BIONUMERICS Tutorial:

Importing peak data from peak table files

1 Aim

Comprehensive tools for processing electrophoresis fingerprints, both from slab gels and capillary sequencers are incorporated into BIONUMERICS. When fingerprints are run on a capillary sequencers the resulting data can have two different formats: curve files (also referred to as electropherograms, chromatogram files or trace files), or peak tables. In this tutorial we will focus on the import of peak tables.

2 Sample data

Text files containing a listing of peaks can be imported in BIONUMERICS. An example peak file can be downloaded from the Applied Maths website (`https://www.applied-maths.com/download/sample-data`, click on "VNTR sample peak table"). This example file will be used to illustrate the import steps in this tutorial.

3 Importing peak data

1. Create a new database (see tutorial "Creating a new database") or open an existing database.

2. Select ***File*** > ***Import...*** (, **Ctrl+I**) to call the *Import* dialog box, choose ***Import peak table*** under ***Fingerprint type data*** and press <***Import***>.

3. Browse to the downloaded and unzipped example data folder `VNTR Peak table` and select the `Beckman_Sample.txt` sample file. Press <***Open***>.

The path is displayed in the *Input* wizard page.

4. Check ***Import as fingerprint file***, specify a name (e.g. **Beckman1**) and press <***Next***>.

The way the information should be imported in the database can be specified with an import template. In the example Beckman peak file, the dye, sample and pool information is provided.

5. Select the predefined template **Beckman with pools** and press <***Edit***> to call the *Import rules* dialog box.

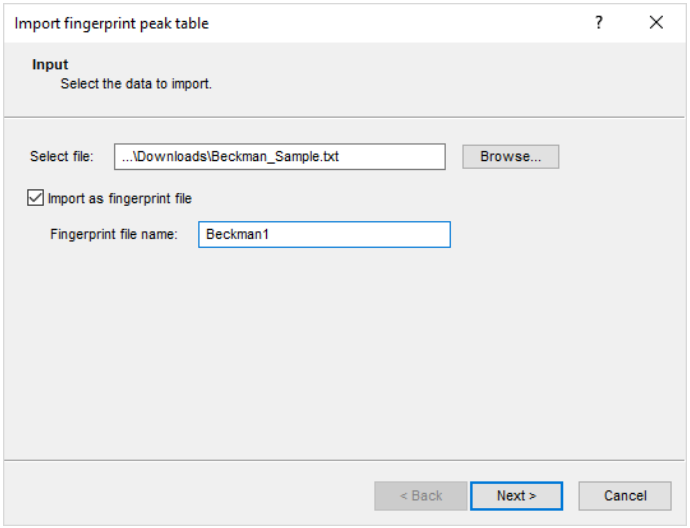
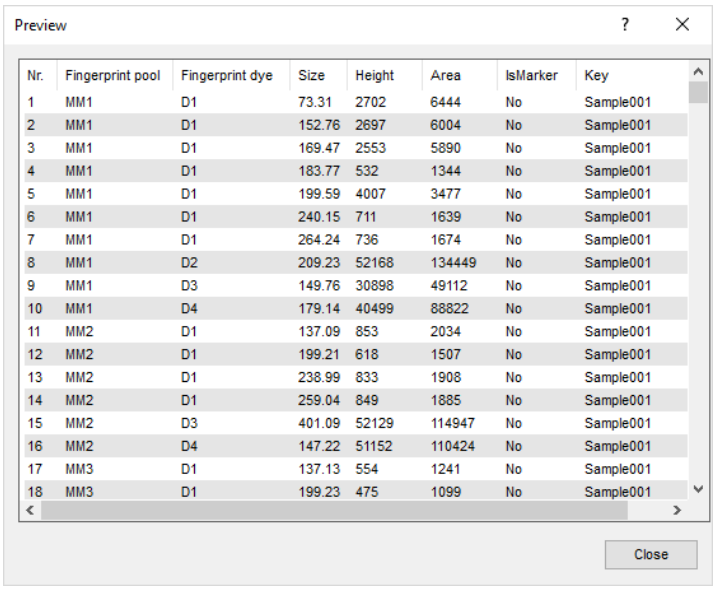


Figure 1: Selected peak table file.

The *Import rules* dialog box lists the import rules defined for the import template **Beckman with pools**.

6. Press the <***Preview***> button to check the parsing of the file information based on the rules defined for the template.

From the preview (Figure 2), it can be seen that all information from the example file is parsed correctly.



Nr.	Fingerprint pool	Fingerprint dye	Size	Height	Area	IsMarker	Key
1	MM1	D1	73.31	2702	6444	No	Sample001
2	MM1	D1	152.76	2697	6004	No	Sample001
3	MM1	D1	169.47	2553	5890	No	Sample001
4	MM1	D1	183.77	532	1344	No	Sample001
5	MM1	D1	199.59	4007	3477	No	Sample001
6	MM1	D1	240.15	711	1639	No	Sample001
7	MM1	D1	264.24	736	1674	No	Sample001
8	MM1	D2	209.23	52168	134449	No	Sample001
9	MM1	D3	149.76	30898	49112	No	Sample001
10	MM1	D4	179.14	40499	88822	No	Sample001
11	MM2	D1	137.09	853	2034	No	Sample001
12	MM2	D1	199.21	618	1507	No	Sample001
13	MM2	D1	238.99	833	1908	No	Sample001
14	MM2	D1	259.04	849	1885	No	Sample001
15	MM2	D3	401.09	52129	114947	No	Sample001
16	MM2	D4	147.22	51152	110424	No	Sample001
17	MM3	D1	137.13	554	1241	No	Sample001
18	MM3	D1	199.23	475	1099	No	Sample001

Figure 2: Preview.

7. Close the preview and press <***Next***> twice and <***Finish***>.

8. Make sure ***Create new*** is selected as base fingerprint type experiment, select the **Beckman with pools** template and press <***Next***>.

9. Specify a name for the new base fingerprint type experiment (e.g. **MLVA**) and press <***OK***>. Confirm the creation of the new experiment in the database.

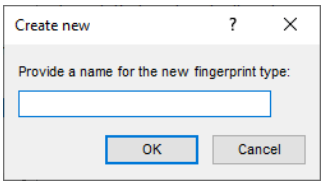


Figure 3: New base fingerprint type experiment.

Since a new fingerprint type experiment is created and added to the database, the *Experiment settings* wizard page pops up prompting for some settings.

10. For this exercise, enter an ***Intensity range*** of “65536” (= 16-bit), a ***Min. fragment length*** of “10”, and a ***Max. fragment length*** of “700” (see Figure 4). Press <***OK***>.

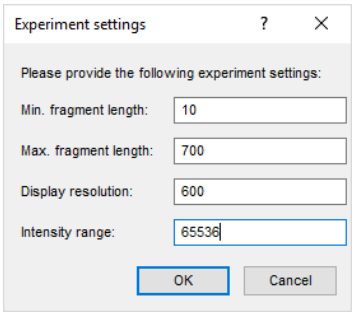


Figure 4: Experiment settings.

A fingerprint type needs to be present in the database for each pool and dye combination. The names of these fingerprint types are composed of the base fingerprint type name, followed by the pool name, and the name of the dye. A new dialog box pops up, listing all missing fingerprint types (see Figure 5).

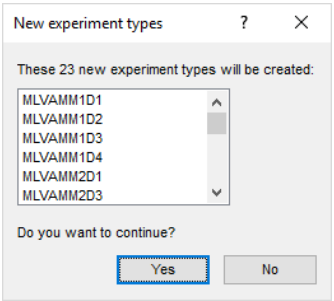


Figure 5: Missing fingerprint types.

11. Confirm the creation of the missing fingerprint type experiments.

12. Press <***Finish***> to confirm the creation of new entries in the database.

For each import dye, a new fingerprint file is created, composed of the file name specified and the name of the dye (e.g. Beckman1_D1). These files are displayed in the *Fingerprint files* panel.

BIONUMERICS reads the band positions from the mapped ”SIZE” column, the peak heights from the mapped ”HEIGHT” column, the area information from the mapped ”AREA” column and generates densitometric curves using this information. The imported fingerprint lanes are linked to new entries in the database. The lanes are linked to the corresponding fingerprint ”dye” type. The

names of these fingerprint types are composed of the base fingerprint type name, followed by the pool name, and the name of the dye. The fingerprint type experiments are displayed in the *Experiment types* panel.

If no reference system has been specified for the base fingerprint type, BIONUMERICS creates for all missing fingerprint types and the base fingerprint type, a linear reference system between the user-defined ***Minimum*** and ***Maximum fragment length*** positions, and copies the reference system to a calibration system.

Entries for which fingerprint data was imported are selected in the database.

After data import, the *Main* window looks as in Figure 6.

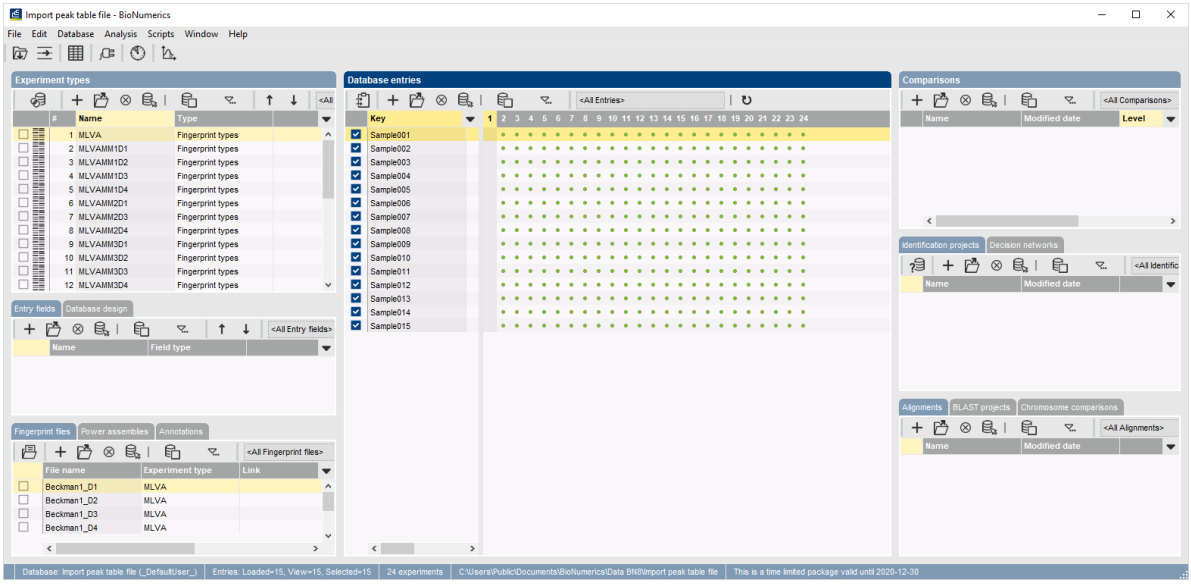


Figure 6: The *Main* window after import of the data.

4 Conclusion

In this tutorial you have seen how easy it is to import data from peak table files into BIONUMERICS. Peak tables have been processed by the software which controls the capillary electrophoresis equipment so no processing is required. Comparison functions such as band matching, clustering, etc. can directly be applied on the data. More information about these functions can found in the analysis tutorials on our website.