td>alpha numerical, max. 3 characters. If an error occurred during pipetting one of the following characters is displayed here:</td>
</tr>
<tr>
<td></td>
<td>First character</td>
</tr>
<tr>
<td></td>
<td>&lt;Space&gt; no liquid error</td>
</tr>
<tr>
<td></td>
<td>L: no or not enough liquid</td>
</tr>
<tr>
<td></td>
<td>Second character</td>
</tr>
<tr>
<td></td>
<td>&lt;Space&gt; no barcode error</td>
</tr>
<tr>
<td></td>
<td>M: manually entered barcode</td>
</tr>
<tr>
<td></td>
<td>Third character</td>
</tr>
<tr>
<td></td>
<td>&lt;Space&gt; no timer overrun</td>
</tr>
<tr>
<td></td>
<td>O: timer overrun</td>
</tr>
</tbody>
</table>

The lines are separated by CR + LF.

**Example**

H;29-02-94;12:47:11
D;1;NEG;A1;1.0;
D;1;POS;B1;1.0;
D;1;0001;C1;1.0
L;

**Interpretation**

When magellan is processing a .tpl-file

- Number of sample IDs is set to 1
- Sample ID or control name is set as sample ID in well position
- Error flags are stored for every well
- Pre-dilution is used as the dilution of the well position
5. Create/Edit a Sample ID List Wizard

DD1-Files .dd1

These files consist of lines, which contain parameters of a fixed length.
The format is:
First line: Date (DD-MM-YY)
Second line: Time (HH:MM:SS)

<table>
<thead>
<tr>
<th>Field</th>
<th>Pos</th>
<th>Length</th>
<th>Format / Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>TestNr</td>
<td>1-3</td>
<td>3</td>
<td>number (001-049)</td>
</tr>
<tr>
<td>TestName</td>
<td>4-23</td>
<td>20</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>SampleID</td>
<td>24-35</td>
<td>12</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>ControlName</td>
<td>36-43</td>
<td>8</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>PlateID</td>
<td>44-51</td>
<td>8</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>PlatePos</td>
<td>52-55</td>
<td>4</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>Errors</td>
<td>56-61</td>
<td>6</td>
<td>Alphanumeric</td>
</tr>
</tbody>
</table>

The lines are separated by CR + LF.

Example
13-04-1999
11:01:32

<table>
<thead>
<tr>
<th>TestName</th>
<th>PlatePos</th>
<th>SampleID</th>
<th>ControlName</th>
<th>PlateID</th>
<th>PlatePos</th>
</tr>
</thead>
<tbody>
<tr>
<td>953test1</td>
<td>KBR</td>
<td>KBR3</td>
<td>H1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>953test1</td>
<td>KBR</td>
<td>KBR3</td>
<td>G1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>953test1</td>
<td>KBR</td>
<td>KBR3</td>
<td>C1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>953test1</td>
<td>KBR</td>
<td>KBR3</td>
<td>B1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>953test1</td>
<td>KBR</td>
<td>KBR3</td>
<td>A1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>953test1</td>
<td>KBR</td>
<td>KBR3</td>
<td>H2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>953test1</td>
<td>KBR</td>
<td>KBR3</td>
<td>G2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>953test1</td>
<td>KBR</td>
<td>KBR3</td>
<td>F2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>953test1</td>
<td>KBR</td>
<td>KBR3</td>
<td>E2</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Interpretation
When magellan is processing a .dd1-file
- Number of sample IDs is set to 1
- <Testname> specifies the magellan method name at the well
- <PlatePos> specifies the well
- <SampleID> or <ControlName> specifies the magellan sample ID
- <Errors> specifies the pipetting flag: L: Liquid error, C: Clot error, E: Manually entered

When a .dd1-file is read the current layout will be modified using the layout defined in the different methods where the names are specified in the .dd1-file. The final layout will be handled like strip methods.
5. Create/Edit a Sample ID List Wizard

Hamilton-Files .pro

These files consist of lines that contain the sample-ID and the well name. A header information is available, too.
Well name: alpha numeric, max. 3 characters
Sample-ID: alpha numeric, max. 20 characters
The lines are separated by CR + LF.

Example

<table>
<thead>
<tr>
<th>Line</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>14ESP-AK-Bommeli</td>
<td>-&gt; Header</td>
</tr>
<tr>
<td>08403009070</td>
<td>-&gt; Header</td>
</tr>
<tr>
<td>SendInfoHost=00</td>
<td>-&gt; Header</td>
</tr>
<tr>
<td>SendInfoPrnt=00</td>
<td>-&gt; Header</td>
</tr>
<tr>
<td>SendInfoDisk=00</td>
<td>-&gt; Header</td>
</tr>
<tr>
<td>A01091111111110</td>
<td></td>
</tr>
<tr>
<td>A02090325228840</td>
<td></td>
</tr>
<tr>
<td>A03090325228930</td>
<td></td>
</tr>
<tr>
<td>A04090325235730</td>
<td></td>
</tr>
<tr>
<td>A05090336975200</td>
<td></td>
</tr>
</tbody>
</table>

Interpretation

When **magellan** is processing a .pro-file
- Number of sample IDs is set to 1
- Sample ID is set as sample ID in well
- Header information is ignored

APL-Files .apl

Description of .apl-files created by MiniSwift 1.3 or later or Minilyser 5.30 or later. The file format is defined as follows:

<table>
<thead>
<tr>
<th>Field</th>
<th>Pos</th>
<th>Length</th>
<th>Format / Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>PlateID</td>
<td>1-8</td>
<td>8</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>PlatePos</td>
<td>9-12</td>
<td>4</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>TestNumber</td>
<td>13-15</td>
<td>3</td>
<td>Number</td>
</tr>
<tr>
<td>TestName</td>
<td>16-27</td>
<td>12</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>SampleID</td>
<td>28-39</td>
<td>12</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>ControlName</td>
<td>40-47</td>
<td>8</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>Result_1</td>
<td>48-55</td>
<td>8</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>Result_2</td>
<td>56-63</td>
<td>8</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>Errors</td>
<td>64-69</td>
<td>6</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>Date</td>
<td>70-79</td>
<td>10</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>Time</td>
<td>80-87</td>
<td>8</td>
<td>Alphanumeric</td>
</tr>
<tr>
<td>CutOff</td>
<td>88-95</td>
<td>8</td>
<td>Alphanumeric</td>
</tr>
</tbody>
</table>

The lines are separated by CR + LF.
5. Create/Edit a Sample ID List Wizard

Example

<table>
<thead>
<tr>
<th>Sample ID</th>
<th>Test</th>
<th>Sample ID</th>
<th>Date/Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>990520S1A1</td>
<td>2</td>
<td>test1_2</td>
<td>BLANK</td>
</tr>
<tr>
<td>990520S1B1</td>
<td>2</td>
<td>test1_2</td>
<td>BLANK</td>
</tr>
<tr>
<td>990520S1C1</td>
<td>2</td>
<td>test1_2</td>
<td>NC1, L, R</td>
</tr>
<tr>
<td>990520S1D1</td>
<td>2</td>
<td>test1_2</td>
<td>PC1</td>
</tr>
<tr>
<td>990520S1E1</td>
<td>2</td>
<td>test1_2</td>
<td>00000000010</td>
</tr>
<tr>
<td>990520S1F1</td>
<td>2</td>
<td>test1_2</td>
<td>00000000010, V</td>
</tr>
</tbody>
</table>

Interpretation

When magellan is processing an .apl-file

- Number of sample IDs is set to 3
- <Testname> specifies the magellan method name at the well
- <PlatePos> specifies the well
- <SampleID> specifies the magellan Sample ID 1
- <ControlName> specifies the magellan Sample ID 2
- <Errors> specifies the magellan Sample ID 3
- <Errors> specifies the pipetting flag: pipetting errors L, B, N at position 1 are uncritical for samples but critical for controls, verification read and barcode errors are uncritical, too.

Gemini-Files .csv

Description of .csv-files created by Gemini 3.40 and 3.60. The following is an example of an output file in Excel format:

<table>
<thead>
<tr>
<th>Position</th>
<th>Tube ID</th>
<th>ScanError</th>
<th>SRCRack</th>
<th>SRCPos</th>
<th>SRCTubeID</th>
<th>Volume</th>
</tr>
</thead>
<tbody>
<tr>
<td>Error</td>
<td>SRCRackID</td>
<td>GridPos</td>
<td>SiteOnGrid</td>
<td>TipNumber</td>
<td>DetectVol</td>
<td>Time</td>
</tr>
<tr>
<td></td>
<td>Version 2.00</td>
<td>3091</td>
<td>Microplate</td>
<td>12</td>
<td>8</td>
<td></td>
</tr>
<tr>
<td>0</td>
<td>9900001</td>
<td>18</td>
<td>1</td>
<td></td>
<td></td>
<td>3.8.1.998</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
<td>0</td>
<td>Tube 13*85mm</td>
<td>1</td>
<td>0001</td>
<td>10</td>
</tr>
<tr>
<td>0</td>
<td>013_000064</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>11:55:42</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>0</td>
<td>0</td>
<td>Tube 13*85mm</td>
<td>2</td>
<td>0002</td>
<td>20</td>
</tr>
<tr>
<td>0</td>
<td>013_000064</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>11:55:42</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>0</td>
<td>0</td>
<td>Tube 13*85mm</td>
<td>3</td>
<td>0003</td>
<td>30</td>
</tr>
<tr>
<td>0</td>
<td>013_000064</td>
<td>1</td>
<td>1</td>
<td>3</td>
<td>11:55:42</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>0</td>
<td>0</td>
<td>Tube 13*85mm</td>
<td>4</td>
<td>0004</td>
<td>40</td>
</tr>
<tr>
<td>0</td>
<td>013_000064</td>
<td>1</td>
<td>1</td>
<td>4</td>
<td>11:55:42</td>
<td></td>
</tr>
</tbody>
</table>

The file format is defined as follows:

The first line contains the column headers, which are the same for all formats, except for some which support only upper-case characters. The second line shows information about the rack / striprack, for which that file was created. Only the column Tube ID, SRCRack, SRCPos, SRCTubeID, Error, SRCRackID, GridPos, SiteOnGrid and Time are valid.

With Gemini 3.60 the SRCPos contains the number of x wells, the SRCTubeID contains the number of y wells and the Volume contains the line to read.
5. Create/Edit a Sample ID List Wizard

The third and following lines are entries for the used wells of a rack / used tubes of a striprack. The columns contain the following information (Column\Range\Explanation):

- **Position**: number of wells\Position of the well in the rack. The numbering sequence is rear to front and then left to right. (1 = A1, 2 = B1, ...) If the microplate has been pipetted in portrait mode (e.g. dimensions 8x12, iso. 12x8), the numbering sequence is left to right and then front to rear. (1 = H1, 2 = H2, ...)
- **TubeID**: Max. 32 characters\This column is only filled for stripracks and when the tube barcodes were scanned with a POSID command. In row 2 this column shows the version of Gemini.
- **ScanError**: 0 .. 4294967295\This column contains possible scanning errors. Please note the table with the error codes below. In row 2 this column shows the serial number of Genesis.
- **SRCRack**: Max. 32 characters\Here Gemini reports for dispense commands the configuration name of the source rack. In row 2 this column shows the configuration name of the rack, for which the output file was written.
- **SRCPos**: number of wells\This column states for dispense commands the position in the source rack, where the liquid came from.
- **SRCTubeID**: Max. 32 characters\If the source for a dispense command was a striprack, Gemini reports here the barcode of the source tube.
- **Volume**: -7158278 .. +7158278\This column contains the volume in µl, which was dispensed (positive value) or aspirated (negative value).
- **Error**: 0 .. 4294967295\This column contains possible pipetting errors. Please note the table with the error codes below. In row 2 this column shows the scanning errors.
- **SRCRackID**: max. 32 characters\For dispense commands this is the source rack barcode. In row 2 this column shows the barcode of the rack, for which the output file was written.
- **GridPos**: 1 .. 67\This is the grid position of the source rack for dispense commands.
- **SiteOnGrid**: 1 .. 128\Here Gemini shows the y-position (site on the carrier) of the source rack for dispense commands.
- **TipNumber**: 1 .. 8\Here Gemini reports the tip number, which was used for pipetting into / from this well.
- **DetectVol**: 0 .. +7158278\If liquid detection was used, the detected volume in the well before the aspirate / dispense command is listed here.
- **Time**: hh:mm:ss\This is the time (format hh:mm:ss) when the well was used.

The lines are separated by CR + LF. The columns are separated by either commas or semicolons. The columns separator is detected from the first header line.

**Interpretation**

The number of lines separated by newline is counted. This number reduced by 2 is used to define the plate format, which can be 8x12, 16x24, 24x36, 32x48 (rows x columns).

With Gemini 3.60 the format information is extracted from the second line, SRCPos and SRCTubeID. Multiple lines per well are possible. The number in the second line, Volume, defines the line to use. If the indicated line does not exist, the sample ID list cannot be read. If any line contains an error number greater than zero, depending on the error number either a critical or an uncritical error is set.

- **Position**: Well position (e.g. 1 = A1, 2 = B1, ...)
- **Tube ID**: ignored
- **Scan error**: if the error number is greater than zero a critical error is set
5. Create/Edit a Sample ID List Wizard

- SRCRack: sample ID 2
- SRCPos: if SRCTubeID is empty, used as sample ID 1 (SRCRackID + "_" + SRCPos)
- SRCTubeID: if not empty used as sample ID 1
- Volume: ignored
- Error: sample ID 3, if the error number is greater than zero a critical error is set
- SRCRackID: if SRCTubeID is empty, used as sample ID 1 (SRCRackID + "_" + SRCPos)
- GridPos: ignored
- TipNumber: ignored
- DetectVol: ignored
- Time: ignored

Custom Format Files *.*

When importing custom format files the Custom Format dialog box is displayed. The Custom Format dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Plate type group box</th>
<th>In the plate type group box the plate format can be specified. If the format is already specified the edit fields are disabled.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rows</td>
<td>Enter the number of rows.</td>
</tr>
<tr>
<td>Columns</td>
<td>Enter the number of columns.</td>
</tr>
<tr>
<td>File format group box</td>
<td>In the File format group box the format of the specified file can be defined.</td>
</tr>
<tr>
<td>File extension</td>
<td>In the File extension field the file extension is displayed and the field is disabled.</td>
</tr>
</tbody>
</table>

**Note**

*Using this feature in the Create/Edit a method wizard, the file extension field is enabled and the file extension has to be specified.*

<table>
<thead>
<tr>
<th>Column separator combo box</th>
<th>Select the column separator used in the file. The row separator must be CR+LF.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Start with line</td>
<td>Enter a number greater than 1 if header lines shall be ignored.</td>
</tr>
</tbody>
</table>
Example
Assume following settings:
Plate type
- 2 rows
- 3 columns
Format
- column separator = Tabulator
- start with line = 2
- column 1 = Plate position (A1, A2, ...)
- column 2 = Sample ID 1
- column 3 = pipetting status

<table>
<thead>
<tr>
<th>Example:</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Tecan custom file</strong></td>
<td></td>
</tr>
<tr>
<td>A1</td>
<td>BLANK</td>
</tr>
<tr>
<td>A2</td>
<td>NC</td>
</tr>
<tr>
<td>A3</td>
<td>SM001</td>
</tr>
<tr>
<td>B1</td>
<td>SM002</td>
</tr>
<tr>
<td>B2</td>
<td>SM003</td>
</tr>
<tr>
<td>B3</td>
<td>SM004</td>
</tr>
</tbody>
</table>

**EXPERT’S KNOW HOW**

**IMPORT SAMPLE-IDS FROM SAMPLE TRACKING (.CSV)**

The option **Investigate Checksum** is available for the import of Sample IDs from sample tracking (*.csv) only.

*Note*

*These Sample ID files have to be imported as custom format files. The checksum is part of the file.*

When importing such a list, the checksum is verified by **magellan**. The import fails if the list has been manipulated in some way afterwards (error: “Failed to load: … Checksum incorrect.”)

For performing the checksum verification, select **Investigate checksum** in the **Custom Format** dialog.
5. Create/Edit a Sample ID List Wizard

5.2.4 Saving the Sample ID List

Click Next in the Import/Edit a Sample ID List window and the Save as window appears, in which the created or modified sample ID list can be saved.

**magellan Tracker:**

**magellan Standard:**
5. Create/Edit a Sample ID List Wizard

The **Save as** window contains the following elements:

<table>
<thead>
<tr>
<th>Field</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Filename field</strong></td>
<td>This field is intended for entering or modifying the file name of the sample ID list (.smp).</td>
</tr>
<tr>
<td><strong>File remarks field</strong></td>
<td>The <strong>File remarks</strong> field allows adding some comments to the file, which will be displayed for example in the <strong>Open File</strong> dialog boxes.</td>
</tr>
<tr>
<td><strong>Audit trail comment field</strong></td>
<td>The <strong>Audit trail comment</strong> field allows adding some comments, which will be stored in the audit trail (only available for magellan Tracker).</td>
</tr>
<tr>
<td><strong>Audit trail… button</strong></td>
<td>Displays the audit trail of the sample ID list (only available in magellan Tracker). See 4.4 Saving the Method - Audit trail for further information.</td>
</tr>
</tbody>
</table>

The **Save&Finish** button is only enabled when a document has been modified. The modified document can be saved under its current file name or under a different name.

Click **Save&Finish** to save the sample ID list and close the **Create/Edit a Sample ID List** wizard.
6. Start Measurement Wizard

6.1 Introduction

In the **Wizard List** window, click **Start Measurement** to open the wizard. Click **Continue** on the welcome page and the **Select a file** dialog box appears:

| Obtain Raw Data | Is used to generate raw data quickly by setting the required measurement parameters. This wizard is designed to create a new workspace, to set the measurement parameters and to obtain measured values. |
| Run Strip Layout | Enables the user to create one strip method from different methods and to run this combined method. |
| Use Predefined Method | Is used to perform measurements based on already defined methods. The wizard creates a new workspace, that contains the selected method (which consists of all measurement parameters and definitions for evaluation) and enables you to insert a **Sample ID list**. After the measurement, the workspace is completed with the obtained raw data which will be evaluated. |
| Start Favorite | Is used to select one of the most frequently used methods from the list of numbered icons. |
6.2 Obtain Raw Data

Select Obtain Raw Data and click Next; the following wizard page appears:

In the Measurement Parameter dialog box, the following options are available:

<table>
<thead>
<tr>
<th>Endpoint measurement</th>
<th>Use this button to perform a single measurement.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kinetic measurement</td>
<td>For multiple measurements within a specified time interval this type of measurement is used.</td>
</tr>
<tr>
<td>Measurement parameters...</td>
<td>Click this button to define the parameters in the Measurement Parameters dialog box.</td>
</tr>
</tbody>
</table>

**WARNING**

IT IS STRONGLY RECOMMENDED TO CHECK ALL OF THE MEASUREMENT PARAMETERS (EVEN PARAMETERS NOT USED IN THE CURRENT MEASUREMENT), BECAUSE PARAMETERS FROM THE PREVIOUS MEASUREMENT METHOD WILL STILL BE SET.
6. Start Measurement Wizard

6.2.1 Obtain Raw Data with the Infinite Instrument

When an Infinite instrument is connected the following window appears after selecting Obtain Raw Data:

Define the measurement parameters following the list on the left side.

Click Choose Measurement Parameters to finish the definition. Refer to the i-control instructions for use for further information.
6.3 Run Strip Layout

The Strip Method... option allows the user to create one method composed of strips from different methods containing different parameters and to run this combined method.

Observe the criteria for combining strips of methods. The methods involved must be defined with:
- exactly the same measurement parameters
- transformations, concentration and kinetic transformations must have the same name.

The Strip Method Definition dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Field</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Exp. group field</td>
<td>This field displays the experimental group number that is assigned to the next inserted strip method.</td>
</tr>
<tr>
<td>Load button</td>
<td>Click the Load button to open a file selection dialog box where all available method files are displayed. Select the required single strip method from the file list and click Open.</td>
</tr>
<tr>
<td>File name text field</td>
<td>This field displays the name of the currently selected method file.</td>
</tr>
<tr>
<td>Text field</td>
<td>In this field the complete path of the method file name is displayed.</td>
</tr>
<tr>
<td>Undo button</td>
<td>This option cancels the last strip method insertion.</td>
</tr>
<tr>
<td>Strip orientation</td>
<td>Determine how the strips are to be allocated to the plate.</td>
</tr>
<tr>
<td>By columns</td>
<td>If this option is selected, the strips must be allocated in columns to the plate.</td>
</tr>
<tr>
<td>By rows</td>
<td>If this option is selected, the strips must be allocated in rows to the plate.</td>
</tr>
</tbody>
</table>
### Fill pattern option buttons

This option allows the users to decide between allocating every new strip to a new row or column or allocating it to the next available well in the plate.

- **Partial**: If this option is selected, the strips will be allocated to complete new rows or columns in the plate.
- **Continuous**: If this option is selected, the strips will be allocated to the next available well in the plate.

### Final layout graphical display

The graphical display shows the layout of the composition of strip methods. The way, in which wells are transferred from the **Layout of currently loaded method** area to the **Final layout** area depends on the settings of the option buttons **Strip orientation** and **Fill pattern**.

### Layout of currently loaded method graphical display

The graphical display shows the layout of the currently loaded method. Double-clicking on the last available well will add the strip method at this position to the plate. This will be displayed in the **Final layout** area on the left side. Replicates, which are not selected, are automatically added.

This step can be repeated by loading another strip method.

---

### 6.4 Use Predefined Method

Select **Start measurement** from the wizard list. Click **Continue** on the welcome page and the **Select a file** dialog box appears. Select **Use Predefined Method** and select the required method from the **Filename** list:

![Select a File Dialog Box]

The **Show** drop down list is a filter. **All files**, **Files from this instrument**, **My files**, **Signed files** or **Last selected methods** can be selected.
6.5 Start Favorite

In the Select a file dialog box click Start Favorites. Select one of the most frequently used methods from the list of numbered icons:

![Select a File Dialog Box](image)

Click Organize favorites to add to or remove methods from the favorites list.

Organize Favorites

Method files can be dragged from the Method list onto one of the 15 icons in the Favorite list to save it as a favorite.

![Organize Favorites Dialog Box](image)

The Organize Favorites dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Methods list</th>
<th>Lists all available methods. The filename and corresponding remarks - if entered - are displayed.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Set button</td>
<td>After selecting a method from the Methods Filename list and selecting a method icon, click Set to add the selected method to the Favorites.</td>
</tr>
</tbody>
</table>
6. Start Measurement Wizard

<table>
<thead>
<tr>
<th>Remove button</th>
<th>Select a method icon and click <strong>Remove</strong> to delete a method from the <strong>Favorites</strong>.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Infinite M1000, M1000 Pro Instrument Favorite group box</strong></td>
<td>With the Infinite M1000/M1000 Pro instrument, it is possible to start a measurement run with a favorite method directly via the instrument's <strong>Start</strong> button. To define a favorite method click the <strong>Select...</strong> button and select a method. This method will remain the favorite one as long as another method is selected.</td>
</tr>
</tbody>
</table>
6.6 Start Measurement with a Predefined or Favorite Method

Click **Make your selection** respectively **Show Summary** in the **Select a file** dialog box to open the **Start Measurement** dialog box. Before the instrument starts to measure, the user has to (if defined) answer the report prompts and/or to confirm or change the constants. If evaluation settings are defined, the calculation is started right after the measurement.

**Edit Prompts Dialog**

If user prompts were specified in the method, the **Edit user prompts** dialog box is displayed. It contains the following elements:

- **Prompt Answer list**: At each text field of this list any text prompt can be entered.
- **Req. check box**: A **Required** check box next to every **Prompt Answer** text field determines that the measurement can only be started when a text has been entered.

Click **Continue** to close the user prompts dialog; the **Start Measurement** window appears. If set in the method, the **Edit Constants** dialog appears.

**Edit Constants Dialog**

The **Edit Constants** dialog box appears only, if the required flag is set for at least one constant in the selected method.

- **Constants list**: At each text field of this list the value of the constant or the comment can be modified.
- **Req. check box**: A **Required** check box next to every **Constant value** text field determines that this constant value needs to be confirmed. Do this by continuing to the next page.

If the method constants have been modified, the new values can be automatically transferred and saved into the corresponding method. Click **Modify constants in Method** to modify the current method with the new defined constants. Please note that this dialog is available only for **magellan** users with the user right **Edit methods**.

Click **Continue** to close the constants dialog; the **Start Measurement** window appears.

---

**Note**

*Using magellan Tracker or magellan Standard with User administration, a default magellan Operator (refer to chapters 11.4.4 User Rights (magellan Tracker and to chapter 11.5.3 Change User) can edit only the required constants. The constants without required flag set are displayed gray and cannot be edited.*

*A default magellan Administrator can edit also constants without required flag set.*

*For a default magellan Application Specialist it depends on the method he runs. Using an unsigned method he is allowed to edit constant with and without required flag. Using a signed method he can edit only the required constants.*
6. Start Measurement Wizard

After these two optional pages the **Start Measurement** dialog box is displayed.

It contains the following elements:

<table>
<thead>
<tr>
<th>Measurement group box</th>
<th>Workspace text field: The default workspace filename as defined in Automated Data Handling is displayed. The filename of this workspace can be renamed.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Arb. cycle kin. ...</strong> button: This button is available if a kinetic measurement is performed. Click this button to display the Arbitrary Cycle Kinetic dialog box. In this dialog box the measurement can be split up into several sub-measurements with a different number of measurement cycles and interval times. Each of these sub-measurements can be started at any time, for example: the workspace can be saved and the measurement can be continued on another day.</td>
<td></td>
</tr>
</tbody>
</table>

**Note**

This option is not available for Infinite Series instruments.

| Method text field: The filename of the previously selected method is displayed. |
| Modify layout... button: Depending on the user rights, the plate layout can be modified. Click the **Modify layout**...button to open the Modify Layout dialog box. The user can move controls and remove samples, change the concentration or change the measurement parameters. The changes are stored only in the workspace and not in the previously selected method. This button is not available when Obtain Raw Data has been selected and after inserting a sample ID list. |
| Sample ID List text field: The filename of the currently loaded sample ID list is displayed |
6. Start Measurement Wizard

**Insert...** button: see also below. Click this button to open the **Insert Sample ID List** dialog box. After selection of a sample ID list file the **Sample ID List with Plate Layout Preview** dialog appears in which the user has to confirm the selection.

**Instrument group box**

Use stacker: This option is available whenever the **Connect** stacker is used together with the instrument. Check this option in order to measure all plates in the stacker with this method. Refer to the **Connect** Instructions for Use for further information. The workspaces will be stored with default workspace names. After all plates have been measured only the first workspace is open. Use **File Open** or the **Evaluate Results** wizard to open the other workspaces. **It is not possible to use the stacker when performing kinetic measurements.**

**Plate In/Out** button: Click to move the plate carrier. This button changes its text depending on the position of the plate carrier.

---

**Note**

*When Use stacker is selected while using magellan, make sure that the overall runtime does not exceed the time set in the Auto Lock option (see chapter 11.4.5 User Administration Options/ Login Options).*

*When magellan is locked, the stacker run will stop even if the measurements are not finished.*

**Movements** button: Further movements of the instrument can be invoked (filter slide, mirror carriage and so on.)

**Optimize Z-Position** button: The user can optimize the z-position of the reader.

**Injector control**: Refer to the respective instrument’s instructions for use.

**Current Temperature** text field: The current temperature of the instrument is displayed.

**Target Temperature** text field: The target temperature, set in the **Temperature Control** dialog box, is displayed.

**Temperature Control** button: Click this button to open the **Temperature Control** dialog box. See chapter 3.1.2 Temperature Control...

**Measurement parameters** group box

In a text field all configured measurement parameters are listed and can be double-checked.

**Please note** group box

Important information is displayed. Read this information and start appropriate actions before running the method.

A warning is displayed if the layout is defined for wells that will not be measured. Click **Start** to start the measurement. A workspace will be created automatically, which contains all previously entered information and will collect all measurement values. While the measurement is being executed, a measurement status dialog box appears indicating the progress of the measurement.
6. Start Measurement Wizard

If you run a multiplate method, the Run Measurement dialog box appears after clicking Start.

It contains the following elements:

<table>
<thead>
<tr>
<th>Measurement of plate</th>
<th>Displays the number of the currently processed plate.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sample ID List</td>
<td>Insert the appropriate sample ID list for the selected plate. Sample ID lists have to be inserted plate by plate.</td>
</tr>
</tbody>
</table>

**Note**

*Only sample ID lists created in magellan can be inserted. Import of other formats is not supported.*

<table>
<thead>
<tr>
<th>RUN</th>
<th>Click this button to start the measurement.</th>
</tr>
</thead>
<tbody>
<tr>
<td>PAUSE</td>
<td>The Evaluate Results wizard is reached when clicking Pause; further plates can be appended later.</td>
</tr>
<tr>
<td>STOP</td>
<td>The Evaluate Results wizard is reached when clicking Stop; no further plates can be added.</td>
</tr>
</tbody>
</table>

After the measurement is completed, the Results dialog box appears, in which all results and calculations can be viewed. See chapter 7 Evaluate Results Wizard for more information.
Insert Sample ID List

The **Insert Sample ID List** option is used to load a previously defined sample ID list file into a workspace.

The **Insert Sample ID List** dialog box contains the following elements:

<table>
<thead>
<tr>
<th><strong>Filename field</strong></th>
<th>The list displays all available sample ID list files (.smp). Select a sample ID list by clicking a filename.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Remarks field</strong></td>
<td>Available comments and remarks will be displayed.</td>
</tr>
<tr>
<td><strong>Import... button</strong></td>
<td>Click to open a standard Windows <strong>Open</strong> dialog box. External files can be imported. Refer to chapter 5.2.3 Import a Sample ID List for further information.</td>
</tr>
</tbody>
</table>

Select the desired sample ID list from the **Filename** field and click **OK** to view the sample ID list in the **Sample ID List with Plate Layout Preview** window.

If the method and the sample ID list have different plate formats, then an error message is displayed.

When the sample ID list is selected in the printed report setup then it is displayed on the printout.

The **Sample ID List with Plate Layout Preview** dialog box displays the sample ID list together with the defined plate layout. This helps the user to ensure that the correct sample ID list is selected. The dialog box contains the following elements:

<table>
<thead>
<tr>
<th><strong>10% button</strong></th>
<th>Click to resize the displayed plate layout to show 10% of the plate layout on the full screen.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>100% button</strong></td>
<td>Click to resize the displayed plate layout to show 100% of the plate layout on the full screen.</td>
</tr>
<tr>
<td><strong>Zoom check box</strong></td>
<td>When this <strong>Zoom</strong> function is activated the required wells on the plate layout can be marked and the wells are automatically enlarged to fit into the full screen.</td>
</tr>
<tr>
<td><strong>Remove unused samples check box</strong></td>
<td>If an only partly filled sample ID list is loaded, the user can delete all unused samples from the layout by selecting this check box. If a final control (e.g. in well H12) has been defined within the layout, this control is automatically moved to the well after the last used sample well. Per default, the <strong>Remove unused samples</strong> option is selected.</td>
</tr>
</tbody>
</table>
## 6.7 Measurement Status

The **Measurement Status** dialog box is shown during the measurement performance of the instrument and contains the following elements:

<table>
<thead>
<tr>
<th>Element</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Status text field</strong></td>
<td>The text field is updated during the measurement and contains a measurement status information.</td>
</tr>
<tr>
<td><strong>Display in wells group box</strong></td>
<td>Select the mode of representation of data in the wells: <strong>Values</strong> option button: The measured value is displayed in the well. If more than one value is measured (for example: polarization measurement) all values are displayed in one well. <strong>Graph</strong> option button: The option is enabled if a kinetic graph can be displayed. The graph is shown as soon as more than one value is available.</td>
</tr>
<tr>
<td><strong>Pause button</strong></td>
<td>To pause a kinetic measurement run at the next possible moment, click the <strong>Pause</strong> button. In the <strong>Pausing Kinetic</strong> dialog click the <strong>Plate out / Plate in</strong> button to move the plate transport out of or into the instrument. Click the <strong>Continue</strong> button to go on with the kinetic run.</td>
</tr>
<tr>
<td><strong>Break button</strong></td>
<td>Click this button to break the measurement at the next possible time point.</td>
</tr>
<tr>
<td><strong>Plate View display</strong></td>
<td>The <strong>Plate View</strong> display shows a schematic display of the microplate. According to the <strong>Display in wells</strong> option the contents of the wells are customized. The wells are updated as fast as the instrument delivers data. Some instruments support row-wise or even well-wise data transmission; other instruments only plate-wise data transmission. When injection or dispensing is performed, the currently used well is automatically highlighted in a different color.</td>
</tr>
<tr>
<td><strong>Cycle text field</strong></td>
<td>If a kinetic measurement is performed, the <strong>Cycle</strong> text field displays the current cycle number and the maximum number of kinetic cycles.</td>
</tr>
<tr>
<td><strong>Graph display</strong></td>
<td>If a kinetic or multilabel measurement is performed, the kinetic or multilabel graph of the currently selected well is displayed in a larger size at the right side of the <strong>Measurement Status</strong> dialog box.</td>
</tr>
<tr>
<td><strong>Previous cycle group box</strong></td>
<td>As long as the transmission of the data of the current cycle was not started the <strong>Raw data</strong> text field contains the value of the previous measured cycle of the currently selected well. As long as the transmission of the data of the current cycle was not started the <strong>Temperature</strong> text field contains the temperature of the previous measured cycle.</td>
</tr>
</tbody>
</table>
### 6. Start Measurement Wizard

<table>
<thead>
<tr>
<th>Time group box</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>The <strong>Elapsed time</strong> text field displays the time span since the start of the measurement.</td>
<td></td>
</tr>
<tr>
<td>The <strong>Exp. run time</strong> text field displays the time span expected for the whole measurement.</td>
<td></td>
</tr>
</tbody>
</table>

Scaling of the y-axis in the graph is possible by selecting either Auto select range or Select range (MIN/MAX).

**Note**

*It is possible to select multiple wells on the plate to view the selected kinetic curves in a graph. When performing kinetic measurements, the retrieved data is saved automatically every 30 min in the magellan log file directory (refer to chapter 3.3 Log Files).*
7. Evaluate Results Wizard

7.1 Introduction

The Evaluate Results wizard is designed to help the user analyze measurement results. Raw data, evaluation data and evaluation parameters can be viewed and data can be re-evaluated.

Workflow Summary

Start the Evaluate Results wizard. After a welcome dialog box, the Select a File dialog box appears. Select an existing workspace file containing the measurement data to be evaluated.

Click Make your selection and the Results dialog box appears, in which the results can be viewed or printed (Evaluate Results tab).

If necessary, the used method can also be modified (Edit Method tab).

Click Finish and the Save dialog box appears, in which a file name and remarks about the measurement can be entered and saved as a workspace file which contains method definitions, instrument data and sample ID list if configured.

Evaluated data are not stored in the workspace but recalculated every time the workspace is opened.

7.2 Select a File

On the Wizard List page, click Evaluate Results.

Click Next on the welcome page of the Evaluate Results wizard and the Select a file dialog box appears.

The Select a File dialog box contains the following elements:

| Filename list | The Filename list contains the names of all files within the standard workspace directory. Remarks entered for that measurement are displayed. |
| Show combo box | In the Show combo box, the displayed list of files can be modified according to the selection. Possible selections are: |
|               | • All files |
|               | • Files from this instrument |
|               | • My files: This option is available if the user administration is enabled (always enabled in magellan Tracker). |
|               | • Signed files: only available for magellan Tracker. |
|               | • Custom definitions are possible by clicking the button; see File Selection Criteria below. |
|               | • Example files: only available if they have been installed. |
7. Evaluate Results Wizard

7.2.1 File Selection Criteria

Click the button to open the **File Selection Criteria** dialog box.

Select one of the options under **Workspace Criteria**: All files, Files from this instrument, My files, Signed files or enter characters in the Containing text field which must appear in the Filename. The files filtered can be further limited to a specific period of time by selecting one of the options under **Workspace file created/modified**: No time limitation, Today, Last week, Last month or enter a number in the Last ... days field. Click OK to save the settings.

Select the workspace file to be evaluated from the Filename list and click **Make your selection**.

![File Selection Criteria dialog box]

**Note**

*If the proper instrument for the selected file is not connected, the Instrument Mismatch dialog box appears. The dialog offers two options:

- Connect to the proper instrument
- Convert the measurement parameters to the connected instrument.

This option is not available if the measurement mode is not supported by the connected instrument, for example: a Sunrise does not support fluorescence measurements.*
7.3 The Workspace Overview Window

Click the Next button and the Workspace Overview window of the Evaluate Results wizard appears. It displays all available data of the currently selected workspace and helps to easily locate and view instrument data, calculated data, cutoff results, measurement parameters, etc.

If the currently working user has the appropriate rights (refer to chapter 10.4.4 User Rights (magellan Tracker and chapter 10.5.4 User Rights (magellan Standard), it is also possible to make some changes in the method by clicking on the Edit Method tab and perform a recalculation of the measured data.

For more detailed information on the calculation procedure and sequence of calculations, refer to chapter 12 Calculations.

The Workspace Overview is composed of the following elements:

- **Plate Layout** window: data for each well is displayed in the plate layout (for example: raw data). If a multiplate workspace is opened, a “counter” for switching between the different plates is displayed in the right upper corner.

- **Toolbar**: for editing, zooming, switching between kinetic cycles and viewing the summary of one selected well.

- **Data Information** window: data which cannot be assigned to a single well is displayed in the text box window (for example: measurement parameters, cutoff definition, result statistic, etc.).

- **Control Bar of Evaluate Results tab**: all available data set names are displayed. Selecting a data set will either display the data in the plate layout or display the data in the Data Information window.

- **Control Bar of Edit Method tab**: the settings and parameters of the loaded method are displayed.

The size of the latter three windows can be changed by using the splitter bars that separate the windows.
7. Evaluate Results Wizard

Plate Layout

The view displays a schematic layout of a microplate. Rows are marked alphabetically, columns numerically.

In the control bar on the left hand side, all available data is listed. The selected data is displayed in the plate layout, in the text pane or in a separate graph window, according to the type of the selected data.

Context-Sensitive Menu of the Plate Layout

To display a summary of all data of one well, select the well and select Summary from the right mouse button menu.

Toolbar Buttons

Available toolbar buttons are described in the following paragraphs.

Depending on the data selected, different buttons are displayed:

- when Instrument data is selected, the Edit button is available;
- when Concentration or Kinetic data is selected, the Curve/Graph button is available.

The following buttons are only available in the Evaluate results wizard.

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Edit button</td>
<td>Click the Edit button to edit or mask raw data.</td>
</tr>
<tr>
<td>button</td>
<td>Click this button to display the Summary dialog box.</td>
</tr>
<tr>
<td>10% button</td>
<td>Click this button to resize the displayed plate layout to show 10% of the plate layout on the full screen.</td>
</tr>
<tr>
<td>100% button</td>
<td>Click this button to resize the displayed plate layout to show 100% of the plate layout on the full screen.</td>
</tr>
<tr>
<td>Zoom check box</td>
<td>When the Zoom check box is selected, the required wells on the plate layout can be marked and the labeled wells are automatically enlarged to fit into the full screen.</td>
</tr>
</tbody>
</table>

Data Information Window

Click, for example, Miscellaneous data in the Evaluate Results tab to view the corresponding information in the Data Information window.
7. Evaluate Results Wizard

7.4 Evaluate Results Tab

All available data set names are displayed in the Available Data control bar. There are several different viewing options:

- Selected data that presents a value for each well is displayed in the plate layout window. It can be viewed as values or in pseudo-colors together with a colors scale.
- Kinetic data can be viewed as a small graph in each well.
- Selected data that presents a data collection which cannot be assigned to a single well is displayed in the data information window (f.e. QC-Validation criteria).
- If a graph (standard curve, kinetics, enzyme kinetics, dilution series, multilabel, spectra) is selected, the Graph dialog box appears.

If a measurement sequence consisting of individual independent measurements has been executed, the results of each measurement are displayed upon selection of the relevant measurement number from a drop down list in the toolbar (f.e. kinetic cycles in a kinetic run).

If necessary, the measurement results can be modified by clicking the Edit button. Manipulated data is marked with a ~ sign.

⚠️ WARNING
THIS FUNCTION IS FOR RESEARCH USE ONLY AND MUST NEVER BE USED FOR DIAGNOSTIC TESTS.

In each well of the plate layout, three lines of data can be displayed. Depending on which criteria selected in the control panel in the left window, different values are displayed.

7.4.1 Menus

<table>
<thead>
<tr>
<th>File</th>
<th>ASCII File Export…</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>ASTM File Export (LIS)…</td>
</tr>
<tr>
<td></td>
<td>Sample Tracking Export…</td>
</tr>
<tr>
<td></td>
<td>Excel Export…</td>
</tr>
<tr>
<td></td>
<td>Method Export</td>
</tr>
<tr>
<td></td>
<td>Print…</td>
</tr>
<tr>
<td></td>
<td>Print Preview…</td>
</tr>
<tr>
<td></td>
<td>Printer Setup…</td>
</tr>
<tr>
<td></td>
<td>Printout Font…</td>
</tr>
<tr>
<td></td>
<td>Plate to Plate QC…</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Edit</th>
<th>Copy to Excel</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Copy to ASCII Format</td>
</tr>
<tr>
<td></td>
<td>Paste from ASCII Format</td>
</tr>
<tr>
<td></td>
<td>Insert Sample ID List…</td>
</tr>
<tr>
<td></td>
<td>Recalculate with another Method…</td>
</tr>
</tbody>
</table>
### 7. Evaluate Results Wizard

<table>
<thead>
<tr>
<th>Instrument</th>
<th>Movements…</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Temperature Control…</td>
</tr>
<tr>
<td></td>
<td>Optimize Z-Position…</td>
</tr>
<tr>
<td></td>
<td>Injector Control…</td>
</tr>
<tr>
<td></td>
<td>Start Measurement…</td>
</tr>
</tbody>
</table>

#### 7.4.2 Toolbar Menu: File

**ASCII File Export**

In the **File** menu, click **ASCII File Export** to export data as ASCII (.asc) files so that other programs can read and process the data provided by magellan.

Before data can be exported, the data must be selected in the **Data Export** dialog box via **Edit method tab → Data handling → Data export**.

Select the folder, where the exported data shall be stored. Enter a file name (.asc).

Upon clicking **Save** in the **Save as** dialog box, the data sets specified in the **Data Export** dialog box will be saved as an ASCII file.

The **Save as** dialog box is a standard Windows dialog box, with file navigation elements, a text field for entering a file name, a drop down list for the selection of a file type (*.asc) and **Save** and **Cancel** buttons.

**ASTM File Export (LIS)**

In the **File** menu, click **ASTM File Export** to export data to in ASTM format to compatible Laboratory Information Systems.

Select the data to be exported from the **Data Export** dialog box via **Edit method tab → Data handling → Data export**.

**Sample Tracking Export**

In the **File** menu, click **Sample Tracking Export** to export data to the Sample Tracking system.

Select the data to be exported from the **Data Export** dialog box via **Edit method tab → Data handling → Data export**.

**Excel Export**

In the **File** menu, click **Excel Export** to export data to Excel.

Select the data to be exported from the **Data Export** dialog box via **Edit method tab → Data handling → Data export**.

**Method Export**

In the **File** menu, click **Method Export**.

In some cases the user will request to save the method definition of a workspace as a method file. These method files can be opened and modified.

The folder to save the method in must be selected and the desired file name needs to be entered. Additionally some comments can be added in the **Remarks** text field.

Click the **Save** button to save the current measurement data into a method file. **Cancel** will cancel the current operation.

The **Save as** dialog box is a standard Windows dialog box, with file navigation elements, a text field for entering a file name, a drop down list for the selection of a file type (*.tst), **Save** and **Cancel** buttons.

An additional **Remarks** text field provides a possibility to add useful information or remarks to the method file.
7. Evaluate Results Wizard

Print

In the File menu, click Print… or press SHIFT-P to print the data as defined with the Printed Report setup from the method. The standard Windows Print dialog box is opened, where the printer, page range and number of copies can be selected.

Note
After the magellan 30-day demo license has expired, printing will not be possible.

Print Preview

In the File menu, click Print Preview… to see exactly how a print-out will appear without actually having to print the document.

The Print Preview window contains the following elements:

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Print… button</td>
<td>Click this button to close the print preview window and the Print dialog box appears. The current document can be printed.</td>
</tr>
<tr>
<td>Next Page button</td>
<td>Click this button to view additional page(s).</td>
</tr>
<tr>
<td>Prev. Page button</td>
<td>Click this button to view previous page(s).</td>
</tr>
<tr>
<td>One Page / Two Page button</td>
<td>Toggle switch: shows either a single page or two pages of the document.</td>
</tr>
<tr>
<td>Zoom In button</td>
<td>The shown page is zoomed in.</td>
</tr>
<tr>
<td>Zoom Out button</td>
<td>The shown page is zoomed out.</td>
</tr>
<tr>
<td>Close button</td>
<td>Closes the print preview window.</td>
</tr>
<tr>
<td>Document area</td>
<td>In the main area, the pages of the document are shown as they would look when printed.</td>
</tr>
</tbody>
</table>

Printer Setup

In the File menu, click Printer Setup… to change the current printer or modify the printer settings.

The standard Windows Print Setup dialog box appears. Select printer, paper size and orientation of printout.

Printout Font

In the File menu, click Printout Font… to select a specific font, font style, font size, font color etc. for future printouts.

These settings will have no effect on the screen display, so it will be difficult to judge the effect these setting have on the printout. Large fonts should be avoided to prevent errors or misrepresentation of data.

Plate to Plate QC

When Plate to Plate QC is configured in the method definition, magellan compares the currently observed mean value of a control against the mean and standard deviation previously defined for this method. (Refer to chapter 4 Create/Edit a Method Wizard).
7. Evaluate Results Wizard

**Levy-Jennings-Graph**

In the File menu, click *Plate to Plate QC* and the Levy-Jennings-Graph window appears. The Levy-Jennings-Graph displays the trend of the control values.

On the y-axes, the data values (raw data, concentrations, etc.) as set in the method definition) are applied and on the x-axes, the time range in days is applied.

The control values are displayed together with the mean value and the distance lines of the standard deviations (1s, 2s, 3s).

When the cursor is placed on a measurement point, a tool-tip shows additional information (workspace name, measurement date and time and rule violated, if any). Use the check boxes of the single elements of the *Show* list to select various controls to be displayed.

**Time Range**

Beside the graph, next to *Show*, various controls can be selected to be displayed. Click *Time range* and the following window appears:

Select an appropriate time range to be displayed.
7. Evaluate Results Wizard

Select Workspaces

Click **En-/Disable** to enable or disable certain workspaces for evaluation.

![Enable/Disable workspaces dialog box](image)

Data Sheet

Click **View summary** and the **Data sheet** window appears:

![Data sheet dialog box](image)

The **Data sheet** dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Workspace column</th>
<th>Contains a list of the evaluated workspace files. On the left hand side of the workspace name, the result of the multirule Westgard® evaluation is displayed (see below). A green checkmark indicates fulfillment, a red cross indicates failure.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control column</td>
<td>The different controls are listed.</td>
</tr>
<tr>
<td>Value column</td>
<td>The mean value of each control is displayed.</td>
</tr>
</tbody>
</table>
### Westgard® Rules

The Westgard® rules are a multirule QC model:

<table>
<thead>
<tr>
<th>Rule</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1:2s</td>
<td>Control rule to test whether a control measurement exceeds the control limits of ( x + 2SD ) or ( x - 2SD ). This rule is used as a warning rule to trigger careful inspection of the control data by the following control rules. If no control measurements exceed the mean plus 2s or the mean minus 2s control limit, then the measurement procedure is considered &quot;in-control&quot;, regardless whether any of the other rules have been violated. However, if one control measurement exceeds the mean plus 2s or the mean minus 2s control limit, and any of the other rules are violated, the measurement procedure is considered &quot;out-of-control&quot;.</td>
</tr>
<tr>
<td>1:3s</td>
<td>Control rule to test whether a control measurement exceeds the control limits of ( x + 3SD ) or ( x - 3SD ). A run is rejected if a single control measurement exceeds the mean plus 3s or the mean minus 3s control limit.</td>
</tr>
<tr>
<td>2:2s</td>
<td>Control rule to test whether two consecutive control measurements exceed the same control limit of either ( x + 2SD ) or ( x - 2SD ). A run is rejected if 2 consecutive control measurements exceed the mean plus 2s or the mean minus 2s control limit.</td>
</tr>
<tr>
<td>R:4s</td>
<td>Control rule to test whether the range, or difference, between control measurements exceeds 4SD. A run is rejected if 1 control measurement exceeds the mean plus 2s and another exceeds the mean minus 2s. The two control results need not be consecutive.</td>
</tr>
<tr>
<td>4:1s</td>
<td>Control rule to test whether four consecutive control measurements exceed the same control limit of either ( x + 1SD ) or ( x - 1SD ). A run is rejected if 4 consecutive control measurements exceed the mean plus 1s or the mean minus 1s control limit.</td>
</tr>
<tr>
<td>10:x</td>
<td>A run is rejected if 10 consecutive control measurements fall on the same side of the mean. However, if one of these results falls directly on the mean, then the run is not rejected.</td>
</tr>
</tbody>
</table>

![Westgard® rules diagram](https://example.com/westgard_rules_diagram.png)
7. Evaluate Results Wizard

7.4.3 Toolbar Menu: Edit

The Edit menu contains the following selections:

Copy to Excel

In the Edit menu, click Copy to Excel or press CTRL-X.
The Copy to Excel command allows the user to export data directly into an MS Excel worksheet.
The necessary options, regarding the copying of the data to Excel, can be defined in the Options dialog box. Refer to chapter 11.3.2 Copy/Export Options.
First the relevant wells must be selected with the mouse. If more than one non-adjacent well field must be selected, press the Control key while clicking the requested fields. If no wells are selected, all wells will be copied.
Once all wells are selected, the Copy to Excel function transfers the well data into an Excel worksheet.

Copy in ASCII-Format

In the Edit menu, click Copy in ASCII format or press CTRL+C. Additionally, in sample ID list documents Copy in ASCII format can be accessed via the context-sensitive menu.
Select Copy in ASCII format to copy the data, which is contained in the selected wells of the plate layout, to the clipboard.
This function allows transferring the well data to other software applications. The copied data can be pasted into any suitable kind of file.
The necessary options, regarding the style of the data which is copied to the clipboard, can be defined in the Options dialog box. Refer to chapter 11.3.2 Copy/Export Options.
First the relevant wells must be selected with the mouse. If more than one non-adjacent well field must be selected, press the Control key while clicking on the requested fields.
Once all desired wells are selected, the Copy in ASCII format function transfers the well data into the clipboard.
The data can be pasted into any other software application if the application provides the paste function and accepts data in ASCII format.

Paste from ASCII-Format

In the Edit menu, click Paste or press CTRL-V.
The contents of selected data will be pasted from the clipboard using the ASCII data format. The function allows the transferring of data from other software applications (for example: Excel) into the wells.
First, the relevant data has to be selected with the mouse in the other software application. Then the selected data has to be copied and is transferred to the clipboard. The rows have to be separated by linefeed, the columns by tab stops. This is automatically done in Excel when selecting multiple cells.
The Paste function pastes the copied data in ASCII format from the clipboard into the wells. Data is always inserted starting at position A1. If the data is non numerical the value is set to 0.
In case of an unfinished kinetic with defined interval, a question is displayed asking whether the currently selected data should overwrite the original data or append the data. The time interval is taken from the measurement parameters.
For polarization measurement, the parallel and perpendicular RFU values can be changed.
7. Evaluate Results Wizard

Insert Sample ID list
For detailed information see 6.6 Start Measurement - Insert Sample ID List.

Recalculate with another Method
In the Method menu, click Recalculate with another Method....
A recalculation based on the settings of a newly selected method will be performed.
If an error occurs during recalculation, the procedure will be stopped.
Click this option to open the File Open dialog box. In an additional Remarks field, a text description of the file - if entered - will be displayed (available only in magellan Tracker). The method must be selected by either double-clicking the method file or by selecting the method file and clicking the Open button.
After selecting the method, the Calculating... dialog box is displayed. This dialog box is for display only and contains no elements for editing. It closes after the calculation is finished.

7.4.4 Toolbar Menu: Instrument

Movements
For detailed information see 3.1.1 Movements...

Temperature Control
For detailed information see 3.1.2 Temperature Control...

Optimize Z-Position
For detailed information see 3.2.4 Optimize Z-Position.

Injector Control
For detailed information see 3.1.5 Injector Control...

Start Measurement
Using this option the measurement run can be started again with the currently loaded method and current data will be overwritten if YES is selected in the magellan dialog box.
In case of an incomplete kinetic run, cycles can be added (not available for Infinite Series instruments).
For detailed information see 6.6 Start Measurement with a Predefined or Favorite Method.

7.4.5 Plate Layout Window
The data, which is to be displayed within a well when opening a workspace file, can be set when defining the method (Automated data handling → view results after measurement → More...).
In each single well, three lines are visible; the following data is displayed as default:
1st line: layout
2nd line: replicate info
3rd line: in the third line, according to the data selected, the conventions described in the following chapter are used (cf. 7.4.6 Special Characters).
7.4.6 Special Characters

<table>
<thead>
<tr>
<th>Special Character</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>&quot;None&quot;</td>
<td>No data is displayed.</td>
</tr>
<tr>
<td>&quot;~&quot; tilde</td>
<td>A tilde is appended for the manipulated value of a well (simulated, edited); for example: 0.354~</td>
</tr>
<tr>
<td>&quot;( )&quot; parenthesis</td>
<td>Parenthesis are applied for the masked value of a well; for example: (0.354)</td>
</tr>
<tr>
<td>&quot;!&quot; exclamation mark</td>
<td>An exclamation mark is appended for the eliminated value of a well; for example: !0.354</td>
</tr>
<tr>
<td>&quot;#&quot; hash</td>
<td>Concentration values are marked with a '#' when the calculated concentration lies outside of the range of the standard curve that means the concentration value has been extrapolated. For example: #13.75</td>
</tr>
<tr>
<td>&quot; * &quot; asterisk</td>
<td>An asterisk marks values that have been measured using the Use gain regulation option, which corrects (= lowers) the gain.</td>
</tr>
</tbody>
</table>

Corresponding error message is displayed

- The average value of a well is unusable (for example: lamp low, divide by zero, negative logarithm).
- No color, third line is empty
  - No formula is applied to the well or
  - Replicate well if "average s" or "v calculation" or
  - No cutoff result.
- Data of first replicate is masked or eliminated
  - Average value is derived without using the masked data but the average value is displayed in the well of the first replicate
- "< MIN" The calculated concentration lies beneath the lowest standard.
- "MltPt" Multiple points; a unique concentration cannot be calculated.
- "> MAX" The calculated concentration lies above the highest standard.
- "NoCalc" Input data is not found or calculation error; calculation is not possible

Shortcuts

When viewing transformed data, press CTRL-SHIFT to display the defined formula in the second line as long as the key is pressed.
7. Evaluate Results Wizard

7.4.7 Control Bar: Instrument Data

The user can select mean values or statistics of the replicates:
- Raw data (absorbance, fluorescence intensity or luminescence, single wavelength measurement)
- Measurement data/Reference data (absorbance dual wavelength only)
- RFU – parallel/perpendicular
- Raw data statistics (mean, standard deviation, variation coefficient)
- Raw data as colors
- Single raw data as colors for multiple reads per well measurements
- Kinetic graph for kinetic measurements. The graphs are displayed in the plate layout.
- Spectrum data (for scans)
- Label 1, 2 … (for multilabel measurements)
- Count rate (for FLT measurements)

7.4.8 Control Bar: Reduced Data

- Difference data (Reference data subtracted from Measurement data)
- Polarization, Anisotropy, Total Intensity, Intensity – parallel/perpendicular, Blank Reduction – parallel/perpendicular
- Blank-reduced spectra, smoothed spectra, peak intensity, wavelength peak

7.4.9 Control Bar: Transformed Data

The user can select the required transformation to display the calculated results:
- Transformation[n] results
- Transformation[n] – statistics (mean, standard deviation, variation coefficient)
- Transformation[n] as colors
- Transformation[n] kinetic graph for kinetic measurements and transformations with kinetic results
7.4.10 Control Bar: Kinetic Parameters

The user can select the kinetic evaluation as defined:

- Mean slope OD/RFU/RLU/mP / sec
- Mean slope OD/RFU/RLU/mP / min
- Mean slope OD/RFU/RLU/mP / hr
- Goodness of fit (Mean slope)
- Correlation coeff.
- Max slope OD/RFU/RLU /mP/ sec
- Max slope OD/RFU/RLU /mP/ min
- Max slope OD/RFU/RLU /mP/ hr
- Time max. slope sec
- Time Onset OD/RFU/RLU/mP, Basis OD/RFU/RLU/mP, Time Basis OD/RFU/RLU/mP, Time Basis to Onset OD/RFU/RLU/mP and the same for percentage calculation
- Minimum OD/RFU/RLU/mP, Time minimum OD/RFU/RLU/mP
- Maximum OD/RFU/RLU/mP, Time maximum OD/RFU/RLU/mP
- Area OD/RFU/RLU/mP*sec
- Graph: Enzyme Kinetics
  Click this option to open the Graph: Enzyme Kinetics dialog box
- If kinetic transformations have been defined the results of the kinetic transformations can be selected.

Note
Unusable data (e.g. overflow values) are ignored for kinetic data calculation.
7. Evaluate Results Wizard

**EXPERT’S KNOW HOW**

**DEFINE KINETIC DATA REDUCTION WELL SPECIFICALLY**

Select **Edit kinetic settings**… from the right mouse context menu when a well is selected. The Kinetic Data Reduction dialog is displayed (see chapter 4.3.8 Kinetic: Kinetic Data Reduction for further details).

For the selected well, particular parameters can be defined which can also be copied to other well(s) (select **Copy kinetic settings** from the right mouse context menu, click in the well(s) where the settings have to be copied to and select **Paste kinetic settings**…).

Changing the Kinetic Data Reduction settings in the Method tab will overwrite the well specific definitions.

**Graph: Enzyme Kinetics Dialog**

The **Enzyme Kinetics Graph** dialog box enables the user to display the enzyme kinetics graph.

**Context-Sensitive Menu of Enzyme Kinetics Graph**

By right-clicking on the graph, a context-sensitive menu is displayed.

<table>
<thead>
<tr>
<th>Command</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crosshair cursor</td>
<td>A crosshair cursor is displayed in order to assist in placing the cursor on particular points on the graph.</td>
</tr>
<tr>
<td>Copy to Clipboard</td>
<td>Copies the graph into the clipboard as a bitmap; the bitmap can be transferred to any Windows application by using the paste function.</td>
</tr>
<tr>
<td>Save as bitmap</td>
<td>Saves the graph as a bitmap file.</td>
</tr>
<tr>
<td>Print…</td>
<td>Prints the graph.</td>
</tr>
<tr>
<td>Printer setup...</td>
<td>Displays the <strong>Printer Setup</strong> dialog box, in which the printer settings can be defined.</td>
</tr>
<tr>
<td>Zoom to 100%</td>
<td>Sets the graph display back to 100% if the zoom factor has been changed by selecting rectangular regions of the graph.</td>
</tr>
<tr>
<td>Enzyme Kinetics Data…</td>
<td>Opens the <strong>Enzyme Kinetics Data</strong> dialog box. The <strong>Enzyme Kinetics Data</strong> dialog box displays the result of the defined enzyme kinetics analysis.</td>
</tr>
<tr>
<td>Properties…</td>
<td>Select this command to change the graph display properties. The graph title, the axis styles, the curve style etc. can be customized.</td>
</tr>
<tr>
<td>Help…</td>
<td>Opens the <strong>magellan</strong> help dialog box.</td>
</tr>
</tbody>
</table>
7.4.11 Control Bar: Concentrations

Select single concentration, mean or average single concentration to view the results, calculated according to the standard curve:

- **Single conc. (Unit)**
  Concentration of individual replicate.

- **Mean conc. (Unit)**
  The mean value of replicates is used for calculation of concentration. If replicates with different dilutions are defined, the mean concentration will not be available.

- **Average single conc. (Unit)**
  For each replicate the concentration is calculated. Then the concentrations are averaged.

- **Additional concentrations (single, mean and average concentration) if available.**

- **Graph: Standard Curve**
  Click this option to open the **Graph: Standard Curve** dialog box

- **Intercepts**

- **If concentration transformations have been defined the results of the concentration transformations can be selected.**

- **IC 50, r-IC 50, Graph: dilution series**

**Graph: Standard Curve Dialog**

Open this dialog via the control bar or by clicking **Curve** on the toolbar to display and edit the **Standard Curve**.

This dialog box has its own menu with options to save the standard curve, change the analysis type or compare a number of curves. The graph can be exported as a bitmap, which can then be incorporated into documents of other software applications.

The **Graph: Standard Curve** dialog box contains the following elements:

**File menu**

The **File** menu contains the following commands:

- **New** is selected to create a new standard curve, the X and Y values can be defined in a dialog box.
  Enter measured values (Y Value) and concentration (X Value). If the **Exclude** option is selected, the corresponding point will not be incorporated into the calculation of the graph.
  On completion, click the **OK** button.

- **Open** is selected to open a previously saved standard curve.
  A standard curve, saved in the file format .std can be opened. On execution of this command, the graph will be displayed together with the already displayed standard curves.

- **Close**
  If a number of curves are open, individual curves can be closed using this option.
  The relevant curve must be selected from the available list and closed by clicking the **OK** button.
• **Save/Save as** is selected to save a standard curve for further evaluations. A standard curve can be saved as a `.std` file. The file can be included in the method by switching to the Data tab. If the user has selected Save and the curve had previously been saved, it will simply be stored without displaying any prompts. If this is not the case, the user will be invited to enter a name for the new curve.

• **Export** is selected to export a standard curve as a bitmap file.

• **Print...** is selected to print the standard curve. This command will print the current graph.

• **Printer Setup...**
  Selecting this options displays the Printer Setup dialog box.

• **Exit** is selected to exit the standard curve dialog box.
  If any modifications have been made, for example a change of interpolation process, a new calculation will be performed.

---

**Note**

Standard curves added by New or Open are for comparison only. After closing the Standard Curve dialog box, the curves will be removed.

---

**Edit menu**

The **Edit** menu contains the following commands:

• Select **Copy** to copy the graph to the clipboard as a bitmap, which can be transferred to any Windows application by using the copy/paste function.

• Select **Properties** to modify the analysis type, axes, title, etc.

• Select **Standard Curve** to open the standard curve dialog box. In this dialog box, standard points may be excluded or included. Upon selecting the relevant curve from the available list and clicking the **OK** button, all of the base points will be displayed in the appearing window. Activate or exclude a point by clicking on the **Exclude** option. Only those points that have not been marked as excluded will be used when calculating the standard curve.

  Only base points that have been obtained from raw data, have been manually entered, or have been additionally loaded can be modified. Base points obtained from transformation, for example, can only be excluded.

• **Conc. Range:** The **Concentration Range** dialog box is displayed. Choose between **Display all** and **Display range**. If **Display range** is selected and the **Min.** and **Max.** limits are defined, only concentration values in the specified range are displayed in the plate layout window.

---

**View menu**

The **View** menu contains the following commands:

• Select **Audit trail** to display the audit trail of an external standard curve. This option is only available for magellan Tracker.

• Select **Statistics** to display the statistics of the obtained values.
  In order to assess whether any drift or changes have occurred with the reader over a period of time, it is possible to compare a series of standard curves by means of statistics values.
  If a number of curves are loaded, the average, the standard deviation and the variation coefficient will be calculated for each of them.

• **Intercepts...** opens the **Intercepts** dialog box. The **Intercepts** dialog box displays the result of the defined intercept values.
7. Evaluate Results Wizard

- **Average Standard Curve** displays the standard curve averaged over the performed experimental groups. This option can only be activated if a number of curves are present in the window. An average curve will be generated and displayed using the collective curve data.

**Help menu**

Select **Help** to open the **magellan** help dialog box.

**Click on points**

Clicking on points will mask/unmask them within the standard curve. After a point is masked the line of the graph is automatically adjusted accordingly and the point is represented as a transparent symbol instead of a solid symbol. Hint: This can be undone by pressing **CTRL+Z**.

**X, Y cursor tool-tip**

When the cursor is not moved for a short moment, a tool-tip text appears displaying the X and Y coordinates of the current cursor position.

---

**EXPERT'S KNOW HOW**

If more than *six* standard curves are displayed in the graph, only a small legend on the right side shows the label of the graph. To view the fit functions respectively the curve fit parameters, select **Standard Curve Data** from the context-sensitive menu (see below).

**Context-Sensitive Menu of a Standard Curve Graph**

By right-clicking on the graph, a context-sensitive menu is displayed.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Crosshair cursor</strong></td>
<td>A crosshair cursor is displayed in order to assist in placing the cursor on particular points on the graph.</td>
</tr>
<tr>
<td><strong>Single points</strong></td>
<td>View replicate values instead of mean values.</td>
</tr>
<tr>
<td><strong>Copy to Clipboard</strong></td>
<td>Copies the graph to the clipboard as a bitmap, which can be transferred to any Windows application by using the paste function.</td>
</tr>
<tr>
<td><strong>Save as Bitmap</strong></td>
<td>Saves the graph as a bitmap file.</td>
</tr>
<tr>
<td><strong>Print...</strong></td>
<td>Prints the graph.</td>
</tr>
<tr>
<td><strong>Printer Setup...</strong></td>
<td>Displays the <strong>Printer Setup</strong> dialog box.</td>
</tr>
<tr>
<td><strong>Undo changes</strong></td>
<td>Cancels recent actions.</td>
</tr>
<tr>
<td><strong>Zoom to 100%</strong></td>
<td>Sets the graph display back to 100% if the zoom factor has been changed by selecting rectangular regions of the graph.</td>
</tr>
<tr>
<td><strong>Standard Curve Data</strong></td>
<td>Views the curve fit parameters of the displayed standard curve(s).</td>
</tr>
<tr>
<td><strong>Intercepts...</strong></td>
<td>Opens the <strong>Intercepts</strong> dialog box, which displays the result of the defined intercept values.</td>
</tr>
<tr>
<td><strong>Properties...</strong></td>
<td>Changes the graph display properties. The graph title, the axis styles, the curve style etc. can be customized.</td>
</tr>
<tr>
<td><strong>Help...</strong></td>
<td>Opens the standard <strong>magellan</strong> help dialog box.</td>
</tr>
</tbody>
</table>
7. Evaluate Results Wizard

Graph: Dilution Series Dialog

The Graph: Dilution Series dialog box displays the dilution graph with the specified intercept.

Context-Sensitive Menu of Dilution Series Graph

By right-clicking the graph, a context-sensitive menu is displayed.

<table>
<thead>
<tr>
<th>Command</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crosshair cursor</td>
<td>A crosshair cursor is displayed in order to assist in placing the cursor on special points on the graph.</td>
</tr>
<tr>
<td>Copy to Clipboard</td>
<td>Copies the complete graph into the clipboard as a bitmap; the bitmap can be transferred to any Windows application by using the paste function.</td>
</tr>
<tr>
<td>Save as bitmap</td>
<td>Saves the graph as a bitmap file.</td>
</tr>
<tr>
<td>Print…</td>
<td>Opens the Print dialog box from which the graph can be printed.</td>
</tr>
<tr>
<td>Printer Setup…</td>
<td>Opens the Printer Setup dialog box, in which the printer settings can be defined.</td>
</tr>
<tr>
<td>Zoom to 100%</td>
<td>Sets the graph display back to the 100% if the zoom factor has been changed by selecting rectangular regions of the graph.</td>
</tr>
<tr>
<td>Dilution Series Data</td>
<td>Displays the intercept values and correlation coefficients.</td>
</tr>
<tr>
<td>Properties…</td>
<td>Select this command to change the graph display properties. The graph title, the axis styles, the curve style etc. can be customized.</td>
</tr>
<tr>
<td>Help…</td>
<td>Opens the standard magellan help dialog box.</td>
</tr>
</tbody>
</table>

7.4.12 Control Bar: Qualitative Results

The cutoff definition shows an overview of the currently used cutoff ranges and the used cutoff limits. This overview is particularly useful, if the cutoff limits are defined as formulas.

In the data information window on the bottom of the screen, the list of cutoff definitions is displayed. The list contains the experimental groups, the input data for each experimental group, the cutoff ranges, the cutoff formulas, and the calculated cutoff limits.

The user can view the cutoff results.

- Cutoff definition
  - Ranges and limits of the ranges
- Cutoff results
  - Cutoff result for each well
- Cutoff statistic
  - Statistics of the number of hits for each range
7.4.13 Control Bar: Sample IDs

The user can view the sample ID list data.

- Sample ID 1
- Sample ID 2 if available
- Sample ID 3 if available
- Pipetting status if available

7.4.14 Control Bar: Method Layout

The user can view the method layout.

- Well positions for example: A1, B1
- Strip method names Available if a strip method was used
- Original concentrations Concentrations originally assigned to standards
- Dilution factors Dilution factors previously assigned to samples
- Layout Layout of the identifiers
- Replicate Info Replicate number and maximum number of replicates of the corresponding identifiers.
- Measurement parameters

7.4.15 Control Bar: QC Validation

The validations are the criteria that determine the validity of a test. They are defined in the method.

In the data information window, the list of validations is displayed. The list contains the experimental groups, the input data for each validation group, the validation formulas and their results (TRUE or FALSE) are displayed. If the result is TRUE, it indicates that the validation criteria were met for this specific plate, whereas FALSE represents an invalid result for the whole plate.

7.4.16 Control Bar: Miscellaneous

The error protocol logs all errors that occur during the run of a method. Errors can occur during a measurement or during the calculation. Review the error protocol before using data and results.

- Remarks
- Error protocol
- Constants
- Results
7. Evaluate Results Wizard

7.4.17 Color Scale Dialog Box

If values contained within the analysis plate are presented in different colors, the Color scale dialog box is displayed. The colors allow for a fast overview of the measurement results of the individual wells. The colors, as they are used, depend on the settings defined in the color scheme.

7.4.18 Context-Sensitive Menu of a Well

By right-clicking on a well on the plate layout – when having selected the tab Edit Method –, a context-sensitive menu is displayed, offering the following commands:

<table>
<thead>
<tr>
<th>Command</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Summary</td>
<td>The Summary dialog box is displayed.</td>
</tr>
<tr>
<td>Details</td>
<td>The Multipoint Measurement dialog box is displayed to show the single measurement points per well.</td>
</tr>
<tr>
<td>Edit</td>
<td>The Edit dialog box is displayed (for Raw Data only).</td>
</tr>
<tr>
<td>Edit kinetic settings</td>
<td>Opens the Kinetic parameters dialog box and offers the ability to modify the kinetic settings for the selected well(s).</td>
</tr>
<tr>
<td>Copy kinetic settings</td>
<td>Copies the kinetic settings of the selected well(s) into the clipboard.</td>
</tr>
<tr>
<td>Paste kinetic settings</td>
<td>Assigns the kinetic settings from the clipboard to the selected well(s).</td>
</tr>
<tr>
<td>Graph: Multilabel…</td>
<td>The graph displays data of selected well(s).</td>
</tr>
<tr>
<td>Graph: Kinetics…</td>
<td>The graph of the kinetic measurement is displayed for the selected well(s).</td>
</tr>
<tr>
<td>Graph: Multilabel kinetics…</td>
<td>The graph of the multilabel kinetics measurement is displayed for the selected well(s).</td>
</tr>
<tr>
<td>Graph: Spectra…</td>
<td>The graph of the spectra is displayed for the selected well(s).</td>
</tr>
<tr>
<td>Graph: Dilution Series…</td>
<td>The graph of the dilution series is displayed for the selected well(s).</td>
</tr>
<tr>
<td>Mask/Unmask selection</td>
<td>Toggle switch that masks or unmasks measurement values in the selected well.</td>
</tr>
<tr>
<td>Show/Hide layout</td>
<td>Toggle switch to show or hide the graph or measurement values in the individual wells. The information will not be printed or exported. Where information has been blanked out, the word Hidden will appear on the relevant well. The Show/Hide Layout button opens no window or dialog box; the Show/Hide Layout process is executed instantly as a background process.</td>
</tr>
</tbody>
</table>
EXPERT'S KNOW HOW

Setting different kinetic parameters for different wells is only possible when using the context sensitive menu of a well in the plate layout window or when using the context sensitive menu in the kinetic graph dialog. By editing the kinetic parameters on the Edit method tab, the kinetic parameters are set equal for all wells.

Summary Dialog

The Summary dialog box provides an overview of all defined parameters of a selected well.

Information tree

The information tree gives an overview of all defined well-based parameters of the selected well. The tree is filled according to the available information, e.g. if sample ID list information is available the sample ID, the pipetting status, etc. are displayed. If raw data is available, additional information can be displayed depending on the measurement settings and the connected instruments, for example for kinetic measurements the time points are displayed.

Left, right, up and down buttons

The direction buttons can be used to select another well on the plate while leaving the dialog box open.

Expand All / Shrink All

Click this button to display the information tree expanded to the highest level or to shrink to the first level.

OK

Closes the Summary dialog box.

Details Dialog

The Details dialog box displays the multiple reads per well results of one well.

File menu

Save & Exit is selected to save all changes and close the dialog box.

Edit menu

The Edit menu contains the following commands:

- Click Copy to copy the single values into the clipboard, which then can be transferred to any Windows application by using the paste function.
- Select Recalculate to force the recalculation of the statistic data at the bottom of the dialog. This option is disabled if Automatic Recalculation is set.
- If Automatic Recalculation is set, the statistic data is calculated after every mask/unmask action.

View menu

The View menu contains the following commands:

- Values can be selected to display the reads as values.
- Use this option to view multiple reads per well coarsely and quickly. Graphic can be selected to display the read values as colors. Brightness uses one color with different brightness to display the values. Pseudo Colors uses different colors to display the values. A color bar with a slide control is displayed to change the intensity.

Help menu

Click Help to open the magellan help dialog box.
7. Evaluate Results Wizard

Click on points
Clicking reads will mask/unmask them. After a read is masked, the value is put in brackets. If the color display is enabled, the read is displayed in white with a black circular border.

Edit Dialog

Use this command to edit the measured raw data of a selected well.

Edit raw data text field
A new value for the selected well can be entered. Data is then shown with the symbol ~ (refer to chapter 7.4.6 Special Characters). For polarization measurements only the RFU values can be edited.

Reset button
Resets the well to its original value.

Mask check box
Excludes the value of the well from the calculation. Data is then shown in brackets. Select the Mask check box again to include the value again.

Left, right, up and down buttons
The direction buttons are used to select another well on the plate while leaving the dialog box open.

OK
Closes the Edit dialog box.

Graph: Multilabel Dialog

The Graph: Multilabel dialog box displays the data of the selected wells. The raw data versus well IDs is displayed.

Context-Sensitive Menu of Multilabel Graph

By right-clicking the graph, a context-sensitive menu is displayed.

Crosshair cursor
A crosshair cursor is displayed in order to assist in placing the cursor on particular points on the graph.

Copy to Clipboard
Copies the graph to the clipboard as a bitmap, which can be transferred to any Windows application by using the paste function.

Save as bitmap
Saves the graph as a bitmap file.

Print…
Opens the Print… dialog box from which the graph can be printed.

Printer setup..
Opens the Printer Setup dialog box in which the printer settings can be defined.

Zoom to 100%
Sets the graph display back to 100% if the zoom factor has been changed by selecting rectangular regions of the graph.

Properties…
Select this command to change the graph display properties. The graph title, the axis styles, the curve style etc. can be customized.

Help…
This button opens the magellan help dialog box.
Graph: Kinetics Dialog

The Graph: Kinetics dialog box displays the graphs of kinetic measurements of one or more selected wells. The legend contains the calculated kinetic parameters.

Click on points to mask/unmask them within the kinetic graph. After a point is masked the line of the graph is automatically adjusted accordingly and the point is represented as a transparent symbol instead of a filled colored symbol.

Context-Sensitive Menu of Kinetics Graph

By right-clicking on the graph, a context-sensitive menu is displayed.

<table>
<thead>
<tr>
<th>Menu Item</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crosshair Cursor</td>
<td>A crosshair cursor is displayed in order to assist in placing the cursor on particular points on the graph.</td>
</tr>
<tr>
<td>Copy to Clipboard</td>
<td>Copies the graph to the clipboard as a bitmap, which can be transferred to any Windows application by using the paste function.</td>
</tr>
<tr>
<td>Save as bitmap</td>
<td>Saves the graph as a bitmap.</td>
</tr>
<tr>
<td>Print...</td>
<td>Opens the Print... dialog box from which the graph can be printed.</td>
</tr>
<tr>
<td>Printer Setup...</td>
<td>Opens the Printer Setup dialog box in which the printer settings can be defined.</td>
</tr>
<tr>
<td>Zoom to 100%</td>
<td>Sets the graph display back to 100% if the zoom factor has been changed by selecting rectangular regions of the graph.</td>
</tr>
<tr>
<td>Show Kinetic Reduced Data</td>
<td>Calculated kinetic data (slopes, onsets, minima, maxima) can be visualized in the graph of the kinetic curve(s). Slopes are visualized as curves; onsets, minima and maxima as intercept points. The display can be enabled/disabled via the context menu item Show Kinetic Reduced Data in the kinetic graph dialog. The current display state is stored and will be reused for further displays.</td>
</tr>
</tbody>
</table>
# 7. Evaluate Results Wizard

**Temperature curve**
This option shows/hides a curve visualizing the temperature progression during kinetic measurements (if available).

**Kinetic parameters…**
Opens the Kinetic parameters dialog box and offers the ability to modify the kinetic settings for the selected well(s).

**Kinetic Data…**
Select this menu item to show a table of all calculated kinetic data of the selected well(s).

**Y-Axis scaling**
A range for the Y-axis can be selected.

**Properties…**
Select this button to change the graph display properties. The graph title, the axis styles, the curve style etc. can be customized.

**Help**
Opens the magellan help dialog box.

---

**EXPERT’S KNOW HOW**

Setting different kinetic parameters for different wells is possible either by using the context sensitive menu for a well in the plate layout window or by using the context sensitive menu in the kinetic graph dialog. Editing the kinetic parameters in the Edit method tab, the kinetic parameters are set identical for all wells.
Graph: Spectra Dialog

The **Graph: Spectra** dialog box displays the spectrum of a scan measurement.

**Context-Sensitive Menu of 2D Spectra Graph**

By right-clicking on the graph, a context-sensitive menu is displayed.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crosshair cursor</td>
<td>A crosshair cursor is displayed in order to assist in placing the cursor on particular points on the graph.</td>
</tr>
<tr>
<td>Copy to Clipboard</td>
<td>Copies the graph to the clipboard as a bitmap, which can be transferred to any Windows application by using the paste function.</td>
</tr>
<tr>
<td>Save as Bitmap</td>
<td>Saves the graph as a bitmap.</td>
</tr>
<tr>
<td>Save as JCAMP-DX</td>
<td>Select this command to save the graph as a JCAMP-DX 4.24 file.</td>
</tr>
<tr>
<td>Save as ASCII</td>
<td>Select this button to save the graph as a tab separated ASCII file.</td>
</tr>
<tr>
<td>Print…</td>
<td>Opens the Print… dialog box from which the graph can be printed.</td>
</tr>
<tr>
<td>Printer Setup…</td>
<td>Opens the Printer Setup dialog box in which the printer settings can be defined.</td>
</tr>
<tr>
<td>Zoom to 100%</td>
<td>Sets the graph display back to 100% if the zoom factor has been changed by selecting rectangular regions of the graph.</td>
</tr>
<tr>
<td>Spectra Data Reduction…</td>
<td>Select this command to change the Spectra Data Reduction parameters settings.</td>
</tr>
<tr>
<td>Spectra Reduced Data…</td>
<td>Select this command to display a list of reduced spectra data.</td>
</tr>
<tr>
<td></td>
<td><strong>Note!</strong> This command is enabled only when reduced spectra data of type value is available.</td>
</tr>
<tr>
<td>Data as Table</td>
<td>Opens a dialog box showing the spectrum as table. This allows copying the data to Excel.</td>
</tr>
<tr>
<td>Spectrum masked</td>
<td>The spectrum and the reduced data are displayed as masked. This prevents further calculation of this well. Option is available only when raw spectrum is displayed.</td>
</tr>
<tr>
<td>Show Prim. Spectrum</td>
<td>The selected spectrum and the raw spectrum are displayed together. Option is available only when reduced spectrum is displayed.</td>
</tr>
<tr>
<td>Properties…</td>
<td>Select this command to change the graph display properties. The graph title, the axis styles, the curve style etc. can be customized.</td>
</tr>
<tr>
<td>Help…</td>
<td>Opens the <strong>magellan</strong> help dialog box.</td>
</tr>
</tbody>
</table>
7. Evaluate Results Wizard

Context-Sensitive Menu of 3D Spectra Graph

By right-clicking on the upper dialog frame, a context-sensitive menu is displayed.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Copy to Clipboard</td>
<td>Copies the graph to the clipboard as a bitmap, which can be transferred to any Windows application by using the paste function.</td>
</tr>
<tr>
<td>Data as Table</td>
<td>Opens a dialog box showing the spectrum as table. This allows copying the data to Excel or exporting in ASCII format.</td>
</tr>
<tr>
<td>Save as Bitmap</td>
<td>Saves the graph as a bitmap.</td>
</tr>
</tbody>
</table>

Note
To export scan results, go to the context-sensitive menu by right-clicking on the spectra graph. Select Data as Table in the dialog box and copy the data to Excel or save them as ASCII file.

7.5 Edit Method Tab

Note
Click this tab to change to the currently used method and its settings. Every modification of the method results in a re-calculation of all data when changing back to the Evaluate Results tab. These changes can be saved in the workspace, however, will not be applied to the originally inserted method file itself. See chapter 4 Create/Edit a Method Wizard for further information.

Note
The Edit method tab is displayed only if the currently working user has the appropriate rights (cf. chapter 11.4.4 User Rights (magellan Tracker) and chapter 11.5.4 User Rights (magellan Standard)).
### 7.6 Saving the Evaluated Results

Click **Next** on the **Results** dialog box to reach the **Save in** dialog box of the **Evaluate Results** wizard:

![Evaluate Results Wizard](image)

The **Evaluate Results** dialog box has the following elements:

<table>
<thead>
<tr>
<th><strong>Save in group box</strong></th>
<th><strong>Filename</strong> text field: a default name for the file will appear, but can be changed if desired.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>File remarks</strong> text field: enter remarks as necessary.</td>
<td></td>
</tr>
<tr>
<td><strong>Audit trail comment</strong> text field: enter comments to the audit trail as necessary (only available for <strong>magellan</strong> Tracker).</td>
<td></td>
</tr>
<tr>
<td><strong>Save</strong> button: Saves the workspace file using the name entered in the filename field.</td>
<td></td>
</tr>
<tr>
<td><strong>Export</strong> button: Click this button to open the Export dialog (see chapter 4.3.14 Data Handling: Data Export).</td>
<td></td>
</tr>
<tr>
<td><strong>Audit Trail button:</strong> Use to view the <strong>Audit Trail</strong> of the file (only available for <strong>magellan</strong> Tracker). Refer to chapter 4.4 Saving the Method – Audit trail for further information.</td>
<td></td>
</tr>
<tr>
<td><strong>Signatures button:</strong> Use to view the signatures attached to this file (only available for <strong>magellan</strong> Tracker). Refer to chapter 4.4 Saving the Method for further information.</td>
<td></td>
</tr>
<tr>
<td><strong>Sign this workspace now</strong> Select <strong>Sign this workspace now</strong> to open the <strong>Attach Signature</strong> wizard (only available for <strong>magellan</strong> Tracker).</td>
<td></td>
</tr>
</tbody>
</table>

The **Evaluate Results** wizard is finished by pressing the **FINISH** button. In case of unsaved changes a message box appears asking the user to perform the saving.

An additional **Save** button is available for saving the data without closing the wizard.
8. Attach Signature Wizard

8.1 Introduction

Signatures are essential in assuring trustworthy records. Electronic signatures and electronic records have come to carry the same force and effect as handwritten signatures and records.

Several signatures can be applied to one record and are always included in the printed report. Signed records can only be modified by users with the appropriate rights. It is possible to fully control the use of methods by allowing users to run only signed methods. Only Method and Workspace files can be signed.

Note
This wizard is only available with magellan Tracker.

Click Attach signature to start the Attach signature wizard.

After the welcome dialog box, the Select a File dialog box appears. Select a Method or Workspace file for signing.

Show combo box

In the Show combo box the displayed list of files can be modified according to the selection. Possible selections are:

- All files
- Unsigned files
- Signed files

8.2 Sign a File

Click Next and the Sign window appears:
8. Attach Signature Wizard

In the **Signature** group box, the following options are available:

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Review</td>
<td>Can only be signed by a user with the appropriate rights.</td>
</tr>
<tr>
<td>Approval</td>
<td>Can only be applied by a user with the appropriate rights, if a review signature has already been applied to the record. Review and approval cannot be signed by the same user. No changes may be made to the file between review and approval.</td>
</tr>
<tr>
<td>Custom</td>
<td>Enter a custom signature meaning in the text field.</td>
</tr>
</tbody>
</table>

The default user settings only allow administrators to attach signatures to reviews and approvals and to modify signed files. Comments can be added in the **Comment** text box.

In the **User Name** text field, the user name of the currently logged in user must be entered. In the **Password** text field, the password of the currently logged in user must be entered.

Click **Finish** to confirm the entered information and sign the record.

**Note**

*Depending on the standard operating procedures of the company using this software, this signature may be viewed as legally binding. Therefore it is very important that the users keep their passwords secret.*
9. Batch Processing

9.1 Introduction

magellan supports batch processing with the Tecan Connect stacker and supported Tecan readers.

CAUTION
Do not use microplates with covers, when using the Connect stacker to perform batch processing.

9.2 Microplate Requirements for Batch Processing

The use of plate types is limited according to the specifications of the connected instrument. See the respective Instructions for Use for details.

Any common microplate ranging from 6 to 1536 well formats conforming to the ANSI/SBS standards (ANSI/SBS 1-2004; ANSI/SBS 2-2004, ANSI/SBS 3-2004 and ANSI/SBS 4-2004) may be used with the Connect stacker for batch processing.

Microplates with covers cannot be used with the Connect.

<table>
<thead>
<tr>
<th>PARAMETERS</th>
<th>CHARACTERISTICS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overall plate height</td>
<td>From 7.3 mm to 20 mm</td>
</tr>
<tr>
<td>Footprint</td>
<td>Length = 127.76 mm ± 0.5 mm</td>
</tr>
<tr>
<td></td>
<td>Width = 85.48 mm ± 0.5 mm</td>
</tr>
<tr>
<td>Minimum difference between plate height</td>
<td>≥ 6 mm</td>
</tr>
<tr>
<td>and skirt height</td>
<td></td>
</tr>
</tbody>
</table>

9.3 Hardware Connections

See chapter 3. Unpacking and Installation in the Instructions for Use for Connect for complete details about the hardware connections for the reader, stacker and computer.
9.4 Working with Tecan Readers

For **Infinite Series Readers**, see 9.5 Working with Infinite Series Readers.

### 9.4.1 Software Connections

If you want to use the **Connect** stacker with Tecan readers, select the **Stacker port** in the **Setup Port** dialog box to which the **Connect** stacker is connected. Or choose **Find any** to let the software search for a **Connect** stacker and click **OK** (refer to chapter 2.5.4 Connecting a Stacker).

![Setup Port](image)

### 9.4.2 Prepare for Batch Processing

**Measurement Parameter - Read Barcode**

In the **Create/Edit a Method** wizard (refer to chapter 4 Create/Edit a Method Wizard), tabs of the **Measurement Parameter** dialog box might contain different parameter settings, depending on the type of instrument connected.

![Measurement Parameter](image)
Note
The option Read barcode can be selected if either the reader or the Connect stacker has a barcode reader module.

Measurement Parameter - Stacker Tab

The Stacker tab of Measurement Parameter window contains the following elements:

Plates group:
- Don’t read topmost plate
  Select Don’t read topmost plate if this plate has been used as a cover. The topmost plate will not be processed and will be moved to the output stack.
- Restack after last plate:
  Select Restack after last plate to return all plates to their original order in the input stack after all of the plates have been processed.

Optimal gain group:
- Measure each plate
  Measure the gain on each plate.
- Use gain calculated from 1st plate
  Measure the gain only on the first plate and use this gain for all following plates.
9.4.3 **Start Batch Processing**

To run a measurement using the Tecan Connect stacker, click **Use stacker** in the Start Measurement dialog box of Start Measurement wizard (refer to chapter 6.6 Start Measurement) or Create/Edit a Method wizard (refer to chapter 4 Create/Edit a Method Wizard) and click **Start** to start a stacker run.

9.4.4 **Control Stacker Movements**

To control the movements of the Connect stacker, click the **Miscellaneous** icon in the Wizard List dialog box and select **Instrument control**. Click the **Movements...** button in the **Instrument control** dialog box. Depending on the type of instrument connected, **Movements...** dialog box may vary.

If a Connect stacker is connected, the **Movements** dialog box additionally contains a **Stacker** group:

- **Park position** button: The stacker moves the gripper into parking position.
- **Restack now** button: The stacker moves all plates from the output stack into the input stack.
9.5 Working with Infinite Series Readers

9.5.1 Connecting Infinite Series Readers

If an Infinite series reader is selected in the **Port Setup** dialog box, the following dialog box appears when **OK** is clicked:

![Infinite Series Reader Connection Dialog Box]

In the **Connect to Instrument** dialog box select the instrument name.
In the **Additionally connect to** field, select **Connect**, if a **Connect** stacker is connected for batch processing.
Click **OK** to confirm selections.

**Simulated Instrument**

To simulate the use of a **Connect** with an Infinite Series reader, select the **Show simulated instruments** check box and then select the instrument under **Connect to**.
9. Batch Processing

After selecting the simulated instrument, a drop-down list will appear offering several options, depending on the instrument selected above (see screenshot above).

For the Infinite 200, for example, these options are:

- Filter: F200 normal or F200 enhanced or F200 FP Option
- Monochromator: M200 normal or M200 enhanced

In the Additionally connect to field, select ConnectSimulator, to simulate the Connect stacker for batch processing.

Click OK to confirm selections.

For a more detailed description on defining parameters for the respective instrument, please refer to the instructions for use for the connected or simulated instrument.

9.5.2 Prepare for Batch Processing for Infinite Series Readers

Read Barcode

The Read Barcode checkbox appears in the Plate program element of the magellan software, if the Infinite Series reader has a barcode reader or if a Connect stacker is connected and has a barcode reader.

For more information about the Barcode Scanner option for the Infinite Series reader, refer to the Instructions for Use of the corresponding instrument.
9. Batch Processing

9.5.3 Start Batch Processing for Infinite Series Readers

To run a measurement using the Tecan Connect Stacker, click **Use stacker** in the **Start Measurement** dialog box of **Start Measurement** wizard (refer to chapter 6.6 Start Measurement) or **Create/Edit a Method** wizard (refer to chapter 4 Create/Edit a Method Wizard).

Click **Start** and the **Stacker Operations** dialog box appears.

Note
The defined script will be performed on each of the available plates in the input stack. It is not possible to run the entire stack more than once per script.
9. Batch Processing

In the **Stacker Operations** dialog box the **Connect** options have to be set.

- Select **Skip topmost plate** if this plate has been used as a cover. The topmost plate will not be processed and will be moved to the output stack.
- Select **Restack after last plate** to return all plates to their original order in the input stack after all of the plates have been processed.

Click **OK** to confirm the settings and start batch processing of all microplates in the input stack.

After finishing a batch run the **Evaluate Results Wizard** opens with the first measured workspace (.wsp) opened. If **Read barcode** has been selected in the **Plate** program element, the workspaces will be named according to the corresponding barcode number, otherwise they will be named as defined in the **Workspace Name** dialog box (see chapter 4.3.16 Data Handling: Automated Data Handling / More – Workspace Name).

**Note**

*Automatically loaded sample ID lists should contain only IDs for samples and must not contain IDs for non-samples (controls, standards etc.).*

**CAUTION**

If the reader is operated while positioned within the **Connect** but without using the **Connect**, make sure that the gripper is in the park position and does not hinder any of the reader's moveable parts (e.g. plate carrier, cuvette carrier, filter slide, etc.).
9.5.4 **Control Stacker Movements for Infinite Series Readers**

To control the movements of the Connect stacker, click the Miscellaneous icon in the Wizard List dialog box and select Instrument control. If a Connect stacker is connected, the Movements... button in the Connect group box is now available.

Click the Movements... button in the Connect group box to open the Stacker Movements dialog box.

- Select **Restack** to return the processed plates from the output stack to the input stack in their original order. After Restack is selected, a dialog box appears in which the plate type must be selected and confirmed with OK, before the restacking procedure is performed.
- Select **Park** to move the gripper into the park position.
- Select **Teaching** to start the Positioning wizard. For details, see the Instructions for Use for Connect, chapter 5. Positioning Wizard in i-control and magellan.
10. Gas Control Module (GCM) Enhanced Support

10.1 Introduction

The magellan software supports data logging and data display for the GCM Enhanced, which is an optional module for Infinite F200 PRO and Infinite M200 PRO devices.

Note
Data logging and data display do not work in conjunction with stacker applications.

10.2 Prerequisites

In order to enable communication between the GCM Enhanced and magellan, you have to install the Virtual Com Port (VCP) driver from the magellan data carrier (CD-ROM).

Furthermore, you have to connect the GCM Enhanced to your PC via the USB cable enclosed with the module.

In order to verify that the GCM Enhanced is connected properly, navigate to Start > Settings > Control Panel > System, select the Hardware tab and click on the Device Manager button. Within the Device Manager, navigate to Ports (COM & LPT) and check for an entry similar to “Silicon Labs CP210x USB to UART Bridge”.

![Device Manager](image)
10. Gas Control Module (GCM) Enhanced Support

10.3 Connecting to GCM Enhanced

Once the VPC driver is installed and the GCM Enhanced is connected to the PC, the GCM Enhanced appears in the Additionally connect to: section of the Connect to: dialog box:

![Connect to Instrument dialog box](image)

10.4 Data Logging

magellan starts logging data provided by the GCM Enhanced when a measurement is started (and from then on every 30 seconds), until the measurement is finished.

The data is written into a log file called `GCM-log_YYYY-MM-DDThh-mm-ss.txt`. YYYY-MM-DDThh-mm-ss stands for date and time of log file creation.

Log file name example: `GCM-log_2012-01-01T12-34-56.txt`

magellan creates a separate log file for each measurement.

The location of the log file depends on the operating system:

- On Windows XP computers, this log file is stored in `C:\Documents and Settings\All Users\Documents\Tecan\Logfiles\Magellan\Version\Instrument Serial Number`
- On Windows Vista and Windows 7 computers, this log file is stored in `C:\Users\Public\Documents\Tecan\Logfiles\Magellan\Version\Instrument Serial Number`
10. Gas Control Module (GCM) Enhanced Support

A log file line contains the following information, separated by a semicolon:

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Date/Time</td>
<td>Date and time when log entry was created</td>
</tr>
<tr>
<td>Version</td>
<td>Version of the GCM Enhanced</td>
</tr>
<tr>
<td>Mode</td>
<td>This entry can have one of the following values: CO2, O2, DUAL, MANUAL, SETTINGS or STANDBY. SETTINGS indicates that you can select the alias (device name) of the GCM Enhanced and adjust the altitude. STANDBY indicates that no mode is selected or activated. For detailed information about the other modes, refer to Infinite200 PRO manual.</td>
</tr>
<tr>
<td>Alias</td>
<td>Alias name of the device. Possible values: A, B, C or D.</td>
</tr>
<tr>
<td>Conc. O2</td>
<td>Current O2 concentration in %</td>
</tr>
<tr>
<td>Conc. CO2</td>
<td>Current CO2 concentration in %</td>
</tr>
<tr>
<td>Target Conc. O2</td>
<td>Target O2 concentration in %</td>
</tr>
<tr>
<td>Target Conc. CO2</td>
<td>Target CO2 concentration in %</td>
</tr>
<tr>
<td>Altitude</td>
<td>Altitude in m</td>
</tr>
<tr>
<td>Status O2</td>
<td>Possible values for this entry are ValidData or InvalidData. ValidData indicates that the O2 sensor is working InvalidData indicates that the O2 sensor might be missing, unplugged or broken.</td>
</tr>
<tr>
<td>Status CO2</td>
<td>Possible values for this entry are ValidData or InvalidData. ValidData indicates that the CO2 sensor is working InvalidData indicates that the CO2 sensor might be missing, unplugged or broken.</td>
</tr>
<tr>
<td>Status Alarm</td>
<td>Possible values for this entry are Normal or Alarm. Normal indicates that the target concentration is normal or the selected mode does not require a target concentration (e.g. mode Manual) Alarm indicates that the target concentration has not been reached within 20 minutes or deviates for more than 10 minutes during operation.</td>
</tr>
</tbody>
</table>

Log file line example:
2012-01-01 12:34:56;TECAN GCM enh. V1.01;MANUAL;A;20.5;0.1;15;0.5;400;ValidData;ValidData;Normal
10.4.1 Importing Logged Data Into Microsoft Excel

The content of the GCM Enhanced log file can be imported into Microsoft Excel for further evaluation.

In order to make sure that the numeric data imported into Microsoft Excel maintains the correct number format, it may be necessary to define the following in Microsoft Excel:

Custom System Separators
- Define “.” (period) as the Decimal separator.
- Define any other character which is not required as separator, e.g. “,” (comma) as the Thousands separator.

Delimiters
Import the log file (.txt file) to Excel as a Delimited file type.
Select “;” (semicolon) as the Delimiter. The delimiter is the character used to separate fields.

Data Format
Select General as the Column data format. General converts numeric values to numbers, date values to dates, and all remaining values to text.

10.5 GCM Enhanced Data Displayed in Status Bar

When the GCM Enhanced is connected via the magellan software, some of the data is displayed in the magellan status bar at the bottom of the application window. This data is updated periodically every 30 seconds.

Depending on the on the GCM Enhanced configuration and the selected mode, magellan displays either the current CO2 and O2 concentrations or the current CO2 concentration only.

For further information about GCM Enhanced configurations, refer to Infinite200 PRO manual.

If GCM Enhanced is in standby, GCM Standby is displayed.

If connection to the GCM Enhanced is lost (e.g. because the module has been turned off or unplugged while magellan is running), GCM Module Error is displayed.

To remove the error, plug in or turn on the module, Disconnect the Infinite 200 PRO reader and reconnect reader and GCM Enhanced with the magellan software via Connect.
10.6 GCM Enhanced Data Displayed in Measurement Status Dialog

When the GCM Enhanced is connected via the magellan software, the current CO2 and O2 concentrations are displayed in the Environment group box during a measurement.

Depending on the GCM Enhanced configuration and the selected mode, magellan displays the current CO2 and O2 concentrations or the current CO2 concentrations or O2 concentrations only.

During endpoint measurements the Environment group box is displayed in the top right edge of the application window.

During kinetic measurements the Environment group box is displayed below the Time group box on the right side of the microplate, below the kinetic graph.

10.7 Precautions before Starting a Measurement

Heating must switched on before using the GCM to maintain a stable gas atmosphere.

The plate carrier compartment should be closed until the target concentration is reached.

When reconfiguring the Mode setting of the GCM Enhanced, wait at least 30 seconds before starting the measurement, so that magellan can update the GCM Enhanced data properly.
11. Miscellaneous Icon

Click the miscellaneous icon in the wizard window and select between the following actions/definitions:

11.1 Instrument Control

See chapter 3 Instrument Control & Settings.

11.2 File Handling

11.2.1 Archive Files

The Archive Files group box gives an overview and complete control of file backup. It lists all the files (workspaces, methods, sample ID lists or temporary files) saved by magellan.
The files for backup have to be selected from the File Name list. Click Archive to move all selected files to the specified backup directory in the appropriate subfolders.

When files have the attribute read-only, a warning box appears before the files are deleted.

The Archive Files group box contains the following elements:

**Archive path** The Archive path contains the path where the files shall be stored. Click the browse button to change the path.

**File Name list** Lists all files saved by magellan filtered by the options entered via the Filter button. It consists of three columns:

- **File Name** The file names of the workspaces, methods or sample ID lists saved by magellan.
- **Date** The date and time a file was saved last.
- **Remarks** The remarks entered when saving the file.

**Archive button** Click Archive to move all files selected in the File Name list to the backup directory (cut-and-paste function).

**Select All button** Click Select All to select all files displayed in the File Name list.

**Refresh button** Click the Refresh button to cancel the current Filter option and to refresh the file list.
11. Miscellaneous Icon

Filter button

This button is used to display only specific files, or files, that contain a certain string in their file names.

Click the button **Filter** and the Apply Filter dialog box appears:

Enter the filter characters for the filter:

- A question mark `?` can be applied as a wildcard for one single character.
- An asterisk `*` can be applied as a wildcard for no or many characters.

11.2.2 Automatic Archiving

The automatic archiving function copies workspace, method and sample files, which are either automatically or manually saved by the user, to a user-defined directory.

The **Automatic Archiving** option is only available in the magellan Tracker version and can only be enabled by users with **Modify general options** rights.
11. Miscellaneous Icon

<table>
<thead>
<tr>
<th>Automatic archiving group box</th>
<th>Enable archiving check box: select this check box to activate automatic archiving.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Click the file browser button (&quot;...&quot;) to browse for the archiving directory.</td>
</tr>
</tbody>
</table>

**Note**

It may happen that a selected archive directory becomes invalid, e.g. a network drive. In such a case magellan will not explicitly warn the user but will make an entry in the System Audit Trail's log file.

11.2.3 Import Raw Data

In the File handling dialog box, click Import raw data…. to import measurement data in ASCII (.asc) format. A number of ASCII options make sure that the corresponding files can be opened and that the data is converted correctly. By using the ASCII File Import function the user can process ASCII data files in magellan which already contain measurement data and additional transformations. Some data format definitions must be performed in advance to guarantee correct data retrieval. For example, the individual data must be separated from the data list by specified separators.

Further options which must be specified are: Plate format, number of measurements, measurement interval, and type of data order, orientation and physical unit of the values.

Data import fails if the ASCII file does not contain as many entries as specified by the plate format.

Once the required options have been defined, select the desired file from the files selection field. Finally the file appears and the data is retrieved by clicking the Open button.

The Open dialog box is a standard Windows ‘open file’ dialog box with file navigation elements, a text field for entering a file name and a drop down list for the selection of a file type (*.asc).

Additionally, the Open dialog box contains the following elements for setting ASCII-Options:

- **Format** option button
  - The Format option button defines the expected data format:
    - Table (well data in rows) option button
    - Table (well data in columns) option button
    - Matrix (nested) option button
    - Matrix (separated) option button

- **Separator** group box
  - The Separator defines which character is used for the separation of the data fields of the list or matrix:
    - If Tabulator is selected, the separator will be a tabulator.
    - If Tabulator is not selected, the separator will be any character entered in the Other text-field.

- **Orientation** option button
  - The Orientation option button allows a definition of the data in either horizontal or vertical direction.
### Measurement Parameters

<table>
<thead>
<tr>
<th>Info</th>
<th>The box shows the following parameters:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>• Plate format</td>
</tr>
<tr>
<td></td>
<td>• Data unit</td>
</tr>
<tr>
<td></td>
<td>• Number of measurements</td>
</tr>
<tr>
<td></td>
<td>• Measurement interval</td>
</tr>
</tbody>
</table>

| Measurement Parameters button | Select the measurement type, the plate type, kinetic cycle number and interval. |

### 11.2.4 Convert To

**Note**

This option is available only when the current user has local administrator rights for the Windows system.

In the File handling dialog box, click **Convert To…** to open the Convert Documents dialog box.

The Convert Documents – Convert to dialog box enables the user to convert magellan files from the current magellan version to files for previous magellan versions.

**Important**

After conversion, methods must be validated, because the content of the converted files may differ slightly from the original file (e.g. contents of printed report, etc.)

The Convert Documents dialog box contains the following elements:

- **Document type group box**
  - Select the document type for conversion:
    - Sample ID list
    - Method
    - Workspace

- **Select all button**
  - Click this button to select all displayed files in the file list

- **Filename list**
  - All files available for conversion are displayed. Click a file to select it for conversion. By holding the Shift-key, multiple file selections are possible.

- **Source path edit field**
  - The Source path edit field contains the path where the files to be converted are stored. Click the … button on the right of the text field to change the path.

- **Destination path edit field**
  - The Destination path edit field contains the path where the converted files are stored. Click the … button on the right of the text field to change the path.

- **Convert document(s) button**
  - Click this button to start conversion.

- **Version drop down menu**
  - Select from the drop down menu the version of magellan the files shall be converted to.

- **Progress bar**
  - This bar shows the progress of the conversion.
WARNING
THE FILES MAY CONTAIN FEATURES THAT ARE NOT COMPATIBLE WITH THE SELECTED FORMAT. THESE FEATURES ARE THEN UNAVAILABLE.

11.2.5 Convert From

In the File handling dialog box, click Convert From… to open the Convert Documents dialog box.

The Convert Documents – Convert from dialog box allows to convert magellan files from previous versions to the current file format. Standard magellan files can also be converted to magellan Tracker files.

**Note**
Files for conversion are displayed only if magellan is connected with the instrument (measurement or demo mode) for which the files were generated.

**Note**
Files from magellan versions earlier than 4.0 must be converted in order to be used.

**Note**
Files from magellan Standard must be converted in order to be used with magellan Tracker.

**Important**
After conversion, methods must be validated, because the content of the converted files may differ slightly from the original file (e.g. contents of printed report, etc.)

The Convert Documents dialog box contains two tabs.
The magellan 2.x/ magellan 3.x tab contains the following elements:

**Document type**
- Select the document type for conversion:
  - Sample ID list
  - Method
  - Workspace
  - Test
  - Plate definition

**Customize new method specific options**
- Several global options – in magellan versions lower than V4.0 – are now method specific. In order to set this options correctly in the method and workspace files, use one of the following buttons:
  - Export to ASCII file… button
  - Export Options… button
  - Export to Excel… button
  - Workspace name.. button

**Select all**
- Click this button to select all displayed files in the file list
11. Miscellaneous Icon

**File name list**
All files available for conversion are displayed. Click a file to select it for conversion. By holding the Shift-key, multiple file selections are possible.

**Note!** Only workspaces and methods created with the currently connected instrument are displayed.

**Source path edit field**
The **Source path** edit field contains the path where the files to be converted are stored. Click the ... button on the right of the text field to change the path.

**Destination path edit field**
The **Destination path** edit field contains the path where the converted files are stored. Click the ... button on the right of the text field to change the path.

**magellan** Tracker: this path cannot be modified.

**Convert document(s) button**
Click this button to start conversion.

**Progress bar**
This bar shows the progress of the conversion.

---

**WARNING**

TESTS DO NOT CONTAIN MEASUREMENT PARAMETERS. WHEN CONVERTING A TEST TO A METHOD THE MEASUREMENT PARAMETERS HAVE TO BE DEFINED. MAKE SURE THE MEASUREMENT PARAMETERS FIT TO THE SELECTED TEST.

The **magellan** 4.x / 5.x tab—available only with **magellan** Tracker—contains the same window elements as the previously described tab, except that the following options are not necessary:

- Document type test: Tests are not available with **magellan** 4.x / 5.x.

Customize new method specific options: These options are already customized in **magellan** 4.x / 5.x files.

### 11.2.6 Save LogFiles

All log files can be saved as zip archive by clicking the **Save Logfiles...** button. The zip archive can now be named and saved in a defined directory. In case of any measurement or status error during performance of **magellan**, this archive contains well data, status (e.g. overflow, lamp low) or calculation error(s) and can be easily sent to Expertline-at@tecan.com for support request.
11.3 Options

Several selections and adjustments which are valid throughout the complete menus and wizards of magellan are defined in the Options dialog box. If magellan user administration is activated, several settings are user dependent. The Options dialog box is divided into individual tabs:

- Paths tab
- Copy tab
- Plate View tab
- Miscellaneous tab

The requested options have to be entered in the corresponding tabs. Click OK to save the changes and to close the dialog box.

User dependent options (every user can modify the options for his convenience) are:

- Default paths (only in magellan Standard)
- Copy to clipboard and Excel options
- Plate view
- Skip welcome page
- Start with wizard list or favorites page
- Move plate in after startup

The following user dependent options can not be set in the options dialog box:

- Selected Printer
- Printout orientation.
- Printout paper size and source.
- Printout font and color.
- Default identifier types.
- Jumping direction for sample ID input.
- Import raw data settings.
- Default for Export options, Export to ASCII file, Export to Excel, and Workspace Name.
- Use stacker
- Graph dialog box size

The following options can only be modified by a user with the appropriate right. These options are then valid for all users:

- Language
- Demo mode allowed
- Suppress 'not monotone' warning for standard curve
- Favorites
- Accepted HUIDs

**Note**

*In magellan Standard the data path can be set by the user, in magellan Tracker the data path is a general setting, valid for all users.*
11. Miscellaneous Icon

11.3.1 Default Data Paths

This tab defines the default paths the different file types used in magellan are to be saved in. These predefined paths are set upon the software installation of magellan and can be changed in the corresponding data fields of the Paths tab.

The Paths tab contains the following elements:

<table>
<thead>
<tr>
<th>Default paths text fields</th>
<th>A text field for each of the following file types is displayed, containing the corresponding default paths:</th>
</tr>
</thead>
<tbody>
<tr>
<td>Workspace</td>
<td>• Workspace</td>
</tr>
<tr>
<td>Method</td>
<td>• Method</td>
</tr>
<tr>
<td>Sample ID list</td>
<td>• Sample ID list</td>
</tr>
<tr>
<td>Export</td>
<td>• Export: for measurement data exported to ASCII files.</td>
</tr>
<tr>
<td>Standard curve</td>
<td>• Standard curve: The path for standard curves is always the same as the path for workspaces.</td>
</tr>
<tr>
<td>Bitmaps</td>
<td>• Bitmaps: for bitmaps created from graph dialog boxes.</td>
</tr>
</tbody>
</table>

| buttons                   | Click the … buttons next to the text fields, to open a standard Window dialog box, where a different path for the generated files can be selected. |

| Change default data path button | Only available in magellan Tracker. Click this button to change the default data path for saving workspaces, methods, sample ID lists and standard curves files. magellan Administrator and System Administrator rights are necessary to modify default data paths. |
11. Miscellaneous Icon

WARNING
THE SOFTWARE MAY NOT BE ABLE TO ASSIGN THE CORRECT FILE SYSTEM RIGHTS FOR A USER-DEFINED DEFAULT DATA_PATH!
THIS MUST BE DONE MANUALLY BY THE SYSTEM ADMINISTRATOR. DELETING OR MODIFYING FILES IN THE DEFAULT DIRECTORIES MUST NOT BE ALLOWED.

Note
In magellan Tracker, only the Export and the Bitmap paths can be modified.

11.3.2 Copy/Export Options

In a workspace document the Edit – Copy and Edit – Copy to Excel commands allow the user to export measurement data to the clipboard or directly into an Excel worksheet. In the Copy tab is specified in which way the content of a plate is handled in case of a data transfer.

The Copy tab contains the following elements:

Matrix format group box

The user also has the following opportunities to define how he would like the data to be displayed.

- **Rows in horizontal order** option button
  Rows of data from the microplate will be copied in horizontal order.

- **Rows in vertical order** option button
  Rows of data from the microplate will be copied in vertical order. This results in a transposed matrix.

- If the **Add row/column labels** check box is selected, the row and column information like in XFluor is added when copying data.
### 11. Miscellaneous Icon

<table>
<thead>
<tr>
<th>Copy to clipboard options group box</th>
<th>A format for the decimal point of numbers must be selected for the transferred data:</th>
</tr>
</thead>
</table>
|                                     | • **Point (x.xxx)** option button  
|                                     | Example: 7.893  
|                                     | • **Comma (x,xxx)** option button  
|                                     | Example: 7,893 |

<table>
<thead>
<tr>
<th>Copy to Excel options group box</th>
<th>The option buttons enable to define where to position the transferred data within Excel.</th>
</tr>
</thead>
</table>
|                                  | • **New workbook** option button  
|                                  | Transferred data will be stored in the first worksheet of a new workbook. A new file will always be created, no matter if Excel is started or not. |
|                                  | • **New worksheet** option button  
|                                  | Transferred data will be put into a new worksheet within an open, active Excel workbook.  
|                                  | If Excel is not open when selecting this option, it will be opened and a new workbook will be created, the requested data is inserted into the first worksheet. |
|                                  | • **Insert into worksheet at cell** option button and cell coordinates text field  
|                                  | Transferred data will be placed into the cell indicated (default is cell A1) of an open, active Excel worksheet.  
|                                  | If Excel is not open when selecting this option, it will be opened and a new workbook will be created, the requested data is inserted into the first worksheet. |
|                                  | • **Append to current worksheet** option button  
|                                  | This option will simply append the data to the current worksheet.  
|                                  | If Excel is not open when selecting this option, it will be opened and a new workbook will be created, the requested data is inserted into the first worksheet. |
11. Miscellaneous Icon

11.3.3 Plate View Settings

In the Plate View tab the look of the plate view can be customized. The colors can be changed for the different regions by selecting the desired color from a drop down list. The selection mode for marking wells can also be defined here. The font size can be adjusted as well.

![Plate View Settings](image)

The Plate View tab contains the following elements:

<table>
<thead>
<tr>
<th>Element</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Background button</td>
<td>The background color of the Plate view window can be selected.</td>
</tr>
<tr>
<td>Plate bottom button</td>
<td>The frame color of the displayed plate can be selected.</td>
</tr>
<tr>
<td>Plate surface button</td>
<td>The surface color of the displayed plate can be selected.</td>
</tr>
<tr>
<td>Font height drop down list</td>
<td>The font height for the text within the wells can be selected:</td>
</tr>
<tr>
<td></td>
<td>• Small</td>
</tr>
<tr>
<td></td>
<td>• Medium</td>
</tr>
<tr>
<td></td>
<td>• Large</td>
</tr>
<tr>
<td>Light shadow button</td>
<td>The light-shadow color of the plate frame can be selected.</td>
</tr>
<tr>
<td>Dark shadow button</td>
<td>The dark-shadow color of the plate frame can be selected.</td>
</tr>
<tr>
<td>Selection mode option buttons</td>
<td>Here the selection mode for marking wells with the mouse is established:</td>
</tr>
<tr>
<td></td>
<td>• Union allows selecting wells only when the mouse has marked the complete area of the well.</td>
</tr>
<tr>
<td></td>
<td>• Intersect allows for the selection of wells when only a part of the well has been marked with the mouse.</td>
</tr>
</tbody>
</table>
11. Miscellaneous Icon

11.3.4 Miscellaneous

The **Miscellaneous** tab contains the following elements:

**Wizard group box**

When selecting the **Skip welcome page** check box, the welcome page of the wizard is not displayed when opening a wizard. The wizard starts at the second of its windows.

**Start at startup group box**

Selecting the **Favorites dialog box** check box defines that instead of the **Wizard List** the **Favorite dialog** will show up after the start of the **magellan** software.

**Group box**

- **Demo mode allowed** check box: Select this option in order to allow connecting to a simulated instrument. This option is helpful if already measured data shall be evaluated. Then, no instrument is needed.
- **Move plate in after startup** check box: If the checkbox is selected and an instrument is connected, the plate carrier is moved in automatically after startup.
- **Suppress ‘not monotone’ warning** check box: Select this option to suppress the ‘not monotone’ warning. This option is useful if in a standard curve several points are taken in a flat area and it is very likely that monotony is not given (i.e. the flat part of a logarithmic curve or other curve where a limit is approached). **Note!** This option is disabled in **magellan** Tracker.

**Set next counter value group box**

Two options are offered:

- **Total counter** spin control enables to set the counter to any value. Displays the number which will appear in the name of the next workspace file created.
- **Counter with daily reset** spin control enables to set the counter to any value. Displays the current number of workspace files that have been created during the course of one day.
### 11. Miscellaneous Icon

<table>
<thead>
<tr>
<th><strong>Language group box</strong></th>
<th>The text field displays the applied language. A different language can be selected from the drop down list. See <strong>Set</strong> below.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Set button</strong></td>
<td>Select a different language and click the <strong>Set</strong> button to restart the program with the selected language.</td>
</tr>
<tr>
<td><strong>Change password button</strong></td>
<td>Click this button to open a dialog box, where the user can change his password (only available with <strong>magellan</strong> User Administration activated).</td>
</tr>
<tr>
<td><strong>Add HUIDs button</strong></td>
<td>A list of additional HUIDs can be defined which allows the user to open files created on another computer (only available in <strong>magellan</strong> Tracker).</td>
</tr>
<tr>
<td><strong>Options and default settings audit trail… button</strong></td>
<td>Click this button to show the audit trail for options and default settings. The audit trail can be saved to an ASCII file (only available in <strong>magellan</strong> Tracker). Click <strong>Save as file</strong> to save this information as a .log or .txt file. The text can also be copied to a word processing program for printing.</td>
</tr>
</tbody>
</table>
11.4 User Administration (magellan Tracker)

There are three types of administrators mentioned in this publication:

**System Administrator** is responsible for any changes made to the computer's operating system.

The **Administrator** is responsible for user rights in the magellan software.

**magellan Administrator** has access to all features of the magellan software, but cannot change user rights.

magellan offers password protection to prevent misuse of the software and to restrict access to parts of the software based on user rights.

**Caution**

To prevent the misuse of user rights and falsification of data, it is recommended that the User Administrator does not have magellan rights (i.e. does not belong to a magellan User Group).

Ideally, the User Administrator should belong to the IT department.

Select **miscellaneous** in the wizard window and click the **User administration** icon. The **Manage Users and Role** dialog box is displayed:

Users and roles can be added and modified, user rights can be defined. Options for login, password, and email can be customized.

The **Manage Users and Role** dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Roles</th>
<th>The Roles list shows all existing user groups (user levels).</th>
</tr>
</thead>
<tbody>
<tr>
<td>Add Role</td>
<td>A new group with corresponding rights can be created.</td>
</tr>
<tr>
<td>Modify Role</td>
<td>Rights of an existing group can be modified.</td>
</tr>
<tr>
<td>Users</td>
<td>The user list shows all existing users and which group they are member of.</td>
</tr>
<tr>
<td>Add User</td>
<td>A new user can be created.</td>
</tr>
<tr>
<td>Modify User</td>
<td>Full name, user level (group) or password of an existing user can be changed.</td>
</tr>
</tbody>
</table>
11. Miscellaneous Icon

<table>
<thead>
<tr>
<th>Lock User</th>
<th>A user account can be enabled/ disabled. The button is visible only if a username is selected.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Audit Trail</td>
<td>All modifications of the user administration database (e.g. creation of groups/users, change of rights, change of options, ...) are recorded in the user management audit trail written by the user management server.</td>
</tr>
<tr>
<td>Options</td>
<td>General login, password or email options can be modified</td>
</tr>
<tr>
<td>Summary</td>
<td>A detailed description of all existing users and user groups as plain text</td>
</tr>
</tbody>
</table>

11.4.1 Add/Modify User (magellan Tracker)

Click Add User in the Manage Users and Roles dialog box and the Create User dialog box appears:

![Create User Dialog Box](image)

The Create User dialog box contains the following elements:

<table>
<thead>
<tr>
<th>User Name</th>
<th>A unique user name has to be entered when a new user is created. This name cannot be modified afterwards.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Full Name</td>
<td>Enter the full name of the user. This can be changed later.</td>
</tr>
<tr>
<td>Password</td>
<td>Enter the initial password. The password must be changed at the next login.</td>
</tr>
</tbody>
</table>
Click OK and the Modify User dialog box appears:

The Modify User dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Element</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Full Name</td>
<td>Enter the full name of the user.</td>
</tr>
<tr>
<td>Roles</td>
<td>Select from one of the existing user groups. The rights associated with that group are assigned to the user.</td>
</tr>
<tr>
<td>Change picture</td>
<td>User’s picture can be added or changed.</td>
</tr>
<tr>
<td>Delete picture</td>
<td>Delete the user’s picture.</td>
</tr>
<tr>
<td>Change Password</td>
<td>A new user’s password can be defined. Note that the administrator needs not to provide the old password.</td>
</tr>
</tbody>
</table>

To modify a user, click Modify User in the Manage Users and Roles dialog box. In the Modify User dialog box proceed as described above.
11.4.2 Add/Modify Role

Click **Add Role** in the *Manage Users and Roles* dialog box and the *Create New Role* dialog box appears. Define a unique **Role Name**. Note that this name cannot be modified afterwards. Close the *Add Role* dialog box by clicking **OK**. Open the *Modify Role* dialog box:

![Modify Role dialog box](image)

The *Modify Role* dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Role Name</th>
<th>The role name is defined in the <em>Add Role</em> dialog box.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Application</td>
<td>Tecan software component, i.e. <strong>magellan</strong>.</td>
</tr>
<tr>
<td>Rights</td>
<td>The role represents a specific user level and corresponding user rights can be selected.</td>
</tr>
</tbody>
</table>
11.4.3 User Administration Audit Trail

Click Audit Trail in the Manage Users and Roles dialog box and the Audit Trail dialog box appears:

![Audit Trail dialog box]

All modifications of the user administration database are recorded in the user management audit trail written by the user management server.

11.4.4 User Rights (magellan Tracker)

There are three different security levels of user rights, the highest level of which is magellan Administrator, who has access to all program functions. The Application Specialist and Operator levels are increasingly limited.

- magellan Standard: The default rights are assigned as stated below.
- magellan Tracker: Each right can be assigned or withdrawn by an Administrator and by default are assigned as stated below. The default set of rights is based on a typical laboratory environment.

<table>
<thead>
<tr>
<th>Caution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Administrators have the responsibility to make sure that the settings (and any modifications) match the laboratory environment defined by the user SOPs (standard operating procedures) and comply with applicable laws.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Note</th>
</tr>
</thead>
<tbody>
<tr>
<td>For clinical diagnostic applications, the operating authority must validate all methods to ensure the safety of the results. A method is considered validated when signed by the operating authority. The operating authority is fully responsible for any results obtained.</td>
</tr>
</tbody>
</table>
## 11. Miscellaneous Icon

<table>
<thead>
<tr>
<th>User Rights</th>
<th>magellan Administrator</th>
<th>magellan Application Specialist</th>
<th>magellan Operator</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Sample ID List</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Create sample ID lists</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Create a new sample ID list or save an existing one with a new name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Edit sample ID lists</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Edit an existing sample ID list and save it with the same name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sign sample ID lists</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Sign an existing sample ID list for review/approval.</td>
<td></td>
<td></td>
<td>Reserved for future use.</td>
</tr>
<tr>
<td>Modify signed sample ID lists</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Edit or change sample IDs in a signed sample ID list.</td>
<td></td>
<td></td>
<td>Reserved for future use.</td>
</tr>
<tr>
<td><strong>Method</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Create methods</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Create a new method or save an existing one with a new name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Edit methods</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Edit an existing method and save it with the same name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sign methods</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Sign an existing method for review/approval.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Modify signed methods</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Edit a signed method and save it with the same name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Run unsigned methods</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Run methods that haven’t been signed.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Note: Each signature (review, approval, custom) allows operators to run those methods!</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Setup favorites</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Add/Remove methods from the favorite list.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Define multilabel measurement</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Define methods using multilabel measurements.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Define kinetic transformations</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Define methods using kinetic transformations.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Define concentration transformations</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Define methods using concentration transformations.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Define alias</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Define methods using aliases for identifiers.</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
### 11. Miscellaneous Icon

<table>
<thead>
<tr>
<th>User Rights</th>
<th>magellan Administrator</th>
<th>magellan Application Specialist</th>
<th>magellan Operator</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Workspace</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Create workspaces</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Perform a measurement and save the workspace with a new name – or – save an existing workspace with a new name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Edit workspaces</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Edit an existing workspace and save it with the same name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sign workspaces</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Sign an existing workspace for review/approval.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Edit signed workspaces</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Edit a signed workspace and save it with the same name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Continue evaluation when error</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Continue calculation after errors have occurred</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Modify raw data (samples)</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Edit or mask measurement data of samples.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Modify raw data (standards)</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Edit or mask measurement data of standards, controls, blanks.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Import raw data</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Import raw data from ASCII file in an existing workspace.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Modify evaluation</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Change evaluation (method) settings in an existing workspace.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Reevaluate with another method</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Reevaluate an existing workspace with another method.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Modify layout</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Change measurement parameters, concentration and layout before starting a measurement.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Standard curve</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Create standard curve files</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Create a new standard curve and save it with a new name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Edit standard curve files</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Edit an existing standard curve and save it with the same name</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sign standard curve files</td>
<td>Reserved for future use.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sign an existing standard curve for review/approval.</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
## 11. Miscellaneous Icon

<table>
<thead>
<tr>
<th>User Rights</th>
<th>magellan Administrator</th>
<th>magellan Application Specialist</th>
<th>magellan Operator</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Modify signed standard curve files</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Edit and change settings in a signed standard curve file.</td>
<td></td>
<td></td>
<td>Reserved for future use.</td>
</tr>
<tr>
<td><strong>General</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Archive files</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Move files to an archive location</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td><strong>Define filter slides</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Change the filter definition of the instrument</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td><strong>Modify general options</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Select language, suppress not monotone warning, allow demo mode.</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td><strong>Print unsigned workspaces</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>The results of an unsigned workspace can be printed.</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td><strong>Run not approved methods</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Reviewed methods can be used for a measurement run.</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Note: This right can be used in combination with the right Run unsigned methods to allow the user to run already reviewed, but still not approved methods.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Reader Server</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Save plate definition files</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Create or edit plate definition files.</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td><strong>Save spin profile</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Create or edit spin profile files.</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
</tbody>
</table>
11.4.5 User Administration Options

Click Options in the Manage Users and Roles dialog box and the Edit Options dialog box appears.

Login Options

If the user doesn’t use the application for a specified time (1 min – 36500 hours), the application is automatically locked and the user has to reenter the password.

Unsuccessful logins

After a number of consecutive unsuccessful logins (1 – 100), the user account is locked and optionally an alert email is sent to the system administrator.

If the user account of a user administrator has been locked due to unsuccessful logins, this account remains locked for an idle time of 45 minutes. After this waiting time the account is unlocked and can be used again.

If the application has not been in use for the specified maximum time it will be locked. The password must be entered to unlock the application. See Auto Lock above.
11. Miscellaneous Icon

Caution
If the User Administrator password is forgotten, User Administration settings cannot be changed. In that case please uninstall magellan first and perform a new installation afterwards (see chapter 1.4 Software Installation Procedure).

Note
When uninstalling magellan, NO existing magellan files will get lost. All previous files can be found in a backup folder generated during the new installation procedure.

Password Options

Passwords have to contain a specific minimum number of characters. Passwords can be defined to contain non-alphanumeric characters and/or numeric digits. Password cannot be reused.

Minimum password length:
Specify the required number of characters.

Minimum required number of non-alphanumeric characters:
Specify the required number of non-alphanumeric characters.

Minimum required number of numeric digits:
Specify the required number of numeric digits.

Password expires after the specified number of days:
User passwords expire after a configurable number of days. The user must then choose another password. Specify the required number of days (range: 1 to 36500 days).

Allow empty password:
Select this checkbox if it is allowed to have an empty password for a user except for the administrator.
When the password expires, the user will be prompted to enter a new password.

The old password has to be entered. The new password must comply with the specified password rules and has to be entered twice to prevent typing errors.

Email Options

An administrator can be notified in case of potential security attacks (a user account has been locked because a number of unsuccessful logins).

An email can be sent to the entered email address: Select one of the options:

- **SMTP server**: the IP address of the SMTP server has to be entered (f.e. SEUATEXCH01.eu.tecan.net)

Click **Test Mail** to send a test mail to verify that the settings are correct.

**Note**

The notification via e-mail requires an SMTP server without authentication.
11. Miscellaneous Icon

11.4.6 User Administration Summary

A detailed description of all existing users and user groups as plain text can be obtained by clicking Summary in the Manage Users and Roles dialog box.

The text can be copied to a word processing program for printing.
11.5 User Administration (magellan Standard)

Click the miscellaneous icon in the wizard window and select User administration in the next window to open the user administration dialog box.

The magellan software offers protection against misuse of the software or access to the software from unauthorized users by providing a password protection facility.

Users can be added, edited, or deleted and their rights can be defined. Password protection can also be enabled.

User profiles can be defined at three different security levels. The highest level of security within the software is that of the magellan Administrator. This level gives access to all of the program’s functions and data editing facilities. For Application Specialist and Operator level, options are increasingly restricted.

Only the User Administrator has the ability to enable or disable the software’s password protection, define new users or delete old users. If the users are logged in under their user name, the system will only give access to options according to their user rights definition.

The user list is maintained via the following three buttons: Add User, Modify and Disable. These buttons should be accessible only to personnel like department managers or data administrators.

The User administration dialog box contains the following elements:

<table>
<thead>
<tr>
<th>Button</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Login button</td>
<td>The Login dialog box is displayed. A user can log in with his user name.</td>
</tr>
<tr>
<td>User list</td>
<td>All currently setup users are displayed within this list.</td>
</tr>
<tr>
<td>Add User button</td>
<td>The Add User button opens the User Rights dialog box, in which a password, name, and user ID can be entered to define a new user.</td>
</tr>
</tbody>
</table>

User profiles can be defined at three different security levels. The highest level of security within the software is that of the magellan Administrator. This level gives access to all of the program’s functions and data editing facilities. For Application Specialist and Operator level, options are increasingly restricted.

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</tr>
<tr>
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</tr>
</tbody>
</table>
11. Miscellaneous Icon

<table>
<thead>
<tr>
<th>Button Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Modify button</td>
<td>The Modify button opens the User Rights dialog box for modifying the selected user in the user list.</td>
</tr>
<tr>
<td>Disable button</td>
<td>The Disable button will disable the selected user in the current user list. (He can no more user the application).</td>
</tr>
<tr>
<td>Password protection (on/off) check box</td>
<td>This check box has to be selected to enable or disable the software’s password protection facility. If enabled, the Login dialog box will be displayed upon starting magellan.</td>
</tr>
</tbody>
</table>

11.5.1 Add/Modify User (magellan Standard)

This dialog allows adding or editing of users and assigning them to a User group. For the rights of different user groups see chapter 11.5.4 User Rights (magellan Standard).

The User Rights dialog box contains the following elements:

- **User name** text field: In this field, the full name of the user – as it shall be displayed – has to be entered.
- **UserID** text field: Here, the user ID the user has to enter for login, has to be defined.
- **User rights** option buttons: Here has to be determined which level of access to the software’s facilities the user will be given:
  - Operator
  - Application Specialist
  - Administrator
- **Password** text field: The password of the user has to be entered. It must consist of at least 5 characters.
- **Confirm password** text field: The password will be required a second time as a precautionary measure. For security concerns, in this field, the password is not shown during entering. Every character is displayed as symbol.

Click the OK button to close the dialog box and the entered settings are saved.
Click the Cancel button to close the dialog box without saving the entered settings.

**Note**

If no users have been defined at all and the user administration shall be used, an administrator has to be defined first. Therefore, upon clicking the Login button, a short message is displayed. After that, the User Rights dialog box is displayed for entering the user information of the administrator (see chapter 2.4 Starting magellan/ Login).
11. Miscellaneous Icon

11.5.2 Login

This button is only enabled if user administration is activated but **Password protection** was not selected. Therefore at startup the Login dialog was not displayed. In order to activate the password protected user administration, click the Login button. The Login dialog box (see chapter 2.4.2 Starting Tracker Version / Login) will be displayed.

11.5.3 Change User

To change the active user, click the Change user icon in the wizard window. The Login dialog box is displayed (see chapter 2.4 Starting magellan/ Login).

11.5.4 User Rights (magellan Standard)

<table>
<thead>
<tr>
<th>User Rights</th>
<th>magellan Administrator</th>
<th>magellan Application Specialist</th>
<th>magellan Operator</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Sample ID List</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Create sample ID lists</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Create a new sample ID list</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>or save an existing one with</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>a new name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Method</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Create methods</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Create a new method or save a</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>existing one with a new name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Edit methods</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Edit an existing method and</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>save it with the same name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Setup favorites</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Add/Remove methods from the</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>favorite list.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Define multilabel</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>measurement</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Define methods using</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>multilabel measurements.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Define kinetic</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>transformations</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Define methods using</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>kinetic transformations.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Define concentration</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>transformations</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Define methods using</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>concentration transformations.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Define alias</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Define methods using</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>aliases for identifiers.</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
## 11. Miscellaneous Icon

<table>
<thead>
<tr>
<th>User Rights</th>
<th>magellan Administrator</th>
<th>magellan Application Specialist</th>
<th>magellan Operator</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Workspace</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Create workspaces</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Perform a measurement and save the workspace with a new name – or – save an existing workspace with a new name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Edit workspaces</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Edit an existing workspace and save it with the same name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Continue evaluation when error</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Continue calculation after errors have occurred</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Modify raw data (samples)</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Edit or mask measurement data of samples.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Modify raw data (standards)</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Edit or mask measurement data of standards, controls, blanks.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Import raw data</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Import raw data from ASCII file in an existing workspace.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Modify evaluation</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Change evaluation (method) settings in an existing workspace.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Reevaluate with another method</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Reevaluate an existing workspace with another method.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Modify layout</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Change measurement parameters, concentration and layout before starting a measurement.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Standard curve</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Create standard curve files</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Create a new standard curve and save it with a new name.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Edit standard curve files</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Edit an existing standard curve and save it with the same name</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>General</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Archive files</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Move files to an archive location</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Set default paths</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Set individual paths for saving workspace, method, sample ID list, export and bitmap files.</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
11. Miscellaneous Icon

### User Rights

<table>
<thead>
<tr>
<th>Define filter slides</th>
<th>magellan Administrator</th>
<th>magellan Application Specialist</th>
<th>magellan Operator</th>
</tr>
</thead>
<tbody>
<tr>
<td>Change the filter definition of the instrument</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Modify general options</th>
<th>magellan Administrator</th>
<th>magellan Application Specialist</th>
<th>magellan Operator</th>
</tr>
</thead>
<tbody>
<tr>
<td>Select language, suppress not monotone warning, allow demo mode.</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
</tbody>
</table>

### Reader Server

<table>
<thead>
<tr>
<th>Save plate definition files</th>
<th>magellan Administrator</th>
<th>magellan Application Specialist</th>
<th>magellan Operator</th>
</tr>
</thead>
<tbody>
<tr>
<td>Create or edit plate definition files.</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Save spin profile</th>
<th>magellan Administrator</th>
<th>magellan Application Specialist</th>
<th>magellan Operator</th>
</tr>
</thead>
<tbody>
<tr>
<td>Create or edit spin profile files.</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
</tbody>
</table>

### 11.6 About magellan

Click the **miscellaneous** icon in the wizard window and select **About magellan**.

Copyright information and software disclaimer are displayed. A window showing copyright information and software disclaimer is displayed. In the **About magellan** dialog box, information about the currently installed version of the **magellan** software, the version numbers of the components (tab **components**), and the program license of the user are displayed (tab **license**).

### Register Wizard

For further details on the **Register magellan Wizard** see chapter 2.6.1 Registration Wizard.
12. Additional Features for magellan Tracker

12.1 User Administration

In magellan Tracker a user administration is obligatory. Refer to chapter 11.4 User Administration (magellan Tracker) for further details.

12.1.1 Audit Trail

To become compliant with the FDA Regulation 21 CFR part 11 every step done in magellan Tracker is documented. In the Audit Trail all modifications concerning the following data are listed:

- a method file
- a workspace file
- a Sample ID list
- a standard curve file
- the user administration database or
- options and default settings.

Each entry consists of the user (name and full name), date and time of change, whether the file was created or modified, and any audit trail comments.

Audit Trail of Methods, Workspaces, Sample ID lists

You can view the Audit trail using the Audit trail button at the save page of the wizards.

Audit Trail of a Standard Curve

Standard curves can be saved and afterwards be used for evaluation of data from another workspace. For the feature to load a standard curve from external file refer to chapter 4.3.10 Concentrations: Standard Curve of the Create/Edit a Method Wizard. For opening a previously saved standard curve in the standard curve graph refer to chapter 7.4.11 Control Bar: Concentrations.

To view the audit trail of the loaded standard curve select Audit trail from the View menu in Standard Curve Graph dialog box.

Audit Trail of the User Administration Database

To view the Audit trail of the User Administration Database select Miscellaneous icon in the Wizard List starting page and click User Administration.

Audit Trail of Options and Default Settings

To view the Audit trail of all options and default settings select miscellaneous icon in the Wizard List starting page and click Options. In the Miscellaneous tab the Audit trail button can then be selected.
12. Additional Features for magellan Tracker

12.2 File Handling

The measured data is always saved directly after the measurement.

12.2.1 Saving a File

A file, created and saved in magellan Tracker, is indicated with a “#” sign in its file name. The added “#” sign can only be seen in the appropriate subdirectory of magellan.

Example
method#1.mth
workspace#1.wsp
sampleIDlist#1.smp

12.2.2 Changing a Method or Workspace File

Every time a method or workspace file is modified and saved, the number behind the “#” in the file name is automatically increased (e.g.: first version of a workspace: name#1.wsp; edit and save the new version to get name#2.wsp; After the next change name#3.wsp is created…). All versions of a file are listed in the appropriate subdirectories of magellan.

Note
When transferring Tracker files it is necessary to transfer all versions of the file.

12.2.3 Opening a File

Only the last saved version of a file is available in the wizards of create/edit a method, create/edit a sample ID list, evaluate results and start measurement.

To view a previous version of a file, open the Audit trail in the saving page of the file, select the preferred version of the file by clicking once on the number and click Save previous version as… button. Rename the file and add some file remarks or Audit trail comments and open the file with the Create/Edit a Method wizard.

Note
If you want to compare a method with its previous versions a printout must be made, because two print preview windows cannot be opened simultaneously.
12. Additional Features for magellan Tracker

12.2.4 Opening a File Created on Another PC – Add HUIDs

In the licensing process of magellan, three numbers are involved:

- Serial number of the software
- HUID (Hardware Unit Identification Number) and
- License number (refer to chapter 2.6 Licensing magellan).

The HUID of a Personal Computer is configured during magellan registration and all files created and saved on this PC are linked to this special HUID.

If there is the need to work with magellan Tracker files, which were created on another PC, the HUID of this other PC must be accepted.

When a user with the right to Modify general options tries to open a document (sample ID list, method, workspace) from another PC, i.e. with a different HUID number, the user is automatically asked to add that number to the list of known HUID numbers. If the button Accept HUID is clicked, the HUID number will be added to the list and the document will be opened without further interactions. Hence this HUID number is always accepted.

To view the list of accepted HUID numbers of other PCs click Miscellaneous icon in the wizard list starting page → Options → Miscellaneous tab. Click the Add HUID button and the dialog box with the other PCs HUID numbers is displayed.
12. Additional Features for magellan Tracker

12.3 System Audit Trail

The system audit trail is only available in the magellan Tracker version. The system audit trail function writes several magellan events into a log file (see table below). A new log file is created once per week and is stored under

**Windows XP:**

C:\Documents and Settings\All Users\Documents\Tecan\LogFiles\SystemAuditTrail

**Windows Vista and Windows 7:**

C:\Users\Public\Documents\Tecan\LogFiles\SystemAuditTrail

A checksum, computed over the entire log file, is used to guarantee log file consistency and to protect the files against intentional and accidental changes. Log file consistency is always checked at start up. Invalid files will be immediately closed, marked as invalid by appending ".invalid" to the log file’s name, and a new one will be created in its place.

**Magellan Events to be Tracked**

<table>
<thead>
<tr>
<th>Event</th>
<th>Event Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Magellan Start</td>
<td>StartUp</td>
<td>Magellan was started.</td>
</tr>
<tr>
<td>Magellan Exit</td>
<td>Exit</td>
<td>Magellan was closed.</td>
</tr>
<tr>
<td>Successful User LogOn</td>
<td>Login</td>
<td>A user logged in successfully.</td>
</tr>
<tr>
<td>Failed User LogOn</td>
<td>FailedLogin</td>
<td>Login failed, due to wrong username or password.</td>
</tr>
<tr>
<td>User LogOff</td>
<td>Logout</td>
<td>A user logged out.</td>
</tr>
<tr>
<td>New Workspace</td>
<td>New</td>
<td>A new workspace was created.</td>
</tr>
<tr>
<td>Load Workspace</td>
<td>Load</td>
<td>An existing workspace file was loaded into Magellan.</td>
</tr>
<tr>
<td>Save Workspace</td>
<td>Save</td>
<td>A workspace was saved.</td>
</tr>
<tr>
<td>New Method</td>
<td>New</td>
<td>A new method was created.</td>
</tr>
<tr>
<td>Load Method</td>
<td>Load</td>
<td>An existing method file was loaded into Magellan.</td>
</tr>
<tr>
<td>Save Method</td>
<td>Save</td>
<td>A method was saved.</td>
</tr>
<tr>
<td>New Sample ID List</td>
<td>New</td>
<td>A new sample ID list was created.</td>
</tr>
<tr>
<td>Load Sample ID List</td>
<td>Load</td>
<td>An existing sample ID list was loaded.</td>
</tr>
<tr>
<td>Save Sample ID List</td>
<td>Save</td>
<td>A sample ID list was saved.</td>
</tr>
<tr>
<td>Start Measurement</td>
<td>Measure</td>
<td>A new measurement was started.</td>
</tr>
<tr>
<td>Attach Signature</td>
<td>Signature</td>
<td>A workspace or method file was signed.</td>
</tr>
</tbody>
</table>
# 12. Additional Features for magellan Tracker

<table>
<thead>
<tr>
<th>Feature</th>
<th>Action</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Export Results</td>
<td>ExportASCII</td>
<td>Results were exported.</td>
</tr>
<tr>
<td></td>
<td>ExportExcel</td>
<td></td>
</tr>
<tr>
<td></td>
<td>ExportASTM</td>
<td></td>
</tr>
<tr>
<td></td>
<td>ExportSampleTracking</td>
<td></td>
</tr>
<tr>
<td>Prints Results</td>
<td>Print</td>
<td>Results were printed.</td>
</tr>
<tr>
<td>Automatic Archive</td>
<td>ArchiveFailed</td>
<td>The archiving of a workspace, method or sample ID list file failed.</td>
</tr>
<tr>
<td>CRC Failure</td>
<td>CRCFailed</td>
<td>Checksum of the previous log file was invalid.</td>
</tr>
</tbody>
</table>
13. Calculations

13.1 Evaluate Results – Calculation Procedure

Depending on the settings the calculation follows the procedure below:

1. Precalculation
   1.1 G-Factor calculation, polarization calculation (blank reduction, intensity, total intensity and anisotropy calculation)
   1.2 Cuvette data reduction
   1.3 Spectra calculation

2. Check if data and evaluation settings fit together

3. Raw data statistic calculation

4. Transformation calculation

5. Kinetic parameter calculation

6. Kinetic transformation calculation

7. Concentration calculation

8. Concentration transformation calculation

9. Cutoff range determination

10. QC Validation

11. Statistic calculation

The procedure is repeated if

- QC Validation eliminated values using the eliminate functions.
- Interpolation parameters in the transformations are required.

Equal values for transformations in kinetic and multilabel measurements will be suppressed.

For calculations with different dilutions the Mean concentrations will be discarded.

In case the evaluation procedure is aborted through errors, results calculated until that point can be displayed.

In case some values are found to be FALSE, the following Occurred Errors dialog box will appear:

<table>
<thead>
<tr>
<th>Message text field</th>
<th>The error message and a short explanation is displayed in a text field.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Save as file button</td>
<td>Click the Save as file button and the error protocol can be stored in an ASCII file.</td>
</tr>
</tbody>
</table>

In case the curve fit failed, depending on the user right, a question is displayed, where the user can decide to change the Analysis Type settings. After changes the evaluation procedure will be started from beginning.

In case the validation failed, depending on the user right, an error message box is displayed or a question message box is displayed, where the user can decide to continue the calculation anyway. If the calculation is aborted, cutoff results cannot be accessed. However, on a printout a validation failed message will be included.
In case values or settings have been changed, a message box will appear.

<table>
<thead>
<tr>
<th>Message</th>
<th>The instrument values have been changed. Do you want to re-start the result calculation?</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yes button</td>
<td>Click the Yes button to re-calculate the evaluation values.</td>
</tr>
<tr>
<td>No button</td>
<td>Click the No button to close the message. No re-calculation will be performed.</td>
</tr>
</tbody>
</table>

### 13.1.1 Statistics

If a statistical value is calculated over e.g. the n replicates with values $x_1...x_n$ of a sample following formulas are used:

<table>
<thead>
<tr>
<th>Name</th>
<th>Formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>mean value, average value</td>
<td>$\bar{x} = \frac{1}{n} \sum_{i=1}^{n} x_i$</td>
</tr>
<tr>
<td>standard deviation</td>
<td>$s = \sqrt{\frac{1}{n-1} \sum_{i=1}^{n} (x_i - \bar{x})^2}$ and $s=0$ for $n=1$</td>
</tr>
<tr>
<td>variation coefficient in percent</td>
<td>$v = 100 \times \frac{s}{\bar{x}}$</td>
</tr>
</tbody>
</table>

For more information refer to chapter 13.4.5 Statistical Functions.

### 13.2 Polarization Data Reduction

#### 13.2.1 Introduction

Fluorescence polarization measurements consist of two fluorescence intensity measurements, one with polarizers in parallel, and one with polarizers in perpendicular position. The G-factor compensates for differences in optical components between parallel and perpendicular measurement. A valid calibration of the instrument resulting in a G-factor is an important requirement for each fluorescence polarization measurement.

#### 13.2.2 Determination of the G-Factor

First, the reader specific G-factor is determined. This occurs by fluorescence intensity measurements of the reference and the reference-blank solution with polarizers in parallel and in perpendicular position. The polarization $P_{\text{ref}} [P]$ for the reference values is known:

$$ G = \frac{(1 + P_{\text{ref}})(RFU_{\text{ref}}^{\text{per}} - RFU_{\text{rbl}}^{\text{per}})}{(1 - P_{\text{ref}})(RFU_{\text{ref}}^{\text{par}} - RFU_{\text{rbl}}^{\text{par}})} $$

$P_{\text{ref}}$  ... reference polarization value

$RFU_{\text{ref}}^{\text{par}}$  ... average of the relative reference fluorescence value

$RFU_{\text{rbl}}^{\text{par}}$  ... average of the relative reference blank fluorescence value
13. Calculations

13.2.3 Blank Correction

If the method contains sample-blanks, a blank reduction process is run, whereby the average of the respective sample-blank is deducted from each sample value.

\[
\Delta RFU_{par} = \begin{cases} 
RFU_{par}^{ref} - RFU_{sbl}^{ref} \\
RFU_{par}^{sbl} - RFU_{sbl}^{sbl} \\
RFU_{par}^{smp} - RFU_{sbl}^{sbl}
\end{cases} \text{ for each well}
\]

\[
\Delta RFU_{per} = \begin{cases} 
RFU_{per}^{ref} - RFU_{sbl}^{ref} \\
RFU_{per}^{sbl} - RFU_{sbl}^{sbl} \\
RFU_{per}^{smp} - RFU_{sbl}^{sbl}
\end{cases} \text{ for each well}
\]

\[
RFU_{smp} \ldots \text{relative sample fluorescence value}
\]

\[
RFU_{sbl} \ldots \text{relative sample blank fluorescence value}
\]

13.2.4 Intensity Calculation

The vertical and horizontal intensities of the raw data, or the result of the blank reduction are then determined using the G-factor.

\[
I_{par} = G \cdot \Delta RFU_{par}
\]

\[
I_{per} = \Delta RFU_{per}
\]

13.2.5 Calculation of the Polarization / Anisotropy / Total Intensity

The following data is calculated using the intensities:

Polarization

\[
P = \frac{I_{par} - I_{per}}{I_{par} + I_{per}}
\]

Anisotropy

\[
A = \frac{I_{par} - I_{per}}{I_{par} + 2 \cdot I_{per}}
\]

Total Intensity

\[
I_{tot} = I_{par} + 2 \cdot I_{per}
\]

Note:

Polarization and Anisotropy are displayed in units of mP; Total Intensity is displayed in units of RFU.
13.3 Spectra Data Reduction

Spectra data contains much more information than single wavelength measurements. Typical information extracted from spectra are intensities at specified wavelengths or at found peaks. During calculation it is also possible to calculate spectral blank reduction and ratio calculation.

13.3.1 Mathematical Description

Blank reduction is performed by subtracting the blank spectrum from the sample spectrum.

Smoothing is done with the Savitzky-Golay algorithm. The filter coefficients are calculated by a polynomial with degree 2. The smooth factor is treated as number of points:

\[ g_i = \sum_{n=n_L}^{n_R} c_n f_{i+n} \text{ where } n_R-n_L+1=\text{number of points} \]

The smoothing window is symmetrical, e.g. for a smooth factor of 5, \( n_L=-2, n_R=2 \).
For the lower and upper border of the spectrum, the window is asymmetrical, thus \( n_L=0, n_R=4 \) or \( n_L=-4, n_R=0 \) respectively.
Before smoothing, all overflow values are removed from the spectrum.

Wavelength pick
• Pick wavelength – Retrieves the intensity of the selected wavelength
• Calculate ratio – Calculates the ratio by dividing the intensities at the selected wavelengths
• Area – Calculates the area under the spectrum within the selected wavelength range
• Custom – Reduces the spectrum using a user defined formula

Normalize
Reduces the spectrum into a range from 0 to 1.

Peak find
The spectrum is differentiated and all null points of the result are treated as potential peaks. The corresponding peaks are sorted by value and all invalid peaks are removed (e.g. overflows, local minima, values below the defined threshold). The highest value of the remaining items is selected as peak.
In practice this is often the maximum value of the spectrum.

Custom formulas
Ability to define various data reductions for the spectra (refer to chapter 13.4.8 Spectra Functions).

WARNING
SINGLE OUTLIERS CAUSED BY NOISE WILL ALSO BE DETECTED AS PEAK! THEREFORE IT IS HIGHLY RECOMMENDED TO SMOOTH THE SPECTRUM BEFORE USING PEAK FIND!
13.4 How to Write a Formula

13.4.1 Introduction

A variety of formulas are necessary for the calculations, the cutoff requirements and the validation. These formulas resemble the syntax of BASIC commands. Therefore, the calculations are relatively easy to define.

All values are calculated in double precision although they are displayed depending on the desired number format.

13.4.2 Formula Variables

All of the previously defined abbreviations for the identifiers contained within the analysis plate can be employed as variables in calculations.

For example:

PC1, SM1_1, BL1...Average values
PC1_1, SM1_1_1, BL1_1...Individual values, individual replicates

**Note**
The program differentiates between lower and upper case letters when dealing with these labels.

It is also possible to work with the well coordinates.

For example: A2, B3, H12

**Note**
Well coordinates must always be written using upper case letters.

The symbol \( x \) refers to the current value within a well. For example: \( x-BL1 \)...subtracts the empty value (blank) from the current value.

**Note**
The different cycles for kinetic measurements can be accessed by indices [], where “0” indicates the first cycle.

For example:

SM1_1[0]... Average value of sample 1 of the first cycle
\( x[1] \)... value of current well of the second cycle
\( x[i] \)... value of the current well and the current cycle

**Serial Kinetic Subtraction – Calculation of Difference between Kinetic Cycles**

Calculations over kinetic data can be defined by using the iteration variable ‘\( i \)’ in formulas. For instance a numerical derivative of a kinetic curve can be performed using the formula \( x[i]-x[i-1] \), which subtracts each kinetic cycle by the previous. But use of that formula would automatically lead to an error for cycle number 1. Therefore, set the formula if(\( i>0 \) then(\( x[i]-x[i-1] \)) else ignore() in the transformation edit field to prevent the subtraction of the first cycle.
13. Calculations

The use of constants in formulas is identical to all other variables, the only difference being that a constant can contain characters (f.e. alpha, dilution).

There are two predefined accessors.

- **concX ...**
  returns the concentration of the standard of the current well

- **dilX ...**
  returns the dilution of the sample or control of the current well

### Note

If more than one set of input data shall be used for calculations, select the appropriate data from the available data drop down list, activated in transformation edit fields of the Create/edit a method tab (refer to chapter 4.3.7 Transformed Data: Add New Transformation and chapter 7.4.9 Control Bar: Transformed Data).

### Note

Using one of the mathematical functions described in the following chapters, an “intellisense” help is activated to support correct writing of special formulas.

### Formula Operators

<table>
<thead>
<tr>
<th>Operator</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>+</td>
<td>Plus</td>
</tr>
<tr>
<td>-</td>
<td>Minus</td>
</tr>
<tr>
<td>*</td>
<td>Multiplication</td>
</tr>
<tr>
<td>/</td>
<td>Division</td>
</tr>
</tbody>
</table>
| ^        | To the power of the exponent
  The symbol used to represent the expression “to the power of” is ‘^’. This character can be obtained by pressing the SHIFT key together with the number 6 key (but not on the numerical keypad.)
  Example: x^3 The value of the well will be increased to the power of three.
| <        | Less than            |
| <=       | Less than or equal to|
| >        | Greater than         |
| >=       | Greater than or equal to |
| ==       | Equals               |
| !=       | Is not equal to      |
| =        | Assigned to          |
13. Calculations

Note
The difference between equals (==) and assign to (=).
For example: if \( x \equiv 0.000 \), then \( x = 1.000 \) (If the current value of \( x \) is equal to 0 then set the value of \( x \) to 1)

13.4.3 Formula Functions

The expressions “and” and “or” can be incorporated into the same equation through the use of logic functions. The result from a logical equation will be either TRUE or FALSE and is therefore a Boolean value. The individual equations must be enclosed in brackets.

Logical Expressions

and

In equations of this nature, the result will be TRUE if both expressions are found to apply, otherwise a result of FALSE will be given. Example:

Where the value held by the well is 0.3

\( (x>0.0) \) and \( (x<1) = \text{TRUE} \)

\( (x>0.0) \) and \( (x<0.1) = \text{FALSE} \)

or

In equations of this nature, at least one of the expressions involved must be found to apply in order that a result of TRUE can be given.

Example: where the value held by the well is 0.3

\( (x>0.0) \) or \( (x<0.1) = \text{TRUE} \)

\( (x>0.4) \) or \( (x<0.1) = \text{FALSE} \)

if(…) then(…) else(…)

The following expressions are used in the program and, as an example, can be written in the following manner:

if (statement) then Term A else Term B

The statement:

The statement must be either true or false and written in brackets. If the statement is arrived at by means of logical operators (and/or), then the whole expression must be written here and enclosed in brackets.

Terms A and B:

If the statement is true, Term A will apply and if the statement is false Term B will apply.

It is not always necessary to include the else expression. If it is not present in the equation, no response will be given in the event of a false result.

The “if(…) then(…) else(…)” expression can also be used with Boolean terms for QC Validation.

Example:

Check whether the value of a well lies within a defined range. If the result is yes, the well will be represented by the value 0.0, if the result is no, the value 1 will be used.

if \( ((x>-0.005) \) and \( (x<0.0) \) \) then(0.0) else(1.0)
13.4.4 Basic Functions

abs(argument)  
This function gives the absolute sum of the argument. Therefore (-1 * x) where x < 0 and (x) where x > 0.

Example:
abs(-1) = 1
abs(1) = 1

exp(argument)  
This function raises the Euler (e) value to the power of the argument.

Example: exp(1) = e^1 = 2.718

frac(argument)  
This function separates out the fraction section of argument. frac(): delivers the fraction section of a decimal value.

Example: frac(1.7) = 0.7

int(argument)  
This function separates out the integer sections of argument. int(): delivers the integer section of a decimal value.

Example: int(1.7) = 1

Log(argument)  

log(arg1;arg2)  
This function takes the logarithm of arg2 to the base of arg1.

Example:
The well holds a value of 100.
log(x;10)  
The result here will be 0.5.

ln(argument)  
This function takes the natural logarithm of argument.

Example: ln(10) = 2.303

lg(argument)  
This function takes the logarithm to base 10 of argument.

Example: lg(10) = 1

round(argument)  
This function rounds argument to an integer value.

Example:

To round 12.579 to two decimal places use the following formula:
    round(12.579*100)/100

The result is 12.58.
sqr(argument)  
This function raises argument to the power of 2  
*Example:* $sqr(3) = 9$

sqrt(argument)  
This function takes the square root of argument  
*Example:* $sqrt(9) = 3$

### 13.4.5 Statistical Functions

**Note**  
*Use single and not average or mean data as input data for transformations with statistical functions.*

avg(argument) and mean(argument)  
This function calculates the average value of argument. The argument must be an identifier.  
*Example:*  
$avg(SM1)$  
The average of all the samples in the first experimental group will be formed. Furthermore, the replicates of a value can be averaged:  
$avg(ST1_1)$  
Averages all replicates of the first standard.

median(argument)  
This function determines the median of argument. The argument must be an identifier. The individual replicates are ordered in terms of size and the median determined by taking the middle value in the order. If the number of values is an even number, the average of the two middle values will be determined.  
*Example:*  
Median (NC1)  
Assume NC1_1=0.1, NC1_2=0.05, NC1_3=0.04  
The median value of these negative controls will be determined as follows.  
The order of the values gives:  
0.04 0.05 0.1  
The median is therefore 0.05.

medianPlate()  
The median of the whole plate can be determined using this function. The individual values are ordered in terms of size and the median determined by taking the middle value in the order. If the number of values is an even number, the average of the two middle values will be determined.  
*Example:*  
$medianPlate()$  
Assume BL1=1, NC1=2, PC1=3, SM1_1=4, SM1_2=5 and no other wells defined. The median of the whole plate is 3.
max(argument) and min(argument)
This function calculates the minimum/maximum of argument. The argument must be an identifier.

Example:
max(SM1)
The maximum of all the samples in the first experimental group will be formed.

min(ST1_1)
Determines the minimum of the individual replicates of the first standard.

maxAvg(argument) and minAvg(argument)
This function gives the maximum/minimum average value of argument. The argument must be an identifier.

Example:
minAvg(SM1)
If a number of results are found for SM1, only the minimum average will be given.

PointwiseCV(argument)
The average point wise coefficient of variation (CV) is determined. The result can be used to validate the standard curve. The argument must be an identifier.

Example:
PointwiseCV(ST1)
Assume
ST1_1_1=0.54  ST1_1_2=0.52  cv=2.668  
ST1_2_1=0.72  ST1_2_2=0.77  cv=4.746  
ST1_3_1=1.08  ST1_3_2=0.99  cv=6.148  
The result of pointwiseCV is the average of the CV of ST1_1, ST1_2 and ST1_3 and is 4.5209.

Sum(argument)
This function calculates the sum of argument.

Example:
sum(SM1)
The sum of all the samples in the first experimental group will be formed.

sum(ST1_1)
Determines the sum of the replicates of the first standard.

stddev(argument)
This function calculates the standard deviation of argument. The argument must be an identifier.

Example:
stddev(NC1)
The standard deviation of the negative control in the first experimental group will be formed.
13.4.6 Elimination Functions

The elimination functions will be employed in the validation. In this way the user can make sure that the measurement values lie within a valid interval and delete any rogue values.

Three differing elimination functions can be employed when defining the validity intervals. The identifier that is to be influenced by the function is always the first parameter required when defining the elimination criteria.

All three elimination functions produce a logical result. TRUE is given when there are enough valid measurement values available and FALSE is given when less than the requirement are valid.

Invalid measurement values will be labeled with an exclamation mark.

**eliminate (arg1; arg2; arg3; arg4)**

The validation interval will be defined using a defined value.

This function eliminates values that lie outside of the validation range defined in arg2.

- **arg1**: Identifier name (NC1, PC1).
- **arg2**: Value used to represent the range, dependent upon arg4.
- **arg3**: Number of valid, individual values that must be available in order that an average can be generated. If too few values are available following the elimination, a result of FALSE will be given.

**Note**

For arg3:

- a value of “2” or higher has to be defined. “1” is not accepted.

- **arg4**: Represents the selection of whether testing will use the range average-arg2 to average+arg2 (argument of 1) or it will be checked whether the individual values lie below average+arg2 (argument of 0). In this case (argument of 0) there is no lower limit.

The elimination function here determines the average of arg1. The value with the highest absolute deviation to the average value is then checked to ensure that it lies within the range according to arg4. If the value lying outside of this range it will be viewed as being invalid. In this case the average calculation will begin again, excluding the previously discovered invalid value, and continue in this manner until no more rogue values can be found.

A result of TRUE will be delivered when enough valid individual values are available.

**Example:**

\[
\text{eliminate(NC1;0.15;2;0)}
\]

The average value will be generated for the negative controls. It will then be seen whether the individual negative controls lie above NC1+0.15. (There is no lower limit). If this is the case, the rogue value(s) will be eliminated as described above. If on completion, at least 2 individual values are valid, a result of TRUE will be returned; otherwise a result of FALSE will be given.

**eliminatePerc (arg1; arg2; arg3; arg4)**

The validation interval will be defined using a percentage of the average value.

This function eliminates values as described for function eliminate. The validation range is defined using a percentage (arg2) of the identifier.
13. Calculations

Example:

eliminatePerc(NC1;10;2;1)

Individual values will be invalid if they deviate to an extent of more than 10% below or above the average. On completion, a minimum of 2 individual values must be valid in order that the negative controls are declared as being valid.

eliminateRange (arg1; arg2; arg3; arg4)

This function eliminates values that lie outside of the validation range defined by arguments 2 and 3.

arg1: Identifier name (NC1,PC1)
arg2: Lower limit of the selected range
arg3: Upper limit of the selected range
arg4: The number of valid, individual values that must be to proceed. If too few values are available following the elimination, a result of FALSE will be given.

A result of TRUE will be delivered when enough valid individual values are available.

Example:

eliminateRange(NC1; 0.0 ; 0.1 ; 2)

The individual values for the negative controls must fall within the range of 0.0 and 0.1 in order to be valid. To achieve a result of TRUE, at least 2 of the values must be viewed as being valid.

eliminateCV (arg1; arg2; arg3)

This function eliminates replicates until the CV of the remaining replicates is lower than the given CV (arg2). The replicates are eliminated step by step, beginning with the value with the highest difference to the mean value.

arg1: Identifier name
arg2: Limit of accepted CV value
arg3: The number of valid, individual values that have to be left to deliver a positive result. If too few values are available following the elimination, a result of FALSE will be given.

A result of TRUE will be delivered when enough valid individual values are available.

Example:

eliminateCV(NC1; 15; 3)

The calculated CV of the individual values of the negative control shall be below 15%. After the elimination, at least 3 replicates must be left to get TRUE as result.

countDeleted(arg1; arg2)

This function checks if there are enough valid values available and returns TRUE or FALSE.

arg1: The identifier, whose quantity is to be checked.
arg2: The lowest number of replicates that must be available.

Example:

countDeleted(NC1; 2)

This function works in conjunction with the Eliminate functions in equations: The Validation contains the following line:
if (NC1>0.5) then eliminateRange(NC1; 0; 0.5; 2)
If the average of the negative control lies above 0.5, then all replicates that lie outside of the range should be omitted.

This elimination will be processed once. If values for elimination are found, a new calculation will follow making sure that the average lies under 0.5 and a result of TRUE will be given.

At this point it is not yet certain that the necessary number of replicates is available. This is then determined using the countDeleted function within an else statement:

\[
\text{if (NC1} > 0.5) \text{ then eliminateRange(NC1; 0; 0.5; 2) else countDeleted(NC1; 2)}
\]

The equation process (of the second run following the elimination) uses the else statement. The countDeleted function then checks, whether the given identifier in arg1 is available in the quantity specified in arg2. If this is the case a result of TRUE will be given, if not FALSE.

**Step by step example eliminate respectively eliminatePerc**

The only difference between eliminate and eliminatePerc is the way for calculating the limits for the valid range (see above). The calculation sequence is the same for both functions. For the step by step description, eliminate is used.

\[
\text{eliminate(NC1; 0.15; 2; 0)}
\]

**Individual values:**

\[
\begin{align*}
NC1_1 &= 0.217 \\
NC1_2 &= 0.439 \quad \overline{NC1} = 0.288 \\
NC1_3 &= 0.208
\end{align*}
\]

**Step 1:** The individual values are sorted by their distance to the average.

\[
\begin{align*}
|NC1_1 - \overline{NC1}| &= |0.217 - 0.288| = 0.071 \\
|NC1_2 - \overline{NC1}| &= |0.439 - 0.288| = 0.151 \\
|NC1_3 - \overline{NC1}| &= |0.208 - 0.288| = 0.08
\end{align*}
\]

**Step 2:** Calculation of upper limit: \(0.288 + 0.15 = 0.438\)

**Step 3:** first comparison:

\(0.439 > 0.438\) and therefore out of the valid range → **Step 4:** value of NC1_2 is eliminated and the average and the limit are recalculated.

**Step 4:** New avg = \((0.217 + 0.208)/2 = 0.2125\)

New limit = \(0.2125 + 0.15 = 0.3625\)

**Step 5:** second comparison:

\(0.208 <= 0.3625 \rightarrow \text{valid}\)

\(0.217 <= 0.3625 \rightarrow \text{valid}\)

**Result:**

The replicate NC1_2 doesn’t fit into the given range and therefore has been eliminated.

Function returns TRUE because there are still two replicates left.
13. Calculations

Note: In each calculation cycle (Step 1 to Step 4), only one replicate is deleted (the replicate with the highest distance to the average). The cycle is repeated until no replicate is deleted during the comparison step within the cycle.

13.4.7 Other Functions

ignore()

This function omits the values of chosen wells so they will not be incorporated into the calculations. Ignored values are displayed with a leading ‘!’ and handled like eliminated values.

Example:

if(x<0.9*SM1_1) then ignore()

isInvalid()

This function gives a Boolean value, whether values within the well are valid or not. Invalid values for example can be caused by overflow values of the reader.

Example:

if(isInvalid()) then x=3.0

If the well contains an invalid value, the value 3.0 will be assigned. In this way, further calculations are possible, in spite of such values.

calcAlways(argument)

This function enables to calculate formulas on wells independent of the state of the value. argument can be any valid formula. The formula will be calculated even if the value is masked or invalid. This function can be used to calculate results that do not depend on the value of the used well.

Example:

calcAlways(A)

The value of parameter A of the standard curve formula is returned.

concX

This function can be used in concentration transformations. The result of concX is the original concentration of the well and can therefore only be used in wells with standards as identifier.

Example:

x – concX gives the difference between the calculated and the original concentration of the well.
13.4.8 Spectra Functions

smooth(numPts)  Smoothes with the given number of points.

minimum()  Delivers the minimum as data pair (wavelength, intensity).

maximum()  Delivers the maximum as data pair (wavelength, intensity).

normalize(wl)  Normalizes by using the intensity at the given wavelength.

peak(threshold;wlStart;wlEnd;peakIndex;percLimit)  Delivers the peak as data set (intensity, wavelength, width, area). Peaks lower than the threshold will not be found. Peak search is done in the given wavelength range.

peakIndex = -1 → returns max. peak
peakIndex = -2 → returns min. peak
peakIndex = 0, 1, 2, … → returns peak at the given index
percLimit is a percentage used for calculating width and area.

numPeaks(threshold;wlStart;wlEnd)  Delivers the number of peaks found in the given wavelength range. Peaks lower than the threshold will not be found.

derive(degree)  Calculates the derivate of the given degree. Valid degrees are 1 and 2; e.g. derive(2).

intensity(function)  Delivers the intensity of either a data pair or a peak; e.g. intensity(minimum()).

wavelength(function)  Delivers the wavelength of either a data pair or a peak; e.g. wavelength(maximum())

width(function)  Delivers the width of a peak; e.g. width(peak0.5;450;650;1;50)).

area(function)  Delivers the area of a peak; e.g. area(peak0.5;450;650;1;50)).
13. Calculations

13.4.9 Examples

Transformations

Transformations modify the current value of the well. The result must always be a numerical value.

**Blank reduction:**

\[ x - \text{BL1} \]

The empty value (blank) will be deducted from the current value of the well.

**Blanking of a kinetic run:**

\[ x - x[0] \]

The value of first point of the kinetic is used as blank and will be deducted from the values of all kinetic cycles.

---

**Note**

*The index “0” represents the first measurement of a kinetic run.*

**Ratio:**

\[ \frac{x}{PC1} \times 100 \]

Calculates the ratio between a sample and a control in percentages.

**DNA/Protein ratio:**

\[ \frac{\text{Label1}\times}{\text{Label2}\times} \]

In order to calculate the DNA/protein ratio, a multilabel measurement must be defined. The first measurement uses a wavelength of 260 nm, the second measurement uses a wavelength of 280 nm.

**Conditional result:**

\[ \text{If (x<0.0) then 0 else x} \]

*If the value of the well is less than 0, it will be represented by 0, otherwise it remains unchanged.*

Cutoff

The cutoff dictates the limits to be applied when evaluating. The result must always be a numerical value.

Label: POS

Limit: NC1*1.15

Label: ??

Limit: NC1*0.85

Label: -

The result is positive (POS) when the absorbance is more than 15% above the average of the negative controls and negative (-) when it is more than 15% below the average. A result is declared as open (??) if it lies between these two values.
QC Validation

The validation serves to examine the validity of the test. The result must always be a logical statement, TRUE or FALSE.

\[(BL1>-0.005) \text{ and } (BL1<0.120)\]

If the average value of the empty value falls within the range of -0.005 to 0.12, a result of TRUE will be declared.

\[\text{eliminateRange(NC1;}-0.005;0.12;2)\]

If a minimum of two negative controls fall within the range of -0.005 to 0.12, a result of TRUE will be declared.

\[abs(PC1-NC1)>0.25\]

The distance between the averages of positive controls and the negative controls must be greater than 0.25. If this is the case, a result of TRUE will be declared.
13. Calculations

13.5 Standard Curve Analysis Types

13.5.1 Definitions

Given \( n \) base points \((x_1, y_1), \ldots, (x_n, y_n)\), \( x_1 < \ldots < x_n \)

<table>
<thead>
<tr>
<th>Name</th>
<th>Formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>correlation coefficient</td>
<td>( r = \frac{\sum_{i=1}^{n} (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^{n} (x_i - \bar{x})^2 \sum_{i=1}^{n} (y_i - \bar{y})^2}} )</td>
</tr>
<tr>
<td>average square deviation</td>
<td>( d = \frac{1}{n} \sum_{i=1}^{n} (y_i - f(x_i))^2 )</td>
</tr>
<tr>
<td>goodness of fit</td>
<td>( goodness = 1 - d )</td>
</tr>
</tbody>
</table>

13.5.2 Analysis Type Parameters

The analysis type parameter (e.g. the slope \( A \) and the intercept \( B \) for linear regression) can be used in calculation. The available parameters are described below. **If there is more than one experimental group**, the analysis type parameters have a postfix of “B” for the second experimental group, “C” for the third experimental group and so on. Example: The slope of a linear regression in experimental group 3 can be accessed as “AC”.

13.5.3 Error Messages

If any of the values in the calculated concentrations lie outside of the range stipulated by the standards, the entry \( >\text{Max} \) or \( <\text{Min} \) will be displayed within the plate’s wells respectively. If the user would nevertheless like to incorporate these values into the calculation, the Extrapolation option must be selected.

If the curve is not strictly monotone, an error message is generated.

If there are multiple solutions for a concentration calculation for a measured value, the entry \( \text{MultPt} \) will be displayed within the plate’s wells.

13.5.4 Point to Point

Using this process, the adjacent base points will be joined by means of a straight line.

A minimum of 2 base points is required for this calculation.

Extrapolation is not possible. There are no parameters for use as variables in the transformations.

If no concentration can be calculated the entry \( \text{NoCalc} \) will be displayed within the plate’s wells.
Mathematical Description

Interpolation function:

\[ f : [x_i, x_n] \rightarrow R \]

\[ x \mapsto y_j + \frac{y_{i+1} - y_i}{x_{i+1} - x_j} \cdot (x - x_j) \quad \text{if } x \in [x_j, x_{i+1}] \]

### 13.5.5 Linear Regression

A straight line will be formed, where the sum of the squared deviations of all base points is a minimum.

A minimum of 2 base points is required for this calculation.

If necessary, extrapolation can also be implemented in this process. In an evaluation with one experimental group, the slope and ordinate intercept serve as the variables A and B in the transformations. Furthermore, the correlation coefficient r may also be implemented.

In the Standard Curve dialog box following additional information is displayed:

- Formula with coefficient values A (slope) and B (intercept)
- Average square deviation d
- Absolute value of the correlation coefficient r

Mathematical Description

Approximation function:

\[ f' : [x_i, x_n] \rightarrow R \]

\[ x \mapsto A \cdot x + B \]

where A and B are determined by minimizing the error function

\[ \text{err}(A, B) = \sum_{i=1}^{n} (f(x_i) - y_i)^2 \]

The solution is unique if

\[ \text{rank} \begin{pmatrix} x_i & 1 \\ \vdots & \vdots \\ x_n & 1 \end{pmatrix} = n \]

which is true if \( x_i \neq x_j \forall i, j = 1, \ldots, n \) (see general condition)

### 13.5.6 Non-Linear Regression

This approximation is designed especially for hyperbolical data. Ideally the measured values for low concentrations are high and the measured values for high concentrations are low and the region of interest is in the high concentration range.

The parameter calculation supported by the linear regression \( x/y \) is used for \( y \).

A linear regression is carried out using the transformed data.

The result is expressed as the slope \( k \) and the intercept \( d \).

From this result \( A = 1/k \) and \( B = d/k \) can be determined.

A minimum of 2 base points is required for this calculation.

If necessary, extrapolation can also be implemented in this process. In an evaluation with one experimental group, the coefficients A and B serve as variables in the transformations. Furthermore, the correlation coefficient r may also be implemented. The approximation is always applied to the unscaled base point values.
In the Standard Curve dialog box following additional information is displayed:
Formula with coefficient values A and B
Average square deviation d
Absolute value of the correlation coefficient r

WARNING
THIS APPROXIMATION IS NOT CONTINUOUS AND THEREFORE IMPROPER DATA CAN EFFECT HUGE DEVIATIONS BETWEEN THE GIVEN BASE POINTS AND CALCULATED POINTS!

Mathematical Description

Approximation function:
\[ f : [x_1, x_n] - \{-b\} \to R \]
\[ x \mapsto \frac{A \cdot x}{B + x} \]
where A and B are determined by solving the linear regression problem for the transformed base points
\[(x_1, \frac{x_1}{y_1}), \ldots, (x_n, \frac{x_n}{y_n})\]

Linear regression:
\[ g : [x_1, x_n] \to R \]
\[ x \mapsto k \cdot x + d \]
minimizing
\[ err(k, d) = \sum_{i=1}^{n} \left( g(x_i) - \frac{x_i}{y_i} \right)^2 \]

The parameters A and B are calculated from k and d by
\[ A = \frac{1}{k} \quad \text{and} \quad B = \frac{d}{k} \]
This function f is not continuous at –B.

13.5.7 Polynomial

2\textsuperscript{nd} order: parabolic or quadratic
3\textsuperscript{rd} order: cubic
The user can select between a polynomial of order 2 calculation or a polynomial of order 3 calculation.
A minimum of 3 base points is required for a polynomial of order 2 calculation, whereas a minimum of 4 is required for the polynomial of order 3 calculation.
If necessary, extrapolation can also be implemented in this process. The parameters A = a_0, B = a_1, and C = a_2 can be used in transformations with polynomial of order 2. For polynomial of order 3, the variables A = a_0, B = a_1, C = a_2 and D = a_3 can be implemented.
In the Standard Curve dialog box following additional information is displayed:
Formula with coefficient values A, B and C for polynomial of order 2 or formula with coefficient values A, B, C and D for polynomial of order 2
Average square deviation

**Mathematical Description**

Approximation function:

\[ f : [x_1, x_n] \rightarrow R \]

\[ x \mapsto \sum_{i=0}^{\text{order}} a_i \cdot x^i, \quad \text{order} = 2 \text{ or } 3 \]

\( (n>\text{order}) \)

where \(a_0, ..., a_n\) are determined by minimizing the error function

\[ \text{err}(a_0, ..., a_n) = \sum_{i=1}^{n} (f(x_i) - y_i)^2 \]

The solution is unique if

\[
\begin{bmatrix}
  x_1^{\text{order}} & \cdots & x_1 & 1 \\
  \vdots & & \vdots & \vdots \\
  x_n^{\text{order}} & \cdots & x_n & 1 \\
\end{bmatrix}
= \text{rank} + 1
\]

which is true if \( x_i \neq x_j \forall i, j = 1, ..., n \)

**13.5.8 Cubic Spline**

The adjacent base points will be joined through the polynomial of order 3 calculation. The determination of the parameters is performed through the use of the not-a-knot condition.

A minimum of 3 base points is required for this calculation.

Extrapolation is not possible. There are no parameters for use as variables in the transformations.

**Mathematical Description**

Interpolation function features:

- Piecewise polynomial of order 3.
- Continuous second derivation at all base points.

\[
\int_{x_1}^{x_n} \left( \frac{d^2 f}{dx^2} \right)^2 dx
\]

Minimizes the integral, which is a simplified term for the deformation energy of a spline.

Not-a-knot condition: at \( x_2 \) and \( x_{n-1} \) also the third derivation is continuous.

**13.5.9 Akima**

The Akima interpolation creates in some cases a smoother curve as the spline interpolation.

A minimum of 3 base points is required for this calculation.

Extrapolation is not possible. There are no parameters for use as variables in the transformations.

**Mathematical Description**

This interpolation method uses piecewise polynomials of order 3.

The piecewise interpolation polynomial itself and its first derivation are continuous.
13. Calculations

Method
The slopes \( m_i \) at all base points are estimated from the neighbor points by a special function:

\[
q_i = \frac{y_i - y_{i-1}}{x_i - x_{i-1}}
\]

are the slopes of the linear interpolator between point \( i \) and point \( i-1 \), \( i=2, \ldots, n \)

\[
m_i = \frac{q_i \left| q_{i+2} - q_{i+1} \right| + q_{i+1} \left| q_i - q_{i-1} \right|}{\left| q_{i+2} - q_{i+1} \right| + \left| q_i - q_{i-1} \right|}, \quad i=3, \ldots, n-2
\]

Special cases:

Is \( q_i = q_{i+1} \), set \( p'(x_i) = q_i = q_{i+1} \).

Is \( q_{i-1} = q_i \) and \( q_{i+1} \neq q_{i+2} \), so \( y'_i = q_i \) (analog for \( q_{i+1} = q_{i+2} \)).

Is \( q_{i-1} = q_i \) and \( q_{i+1} = q_{i+2} \), set \( m_i = \frac{q_i + q_{i+1}}{2} \).

For the indexes 1, 2, n-1, n the slopes cannot be estimated by this algorithm.

Now we have the following conditions for the 3\(^{rd}\) order interpolation polynomial \( p_i \), \( i=1, \ldots, n-1 \)

\[
p_i(x_i) = y_i
\]

\[
p_i(x_{i+1}) = y_{i+1}
\]

\[
p'_i(x_i) = m_i
\]

\[
p'_i(x_{i+1}) = m_{i+1}
\]

which are four conditions for each 3\(^{rd}\) order interpolation polynomial \( p_i \).

13.5.10 LogitLog

LogitLog is designed for sigmoid standard curves. LogitLog will always produce an S-shaped curve. The curve will asymptotically reach an upper and a lower limit, which can be independently established as the minimum and maximum limits. If the user has not established any limits here, the minimum and maximum base point value will be used. The approximation is always applied to the unscaled base point values.

A minimum of 4 base points is required for this calculation.

If necessary, extrapolation can also be implemented in this process. The parameters A, B, C and D can be employed as parameters in the transformations.

In the Standard Curve dialog box following additional information is displayed:

Coefficient values A, B, C and D

Average square deviation \( d \)

Absolute value of the correlation coefficient \( r \) (correlation of data and fit)

Restrictions for the Process Application

LogitLog and Four Parameter approximation may only be employed when working with standard curves that meet following requirements:

- Sigmoid process applied to the standard data in relation to the concentrations
- Symmetrically generated curve in relation to the IC-50 value
In order to calculate the curve correctly it is necessary to have a concentration value of zero and a value of infinite standard concentration (saturated value), so that the asymptotes can be determined. If these two values are not present within the standard curve, they can be defined manually using the **More standard curve parameters** option (Min, Max). If no Min and Max values are defined, magellan will base the process on the smallest and largest values present respectively.

---

**WARNING**

*IF THESE REQUIREMENTS ARE NOT MET, APPROXIMATION OF THIS NATURE CANNOT BE CORRECTLY EMPLOYED.*

---

**Mathematical Description**

The LogitLog regression is a function

\[ f : [x_1, x_n] \rightarrow R \]

\[ x \mapsto D + \frac{A - D}{1 + \left( \frac{x}{C} \right)^b} \]

for the description of sigmoid correlation of data.

The parameter can be interpreted as:

- \( A = \lim_{x \to 0} f(x) \)
- \( D = \lim_{x \to \infty} f(x) \)
- \( f(C) = \frac{A + D}{2} \)

A, D are determined as the minimum respectively maximum (or vice versa if the function is decreasing).

Then the linear regression problem is solved for transformed base points.

\[ X = \log_{10} x \]

\[ Y = \ln \left( \frac{D - y}{D - A} \right) \]

\[ g : [X, Y] \rightarrow R \]

\[ x \mapsto k \cdot x + d \]

, minimizing the error function

\[ err(k, d) = \sum_{i=1}^{n} (g(x_i) - Y_i)^2 \]

The parameters B, C are determined from k, d:

\[ B = -m \cdot \log_{10} (e) \]

\[ C = e^b \]

The parameters A,B,C,D, have appealing geometric interpretations.

A = response at a dose (x-value) of zero (keep in mind that x=0 does not appear on logarithmic plots)
13. Calculations

D = response at an infinitely high dose
C = is the point of symmetry on the curve (IC50); and below this point the curve is a mirror image
B = is a measure of the steepness of the curve at the inflection point; in fact it is (within a possible change of sign) the slope of the curve written in its Logit form
Notice that the curve is always decreasing (if A>D) or increasing (if A<D).

13.5.11 Four Parameters

Four parameter approximation needs to fulfill the same base point requirements as LogitLog.
The resulting curve will be produced using the Nelder and Mead Downhill-Simplex method. This method produces an increasingly more accurate approximation of the result throughout the interval. The four-parameter method requires considerably more time to be processed. As with LogitLog, an S-shaped curve is produced.
A minimum of four base points is required for this calculation.
If necessary, extrapolation can also be implemented in this process. The parameters A, B, C, and D can be employed as parameters in the transformations. The approximation is always applied to the unscaled base point values.
In the Standard Curve dialog box following additional information is displayed:
Coefficient values A, B, C and D
Average square deviation \(d\)
Absolute value of the correlation coefficient \(r\) (correlation of data and fit)

Restrictions for the Process Application

Refer to chapter 12.5 Standard Curve Analysis Types – LogitLog for further information.

Mathematical Description

Approximation function:
\[ f : [x_1, x_n] \rightarrow R \]
\[ x \mapsto D + \frac{A - D}{1 + \left(\frac{x}{C}\right)^a} \]

Method

First a LogitLog approximation is calculated.
The parameters A, B, C, D are optimized by the Downhill-Simplex algorithm, a minimization algorithm that needs only function evaluations but no function derivation.
The algorithm stops if an accuracy of 0.001 is reached (success) or the maximum number of 10,000 iterations is exceeded (failure) before the given accuracy is reached.

Bibliography

13. Calculations

13.5.12 Four Parameters – Marquardt

The four-parameter approximation needs to fulfill the same base point requirements as LogitLog.

The resulting curve will be produced using the Levenberg-Marquardt method. This method produces an increasingly more accurate approximation of the result throughout the interval. The four-parameter method requires considerably more time to be processed. As with LogitLog, an S-shaped curve is produced.

A minimum of four base points is required for this calculation.

If necessary, extrapolation can also be implemented in this process. The parameters A, B, C and D can be employed as parameters in the transformations. The approximation is always applied to the unscaled base point values.

In the Standard Curve dialog box following additional information is displayed:
- Coefficient values A, B, C and D
- Average square deviation d
- Absolute value of the correlation coefficient r (correlation of data and fit)

Restrictions for the Process Application

Refer to chapter 13.5 Standard Curve Analysis Types – LogitLog for further information.

Mathematical Description

Approximation function:

\[
 f^* : [x_1, x_n] \to R
\]

\[
x \mapsto D + \frac{A - D}{1 + \left(\frac{x}{C}\right)^B}
\]

Method

First a LogitLog approximation is calculated.

The parameters A, B, C, D are optimized by the Levenberg-Marquardt algorithm, an iterative technique that finds a local minimum of a function that is expressed as the sum of squares of nonlinear functions.

The algorithm stops if an accuracy of 1E-7 (FLT_EPSILON) is reached (success) or the maximum number of 30,000 iterations is exceeded (failure) before the given accuracy is reached.
13.5.13 Five Parameters – Marquardt

The five-parameter approximation basically needs to fulfill the same base point requirements as LogitLog. The sigmoid curve may however be non-symmetric. The resulting curve will be produced using the Levenberg-Marquardt method. This method produces an increasingly more accurate approximation of the result throughout the interval. The five-parameter method requires considerably more time to be processed. As with LogitLog, an S-shaped curve is produced.

A minimum of five base points is required for this calculation. If necessary, extrapolation can also be implemented in this process. The parameters A, B, C, D, and E can be employed as parameters in the transformations. The approximation is always applied to the unscaled base point values.

In the Standard Curve dialog box following additional information is displayed:
- Coefficient values A, B, C, D, and E
- Average square deviation \( d \)
- Absolute value of the correlation coefficient \( r \) (correlation of data and fit)

Restrictions for the Process Application
Refer to chapter 13.5 Standard Curve Analysis Types – LogitLog for further information.

Mathematical Description
Approximation function:

\[
f : [x_1, x_n] \rightarrow R
\]

\[
x \mapsto D + \frac{A - D}{(1 + (\frac{x}{C})^B)^E}
\]

Method
The parameters A, B, C, D, E are optimized by the Levenberg-Marquardt algorithm, an iterative technique that finds a local minimum of a function that is expressed as the sum of squares of nonlinear functions.

The algorithm stops if an accuracy of 1E-7 (FLT_EPSILON) is reached (success) or the maximum number of 30000 iterations is exceeded (failure) before the given accuracy is reached.
13. Calculations

13.5.14 Weighting for Four / Five Parameter Fit – Marquardt / Polynomial Fit

Weighting influences the standard optimization algorithm. The algorithm tries to optimize the weighted sum of least squares. A weighting factor of one means no weighting. Weighting factors greater than one mean that the specified point has higher priority for the resulting fit. Weighting factors smaller than one indicate that the point is taken less into account.

WARNING
WEIGHTS SHOULD ONLY BE USED IF THERE IS SEVERE STATISTICAL EVIDENCE, THAT GATHERED DATA AND ALGORITHM ARE APPROPRIATE.

Mathematical Description
Average weighted square deviation

\[ d = \frac{1}{n} \sum_{i=1}^{n} k_i (y_i - f(x_i))^2 \]

Automatic calculation of weights using variance:
The weights are automatically calculated with 1/SD² where SD is the standard deviation of the replicates of the actual base point.

This means that data with high standard deviation is less weighted than data with low standard deviation.

WARNING
WEIGHTING USING VARIANCE IS DANGEROUS WHEN TOO FEW REPLICATES ARE USED, BECAUSE THE STANDARD DEVIATION CAN THEN HAVE A HIGH RANDOM PORTION WHICH CONSIDERABLY INFLUENCES THE OPTIMIZATION ALGORITHM.

Automatic calculation of weights using relative weights:
The weights are automatically calculated with 1/Y² where Y is the mean value of the actual base point. This means that the algorithm minimizes the relative distances of the data to the curve.
13.6 Calculation of Dilution Series

13.6.1 Detection of Dilution Series

The following criteria have to be fulfilled to force magellan to detect a dilution series on the layout:

- Sample(s) with a minimum of four replicates
- Usage of at least four different dilution factors for the single replicates of a sample

magellan checks the whole layout and picks all found dilution series.

13.6.2 Curve Parameter Calculation

Curve parameters are calculated for every found dilution series using the Four Parameters – Marquardt algorithm. In case of a failure the calculation is redone using the Four Parameters algorithm. Please refer to chapter 13.5 Standard Curve Analysis Types for more detailed information about the algorithms mentioned above.

13.6.3 Calculation of IC Values

First the maximum intensity ($I_{\text{max}}$) and the minimum intensity ($I_{\text{min}}$) of every dilution series is picked.

**Calculation of IC-intensity**

If the 0% value is set to intensity 'Intensity 0'

$$I_{IC} = \frac{ICx}{100.0} \times I_{\text{max}}$$

If the 0% value is set to ‘Min. intensity of dilution series’

$$I_{IC} = I_{\text{min}} + \frac{(I_{\text{max}} - I_{\text{min}}) \times ICx}{100.0}$$

**Calculation of dilution at ICx**

Using the curve parameters calculated in step 12.6.2 and the calculated IC-intensity the resulting dilution is calculated.

$$\text{dilution} = C \times \left(\frac{A - I_{IC}}{I_{IC} - D}\right)^\frac{1}{b}$$
14. Application Example

14.1 Introduction

The magellan example files package provide magellan workspaces and the corresponding Instructions for Use (IFU) to introduce the software and to ease the user’s work with it. The files can be installed separately and include examples for different measurement modes; they are based on commercial available applications. For further information please refer to the IFU for the example files.

14.2 Step-by-Step Example: Quantitative ELISA

A step-by-step example (quantitative test) of how to create a method in magellan is provided in this chapter. By following the instructions you will learn how to define evaluations from a test kit description in magellan.

The method was created using a Sunrise in demo mode, but it is also possible to define the methods with another Tecan instrument connected, if it is able to measure absorbance.

14.2.1 Test Kit Description

In the manufacturer’s test kit description of a quantitative IgM – Antibody detections – ELISA the following instructions are found: Plate Layout

<table>
<thead>
<tr>
<th></th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
<th>12</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>BLK</td>
<td>C3</td>
<td>S1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>NC</td>
<td>C4</td>
<td>S2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>NC</td>
<td>C4</td>
<td>S2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D</td>
<td>C1</td>
<td>C5</td>
<td>S3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>E</td>
<td>C1</td>
<td>C5</td>
<td>S3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F</td>
<td>C2</td>
<td>C6</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>G</td>
<td>C2</td>
<td>C6</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>H</td>
<td>C3</td>
<td>S1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

BLK = Blank, NC = Negative control, C1 – C6 = Calibrators (Standards), S1 – S… = Samples
14. Application Example

Measurement and Evaluation

Read plate at a wavelength of 492nm, reference at 620nm.
Blank reader/plate on well A1.

Concentrations of the Calibrators (Standards):

<table>
<thead>
<tr>
<th>Calibrator</th>
<th>Concentration (UA/mL)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Calibrator 1</td>
<td>5</td>
</tr>
<tr>
<td>Calibrator 2</td>
<td>10</td>
</tr>
<tr>
<td>Calibrator 3</td>
<td>20</td>
</tr>
<tr>
<td>Calibrator 4</td>
<td>40</td>
</tr>
<tr>
<td>Calibrator 5</td>
<td>80</td>
</tr>
<tr>
<td>Calibrator 6</td>
<td>160</td>
</tr>
</tbody>
</table>

After the blank correction the optical densities (OD492–OD620) are plotted versus the concentration. The regression line that goes through these points is the standard curve.

Interpretation of the test results:

<table>
<thead>
<tr>
<th>IgM Concentration</th>
<th>Result</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt; 18 UA/mL</td>
<td>Negative</td>
</tr>
<tr>
<td>18 UA/mL ≤ IgM &lt; 22 UA/mL</td>
<td>Intermediate</td>
</tr>
<tr>
<td>≥ 22 UA/mL</td>
<td>Positive</td>
</tr>
</tbody>
</table>

The calculated IgM concentration of both negative controls must be under 8 UA/mL.

Data Handling

After the measurement, the data file (workspace) is stored automatically and a report containing the measurement parameters, plate layout, blanked values, standard curve, IgM-concentrations, cutoff definition, qualitative results of the samples and validations is created.

Additionally, the layout and the qualitative results are be stored as ASCII file.
14.2.2 Create a Method

In the Wizard List dialog box, select Create/edit a method and click OK. Click next on the Welcome page of the Create/edit a method wizard and the Select a file dialog box appears. Select Create new.

Measurement Parameters

Click Next and the Measurement parameter dialog box appears.

Select Endpoint measurement and click the Measurement parameters button. The following dialog box appears:
On the General tab select **Absorbance**.

On the Wavelengths tab select 492nm as **Measurement wavelength** and 620nm as **Reference wavelength**.

Click **OK** to return to the Measurement parameter dialog box.

Click **Define evaluation** and the Plate layout window is displayed.
14. Application Example

**Design Layout**

Define the plate layout using the **Well Assignment** dialog box on the right side of the screen.

In the **Identifiers** group box, select **BL (Blank)**.

In the **Experimental** group box the number 1 remains.

In the **Replicates** group box, select **All**.

Click well **A1**, which is then marked with a red border.

Click **Fill selection** and the well is labeled with the selected identifier type.

![Well Assignment Dialog Box](image)

Note

*A single well can also be filled by double-clicking it.*

Now choose the following settings in the **Well Assignment** dialog box:

In the **Identifiers** group box, select **NC (Negative Control)**.

In the **Experimental** group box the number 1 remains.

**All** is selected in the **Replicates** group box.

Starting at well **B1** click and drag the mouse to **C1**. The wells **B1** to **C1** are then marked with a red border.

Click **Fill selection** and the wells are labeled with the selected identifier type.

Next, calibrators (standards) must be assigned to wells **D1** to **G2**. Select the following settings in the **Well Assignment** dialog box:

In the **Identifiers** group box, select **ST (Standard)**.

In the **Experimental** group box the number 1 remains.

In the **Replicates** group box, choose between **Fix number** and **All**:

**Fix number**

Only enabled for standards and samples where IDs can be used.

If this **Fix number** button is active a number can be entered in the corresponding text field. This number defines how many replicates are intended for this method.

In the selected wells, the entered number of replicates for every ID is created.

Therefore the number of selected wells must be a multiple of the entered number of replicates.
14. Application Example

All selected wells are defined as replicates. If an existing ID number for the samples and standards is chosen, the selected wells are then added as replicates to the existing replicates. With all other identifier types the selected wells are added as replicates to the existing replicates.

Two arrow buttons define the direction of the replicate and ID number sequence (horizontal or vertical).

In this example select **Fix Number** and **2**.

In the ID-Number box and in the Replicates group box select the vertical arrows.

Then select the wells D1 to G2 and click Fill selection.

---

**Note**

Select the wells as follows: Starting at well D1 click and drag the mouse over the required wells to H1. Then hold down the control (Ctrl) key and drag the mouse over the required wells from A2 to G2.

---

The Plate Layout appears as follows:

Click Select all unused from the toolbar to select all empty wells on the plate. Then hold down the control (Ctrl) key and click the well H12, so that it remains blank and unmarked.

In the Well Assignment dialog box select SM (Sample) under Identifiers.

In the Experimental group box the number 1 remains.

In the Replicates group box choose Fix number and 2.
In the ID-Number box leave 1 and in the Replicates group box select the vertical arrows. Click then Fill selection. The layout definition procedure is complete.

Transformations

In the control bar on the left of the window select the next option, Add new transformation... from the Transformed data item, to define blank reduction.

A dialog box appears asking you if you want to define a blank reduction. Click Yes.

Select Difference Data in the Input data box. By default the transformation is named Transformation1 (see control bar). If you have confirmed the definition of a blank reduction before, the software automatically names it Blank reduction.

In the Formula box automatically appears x-BL1 for this blank reduction, where x refers to the current input data value in a well and BL1 is the mean value of the blank wells of experimental group 1.

Now select the whole plate by clicking the sign in the upper left corner of the microplate and click the green hook next to the formula window to assign the transformations to the wells. Further details and explanations concerning the definition and assignment of transformations, refer to chapter 4.3.7 Transformed Data: Add New Transformation. The following window appears:
14. Application Example

In each well the following information appears (example well A5):

<table>
<thead>
<tr>
<th>SM1_9</th>
<th>Sample, experimental group number 1, sample ID number 4.</th>
</tr>
</thead>
<tbody>
<tr>
<td>2/2</td>
<td>Number of replicate is 2, total number of replicates is 2.</td>
</tr>
<tr>
<td>x-BL1 or 1.000</td>
<td>Assigned transformation x-BL1 (when Transformation is selected) or Dilution Factor value of 1 (when Conc., Dil., Ref.-values is selected).</td>
</tr>
</tbody>
</table>

Concentration / Dilution / Reference Value Definition

In the control bar select Conc., Dil., Ref.-values from the Method layout item to define the respective values as described in the test kit.

<table>
<thead>
<tr>
<th>Calibrator</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>5 UA/mL</td>
</tr>
<tr>
<td>2</td>
<td>10 UA/mL</td>
</tr>
<tr>
<td>3</td>
<td>20 UA/mL</td>
</tr>
<tr>
<td>4</td>
<td>40 UA/mL</td>
</tr>
<tr>
<td>5</td>
<td>80 UA/mL</td>
</tr>
<tr>
<td>6</td>
<td>160 UA/mL</td>
</tr>
</tbody>
</table>

Make sure ST is selected in the Select Identifier list.

In the Identifier list, a list of the standards from the Exp. Group 1 appears. In the corresponding Concentration box of ST1_1 type the number 5 and in the Unit box, type UA/mL. In the corresponding Concentration box of ST1_2 type the number 10. The unit only needs to be defined once and is valid for all standards. Type the values for the ST1_3 to ST1_6 in the same way.

The screen showing the plate layout and the concentration is displayed:
Standard Curve

In the control bar click **Standard curve** from the **Concentrations** item to define the appropriate standard curve.

The following is in the test kit description: After the blank correction, the optical densities (OD 492 – OD 620) are plotted versus the concentration. The regression line that goes through these points is the standard curve.

On the **Data tab**, select **Blank reduction** as input data.

On the **Analysis type tab**, select **Linear regression**.
14. Application Example

On the **Axis tab**, define the labeling and the scaling of the axis as shown below:

![Axis Tab Illustration]

On the **Graph tab**, define the graph title, curves, font and graph display.

![Graph Tab Illustration]
Define Cutoffs

In the control bar select **Cutoff definition** from the **Evaluate data** item to define the limits for the qualitative evaluation.

The test kit description contains the following instructions:

**Interpretation of the test results:**

<table>
<thead>
<tr>
<th>IgM &lt; 18 UA/mL</th>
<th>Negative</th>
</tr>
</thead>
<tbody>
<tr>
<td>18 UA/mL &lt;= IgM &lt; 22 UA/mL</td>
<td>Intermediate</td>
</tr>
<tr>
<td>IgM &gt;= 22 UA/mL</td>
<td>Positive</td>
</tr>
</tbody>
</table>

Use the following procedure to define the appropriate cutoffs:

In the **Input data** box, select **Mean conc. (UA/mL)**.

The **Cutoffs** table represents a scale indicating the high and the low end for the **Limits** and **Labels**. In **Limits**, type 22 as the first (higher) limit and 18 as the second (lower) limit.

In **Labels**, enter the test interpretation (**Positive**, **Intermediate** and **Negative**) into the individual boxes. Use the drop down color palette to assign a color:

- Positive – Red
- Intermediate – Blue
- Negative – Green

The screen contains the following:

Click **Cutoff results selection** to select the identifier types for which the cutoff results must be shown.
Define QC Validations

In the control bar, click **QC Validations** from the **Evaluate data** item. Validation criteria for the test must be defined, so that the validity of the test results is guaranteed.

In this example the following requirement must be fulfilled:
The calculated IgM-concentration of both negative controls must be under 8 UA/mL.

In the Input box, select **Single conc. (UA/mL)**.

In the first row, type **NC1_1<8**, or enter the formula using the available variables, operators and functions.

Note

**NC1_1** means Negative control of experimental group 1, replicate 1.

In the second row, type **NC1_2<8**.

The **QC Validations** dialog box is now displayed as follows:
Organize Printed Report

In the control bar, click **Printed report** from the **Data handling** item. The following screen is displayed:

On the **Data selection** tab, all available report data is contained in the **Available data** box. Using the **Insert** and **Append** buttons, data can be transferred into the **Selected data** box. Data can also be transferred using drag-and-drop.

In the **Print as** box, choose between printing the data as a matrix or as a list with a special orientation.

In this example a report containing the measurement parameters, plate layout, blanked values, standard curve, IgM-concentrations, cutoff definition, qualitative results of the samples and validations should be created.

Before creating the report, the default **Matrix Difference data** must be removed from the **Selected data** box. So only **Measurement parameters** remain in the **Selected data** box.

Select **Method layout/Layout** in the **Available data** box and attach it as a matrix to the report by clicking **Append**. Then insert **Blank reduction, Mean conc. (UA/mL)** and **Cutoff results** into the matrix by selecting the corresponding items and clicking **Insert**.
14. Application Example

Append Graph: Standard curve, Cutoff definition and QC Validation criteria to the selected data. The data setup part of the report definition procedure is complete; the Printed Report dialog box looks like this:

On the Header and Footer tabs, define the layout of the header and the footer of the report (see chapter 4.3.15 Data Handling: Printed Report for further details).

Data Export

In the control bar, select Data export from the Data handling item. In this example, the layout and cutoff results should be stored as ASCII file. Select Layout and Cutoff results from the Available data window; click the → arrow to insert them into the Selected data window. The screen displays the following information:

Note

Exported data should always contain the Layout or Sample ID List.
Automated Data Handling

In the control bar, select **Automated data handling** from the **Data handling** item.

Select **export to ASCII file**, and **view results after measurements**. In **magellan Tracker**, **save workspace** is selected by default and cannot be modified.

**Save the Method**

Click **FINISH** to open the **Save as** window. Enter the method filename and complete any other field if appropriate.

<table>
<thead>
<tr>
<th><strong>Filename</strong> text field</th>
<th>A filename must be entered. A default filename is suggested automatically, but can be changed.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>File remarks</strong> text field</td>
<td>Comments entered here will be saved and displayed with the filename.</td>
</tr>
</tbody>
</table>
## 14. Application Example

### Audit trail comment text field

Comments entered here will be stored in the audit trail. *This option is only available with magellan Tracker.*

### Audit trail button

The **Audit Trail** dialog box appears. *This option is only available with magellan Tracker.*

### Organize Favorites button

The **Organize Favorites** dialog box appears. *(See chapter 6.5 Start Favorite – Organize Favorites).*

### Signatures button

The **Signature** dialog box appears. *This option is only available with magellan Tracker.*

### Method password

Enter a method password if you want to protect the method to be saved *(see chapter 4.4.1 Password Protection of Methods).*

### Run this method now check box

The method will be run immediately after having finished the wizard.

## Audit Trail

Click **Audit Trail** to view the **Audit Trail** dialog box:

![Audit Trail dialog box](image)

The audit trail shows a list of all modifications made to the method. Each entry consists of the user (name and full name), date and time of change, whether the file was created or modified, and any audit trail comments.

Click **Print preview...** to get a preview of the file. To compare a method with its previous versions a printout must be made, because two print preview windows cannot be opened simultaneously.
14.2.3  Run the Method

If Run this method now is selected in the Save as dialog box of the Create/edit a method wizard, the Start Measurement Wizard/Start Measurement dialog box will appear after Save is clicked:

![Start Measurement Wizard/Start Measurement dialog box]

Click Start to start the measurement. A workspace will be created automatically, which contains all previously entered information and will collect all measurement values. While the measurement is being executed, a measurement status dialog box appears indicating the progress of the measurement.

After the measurement is completed, the Results dialog box appears, in which all the results and calculations can be viewed.
14. Application Example

14.2.4 Evaluate the Result

Evaluate results enables you to view and evaluate raw data. The evaluation parameters can be viewed and data can be re-evaluated. This section guides you through the Evaluate Results wizard using the example workspace file created by running the quantitative ELISA method.

Note

Example files automatically appear in the Method List in magellan Standard. For magellan Tracker, these files are available in the default data path and must be converted.

In the Wizard List dialog box, click Evaluate results. Click Next on the Welcome page of the Evaluate Results wizard and the Select a file dialog box appears. Select the workspace Quantitative Elisa example_Sunrise.wsp from the file list and click Make your selection. Calculations are executed and the following plate layout window is displayed:

In each single well the calculated value is displayed. Depending on the selected item in the control bar, the plate layout window changes correspondingly. Parameters and settings can be changed using the items in the control bar. If the method is to be modified, click on the Edit method tab.
Click in the well with the right mouse key and the context-sensitive menu appears:

Selecting **Summary** the following window is displayed providing detailed information of the definition and the settings of the chosen well:

Click **Finish** in the plate layout window and the **Save as** dialog box appears, where you can enter a file name and remarks. Click the small **Save** button on the left of the window to save the file; you can continue working on the method or workspace. Click the **Save** button on the right side at the bottom of the screen to save the file and to close the wizard. The program goes back to the wizard list.
14.2.5 Summary of Definition of Quantitative ELISA in magellan

1. Subtract Blank value

Definitions in magellan
Click on Add new transformation in the control bar and a window appears, asking if you want to define a Blank reduction. Click Yes and the Blank reduction formula is assigned automatically to all wells.

2. Define Concentrations

Definitions in magellan (Control bar – Method layout/ Conc.-, Dil.-, Ref.-values)
Selected identifier: ST
Unit: UA/ml
ST1_1 5 (ST1_1…..Standard 1 first experimental group)
ST1_2 10 (ST1_2…..Standard 2 first experimental group)
ST1_3 20 (ST1_3…..Standard 3 first experimental group)
ST1_4 40 (ST1_4…..Standard 4 first experimental group)
ST1_5 80 (ST1_5…..Standard 5 first experimental group)
ST1_6 160 (ST1_6…..Standard 6 first experimental group)

3. Define Standard Curve

Definitions in magellan (Control bar – Concentrations/ Standard curve)
Input data: blank reduction
Analysis type: linear regression
X-axis: linear
Y-axis: linear

4. Define Cutoffs

Definitions in magellan (Control bar – Evaluate data/ Cutoff definition)
• Input data: Mean conc. (UA/mL)
  Limits: 22 18
  Positive>=22>intermediate>=18>negative
Non competitive test#

5. QC Validation

Definitions in magellan (Control bar – Evaluate data/ QC validation):
• Input data: Single conc. (UA/mL)
  Validation condition 1 NC1_1<8
  Validation condition 2 NC1_2<8

NC1_1………..Negative Control first replicate first experimental group
NC1_2………..Negative Control second replicate first experimental group
# 15. Glossary of Terms

<table>
<thead>
<tr>
<th>Term</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Anisotropy</td>
<td>Data calculated with polarization measurements</td>
</tr>
<tr>
<td>Average single conc. (???)</td>
<td>Concentration calculated by averaging the single concentrations</td>
</tr>
<tr>
<td>Basis ???</td>
<td>Kinetic Parameter: Basis OD/RFU/RLU value of the onset calculation</td>
</tr>
<tr>
<td>Basis ??? %</td>
<td>Kinetic Parameter: Basis value of the onset calculation in %</td>
</tr>
<tr>
<td>Blank Reduction – parallel</td>
<td>Reduced data calculated with polarization measurements</td>
</tr>
<tr>
<td>Blank Reduction – perpendicular</td>
<td>Reduced data calculated with polarization measurements</td>
</tr>
<tr>
<td>Clipboard</td>
<td>The clipboard is the medium by which programs under Windows exchange data with each other. Data can be selected in one Windows application by cutting or copying it to the clipboard and then added into another application by pasting it from the clipboard.</td>
</tr>
<tr>
<td>Correlation coeff.</td>
<td>Correlation coefficient, indicates the strength and direction of a linear relationship between two random variables.</td>
</tr>
<tr>
<td>Cutoff limit</td>
<td>The cutoff limit enables the user to define the limits between two conditions (for example: positive or intermediate). These criteria are used in the evaluation of the results.</td>
</tr>
<tr>
<td>Cutoff results</td>
<td>Name of the cutoff range the value lies in as defined under cutoff definition</td>
</tr>
<tr>
<td>Cutoff definition</td>
<td>Definition of all cutoff ranges and calculated limits</td>
</tr>
<tr>
<td>Dilution factors</td>
<td>Defined dilution factors of the samples and controls.</td>
</tr>
<tr>
<td></td>
<td>A dilution factor of 2 represents a 1:2 dilution.</td>
</tr>
<tr>
<td>Dilution series</td>
<td>A sample with replicates in different dilutions.</td>
</tr>
<tr>
<td>G-Factor</td>
<td>The G-factor is a instrument constant used in calculations of polarization measurements. In order to determine the G-factor a calibration measurement has to be performed.</td>
</tr>
<tr>
<td>Goodness of fit</td>
<td>1 minus average relative square deviations of the base points from the curve</td>
</tr>
<tr>
<td>Graph</td>
<td>Graphs can be displayed for kinetic measurements, enzyme kinetics, multilabel measurements, dilution series or standard curves.</td>
</tr>
</tbody>
</table>
## 15. Glossary of Terms

<table>
<thead>
<tr>
<th>Term</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hidden</td>
<td>Displayed if well data is hidden when printing</td>
</tr>
<tr>
<td>HUID</td>
<td>Hardware Unit Identification Number</td>
</tr>
<tr>
<td>IC 50</td>
<td>The dilution/concentration which results in 50% of the maximum response</td>
</tr>
<tr>
<td>Intensity – parallel</td>
<td>Reduced data calculated with polarization measurements</td>
</tr>
<tr>
<td>Intensity – perpendicular</td>
<td>Reduced data calculated with polarization measurements</td>
</tr>
<tr>
<td>Invalid</td>
<td>Value is invalid, no calculation possible</td>
</tr>
<tr>
<td>Graph: Kinetic</td>
<td>Graph of kinetic measurements</td>
</tr>
<tr>
<td>Lamp low</td>
<td>No values from measurement because of absorbance instrument error.</td>
</tr>
<tr>
<td>Layout, Plate Layout</td>
<td>Defines where samples or controls are placed on the microplate</td>
</tr>
<tr>
<td>Max. slope ??/?hr</td>
<td>Kinetic Parameter: Maximum slopes of the kinetic curves per hour</td>
</tr>
<tr>
<td>Max. slope ??/?min</td>
<td>Kinetic Parameter: Maximum slopes of the kinetic curves per minute</td>
</tr>
<tr>
<td>Max. slope ??/?sec</td>
<td>Kinetic Parameter: Maximum slopes of the kinetic curves per second</td>
</tr>
<tr>
<td>Maximum ??</td>
<td>Kinetic Parameter: Maximum value of the kinetic curves</td>
</tr>
<tr>
<td>Mean slope ??/?hr</td>
<td>Kinetic Parameter: Average slopes of the kinetics curves per hour</td>
</tr>
<tr>
<td>Mean slope ??/?min</td>
<td>Kinetic Parameter: Average slopes of the kinetics curves per minute</td>
</tr>
<tr>
<td>Mean slope ??/?sec</td>
<td>Kinetic Parameter: Average slopes of the kinetics curves per second</td>
</tr>
<tr>
<td>Mean. conc (???)</td>
<td>Concentration calculated from the mean of the replicates of the input data</td>
</tr>
<tr>
<td>Measurement data</td>
<td>Dual wavelength absorbance measurement: Data measured using the measurement filter</td>
</tr>
<tr>
<td>Measurement parameters</td>
<td>Defines measurement mode, wavelength, plate size, shaking, etc.</td>
</tr>
<tr>
<td>Measurement type</td>
<td>The measurement type can be endpoint measurement, kinetic measurement, multilabel measurement or well-kinetic measurement.</td>
</tr>
<tr>
<td>Method</td>
<td>Methods contain of the measurement parameters and the evaluation definition. Running a method leads to a workspace that contains the measured and calculated data.</td>
</tr>
<tr>
<td>Minimum ??</td>
<td>Kinetic Parameter: Minimum value of the kinetic curves</td>
</tr>
<tr>
<td>Term</td>
<td>Definition</td>
</tr>
<tr>
<td>------------------------------------</td>
<td>-------------------------------------------------------------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>Multiple Reads per Well Measurement</td>
<td>A variety of readers have the ability to run a number of measurements within the same well. The average of the individual values will be determined for use in the evaluation and, if required, chosen values can be masked from the calculations of the mean value.</td>
</tr>
<tr>
<td>MultPt</td>
<td>The standard curve is not monotone and delivers more than one concentration at the given input data.</td>
</tr>
<tr>
<td>NoCalc</td>
<td>No value returned from the calculation.</td>
</tr>
<tr>
<td>Original Concentrations</td>
<td>Concentrations of the standard curve defined in the method.</td>
</tr>
<tr>
<td>Overflow</td>
<td>Overflow occurred during measurement in this well</td>
</tr>
<tr>
<td>Pipetting status</td>
<td>If a sample ID list is imported from a pipetting software, the pipetting status can be displayed.</td>
</tr>
<tr>
<td>QC Validation</td>
<td>The QC validation criteria are defined in the method and stipulate whether a measurement is valid or invalid. The criteria can, for example, indicate if the measurement values lie too far apart from each other, or if they deviate too far from an expected value. The program automatically warns the user if the criteria are not met.</td>
</tr>
<tr>
<td>Strip Method Names</td>
<td>File names of the strip methods (useful for export of strip method results)</td>
</tr>
<tr>
<td>Polarization</td>
<td>Data calculated with polarization measurements</td>
</tr>
<tr>
<td>Raw data</td>
<td>Data measured by the instrument.</td>
</tr>
<tr>
<td>Reference data</td>
<td>Dual wavelength absorbance measurement: Data measured using the reference filter</td>
</tr>
<tr>
<td>Results statistics</td>
<td>Summary of the number of values in the different cutoff ranges</td>
</tr>
<tr>
<td>RFU – parallel</td>
<td>Data measured with polarization measurements</td>
</tr>
<tr>
<td>RFU – perpendicular</td>
<td>Data measured with polarization measurements</td>
</tr>
<tr>
<td>Sample ID List</td>
<td>Sample IDs are assigned to each well on the basis that the associated probe can be identified. The IDs are usually barcodes imported from sample ID lists stored by a pipetting software.</td>
</tr>
<tr>
<td>Sample IDs</td>
<td>IDs of the samples</td>
</tr>
<tr>
<td>Single. conc (???)</td>
<td>Concentration calculated from the input data of each replicate</td>
</tr>
</tbody>
</table>
## 15. Glossary of Terms

<table>
<thead>
<tr>
<th>Term</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Test</td>
<td>In previous versions a test contained the evaluation settings but not the measurement parameters. Tests are no longer supported in magellan and are replaced by the more powerful methods.</td>
</tr>
<tr>
<td>Time Basis ???</td>
<td>Kinetic Parameter: Time until the basis value is reached</td>
</tr>
<tr>
<td>Time Basis ??? %</td>
<td>Kinetic Parameter: Time until the basis value % is reached</td>
</tr>
<tr>
<td>Time Basis to Onset ???</td>
<td>Kinetic Parameter: Time between basis value and onset value</td>
</tr>
<tr>
<td>Time Basis to Onset ??? %</td>
<td>Kinetic Parameter: Time between the basis and the onset value %</td>
</tr>
<tr>
<td>Time max. slope sec</td>
<td>Kinetic Parameter: Kinetic Parameter: Time point of the maximum slope</td>
</tr>
<tr>
<td>Time maximum ???</td>
<td>Kinetic Parameter: Time until the maximum is reached</td>
</tr>
<tr>
<td>Time minimum ???</td>
<td>Kinetic Parameter: Time until the minimum is reached</td>
</tr>
<tr>
<td>Time Onset ???</td>
<td>Kinetic Parameter: Time until the defined onset value is reached</td>
</tr>
<tr>
<td>Time Onset ??? %</td>
<td>Kinetic Parameter: Time until the defined onset in % is reached</td>
</tr>
<tr>
<td>Time points</td>
<td>Time stamps of the single measurements of a kinetic measurement</td>
</tr>
<tr>
<td>Total Intensity</td>
<td>Data calculated with polarization measurements</td>
</tr>
<tr>
<td>Unavailable</td>
<td>Requested data is not available</td>
</tr>
<tr>
<td>Unused</td>
<td>No data measured, no layout defined in this well</td>
</tr>
<tr>
<td>User Prompts</td>
<td>User Prompts are references that are setup in the method. They are displayed before the measurement and the user has to add text to them. This text will then be incorporated in a printout.</td>
</tr>
<tr>
<td>Validation criteria</td>
<td>Summary of validation condition results</td>
</tr>
<tr>
<td>Well position</td>
<td>Name of the well, for example: A1, A2, ...</td>
</tr>
<tr>
<td>Workspace</td>
<td>All available data within the program can be found in the Workspace, for example the measurement data, the print definition and the method definition. The Workspace is used for loading methods and running measurements.</td>
</tr>
<tr>
<td>!</td>
<td>Precedes values that have been eliminated during calculation</td>
</tr>
<tr>
<td>#</td>
<td>Precedes concentration values that have been calculated using extrapolation and lie outside the range of the standard curve</td>
</tr>
<tr>
<td>( )</td>
<td>Parenthesis surround values that have been masked</td>
</tr>
<tr>
<td>Term</td>
<td>Definition</td>
</tr>
<tr>
<td>------</td>
<td>------------</td>
</tr>
<tr>
<td>*</td>
<td>An asterisk marks values that have been measured using the <strong>Use gain regulation</strong> option, which corrects (= lowers) the gain.</td>
</tr>
<tr>
<td>??? – Mean</td>
<td>Calculated averages (for example: Raw data – Mean)</td>
</tr>
<tr>
<td>??? – Standard deviation</td>
<td>Calculated standard deviations (for example: Raw data – Standard deviation or s – Raw data)</td>
</tr>
<tr>
<td>s - ???</td>
<td>Calculated variation coefficients (for example: Raw data – Variation coefficient or v – Raw data)</td>
</tr>
<tr>
<td>~</td>
<td>Added to values that have been edited or simulated</td>
</tr>
<tr>
<td>&lt;Min</td>
<td>Calculated concentration is lower than minimum</td>
</tr>
<tr>
<td>&gt;Max</td>
<td>Calculated concentration exceeds maximum</td>
</tr>
<tr>
<td>&lt;Blank&gt;</td>
<td>Printed report: Insert empty matrix or table printout</td>
</tr>
<tr>
<td>&lt;Page break&gt;</td>
<td>Printed report: Print next item on the next page</td>
</tr>
<tr>
<td>&lt;Separator&gt;</td>
<td>Printed report: Print line between two items</td>
</tr>
<tr>
<td>x</td>
<td>Symbol x refers to the current value within a well</td>
</tr>
<tr>
<td>concX</td>
<td>Symbol <strong>concX</strong> refers to the concentration of the standard in the current well.</td>
</tr>
<tr>
<td>dilX</td>
<td>Symbol <strong>dilX</strong> refers to the dilution of the sample or control in the current well.</td>
</tr>
<tr>
<td>‘???’!</td>
<td>Available data set if more than one set of input data shall be used for calculations</td>
</tr>
<tr>
<td>[]</td>
<td>Indices access the different cycles of a kinetic measurement whereas [0] indicates the first cycle</td>
</tr>
<tr>
<td>*</td>
<td>The asterisk marks identifiers that have been set as aliases.</td>
</tr>
</tbody>
</table>
Index

Numbers refer to pages.

A
About magellan ........................................... 221
abs(argument) .............................................. 236
Add HUIDs ................................................. 225
Add New Transformation ............................... 73
Add/Modify Role ........................................... 208
Add/Modify User (magellan Standard) ............... 218
Add/Modify User (magellan Tracker) ................. 206
Administrator .............................................. 13
Akima ....................................................... 249
and – logical expression ................................ 235
Application Examples .................................... 257
Application Locked ..................................... 34, 213
Application Specialist ................................... 13
Approval ................................................. 174
Arbitrary Cycle Kinetic ................................ 137
Archive Files ............................................ 191
area under the kinetic curve .......................... 79
ASCII File Export ....................................... 148
Assign Alias ............................................. 58, 62
ASTM delimiter definition .............................. 99
ASTM Export Settings ................................ 101
ASTM file ................................................. 99, 100, 101
ASTM File Export ........................................ 98, 100, 148
ASTM File Export (LIS) ................................ 147, 148
Attach signature ........................................... 173
Audit Trail .................................................. 223
Autofill Selection ....................................... 116
Automated Data Handling ............................... 98
Automatic Archiving .................................... 193
Available Data .......................................... 80
avg(argument) ............................................. 237

B
Batch Processing ......................................... 175
Microplate Requirements ............................... 175

C
calcAlways(argument) .................................... 242
Calculations ............................................... 229
Polarization Data Reduction ........................... 230
Spectra Data Reduction ................................ 232
Calculations ............................................. 229
Change Password ........................................ 33
Color Scale ................................................ 164
Components & Terms .................................. 25, 28
Conc., Dil. and Ref. Values ............................. 65
Concentrations .......................................... 159
Connecting an Instrument .............................. 35
Context Sensitive Menu of a Well of .................. 164
Evaluate Results Tab ................................... 164
Details Dialog ............................................ 165
Edit Dialog ............................................... 166
Graph-Kinetics Dialog .................................. 167
Graph-Multilabel Dialog ............................... 166
Graph-Spectra Dialog .................................. 169

D
Data Export ............................................... 89
Data Handling .......................................... 89, 171
Default paths ........................................... 199
Define a Plate Layout .................................. 60
Define Constants ....................................... 76, 125
Define Evaluation ...................................... 56
Define Filter Slides ..................................... 43
Dilution Series .......................................... 162

E
Edit Constants ............................................ 136
Edit user prompts ....................................... 136
Edit well .................................................... 115
eliminate (arg1; arg2; arg3; arg4) .................... 239
eliminatePerc (arg1; arg2) ............................. 240
eliminateRange (arg1; arg2; arg3; arg4) .......... 240
Email Options ........................................... 215
Enzyme Kinetics ........................................ 80
Enzyme Kinetics Graph ................................ 158
Evaluate Data ............................................ 86
Evaluate Results ......................................... 143, 171
Excel Export ............................................ 148
exp(argument) ............................................ 236
Export
to ASCII ............................................... 92
to Excel ................................................. 93

F
File Handling ............................................ 224
File Selection Criteria .................................. 144
file type symbols ....................................... 24
File Types Used with magellan ........................ 26
Five Parameters – Marquardt .......................... 254
Folder Handling ......................................... 23
Formula .................................................... 233
Basic Functions ......................................... 236
Index

Elimination Functions ........................................... 239
Functions ......................................................... 235
How to write a formula ......................................... 233
Logical Expressions ............................................. 235
Operators .......................................................... 234
Other Functions .................................................. 242
Spectra Functions .................................................. 243
Statistical Functions ........................................... 237
Variables ............................................................. 233
Four Parameters ............................................... 252
Four Parameters – Marquardt ................................ 253
frac(argument) .................................................... 236

G

Gas Control Module (GCM) Enhanced
Connecting to ....................................................... 186
Data Displayed in Status Bar .................................. 188
Data Logging ......................................................... 186
Importing Logged Data Into Microsoft Excel ............ 188
Precautions before Starting a Measurement .............. 189
Prerequisites ....................................................... 185
Glossary of Terms .............................................. 277

H

Heating Dialog ..................................................... 42
Help Button .......................................................... 31
HUID ................................................................. 20, 21, 37, 225

I

Icons ........................................................................ 28
ICx calculation ....................................................... 67
identifiers .............................................................. 63, 64
if(…) then(…) else(…) – logical expression ........... 235
ignore() ............................................................... 242
Import Raw Data .................................................. 194
Import sample ID list .......................................... 117
Import/edit a sample ID list ................................... 112
In(argument) ........................................................... 236
Initial Password ...................................................... 33
Insert Sample ID List .......................................... 140
Installation
Software ............................................................... 18
Installation Qualification IQ ................................... 19
Instrument Control .............................................. 41
Instrument Data .................................................... 156
int(argument) ........................................................ 236
isInvalid() ............................................................ 242

K

Kinetic Data Reduction ........................................... 76
Kinetic Parameters ................................................. 157
Kinetic transformations ........................................ 80, 85
Kinetics Graph ......................................................... 167

L

Levenberg-Marquardt algorithm .............................. 253
Levenberg-Marquardt method ................................ 254
Levy-Jennings-Graph ............................................. 150
lg(argument) ........................................................... 236
Licensing magellan .................................................. 37
Lock application .................................................... 213
Log(argument) ........................................................... 236
Logical Expressions ............................................. 235
and ........................................................................ 235
if(…) then(…) else(…) ........................................... 235
or ........................................................................ 235
login ................................................................. 218
Login ...................................................................... 34
logins unsuccessful .............................................. 213

M

magellan Standard .................................................. 13
magellan Standard .................................................. 15
magellan Standard .................................................. 18
magellan Tracker .................................................. 13
magellan Tracker .................................................. 15
magellan Tracker .................................................. 18
Manufacturer ......................................................... 3
max(argument) ...................................................... 238
maxAvg(argument) ................................................. 238
mean(argument) .................................................... 237
Measurement Parameters ..................................... 52
Measurement Status ............................................. 141
Measurement Types ............................................. 53
median(argument) .................................................. 237
medianPlate() ....................................................... 237
Menus of the Evaluate Results Tab .................. 147
Method Export ...................................................... 148
Method Layout ......................................................... 163
Method Notes ....................................................... 103
min(argument) ....................................................... 238
Min./Max. ............................................................. 79
minAvg(argument) .................................................. 238
Miscellaneous Icon ............................................... 191
Options ............................................................... 198
Miscellaneous of Evaluate Results Tab ............ 163
Miscellaneous Tab ................................................. 203
Movements
plate carrier, filter slide ......................................... 41
Multilabel Graph ..................................................... 166
Multilabel Measurement ....................................... 54
Multiplate Methods ............................................. 105

N

New Identifier ......................................................... 63
Number Format ....................................................... 102

O

Obtain Raw Data ................................................... 129, 130
Onsets ................................................................. 78
Operation Qualification OQ ..................................... 19
Operator .............................................................. 14
Optimize Z-Position ............................................... 44
or – logical expression ......................................... 235
Organize Favorites .................................................. 134

P

Park ................................................................. 183
Password
Expiration ......................................................... 215
Options ............................................................... 214
Paste from ASCII-Format ..................................... 153
Paste in ASCII-Format ......................................... 117
Paths Tab ............................................................. 199
Plate geometry editor .......................................... 44
Plate layout .......................................................... 60
Plate Layout Window .................. 57, 154
Plate to Plate QC ........................ 88, 149
Plate View Settings ....... 202
Plate View Tab .................. 202
PointwiseCV(argument) ................. 238
Polarization Data Reduction .... 68, 230
Print ........................................ 149
Print Preview ......................... 149
Printed Report ..................... 93
Printer Setup .................. 149
Printout Font .................. 149

Q
QC Validation .................. 87, 163
Qualitative Results ............. 162
Quantitative ELISA Example .... 257

R
Reader Compatibility ............ 17
Recalculate with another Method .... 154
Reduced Data .................. 156
Register Wizard .............. 221
Registration form .............. 39
Restack ......................... 183
Review ......................... 174
round(argument) .................. 236
Run Strip Layout .............. 129

S
sample ID list
  importing .................................. 110, 117
Sample ID list .................. 129
Sample ID List Settings ........... 110
Sample IDs ......................... 163
Saving the Evaluated Results .......... 171
Saving the Method .................. 103
Saving the Sample ID List ......... 126
Shortcuts List ................. 31
Sign a File ......................... 173
Signature ......................... 173
Approval ......................... 174
Review ........................ 174
Simulated Instrument .......... 179
Slopes ................................ 77
SMTP server .................. 215

Software
  Installation .................. 18
  Removal ......................... 22
Special Characters ............... 155
Spectra Data Reduction ....... 69, 232
Spectra Dialog .................. 169
  spectrum of a scan measurement .... 169
  sqr(argument) .................. 237
  sqrt(argument) .................. 237

Standard Curve .................. 81, 159
Standard Curve Analysis Types .... 246
Standard Curve Graph .......... 161
Standard Elements .................. 30
Start Favorite ................... 129
Start Favorites ................. 134
Start Measurement ............ 129, 136
Starting magellan .............. 32
stddev(argument) .................. 238
Strip ......................... 132
Sum(argument) .................. 238
System Audit Trail ............ 226
System Recovery .................. 20

T
Teaching ......................... 183
Temperature Control ........... 29, 41, 138, 154
Test Mail ......................... 215
Transformation
  Add new transformation ................. 73
  Rename Transformation ................. 73
  Transformed Data .................. 73
  Transformed Data .................. 156

U
Unsuccessful logins .................. 213
Use Predefined Method .......... 129, 133
User Administration ............. 205
  Options ......................... 213
User Administration (magellan Standard) .... 217
User Administration (magellan Tracker) ........ 205
  Change User .................. 219
  Login ......................... 219
User Administration Audit Trail ...... 209
User Administration Summary .... 216
User Interface .................. 23
User Prompts ..................... 102
User Rights ..................... 210, 219
table of default rights .............. 209
User Rights (magellan Standard) .... 219
User Rights (magellan Tracker) .... 209

W
Weighting
  Four/Five Parameter Fit – Marquardt/Polynomial Fit .... 83, 255
Welcome Dialog box .......... 31
Well Summary .................. 116
Westgard® rules .................. 152
Wizard
  Standard Elements .................. 30
  Wizard List ..................... 27
Workspace Overview .............. 145
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