

BioNumerics Tutorial:

Importing sequences from GenBank/EMBL files

1 Aim

With the BioNumerics GenBank/EMBL import routine, sequences in GenBank/Embl format can be imported into BioNumerics. In this tutorial you will learn how to use this import tool by importing sequences from an example file.

2 Example data

As an example we will import Influenza A sequences of the hemagglutinin (HA) gene into a new or existing BioNumerics database. The example GenBank file (H1N1 HA gene.gb file) can be found on the download page on our website (<http://www.applied-maths.com/download/sample-data>, "GenBank file"). Note that the steps for the import of an EMBL formatted file are the same.

3 The Import wizard

1. Create a new database (see tutorial "Creating a new database") or open an existing database.
2. In the *Main* window, select **File > Import...** (, **Ctrl+I**) to open the *Import* dialog box.
3. Choose the option **Import EMBL/GenBank sequences from text files** under the *Sequence type data* item in the tree and click **<Import>**.
4. Press **<Browse>**, select the H1N1 HA gene.gb file and press **<Open>**.
5. With the option **Preview sequences** checked, press **<Next>**.

The import wizard now displays a preview of the sequence data in the file (see Figure 1).

6. Press **<Next>**.

The next step of the import wizard lists the templates that are present to import sequence information in the database. As this is the first time we import GenBank formatted sequences in the database, we need to create a new import template by specifying **Import rules**.

7. Click **<Create new>** to create a new import template.
8. Select "OS - SOURCE" in the list and click **<Edit destination>**.
9. Select "[Create new]" under **Entry info field** and click **<OK>**.
10. Enter "Strain" as name for the new information field, press **<OK>** and press **<Yes>**.

The accession number is valuable information which is specific for the sequence (not for the strain), therefore we will store the accession number as a sequence information field.

11. Select "AC - ACCESSION" in the list and click **<Edit destination>** or double-click on "AC - ACCESSION". Under **Sequence info field**, select "[Create new]" and press **<OK>**.

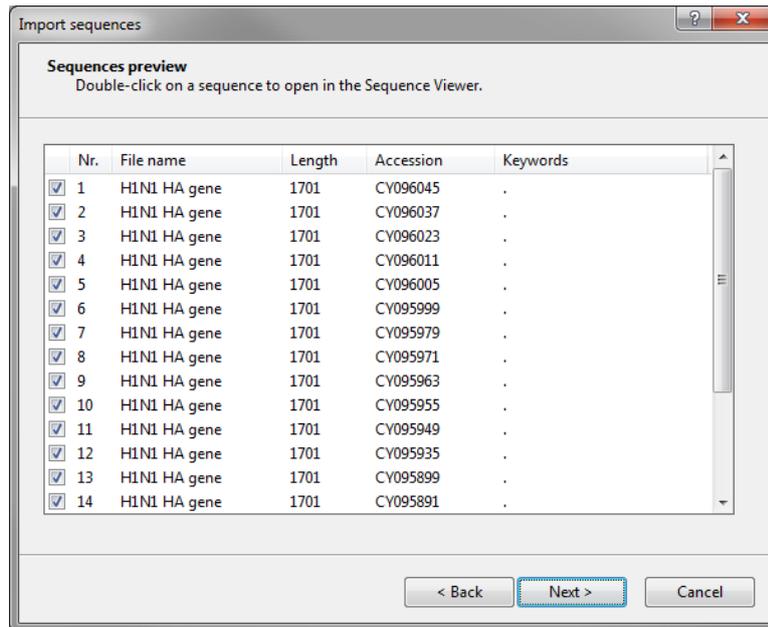


Figure 1: Preview.

12. Change the suggested name ("AC - ACCESSION") for the new information field into "Accession number", press <OK> and confirm with <Yes>.

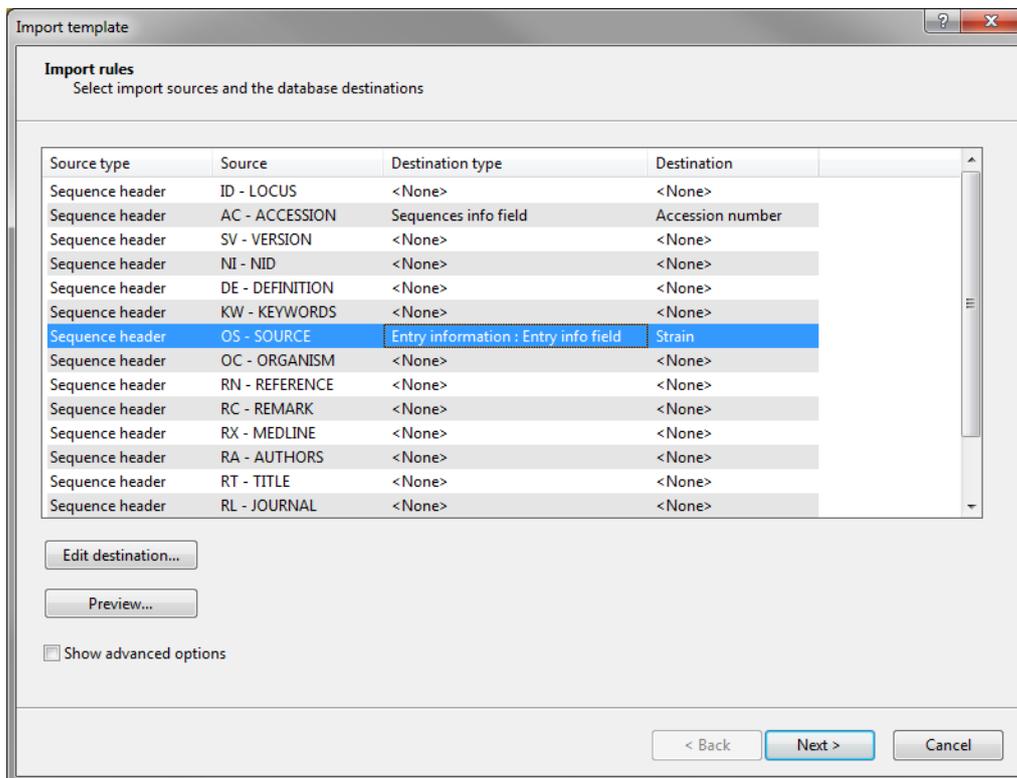


Figure 2: Import template

13. Optionally, you can press <Preview> to obtain a preview of the data you are about to import.

14. Click <Next> to go to the next step.

15. Do not select an *Entry link field* to have the database keys automatically generated. Press <Finish>.
16. Specify a template name (e.g. “GenBank”) and optionally enter a description. Press <OK>.
17. Highlight the newly created template and select “Create new” as *Experiment type* (see Figure 3).

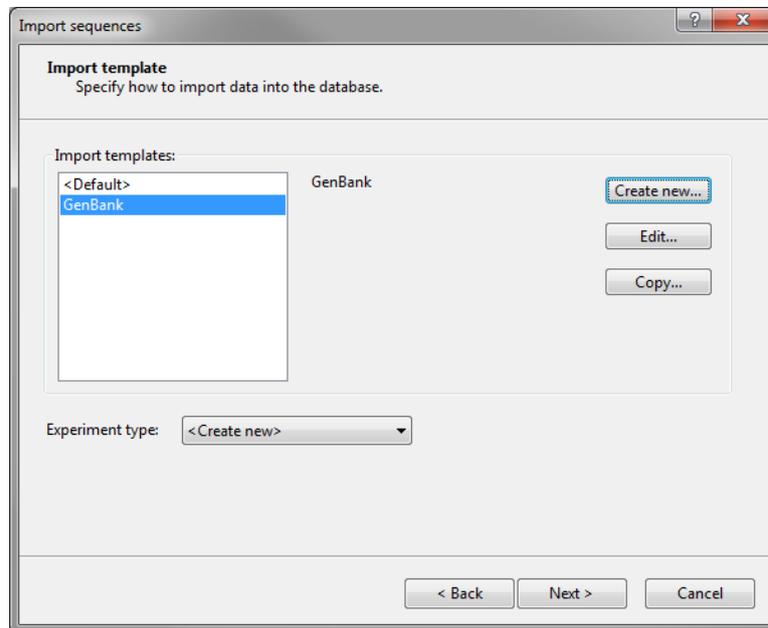


Figure 3: Import template.

18. Press <Next>.
19. Specify a sequence type name (e.g. **HA** or **haemagglutinin**) and press <OK> and confirm the action.

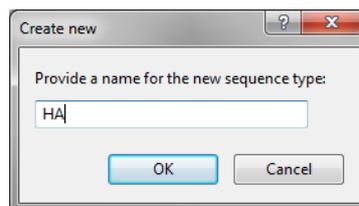


Figure 4: Create a new sequence type.

The *Database links* wizard page will indicate that 20 new entries will be created during import (see Figure 5).

20. Press <Finish>.

Twenty sequences are imported in the database (see Figure 6). All entries for which information was imported are automatically selected.

21. Click on a green colored dot in the *Experiment presence* panel to open the *Sequence editor* window.

The sequence is displayed in the upper panel and a graphical representation of the sequence is displayed in the panel below. The *Annotation* panel (see Figure 7) holds the GenBank features, the header information is stored in the *Header* panel and the accession number is stored in the *Custom Fields* panel.

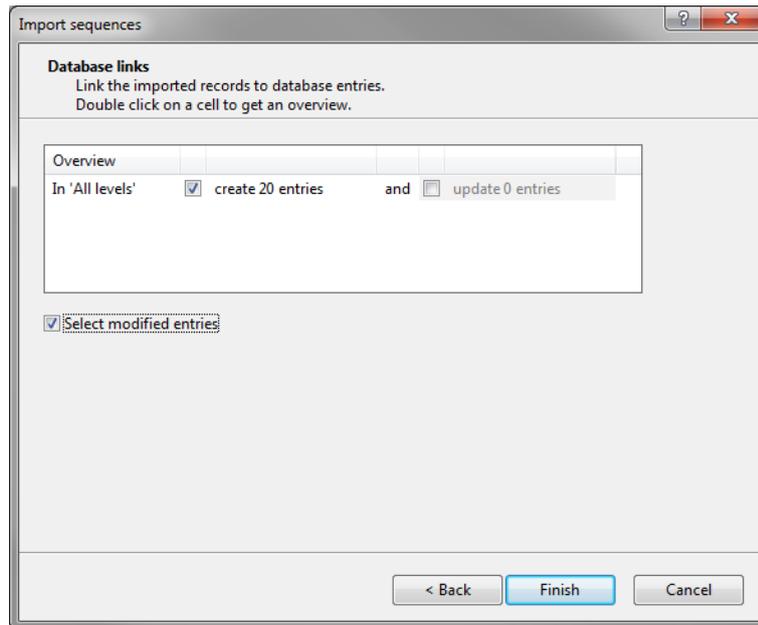


Figure 5: The *Database links* wizard page.

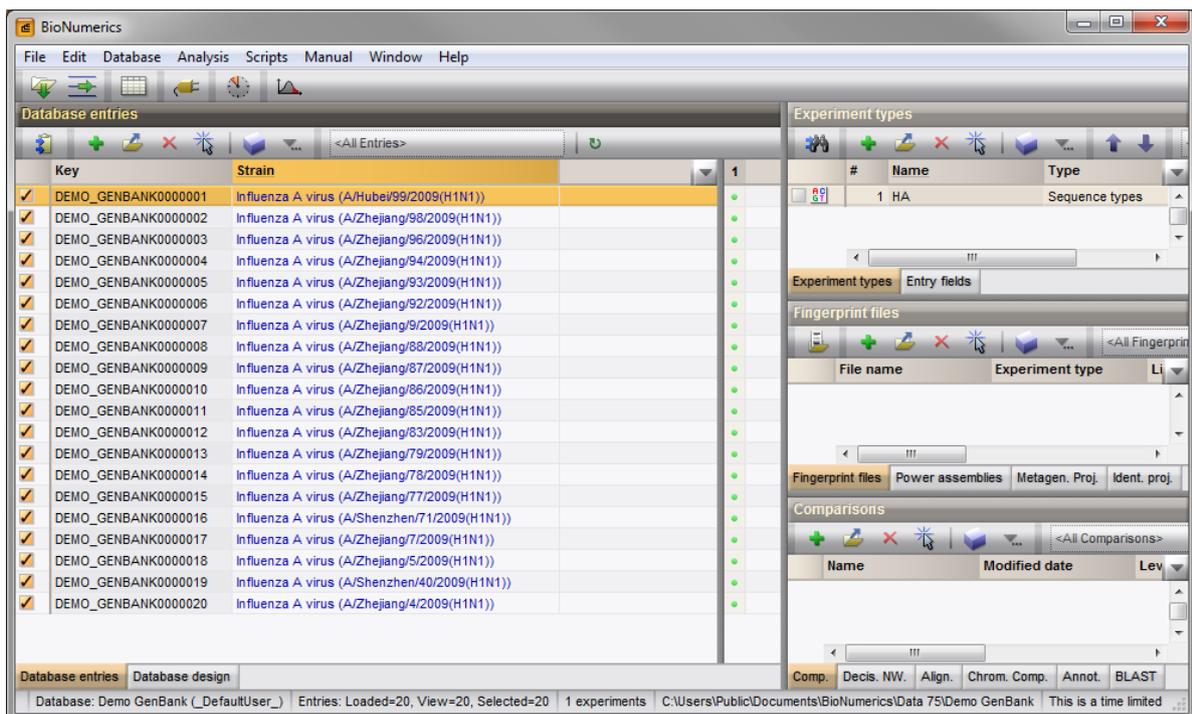


Figure 6: The *Main* window.

4 Conclusion

In this tutorial you have seen how easy it is to import GenBank/Embl formatted sequences in BioNumerics. The sequences can now be analyzed in BioNumerics. More information can be found in the analysis tutorials on our website.

The screenshot displays the 'DEMO_GENBANK000001 (Sequence Viewer)' application window. The interface is divided into several sections:

- Sequence Editor:** Shows a multi-line DNA sequence with positions 1190, 1260, 1330, and 1400 indicated on the right.
- Sequence Viewer:** A graphical representation of the sequence with a blue arrow indicating a specific region.
- Annotation:** A table listing features and their genomic coordinates. The 'CDS' feature is highlighted in yellow.
- Feature list table:**

Feature key	Start	End	Length
1 source	1	1701	1701
2 gene	1	1701	1701
3 CDS	1	1701	1701
4 sig_peptide	1	51	51
5 mat_peptide	52	1032	981
6 mat_peptide	1033	1698	666
- Annotation details:** A text area showing details for the selected feature (1..1701), including gene name ('HA'), function ('receptor binding and fusion protein'), product ('hemagglutinin'), protein ID ('AEN25706.1'), and a full amino acid translation sequence.

The status bar at the bottom indicates: Sequence: DEMO_GENBANK000001 | Experiment: abcZ | 1-1701 | 1701 bp

Figure 7: The Sequence editor window.