BioNumerics®

MICROBIAL DATA ANALYSIS SOFTWARE

# Antibiotics susceptibility plugin

PLUGINS

VERSION 7.6

www.applied-maths.com

# Contents

## NOTES

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- PIL Python library® version 1.1.7 (http://www.pythonware.com/products/pil/).
- The SPAdes genome assembler version 3.7.1 (http://bioinf.spbau.ru/spades).

# Chapter 1

# Starting and setting up BioNumerics

## 1.1 Introduction

This guide is designed as a tutorial for the *Antibiotics Susceptibility plugin* of BioNumerics. With this plugin, *zone diameter interpretive standards* and *equivalent minimal inhibitory concentration (MIC) breakpoints* can be stored in the database. These standards can be imported from a text file or they can manually be entered and edited in the database (see 2.1).

Antibiotic data can be imported from text files, MS Excel or from any ODBC-compatible source (see 3.1.2). Based on the defined standards, the antibiotics data is converted to Sensitive (S), Intermediate (I) and Resistant (R) categories. This setup makes it possible to evaluate antibiotics data with different breakpoints, e.g. in case guidelines change.

The features of the *Antibiotics Susceptibility plugin* will be illustrated using data available on the download page on the Applied Maths website (`http://www.applied-maths.com/download/sample-data`, click on "Antibiotics sample data").

The minimal configuration for the installation of the *Antibiotics Susceptibility plugin* includes the Character data module (import antibiotics data) and the Classifiers and Identification module (use of decision networks for the conversion to categorical data).

## 1.2 Startup program

When BioNumerics is launched from the Windows start panel or when the BioNumerics shortcut (  ) on your computer's desktop is double-clicked, the **Startup program** is run. This program shows the *BioNumerics Startup* window (see Figure 1.1).

A new BioNumerics database is created from the Startup program by pressing the  button.

An existing database is opened in BioNumerics with  or by simply double-clicking on a database name in the list.

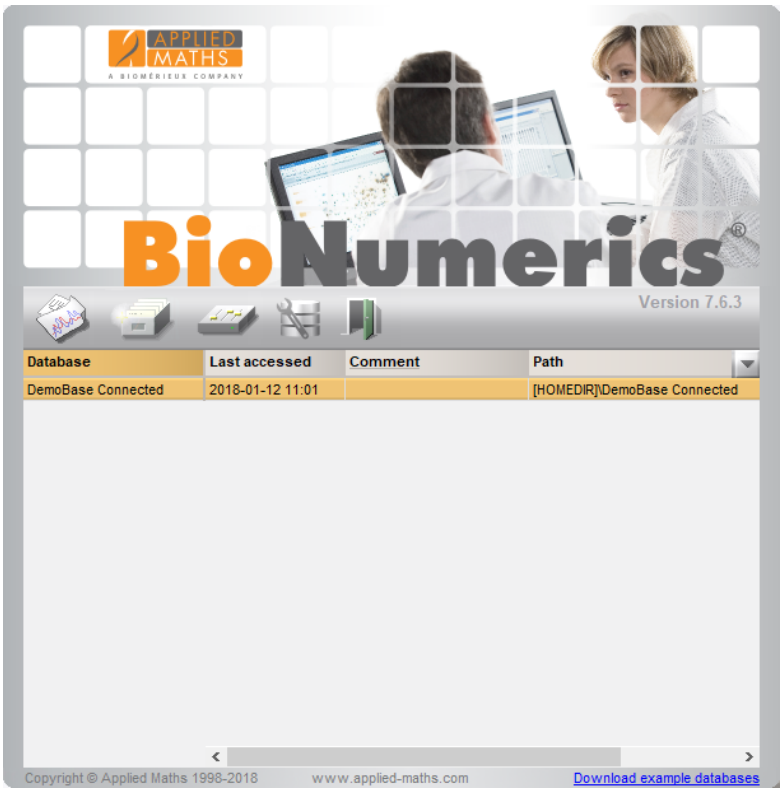


**Figure 1.1:** The *BioNumerics Startup* window.

## 1.3 Creating a new database

3.1 Press the  button in the BioNumerics *BioNumerics Startup* window to enter the *New database* wizard.

3.2 Enter a name for the database, and press <***Next***>.

A new dialog box pops up, prompting for the type of database (see Figure 1.2).

3.3 Since we want to create a new database to demonstrate the features of the plugin, leave the default option selected and press <***Next***>.

A new dialog box pops up, prompting for the database engine (see Figure 1.3).

3.4 Leave the default option selected and press <***Next***>.

3.5 Press <***Finish***> to complete the setup of the new database.

The *Plugins* dialog box appears.

## 1.4 Installing the Antibiotics susceptibility plugin

If a database is opened for the first time, the *Plugins* dialog box will appear by default (see Figure 1.4).

If the database has already been opened previously, the *Plugins* dialog box can be called from the *Main* window by selecting ***File*** > ***Install / remove plugins...*** (  ).

When a particular plugin is selected from the list of plugins, a short description appears in the right panel.

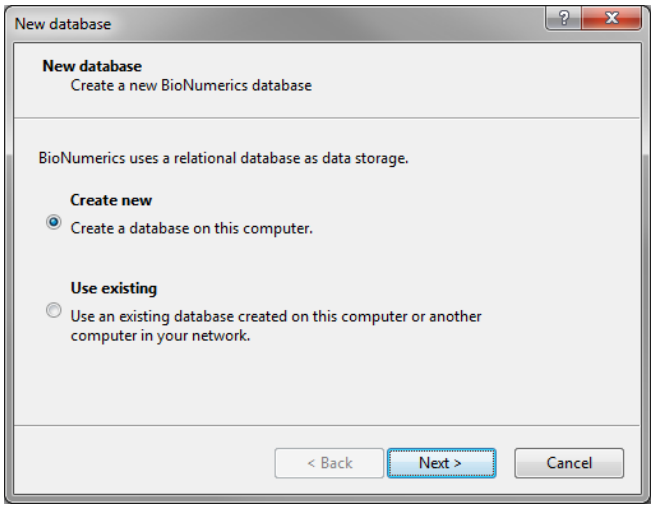


**Figure 1.2:** The *New database* wizard page.

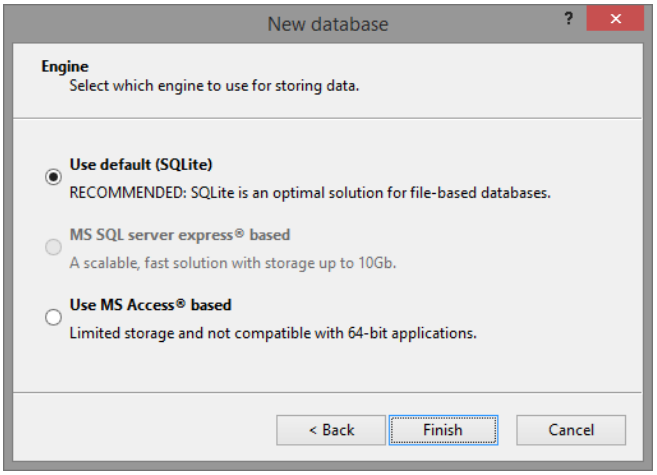


**Figure 1.3:** The *Database engine* wizard page.

A selected plugin can be installed with the <***Activate***> button. The software will ask for confirmation before installation. Some plugins depend on functionality offered by specific BioNumerics modules. If a required module is missing, the plugin cannot be installed and an error message will be generated.

Once a plugin is installed, it is marked with a green V-sign. It can be removed again with the <***Deactivate***> button.

If the selected plugin is documented, pressing <***Show Manual***> will open its manual in the *Help* window.

4.1 Select the *Antibiotics susceptibility plugin* from the list in the *Applications tab* and press the <***Activate***> button.

4.2 The program will ask to confirm the installation of the plugin. Press <***Yes***> and then <***OK***> to confirm the installation.

4.3 Press <***Proceed***> (or <***Exit***>) to close the *Plugins* dialog box and to continue to the *Main* window.

4.4 Close and reopen the database to activate the features of the *Antibiotics susceptibility plugin*.

The *Antibiotics susceptibility plugin* installs itself in a menu of the BioNumerics software (see Figure 1.5).

The ***Import antibiotics data*** items are activated in the *Import* dialog box (see Figure 1.6). This dialog is called when selecting ***File*** > ***Import...*** (, **Ctrl+I**) in the *Main* window.

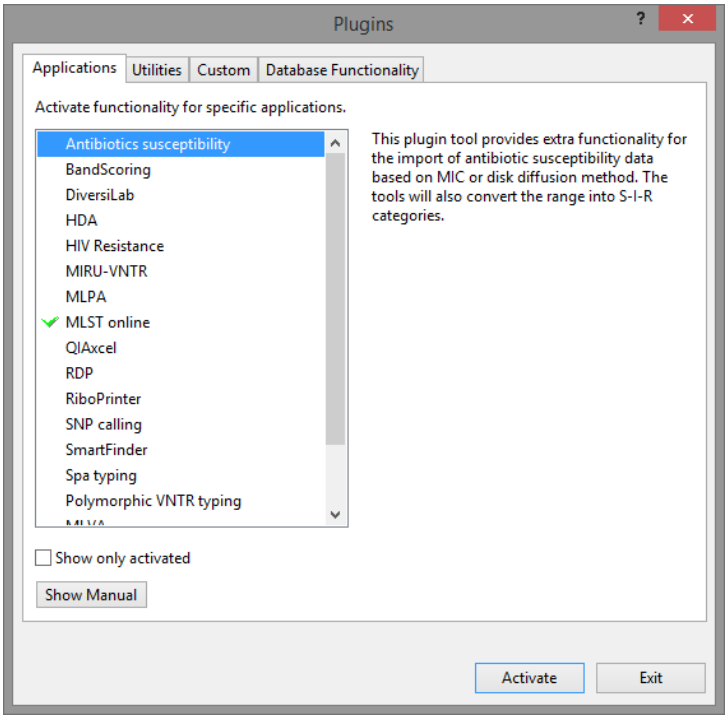


**Figure 1.4:** The *Plugins* dialog box.

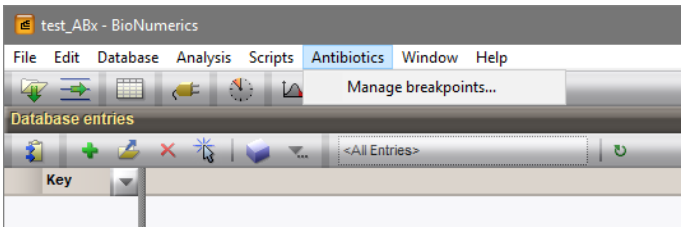


**Figure 1.5:** Antibiotics menu item in the *Main* window.

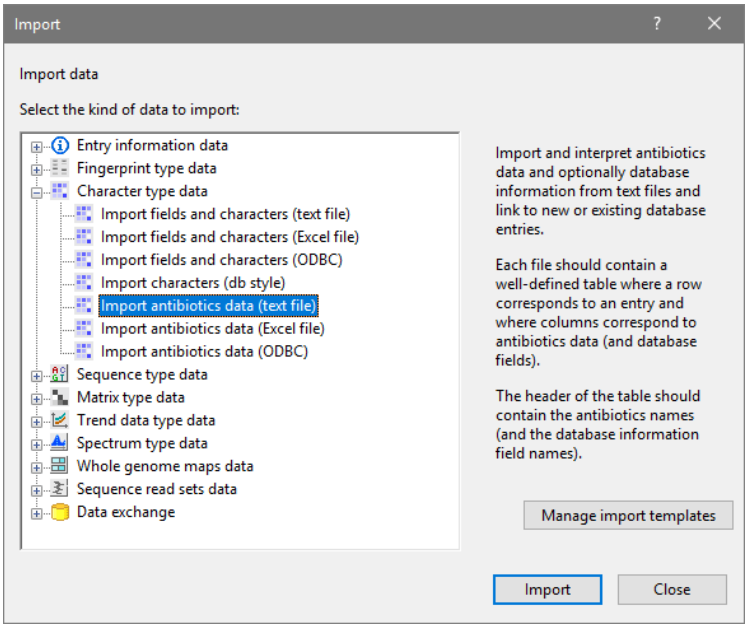


**Figure 1.6:** The ***Import antibiotics data*** items for text files, Excel files and ODBC-compatible sources in the Import tree.

# Chapter 2

# Defining experiment settings

## 2.1 Managing antibiotics breakpoints

In order to classify ”raw” antibiotic resistance data i.e. zone diameters for the disk diffusion method or Minimum Inhibitory Concentration (MIC) values into the categories Sensitive (S), Intermediate (I) and Resistant (R), we first need to specify the cut-off values per antibiotic for the bacteria under study. These values can be imported from a text file or added manually.

1.1 Select ***Antibiotics*** > ***Manage breakpoints...*** in the *Main* window.

The *Add ABx breakpoints* dialog box (see Figure 2.1) pops up in case no breakpoints were specified earlier.

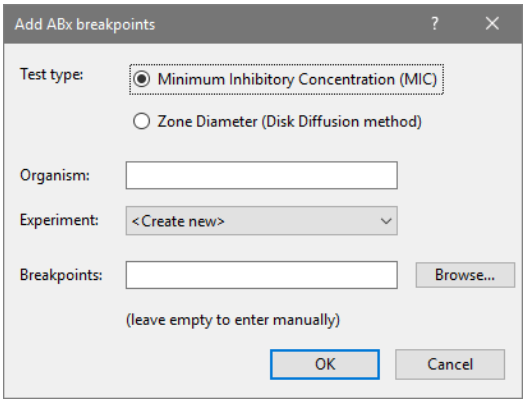


**Figure 2.1:** The *Add ABx breakpoints* dialog box.

For ***Test type***, choose between ***Minimum Inhibitory Concentration (MIC)*** or ***Zone Diameter (Disk Diffusion method)***, depending on the input data available.

Since breakpoints are typically organism-dependent, an ***Organism*** should be specified. The organism name will be used in the decision network name, allowing you to maintain different cut-off values for interpretation of antibiotics resistance data.

From the ***Experiment*** drop-down list, an existing character experiment type can be selected to hold the antibiotics data values. With <***Create new***>, a new character experiment type will be created automatically.

A text file with breakpoints can be browsed for by pressing the <***Browse...***> button next to ***Breakpoints***. Only a text file that contains a table of tab-delimited values can be used for this import routine. The table should contain the data in the following format (see Figure 2.2 for a fictitious example):

- **Header line**: Column names.

- **First column**: Full name of the antibiotic agents.
- **Second column**: Abbreviations of the antibiotics' names.
- **Third column**: Susceptibility cut-off values.
- **Fourth column**: Intermediate values.
- **Fifth column**: Resistant cut-off values.

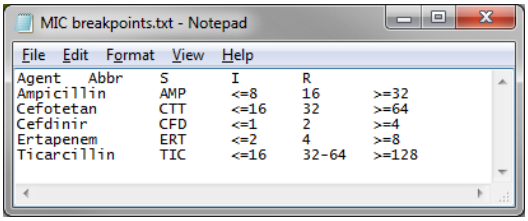


**Figure 2.2:** Example file with equivalent Minimal Inhibitory Concentration (MIC) breakpoints for *Enterobacteriaceae*.

If no text file is provided, the breakpoints can be entered manually in the *Edit ABx breakpoints* dialog box.

Pressing <***OK***> in the *Add ABx breakpoints* dialog box will create following components in the database:

- A decision network to convert MIC values or inhibition zone diameters into Sensitive (S), Intermediate (I), or Resistant (R) categories.
- A character experiment type to store the MIC values or inhibition zone diameters (only if <***Create new***> was selected).
- A character experiment type to store the SIR values. Its name corresponds to the name of the character type that holds the antibiotic data values, with the suffix "_SIR" added.

As an example, we will import (fictitious) MIC breakpoints for *Enterobacteriaceae*. This file can be found on the sample data download page of the Applied Maths website (`http://www.applied-maths.com/download/sample-data`, click on "Antibiotics sample data").

1.2 In the *Add ABx breakpoints* dialog box, check the ***Minimal Inhibitory Concentration (MIC)*** option.

1.3 Enter "Ecoli" in the ***Organism*** text box and select the <***Create new***> option for ***Experiment***.

1.4 Press <***Browse...***>, navigate to the downloaded and unzipped `MIC breakpoints.txt` file and press <***Open***>.

1.5 Press <***OK***> in the *Add ABx breakpoints* dialog box.

As a result, the *Edit ABx breakpoints* dialog box pops up, displaying the breakpoints from the `MIC breakpoints.txt` text file (see Figure 2.3).

To add breakpoints for an additional antibiotic, press <***Add...***>. This action displays the *Add ABx breakpoint* dialog box (see Figure 2.4).

An antibiotic ***Name***, an abbreviation (***Abbr.***) and the breakpoints for Sensitive (***S***), Intermediate (***I***) and Resistant (***R***) need to be entered. If no intermediate resistances should be assigned, the (***I***) values can be left empty.

Pressing <***OK***> will add the breakpoints for this antibiotic to the list in the *Edit ABx breakpoints* dialog box.

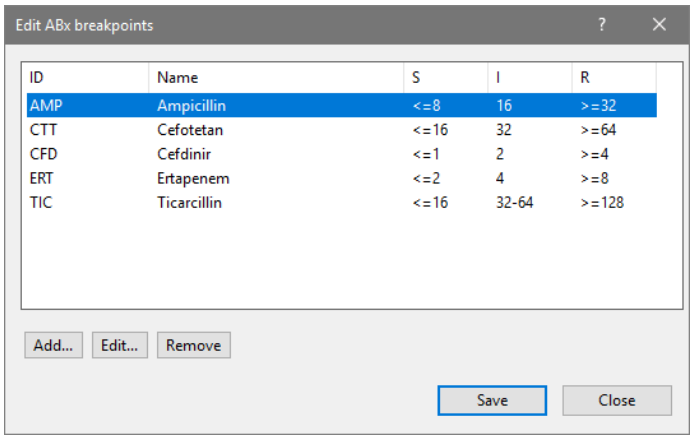


**Figure 2.3:** The *Edit ABx breakpoints* dialog box, displaying the breakpoints from the sample `MIC breakpoints.txt` text file.

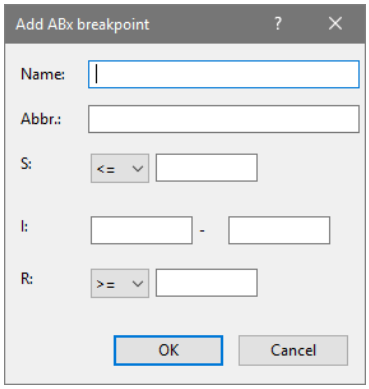


**Figure 2.4:** The *Add ABx breakpoint* dialog box.

To edit the breakpoints for an already listed antibiotic, highlight it from the list and press <***Edit...***>. Alternatively, simply double-click the antibiotic in the list. The *Edit ABx breakpoint* dialog box pops up (see Figure 2.5).

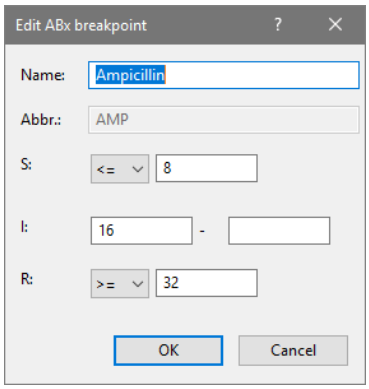


**Figure 2.5:** The *Edit ABx breakpoint* dialog box, to modify the breakpoints for a single antibiotic.

The antibiotic ***Name*** and the breakpoints for Sensitive (***S***), Intermediate (***I***) and Resistant (***R***) can be altered. If no intermediate resistances should be assigned, the (***I***) values can be left empty. The antibiotic abbreviation (***Abbr.***) is inactive and cannot be modified since it is used as a character name.

Pressing <***OK***> will save the modified breakpoints for this antibiotic. The new values will be listed in the *Edit ABx breakpoints* dialog box.

The breakpoints for an antibiotic can be removed by highlighting the antibiotic in the list and pressing <***Remove***>. The software will ask for confirmation before actually removing the breakpoints.

Press <***Save***> to save any changes made to the antibiotics breakpoints in the database.

If the dialog box is closed, the software will detect if breakpoints were changed and will prompt you to save these changes.

When one or more sets of antibiotics breakpoints are present in the database, selecting ***Antibiotics*** > ***Manage breakpoints...*** will display the *Manage ABx breakpoints* dialog box (see Figure 2.6).

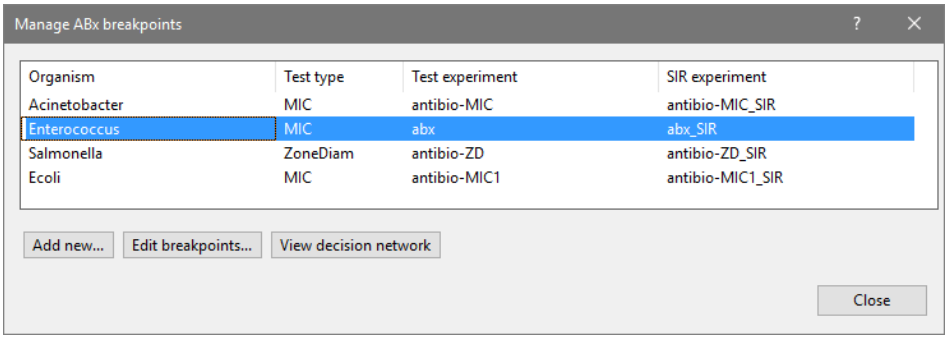


**Figure 2.6:** The *Manage ABx breakpoints* dialog box, displaying sets of antibiotics breakpoints for four different organisms.

Pressing <***Add new...***> will pop up the *Add ABx breakpoints* dialog box, from which a new set of breakpoints can be added.

The highlighted set of breakpoints can be edited by pressing <***Edit breakpoints...***> or simply double-clicking the item in the list. This action opens the *Edit ABx breakpoints* dialog box.

Pressing <***View decision network***> will open the *Decision Network* window, for closer examination of the decision network that converts MIC values or zone diameters into S, I and R for the highlighted set of breakpoints.

## 2.2 Character types and decision networks

In the *Experiment types* panel, the two character types are listed (see Figure 2.7).

2.1 Select the *Decision networks* panel in the lower right part of the *Main* window (see Figure 2.7).

In this example, the network is named **ABX_MIC_Ecoli_antibio-MIC**. All imported breakpoint information is contained in this decision network. The information is written to the *Antibiotics values* experiment type (in this example **antibio-MIC**) and to the *SIR categorical* experiment type (in this example **antibio-MIC_SIR**).

2.2 Double-click on the **antibio-MIC_SIR** experiment type in the *Experiment types* panel.

2.3 Make sure the *Characters* panel is displayed in the *Character type* window (see Figure 2.8).

The abbreviations of the antibiotics names are listed in the first column. The **Name** column lists the full names of the antibiotics. This column is used as the default field in the *Comparison* window (column highlighted in pale green; see Figure 2.8). The 'Min.' and 'Max.' columns list the minimum and maximum categorical values for each category. The default color scale ranges from white (category 0), over green

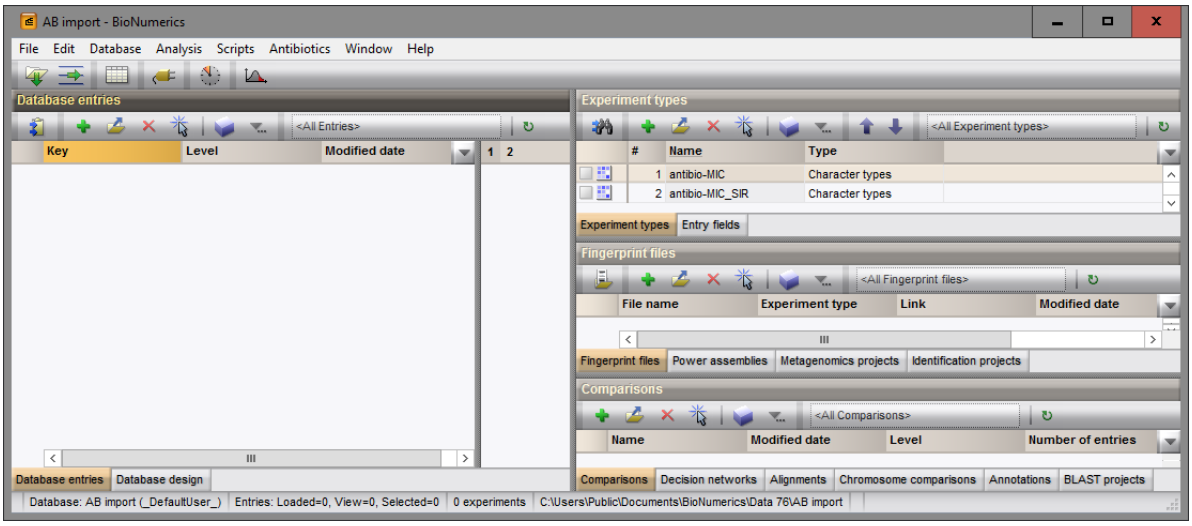


**Figure 2.7:** The *Main* window, after adding a new antibiotics experiment.

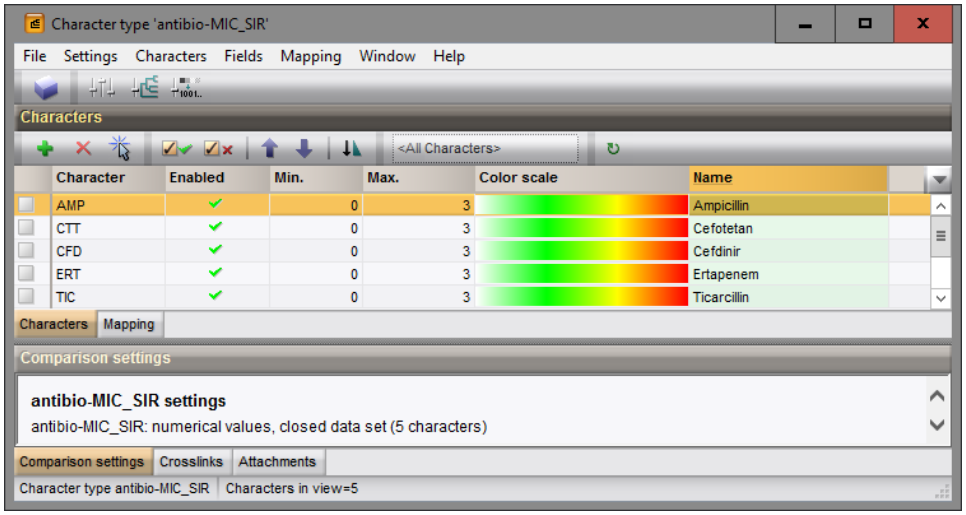


**Figure 2.8:** The **antibio-MIC_SIR** character type.

(category 1), over yellow (category 2), to red (category 3).

2.4 Select the *Mapping* panel in the *Character type* window (see Figure 2.9).

Four mapping names are defined for the four different categories: N/A (not available) if the categorical value is 0 (absent value); S (susceptible) if the categorical value is 1; I (intermediate) if the categorical value is 2; R (resistant) if the categorical value is 3.

2.5 Close the *Character type* window with ***File*** > ***Exit***.

## 2.3 Additional exercise

As an exercise, import the (fictitious) breakpoints for *Enterobacteriaceae* based on the *disk diffusion method* using the text file `Zone diameter breakpoints.TXT`.

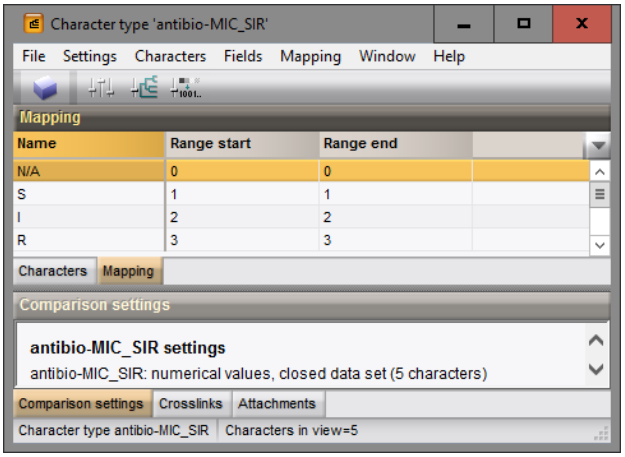


**Figure 2.9:** The *Mapping* panel.

# Chapter 3

# Antibiotics data import and conversion

## 3.1 Import procedure

### 3.1.1 Overview of the import procedure

After importing the antibiotics breakpoints (see 2.1), MIC values or inhibition zone diameters (referred to as "antibiotics data" in this text) can be imported in the database. The original values will be stored in the **antibio-MIC** character type and will be automatically converted to SIR categories by the corresponding decision network (see 2.2). Whether a given strain is Sensitive (S), Intermediate (I) or Resistant (R) against a given antibiotic, will be stored in the **antibio-MIC_SIR** character type. This setup allows you to easily re-evaluate already imported antibiotics data with different breakpoints.

The import of antibiotics data works via the general ***File*** > ***Import...*** (  , **Ctrl+I**) functionality, since the *Antibiotics Susceptibility plugin* add additional items to the Import tree (see also 1.4).

Before any data can be imported, an **import template** should be created (see 3.1.3). An import template specifies where and how the information contained in an external file should be stored in the BioNumerics database. Once an import template is created, it can be used over and over again for all data files with the same format (see 3.1.4).

### 3.1.2 Compatible data formats

MIC values and inhibition zone diameters can be imported from **text files**, **MS Excel files** or from any **ODBC-compatible source**. In any case, the data should be arranged in a grid containing a header row. One column should contain a strain identifier, which could correspond to the key or a unique database field such as an isolate or strain number. Optionally, one or more columns can contain strain descriptive information. Additional columns should represent MIC values or inhibition zone diameters of individual antibiotics. Greater-or-equal (>=) or smaller-or-equal signs (<=) preceding the values are optional. The header row should contain only unique column names, i.e. information field names or antibiotics names or abbreviations. See Figure 3.1 and Figure 3.2 for an example of the expected format.

With the antibiotics data stored as Comma Separated Values (CSV) or in tab-delimited **text files** as illustrated in Figure 3.1, the corresponding item ***Import antibiotics data (text file)*** should be selected from the Import tree. The only required input is the file path of the text file, which can be browsed for by pressing the <***Browse***> button.

With the antibiotics data stored in an **MS Excel file** (`*.xls` or `*.xlsx` files) as illustrated in Figure 3.2, the corresponding item ***Import antibiotics data (Excel file)*** should be selected from the Import tree. In addition to the file path of the Excel file, a ***Data range*** should be specified from the drop-down list. This corresponds to a Excel sheet name or a named range that contains the antibiotics data.

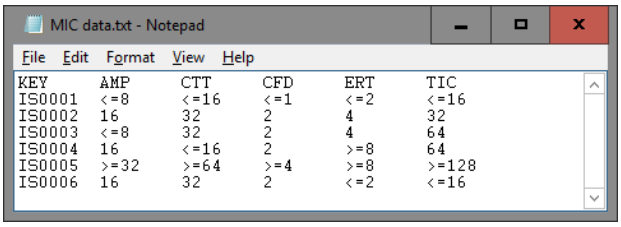


**Figure 3.1:** MIC values for *E. coli* entries with key IS0001-IS0006: text file.

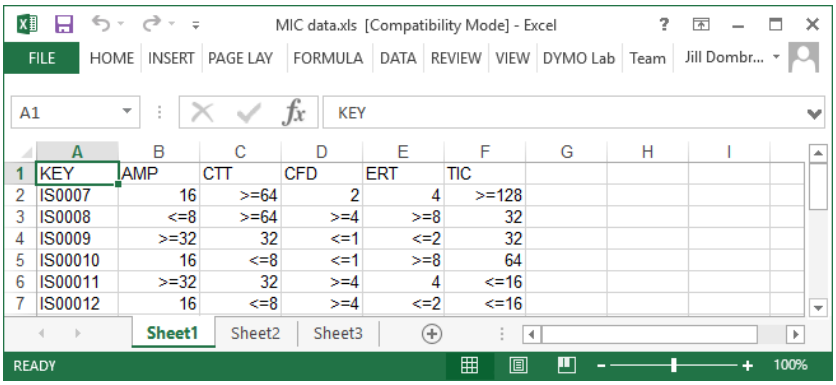


**Figure 3.2:** MIC values for *E. coli* entries with key IS0007-IS00012 : Excel file.

With the antibiotics data stored in an **ODBC-compatible database**, the corresponding item ***Import antibiotics data (ODBC)*** should be selected from the Import tree. This option requires you to build an ODBC connection string to the database and specify the ***Database table*** in which the antibiotics data are stored.

### 3.1.3 Creating an ABx import template

A new import template can be created by pressing the <***Create new...***> in the *Antibiotics data import template* wizard page (see 3.1.4). If no import template is available yet, the *Import rules* dialog box (see Figure 3.3) will open automatically.

Each column in the selected file corresponds to a row in the grid (column 1 in the file corresponds to row 1 in the grid, column 2 corresponds to row 2, etc.). The text ***File field*** is specified in the ***Source type*** column and the column names are displayed in the ***Source*** column.

The rows in the grid can be associated with new or existing entry information fields, antibiotics experiments, or character type information fields. Initially the rows are not linked to any information in the database (the ***Destination type*** and ***Destination*** for all rows is set to <***None***>).

Specifying a *destination* for one or more selected rows can be done by pressing the <***Edit destination...***> button or by double-clicking. This action pops up a new dialog box prompting for the new destination for the selected row(s).

To select multiple rows, hold the **Ctrl**-key on the keyboard and click the rows to be selected. To select a complete range of rows at once, select the first row, hold the **Shift**-key and click the last row.

With more than one row selected, the last-clicked row should be double-clicked to edit the destinations.

When only one row is selected in the grid, the information of this row can be linked to (see Figure 3.4):

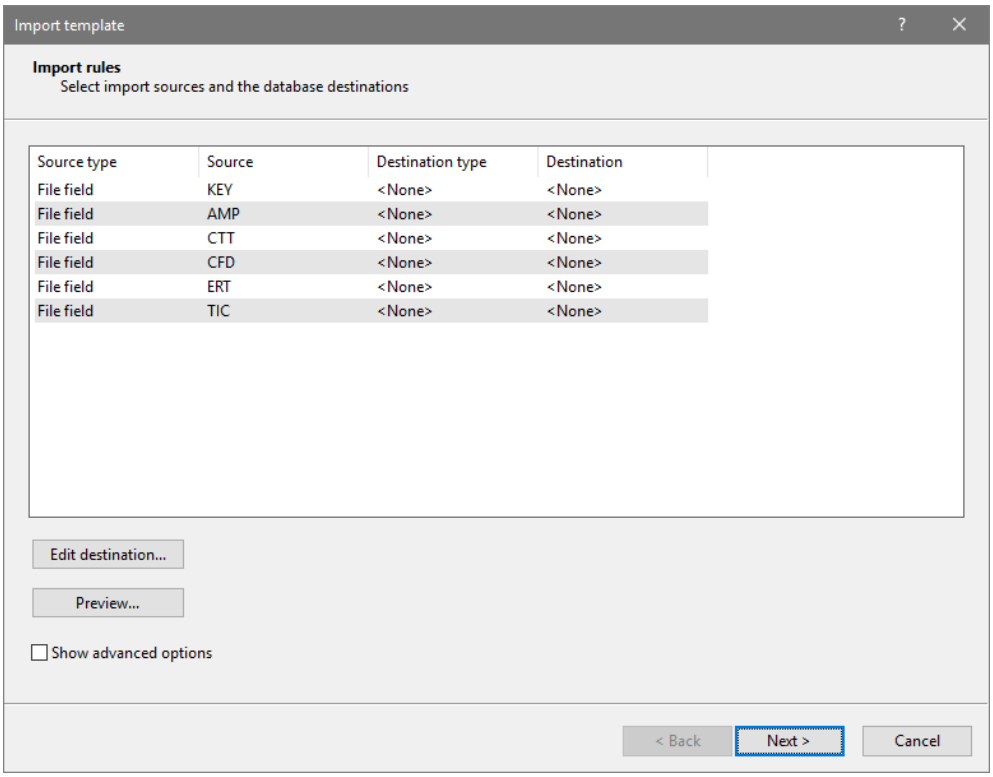


**Figure 3.3:** The *Import rules* dialog box for antibiotics data.

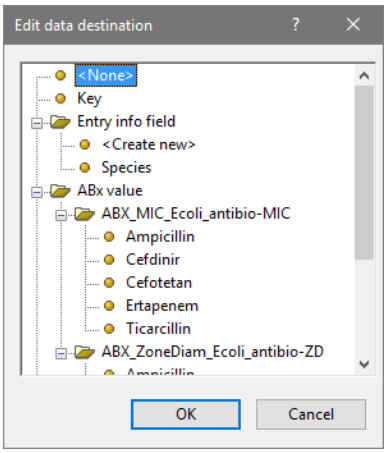


**Figure 3.4:** Edit data destination for a single selected row entry.

- The default information field ***Key***.
- A new or existing non-default entry information field (select the <***Create new***> option or an existing field under the topic ***Entry info field***, respectively).
- A value of an antibiotic in an existing antibiotics experiment. The latter are listed under ***ABx values*** as the name of the decision network that performs the conversion from MIC values or zone diameters to SIR (see 2.2).
- A mapped value of an antibiotic in an existing antibiotics experiment. In order to import the mapped values correctly, the mapping rules need to be defined in the experiment type before the import. This can be done in the *Character type* window and is described in detail in the Reference manual, Chapter Setting up character type experiments.

- A new or existing character type information field (select <***Create new***> or select an existing field under the topic ***Character set info field***, respectively).

If a row is linked to a new entry information field or a new character type information field, a new dialog box pops up when pressing the <***OK***> button. This new dialog box prompts for the name of the new field.

When multiple rows are selected in the grid, the information of these rows can be linked to (see Figure 3.5):

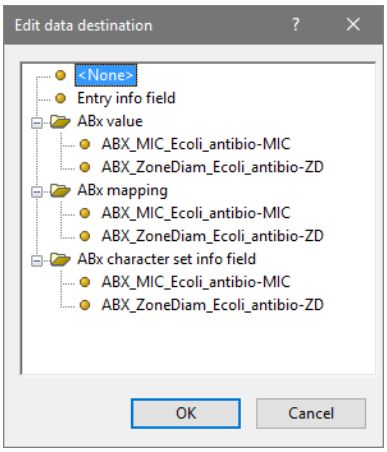


**Figure 3.5:** Edit data destination for multiple selected row entries.

- Non-default entry information fields (select the ***Entry info field*** option).
- Values of antibiotics in an existing antibiotics experiment. The latter are listed under ***ABx values*** as the name of the decision network that performs the conversion from MIC values or zone diameters to SIR (see 2.2). Antibiotics will be automatically linked if their name or abbreviation matches with the one defined in the character type. An error message will be generated if this is not the case.
- Mapped values of antibiotics in an existing antibiotics experiment. In order to import the mapped values correctly, the mapping rules need to be defined in the character type experiment before the import. This can be done in the *Character type* window and is described in detail in the Reference manual, Chapter Setting up character type experiments.
- Character information fields of a character type experiment (select the character type experiment under the topic ***Character set info field***).

When pressing the <***OK***> button, the plugin checks if the selected rows can automatically be mapped to existing entry information fields or character information fields in the database. If no entry information fields or character information fields exist with the same name, a new dialog box pops up prompting for the names.

When a row in the grid is linked to the ***Key*** field, the ***Destination*** column in the grid displays the name ***Key***. Rows that are linked to entry information fields in the database display the text ***Entry info field*** in the ***Destination type*** column; the ***Destination*** column holds the name of the entry information field. Rows linked to antibiotics, defined in an antibiotics experiment, hold the name of the corresponding decision network (preceded with ***ABx value:***) in the ***Destination type*** column; the name of the antibiotic is displayed in the ***Destination*** column. When rows are linked to character type information fields, the text ***ABx character set info field***, followed by the name of the decision network, is displayed in the ***Destination type*** column; the name of the character information field is listed in the ***Destination*** column.

Pressing <***Preview***> opens the *Preview* dialog box displaying the parsed information using the template settings. The preview can be closed with the <***Close***> button.

When the <***Show advanced options***> check box is enabled, three more columns appear inside the grid and eight extra buttons appear below the grid.

Pressing the <***Cancel***> button cancels the operation and the template settings are not saved to the database.

Pressing the <***Next***> button calls a new dialog where the entry link field needs to be defined.

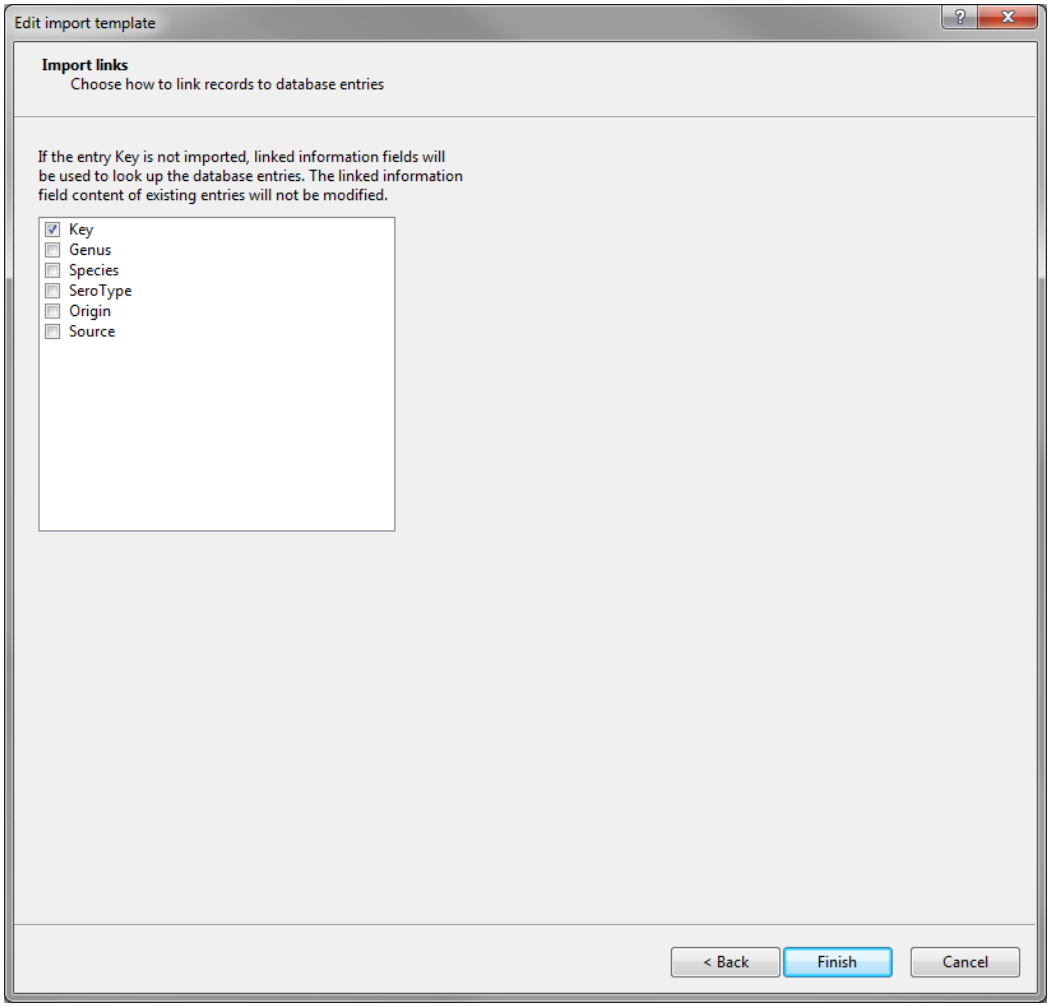


**Figure 3.6:** Specify the entry link field.

- If a row in the grid is linked to the ***Key*** field in the database, ***Key*** is automatically selected as the entry link field. If entries are already present in the database with the same (parsed) key information, the import tool will link the data to these entries. If the ***Key*** field was linked for several levels, the import tool will link to each of these levels and also create cross links between the levels.

- If no row entry in the grid is linked to the ***Key*** field, but one or more rows are linked to an entry information field in the database, these fields can be selected from the list. If entries are already present in the database with this linked information, the import tool will link the data to these entries (Note: If the linked field content is not unique in the database, the data is linked to only one entry in the database, i.e. the first entry in the database holding the linked field content). If the entries are not yet present in the database, the data will be linked to new entries in the database.

- If no fields are selected from the list, no check for existing entries will be performed, and all data will be linked to new entries in the database (if the option ***Create x entries*** is checked in the last step of the wizard). New keys are automatically generated during import.

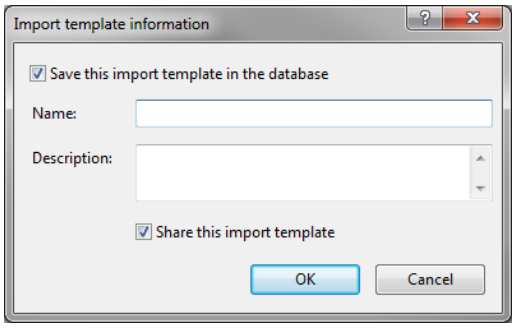


**Figure 3.7:** The *Import template information* dialog box.

Pressing <***Finish***> brings up the last step of the wizard.

Each import template has its own unique ***Name***.

Optionally, a descriptive text string can be entered in the ***Description*** input field. This descriptive text will be displayed when the template is selected from the template list.

The import template is saved to the database when the option ***Save this import template in the database*** is checked.

Check or uncheck the option ***Share this import template*** when the import template should be shared with other database users or when the template is intended exclusively for the current database user, respectively. Shared templates can be used and modified by all other database users.

When pressing the <***OK***> button, all template settings are saved to the database.

### 3.1.4 Applying an ABx import template

Once an import template for antibiotics data is created (see 3.1.3), the *Antibiotics data import template* wizard page will appear, from which the import template can be selected and applied on the antibiotics data file (see Figure 3.8).

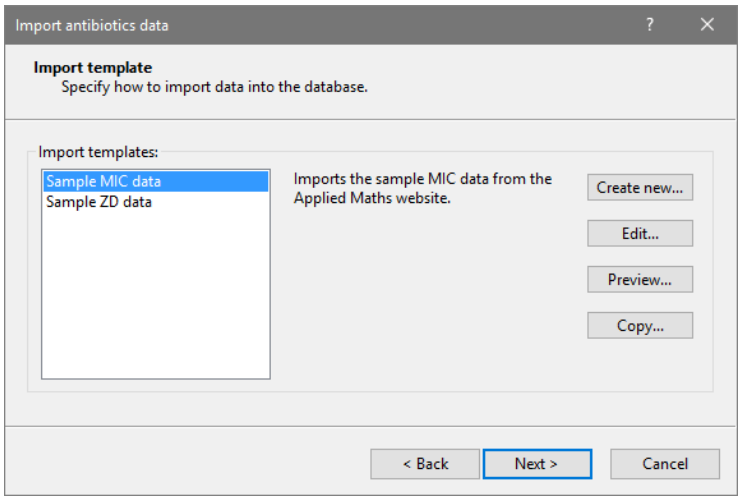


**Figure 3.8:** The *Antibiotics data import template* wizard page.

The way the character and entry information should be imported in the database can be specified with an import template. The *Antibiotics data import template* wizard page lists all antibiotics data import templates that have been created and stored in the database.

Pressing the <***Create new...***> button brings up a new dialog box, allowing you to define a new import template (see 3.1.3).

When an import template has been created, the template ***Name*** is shown in the list on the left and automatically selected. The template's ***Description*** is shown in the middle part of the dialog.

A highlighted import template can be copied and saved under a different name by pressing <***Copy...***>.

Pressing the <***Edit...***> button brings up the *Import rules* dialog box again (see 3.1.3). If a conversion rule could not be applied to a selected file (e.g. a template column name could not be found in the selected file), the tag <***Absent***> is shown in the ***Source*** column next to the source name. Only if all conversion rules of a template can be applied to the selected file(s), the template can be used to import data in the database.

The *Preview* dialog box is displayed when pressing the <***Preview...***> button. The *Preview* dialog box displays the parsed information using the template settings. The preview can be closed with the <***Close***> button.

Pressing <***Next***> opens the last step of the wizard, prompting for some final settings.

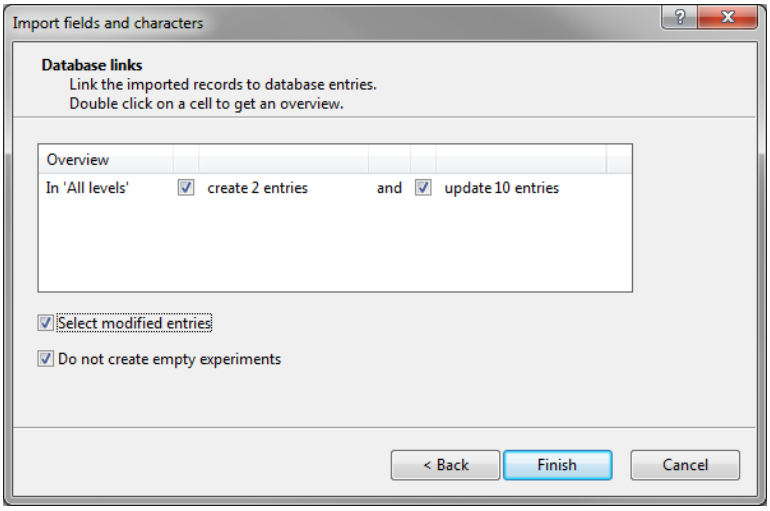


**Figure 3.9:** The *Database links* wizard page.

- When ***Create x entries*** is checked, the import tool is allowed to create the new entries in the database.
- Check the option ***Update x entries*** if you want the software to be able to update the entry and character information for existing entries.
- If the option ***Select modified entries*** is checked, entries in the database that were modified during the import routine will be selected after import.

When ***Do not create empty experiments*** is enabled, the import routine will not create experiment links for entries that are present in the selected file for which no character values are present.

When mapped ***Key*** information exceeds the maximum number of allowed characters (i.e. 60 characters), the ***Create x entries*** option will have a red background. The entries with a ***Key*** exceeding the maximum number of allowed characters will not be created in the database. Double-clicking on the red menu item opens the *Entry key import* dialog box.

Pressing <***Finish***> will start the import.

Mapped entry field information, exceeding the maximum number of allowed characters (i.e. 79 characters) will be truncated to 79 characters during import. A message pops up asking the user to confirm the import action.

Mapped character field information, exceeding the maximum number of allowed characters (i.e. 79 characters) will be truncated to 79 characters during import. A message pops up asking the user to confirm the import action.

## 3.2 Tutorial: Importing antibiotics data from a text file

As an illustration, we will import MIC values from a text file. The import from an Excel file is identical, except that an Excel sheet should be selected as ***Data range*** (see 3.1.2). The example files can be downloaded from the sample data download page on the Applied Maths website (`http://www.applied-maths.com/download/sample-data`).

2.1 Select ***File*** > ***Import...*** (  , **Ctrl+I**) in the *Main* window to call the *Import* dialog box.

2.2 Select ***Import antibiotics data (text file)*** from the Import tree under ***Character type data*** and press <***Import***>.

2.3 Press the <***Browse...***> button, browse for the `MIC data.txt` text file (see Figure 3.10) and press <***Open***>.

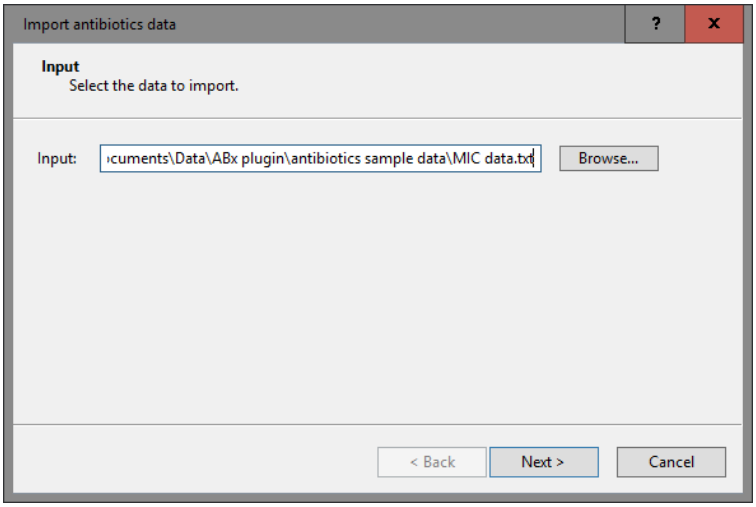


**Figure 3.10:** Browse for the text file containing the data.

2.4 Press <***Next***> in the *Input* dialog box.

Since no import template for antibiotics data is present yet, the *Import rules* dialog box will open.

2.5 Double-click on the "KEY" row, select ***Key*** as data destination and press <***OK***>.

2.6 Click on the "AMP" row, hold the **Shift**-key and click on the "TIC" row to select all antibiotics rows simultaneously.

2.7 Press <***Edit destination...***>, select ***ABX_MIC_Ecoli_antibio-MIC*** under ***ABx value*** (see Figure 3.11) and press <***OK***>.

The software will automatically link the MIC values to the corresponding antibiotics in the antibiotics experiment via their abbreviations. The *Import rules* dialog box should now look like Figure 3.12.

2.8 Press <***Next***>.

2.9 Leave ***Key*** checked and press <***Finish***>.

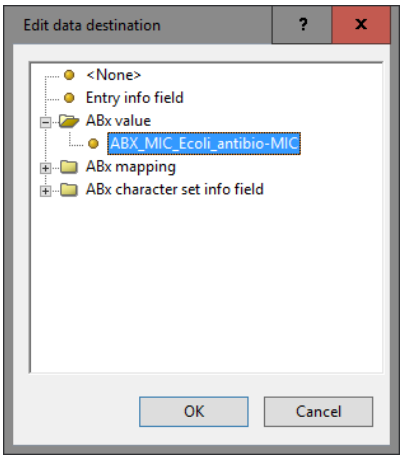


**Figure 3.11:** Edit data destination.

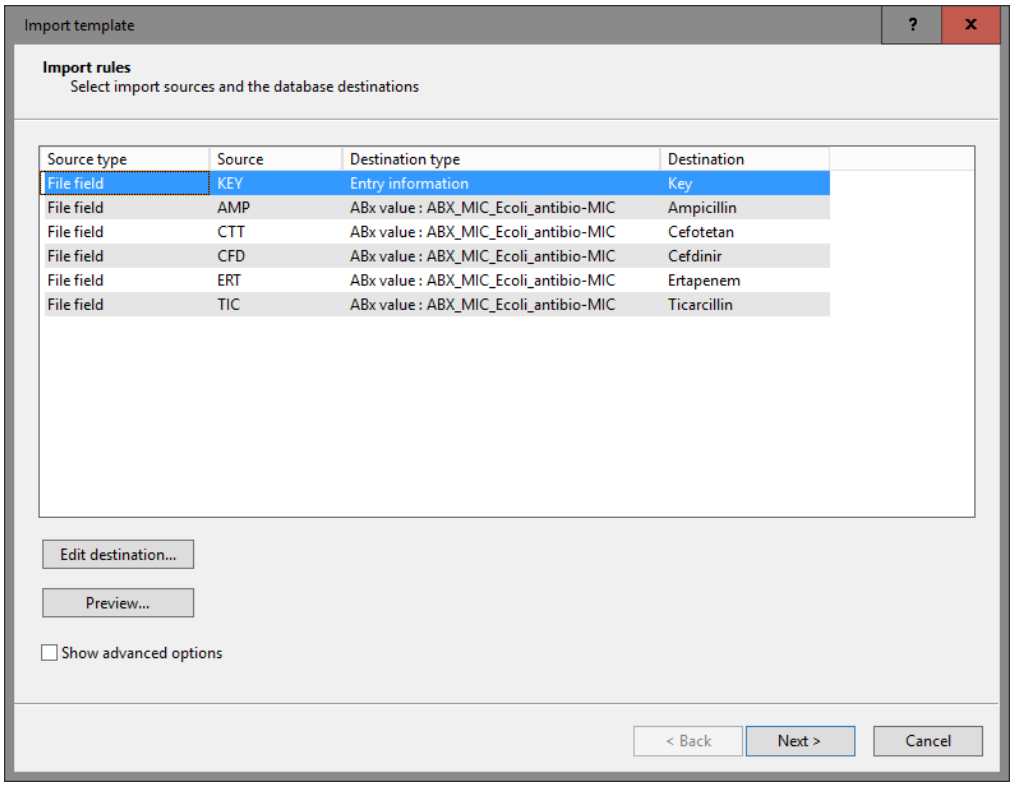


**Figure 3.12:** The *Import rules* dialog box, showing the import rules for the `MIC data.txt` example data file.

2.10 Enter a name for the import template (e.g. “Sample MIC data”) and press <***OK***>.

The new import template is now added to the database and is listed in the *Antibiotics data import template* wizard page (see Figure 3.13).

2.11 Press <***Next***>.

The last dialog will indicate that 6 new entries will be added to the database (see Figure 3.14).

2.12 Press <***Finish***>.

The entries are imported in BioNumerics. Their values (stored in the **antibio-MIC** experiment type) are

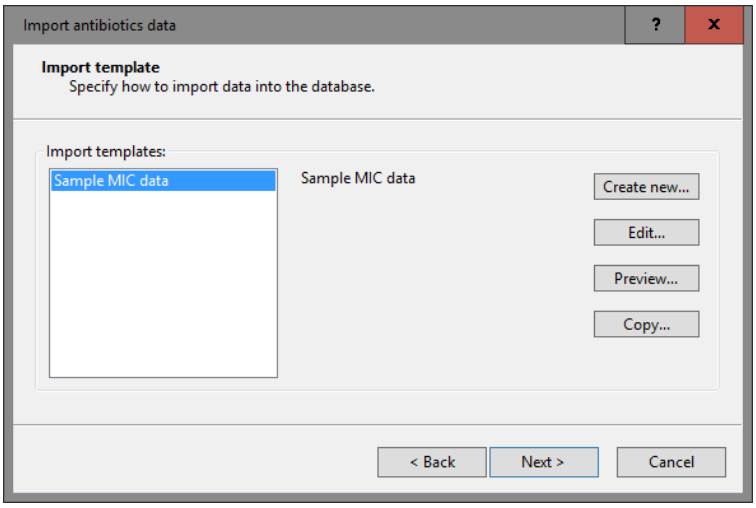


**Figure 3.13:** Import template.

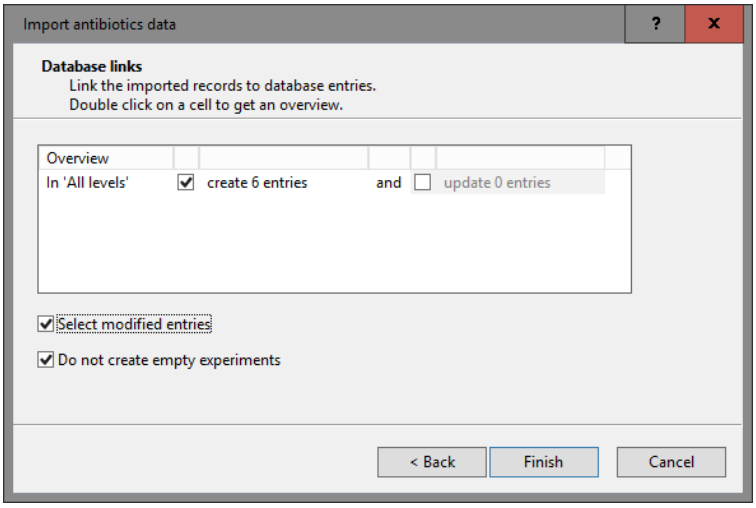


**Figure 3.14:** Database links.

automatically converted to categories (stored in the **antibio-MIC_SIR** experiment type).

## 3.3 Additional exercise

As an exercise, import the example data files based on the disk diffusion method and link them to the corresponding character type (see 2.1). Two example files with zone diameter values are present in the `Antibiotics data` folder, downloaded from the Applied Maths website: `Zone diameter data.txt` and `Zone diameter data.xls`.

# Chapter 4

# Comparison

## 4.1 The Comparison window

1.1 In the *Database entries* panel of the *Main* window, press **Ctrl+A** on the keyboard to select all database entries at once.

Check boxes for selected entries are indicated as ☑.

1.2 Highlight the *Comparisons* panel in the *Main* window and select ***Edit*** > ***Create new object...*** (  ) to create a new comparison for the selected entries.

A *Comparison* window is created, with the selected database entries.

1.3 You can drag the vertical separator lines between the panels to the left or to the right, in order to divide the space among the panels optimally.

1.4 Click on the eye button  next to **antibio-MIC_SIR** in the *Experiments* panel.

The pattern images are displayed in the *Experiment data* panel. Initially, the character values are displayed as colors according to the color scale defined for each character.

1.5 Select ***Characters*** > ***Show values+colors*** () to show the colors in overlay with the values in the *Experiment data* panel.

1.6 To export the character values, select ***Characters*** > ***Export character table***.

1.7 Select a character in the header of the *Experiment data* panel (e.g. Ampicillin) and select ***Characters*** > ***Sort by character value*** (  ).

The entries are now sorted by increasing value of the selected character.

1.8 Select ***Characters*** > ***Show mappings*** to show the corresponding mappings for all entries in the *Experiment data* panel.

## 4.2 Cluster analysis

2.1 In the *Experiments* panel of the *Comparison* window, make sure **antibio-MIC_SIR** is selected.

2.2 Select ***Clustering*** > ***Calculate*** > ***Cluster analysis (similarity matrix)...***.

2.3 Select ***Categorical (mappings)*** from the list and press <***Next***> and <***Finish***>.

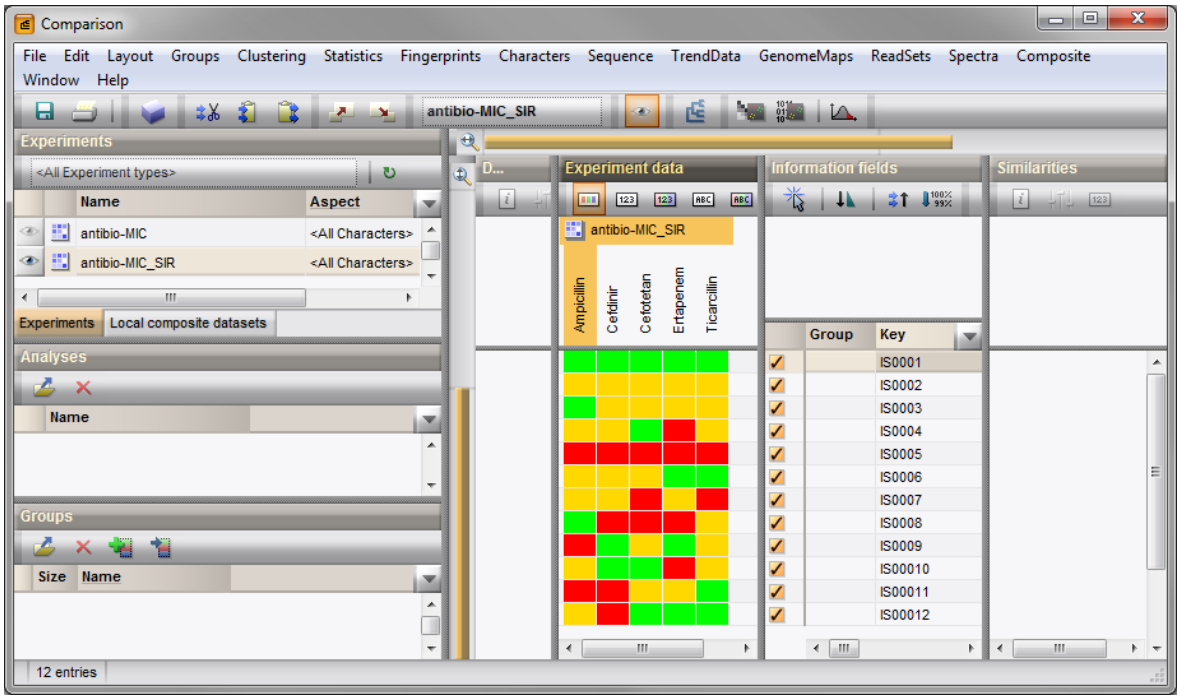


**Figure 4.1:** The *Comparison* window.

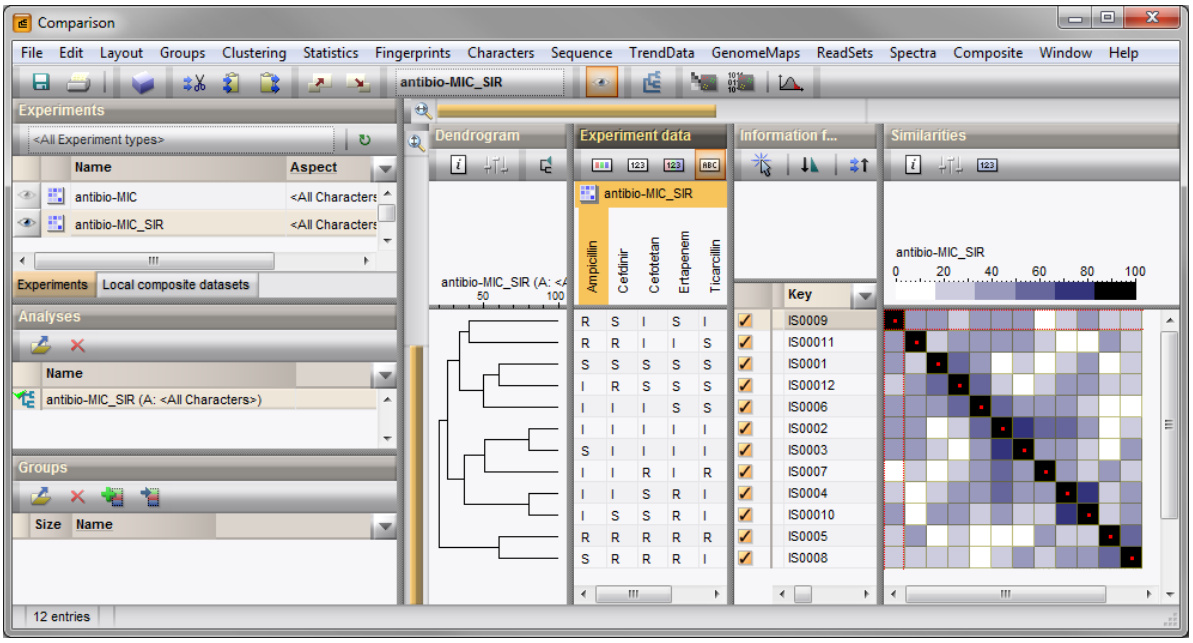


**Figure 4.2:** The *Comparison* window with dendrogram, image, entry names and similarity matrix.

When finished, the dendrogram and the similarity matrix are shown in the *Comparison* window (see Figure 4.2).

A comparison can be saved and all calculations done on the data it contains will be stored along. This includes similarity matrices in all experiment types where they have been calculated and any dendrogram that has been calculated.

2.4 Select ***File*** > ***Save*** ( , **Ctrl+S**) to save the comparison.

2.5 Enter a name, e.g. “MyComp” and press <***OK***>.

2.6 Close the comparison with ***File*** > ***Exit***.

The comparison **MyComp** is listed in the *Comparisons* panel of the *Main* window.

2.7 To open an existing comparison, highlight the comparison in the *Comparisons* panel and select ***Edit*** > ***Open highlighted object...*** (  , **Enter**). Alternatively, just double-click on the comparison name.

APPLIED MATHS

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Please contact us for any additional information you might require, we will gladly help you!

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