BIONUMERICS Tutorial:

Concatenating sequences

1 Aim

A script is available at the BIONUMERICS scripts website that joins two or more (nucleic or amino acid) sequences. The resulting concatenated sequence is stored in an appointed sequence type experiment. In this tutorial you will learn how to use this script.

2 Importing individual sequences

Sequences can be imported in your BIONUMERICS database using one of the import routines available in the software. For most import formats and data sourcees a tutorial is available on our website with some example data:

- "Importing sequences from FASTA files"

- "Importing sequences from GenBank/EMBL files"

- "Importing sequences from online repositories"

- "Importing and assembling sequences in batch"

3 Creating a sequence type experiment

Before running the script a sequence type needs to be available in the database that will be used to store the merged sequence.

1. To create a new sequence type, click on the *Experiment types* panel to activate it and select *Edit* > *Create new object...* (+).

2. From the *Create a new experiment type* dialog box that pops up, select *Sequence type* to start the *New sequence type* wizard.

3. The first page prompts you to enter a name for the new sequence type. Pressing <*Next*> will bring you to the second page of the *New sequence type* wizard.

4. Check the radio button that corresponds to the kind of the sequences: *Nucleic acid sequences* or *Amino acid sequences* and press the <*Finish*> button to complete the setup of the new sequence type.

The sequence type will be listed in the *Experiment types* panel of the *Main* window.

4   Concatenating the sequences

1. In the *Main* window, select the entries for which you want to concatenate the sequences.

2. Select **Scripts** > **Browse internet...** and click on the "Sequence related tools" link.

3. Click on "Concatenate sequences" to run the script.

4. Select the sequence types to merge in the list on the left and use the > button to add the experiments to the list on the right. Use the arrow up and down buttons to change the order of the experiments.

5. Select the **Merged sequence type** experiment from the drop-down list.
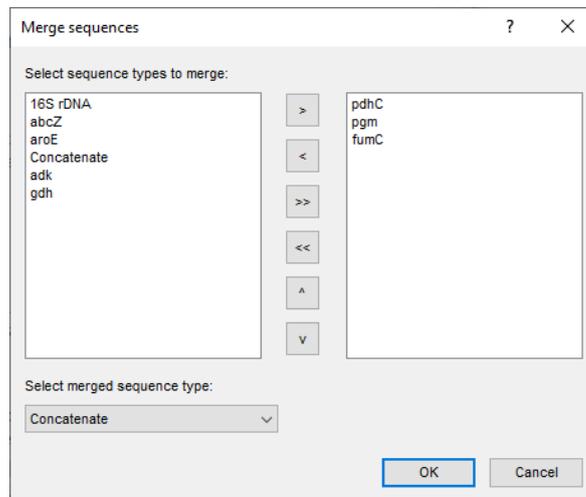
Figure 1: Select the sequence type experiments.

6. Press <**OK**> to run the script.

The sequences are merged based on the order of the sequence types as they appear in the list on the right and stored in the appointed sequence type experiment.