



BIONUMERICS Tutorial:

Importing spectrum data in a database with levels

1 Aim

Comprehensive tools for the import of spectrum data, both raw spectrum data as processed spectrum data are incorporated into BIONUMERICS. In this tutorial we will focus on the import and preprocessing of raw spectrum data in a leveled BIONUMERICS database.

2 Sample data

As an exercise, we will import a set of MALDI-TOF spectra from different isolates and species. The set can be downloaded from the Applied Maths website: go to <https://www.applied-maths.com/download/sample-data> and click on "Demo raw spectra". When the download is complete, unzip the file.

3 Preparing a sample database

3.1 Creating a new database

For this example we will be importing the raw spectra to a database with levels. We will start by creating a new, empty database.

1. Double-click on the BIONUMERICS icon () on the desktop.
2. In the *BIONUMERICS Startup* window, press the  button to enter the *New database* wizard.
3. Enter a database name, e.g. "Demo Spectra".
4. Click <**Next**>.

A new dialog box pops up, asking whether to create a new relational database for data storage or to use an existing one.

5. Leave the default option **Create new** enabled and press <**Next**>.

The next dialog asks which database engine should be used for storing data.

6. Select the default option and press <**Finish**>.

The *Main* window opens with an empty database.

3.2 Creating a spectrum type experiment

Before importing spectrum data, we will first create a spectrum experiment type.

7. In the *Main* window, click on  in the toolbar of the *Experiment types* panel and select **Spectrum type** from the list (see Figure 1). Press <**OK**>.

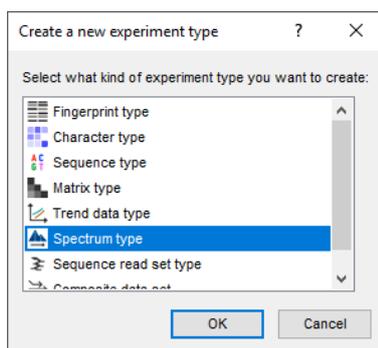


Figure 1: Create a new Spectrum type.

8. Enter a name, for example **Maldi**, leave the units for the horizontal and vertical axis at their defaults and press <**Next**> (see Figure 2).

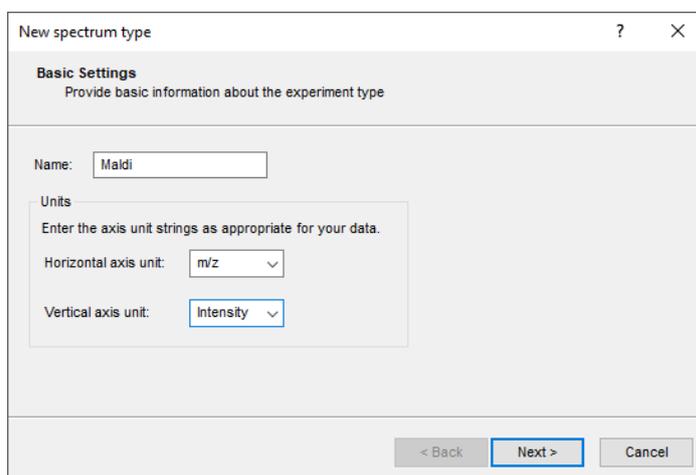


Figure 2: Basic settings.

Three predefined preprocessing templates are included: **Preprocessing (Default)**, **Preprocessing (Relaxed)**, and **Preprocessing (Strict)**. The settings of each template can be changed in the *Spectrum Preprocessing* window (see 5) and saved to the database.

9. Select the template *Preprocessing (strict)* and press <**Finish**> to complete the creation of the new spectrum type experiment.

The *Experiment types* panel now lists the spectrum type **Maldi** (see Figure 4).

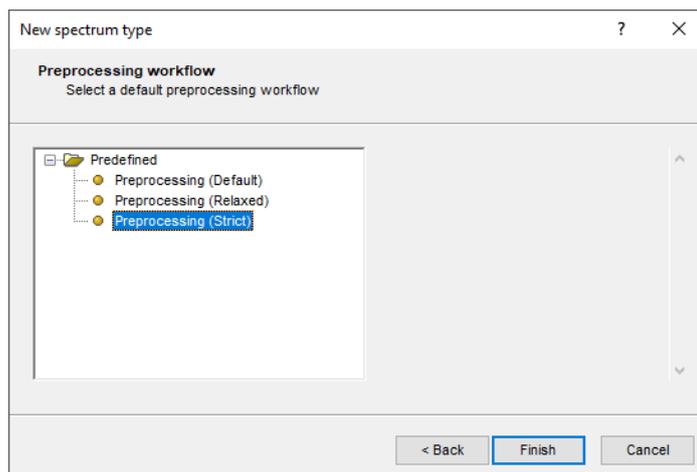


Figure 3: Preprocessing template.

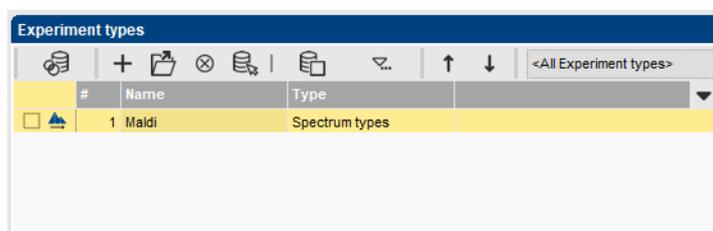


Figure 4: The *Experiment types* panel.

3.3 Creating levels

Next, we need to create the correct levels in the database. Database levels are schematically visualized in the *Database design* panel. This panel appears by default as a tab behind the *Entry fields* panel.

When working with levels, it is easier to switch between levels if the *Database design* panel is docked above the *Database entries* panel:

10. Click on the *Database design* tab and - while keeping the mouse button pressed - drag it inside the *Database entries* panel. Drop the floating panel on the top part of the docking guide that appears (see Figure 5).

The *Database design* panel is now shown above the *Database entries* panel.

11. In the *Database design* panel, click on "All levels" and select **Database > Levels > Add new level... (+)**. This will show the *Level information* dialog box. Fill in **Species** and press <OK>.
12. Next, click on the new level "Species" and select **Database > Levels > Add new level... (+)**, fill in **Isolate** and press <OK>. Finally, click on the new level "Isolate" and select **Database > Levels > Add new level... (+)**, fill in **Raw spectra** and confirm.

After making the levels, the structure of the database should look like Figure 6.

3.4 Creating information fields

Level-specific information fields can be created during the import of the spectra (see 4), during import of entry information from an external Excel or text file (see tutorial: "Adding entry information")

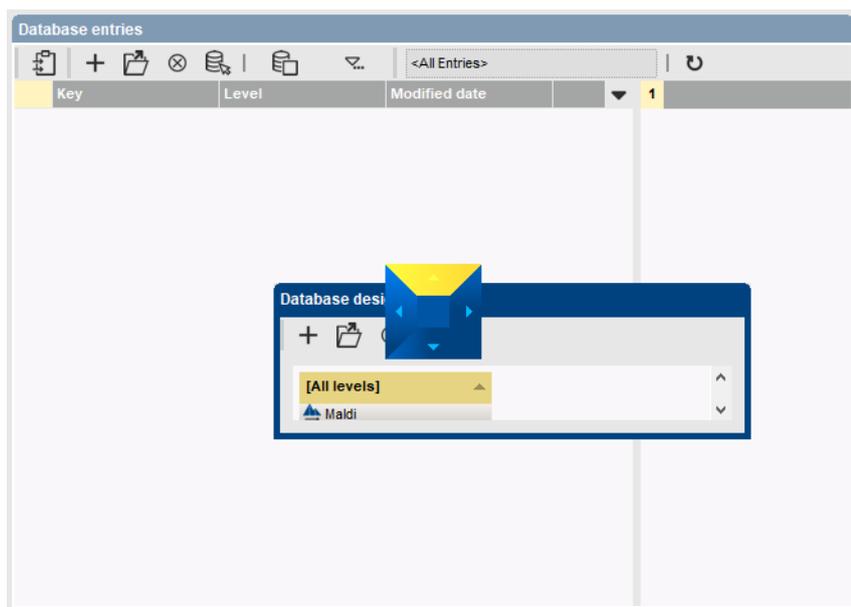


Figure 5: Docking guide.

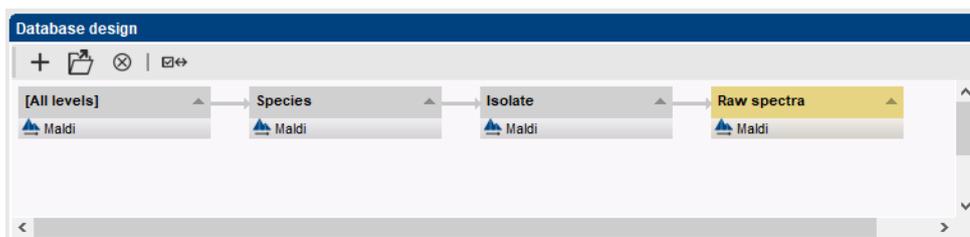


Figure 6: Database design after creating levels.

or manually with the menu-items.

To manually add level specific information fields with the menu-items follow these steps:

- Click on the correct level in the *Database design* panel.
- Select **+** in the *Entry fields* panel.
- Enter a name for the new information field and press **<OK>**.

4 Importing spectra

When importing data (descriptive information and/or experimental data) in a database with levels, it is important to highlight the corresponding level first. Typically, information will most often be imported at the deepest child level (i.e. **Raw spectra** in our example database).

1. Make sure the 'Raw spectra' level is highlighted, select **File > Import...** (⌘, **Ctrl+I**), highlight **Spectrum type data > Import spectrum data** and press **<Import>** (see Figure 7).
2. Browse to the folder, select all files in this folder and press **<Open>** and **<Next>**.
3. In the *Import template* wizard page of the wizard, press **<Create new>**.

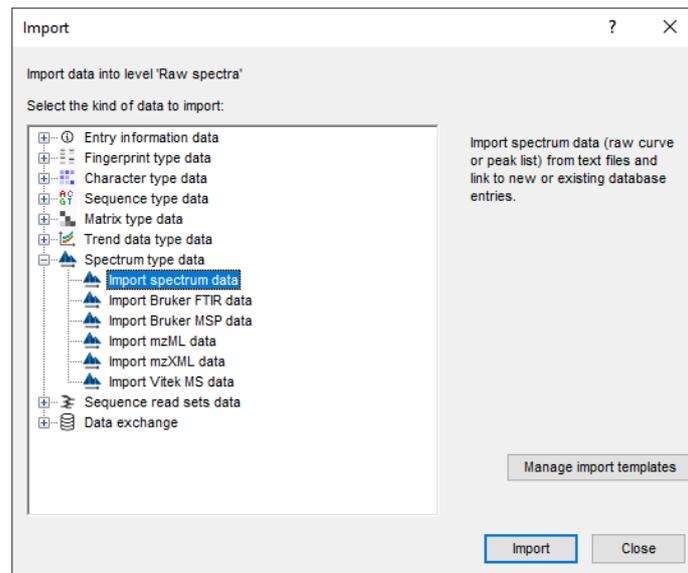


Figure 7: The Import tree.

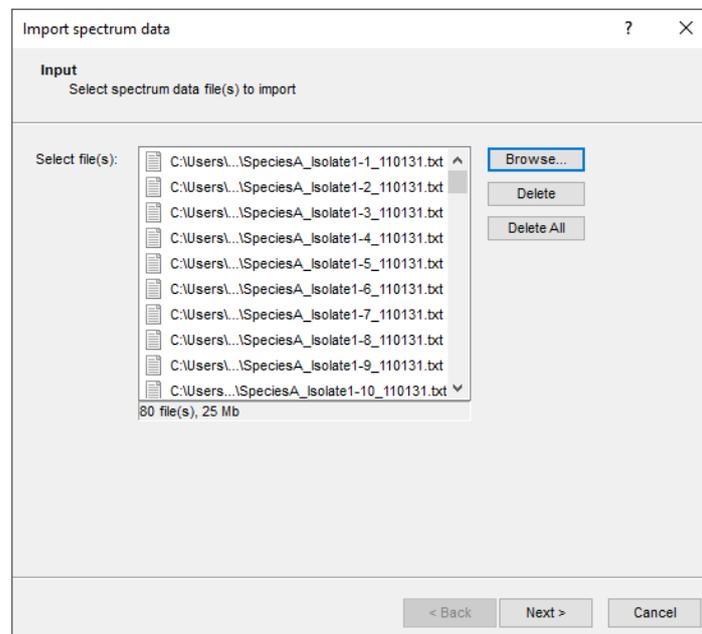


Figure 8: Select files.

The only source of information available in the newly created import template is the file name.

4. Double-click on the only row available in the grid or press **<Edit Destination>**.
5. Select **Raw spectra key** in the *Edit data destination* dialog box (see Figure 9).
6. Press **<OK>**.
7. Visualize the advanced options for the *Import template* dialog box by clicking on the check box next to **Show advanced options**.
8. Press **<Add rule>** to open the *Add data conversion rule* wizard.

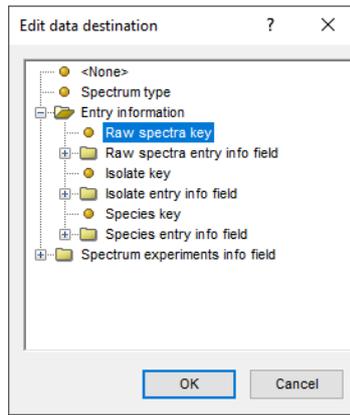


Figure 9: Select the destination

9. In the first page of the *Add data conversion rule wizard* select **File** > **Name** (Figure 10) and press <**Next**>.

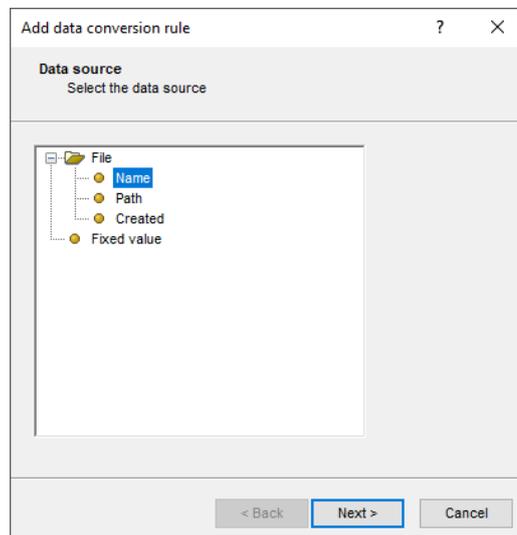


Figure 10: Adding a new rule to the import template.

10. In the second page of the *Add data conversion rule wizard*, select **Isolate key** and press <**Next**> (see Figure 11).
11. In the *Data parsing* dialog box, fill in following data parsing string: “[DATA]-*”. Press the <**Preview**> button (see Figure 12).
12. When the information is parsed correctly press <**Next**> and <**Finish**>.
13. Press <**Add rule**> again to open the *Add data conversion rule wizard*.
14. In the first page of the *Add data conversion rule wizard* select **File** > **Name** and press <**Next**>.
15. In the second page of the *Add data conversion rule wizard*, select **Species key** and press <**Next**> (see Figure 13).
16. In the *Data parsing* dialog box, fill in following data parsing string: “[DATA]-*”. Press the <**Preview**> button (see Figure 14).
17. When the information is parsed correctly press <**Next**> and <**Finish**>.

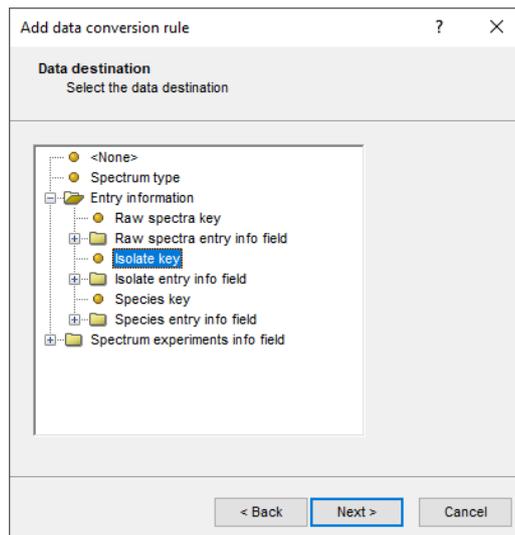


Figure 11: Isolate key.

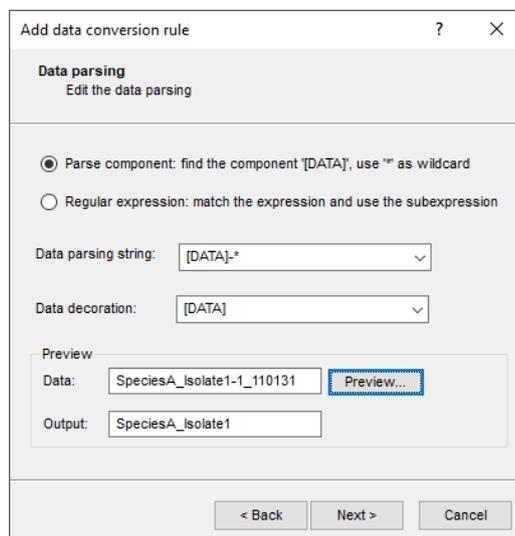


Figure 12: Parsing string.

18. Press <**Add rule**> again to open the *Add data conversion rule* wizard.
19. In the first page of the *Add data conversion rule* wizard select **File** > **Name** and press <**Next**>.
20. In the second page of the *Add data conversion rule* wizard, select **Create new** under **Raw spectra entry info field** and press <**Next**>, specify a name (e.g. **Date**) and confirm (see Figure 15).
21. In the *Data parsing* dialog box, fill in following data parsing string: "*_*_[DATA]". Press the <**Preview**> button (see Figure 16).
22. When the information is parsed correctly press <**Next**> and press <**Finish**>.

The grid is updated.

23. In the *Import template* dialog box, press <**Preview**> and verify the preview of the import (see Figure 17). Close the preview and press <**Next**> and <**Finish**>.

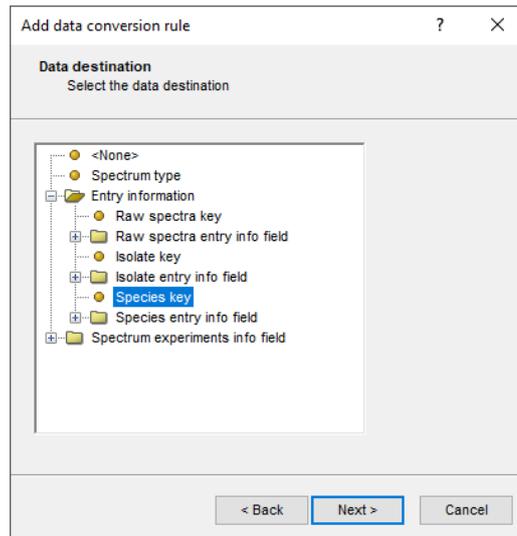


Figure 13: Species key.

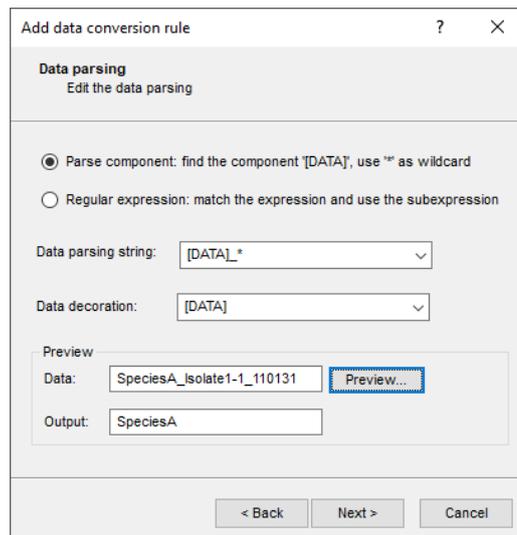


Figure 14: Species key.

24. Name the import template (e.g. "Import to levels") and optionally give it a description. Press **<OK>**.
25. With the new import template highlighted, and the **Maldi** experiment selected press **<Next>** to go the next step where an overview of the actions that will be performed during the import is displayed (see Figure 18).
26. Press **<Next>**, check **Do preprocessing**, select **Preprocessing template (strict)** as **Preprocessing** option, leave all other settings at default and press **<Finish>**.

The raw spectra will be imported. Depending on the performance of your computer, this may take a few minutes.

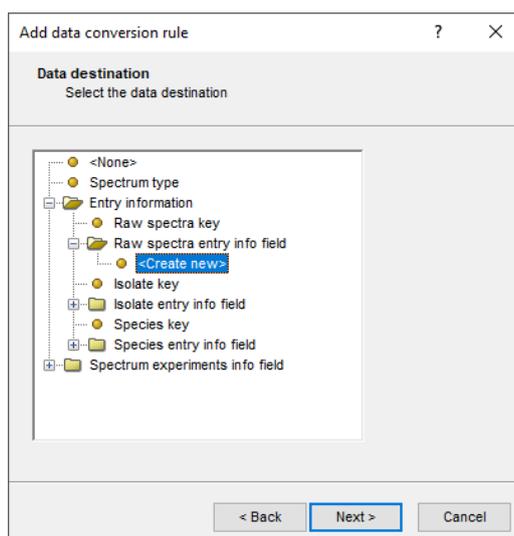


Figure 15: Create new information field.

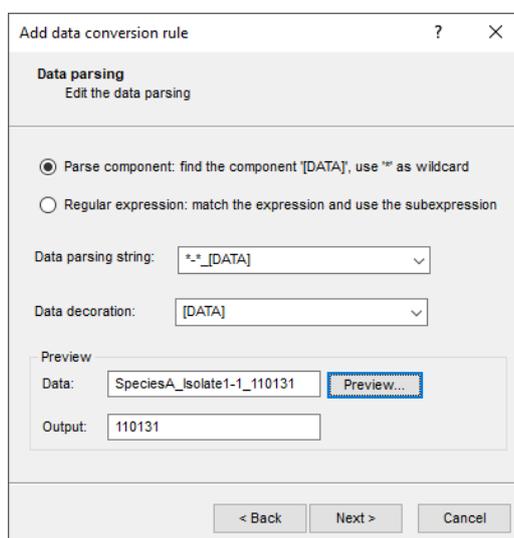


Figure 16: Parsing string.

5 Preprocessing of spectra

Upon completion of the import, the *Spectrum Preprocessing* window will open automatically. If it does not open automatically, you can select all entries on the lowest level "Raw spectra", and use **Analysis > Spectrum types > Open preprocessing window...** to open the *Spectrum Preprocessing* window.

All the imported spectra are loaded in the *Spectrum Preprocessing* window with the preprocessing template selected in the last step of the *Import spectrum data wizard* (see Figure 19).

Because there is a slight difference in the range of the different spectra, we will be adding a trimming step to this template.

1. With the **Import & Resample** step of the preprocessing template highlighted in the *Workflow* panel, select **Workflow > Show flow chart....** This will open the *Workflow* window for this step of the template.

Nr.	Raw spectra key	Date	Isolate key	Species key
1	SpeciesA_Isolate1-1_110131	110131	SpeciesA_Isolate1	SpeciesA
2	SpeciesA_Isolate1-2_110131	110131	SpeciesA_Isolate1	SpeciesA
3	SpeciesA_Isolate1-3_110131	110131	SpeciesA_Isolate1	SpeciesA
4	SpeciesA_Isolate1-4_110131	110131	SpeciesA_Isolate1	SpeciesA
5	SpeciesA_Isolate1-5_110131	110131	SpeciesA_Isolate1	SpeciesA
6	SpeciesA_Isolate1-6_110131	110131	SpeciesA_Isolate1	SpeciesA
7	SpeciesA_Isolate1-7_110131	110131	SpeciesA_Isolate1	SpeciesA
8	SpeciesA_Isolate1-8_110131	110131	SpeciesA_Isolate1	SpeciesA
9	SpeciesA_Isolate1-9_110131	110131	SpeciesA_Isolate1	SpeciesA
10	SpeciesA_Isolate1-10_110131	110131	SpeciesA_Isolate1	SpeciesA
11	SpeciesA_Isolate2-1_110131	110131	SpeciesA_Isolate2	SpeciesA
12	SpeciesA_Isolate2-2_110131	110131	SpeciesA_Isolate2	SpeciesA
13	SpeciesA_Isolate2-3_110131	110131	SpeciesA_Isolate2	SpeciesA
14	SpeciesA_Isolate2-4_110131	110131	SpeciesA_Isolate2	SpeciesA
15	SpeciesA_Isolate2-5_110131	110131	SpeciesA_Isolate2	SpeciesA
16	SpeciesA_Isolate2-6_110131	110131	SpeciesA_Isolate2	SpeciesA
17	SpeciesA_Isolate2-7_110131	110131	SpeciesA_Isolate2	SpeciesA
18	SpeciesA_Isolate2-8_110131	110131	SpeciesA_Isolate2	SpeciesA
19	SpeciesA_Isolate2-9_110131	110131	SpeciesA_Isolate2	SpeciesA

Figure 17: Preview.

Import spectrum data

Database links
Link the imported records to database entries.
Double click on a cell to get an overview.

Overview				
In 'Raw spectra'	<input checked="" type="checkbox"/> create 80 entries	and	<input type="checkbox"/> update 0 entries	
In 'Isolate'	<input checked="" type="checkbox"/> create 8 entries	and	<input type="checkbox"/> update 0 entries	
In 'Species'	<input checked="" type="checkbox"/> create 3 entries	and	<input type="checkbox"/> update 0 entries	

Select modified entries

< Back Next > Cancel

Figure 18: Import actions.

- In the left panel, highlight the operator **Processing** > **X-axis** > **Trimming** and select **File** > **Add operator...** (📎).
- In the resulting dialog box (see Figure 20), fill in **2000** as X-axis minimum, do not use an upper limit and press < **Next**>.

The trimming operator is added to the end of the workflow, resulting in the workflow shown in Figure 21.

- After the operator has been added, close the *Workflow* window.
- Select **File** > **Save workflow as template...**, enter a name for the new template (e.g. "Strict with trimming") and press < **OK**>.

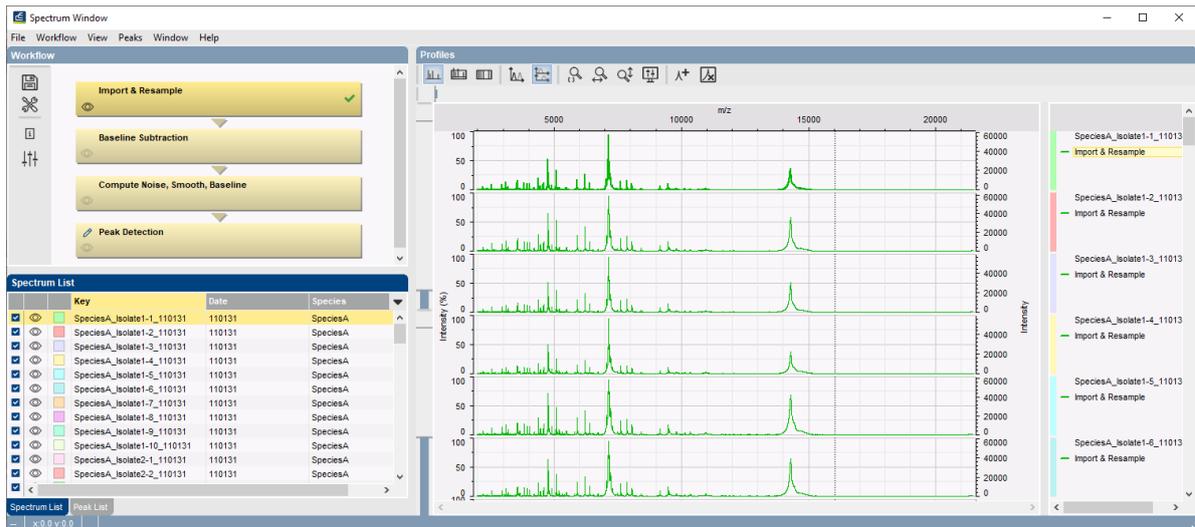


Figure 19: Preprocessing window after import of spectra.

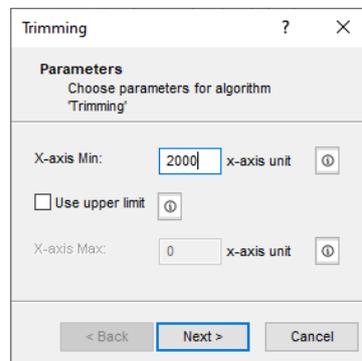


Figure 20: Parameters of the trimming operator.

This template will now be available for future import and preprocessing of spectra.

- Press the last step of the preprocessing template in the *Workflow* panel, i.e. **<Peak Detection>**, to execute the entire preprocessing workflow. Leave the limit for the signal to noise ratio at default and press **<Next>**.

Depending on the performance of your computer, the execution might take a few minutes.

With the "Peak Detection" step still selected in the *Workflow* panel, the preprocessed spectra are displayed in the *Profiles* panel. The detected peaks are indicated with circles on top of the peaks.

- Click on a spectrum in the *Profiles* panel to make it the active spectrum in the window.
- Click on the *Peak List* panel to display the Peak List table.
- Double-click on a peak in the *Peak List* panel: the peak is highlighted in *Profiles* panel and the view is updated.
- Use the zoom sliders in the *Profiles* panel to obtain the best view.
- Save the results by selecting **File > Save spectrum data** (). Close the *Spectrum Preprocessing* window.

The preprocessed spectra are now available in the database and further analysis, such as creating summary spectra or comparing the spectra, can be performed.

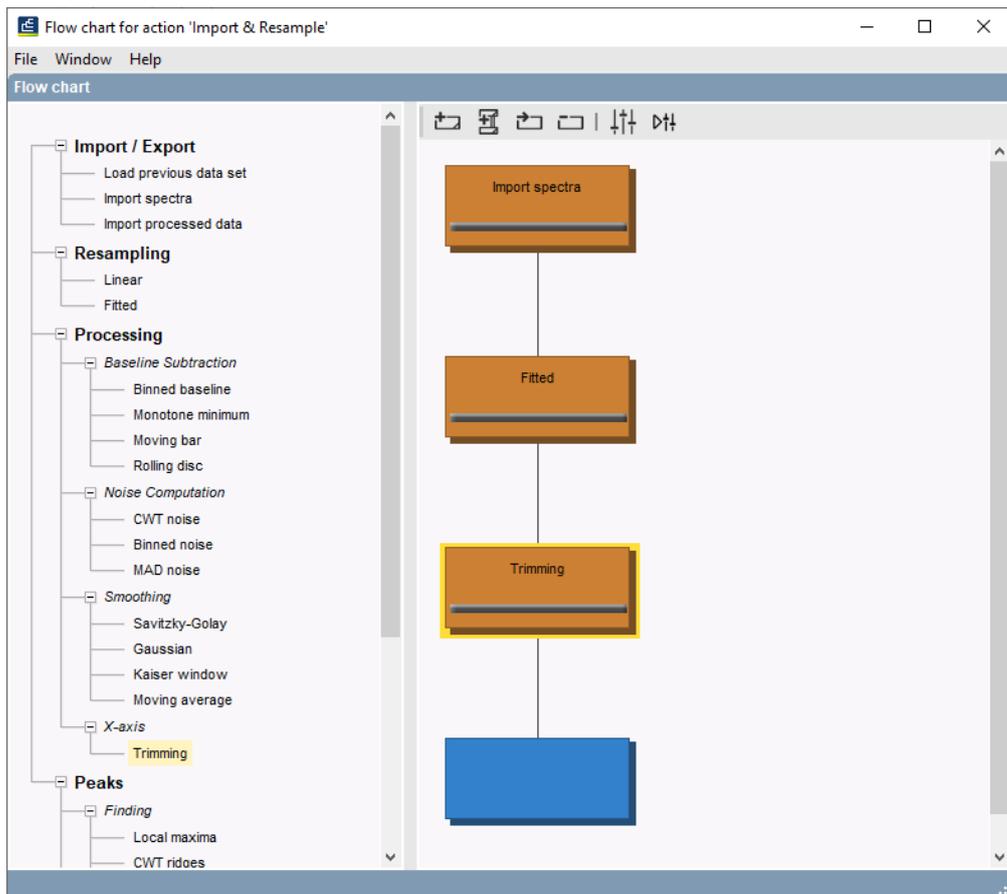


Figure 21: Final workflow with trimming operator.