

BioNumerics Tutorial:

Selecting entries in a database

1 Aim

Selections are very important in BioNumerics since they form the basis for the creation of comparisons, comprising a host of analysis tools such as clustering, PCA analysis, band matching, etc. Furthermore, the creation of identification, alignment, chromosome comparison and genome annotation projects are based on a selection of entries, as well as the exchange of information with other users. In this tutorial you will learn how you can make selections in your BioNumerics database using the keyboard and the powerful google-like BioNumerics search window.

2 Preparing the database

The **DemoBase Connected** will be used in this tutorial and can be downloaded directly from the *BioNumerics Startup* window or restored from the back-up file available on our website:

1. To download the database directly from the *BioNumerics Startup* window, click the **Download example databases** link, located in the lower right corner of the *BioNumerics Startup* window. Select **DemoBase Connected** from the list and select **Database > Download**. Confirm the download action.
2. To restore the database from the back-up file, first download the file `DemoBase_Connected.bnbk` from <http://www.applied-maths.com/download/sample-data>, under 'DemoBase Connected'.

In the *BioNumerics Startup* window, press the  button, select **Restore database**, browse for the downloaded file and select **Create copy**. Specify a name and click **<OK>**.



In contrast to other browsers, some versions of Internet Explorer rename the `DemoBase_Connected.bnbk` database backup file into `DemoBase_Connected.zip`. If this happens, you should manually remove the `.zip` file extension and replace with `.bnbk`. A warning will appear ("If you change a file name extension, the file might become unusable."), but you can safely confirm this action. Keep in mind that Windows might not display the `.zip` file extension if the option "Hide extensions for known file types" is checked in your Windows folder options.

3 Manual selection of entries

1. In the *BioNumerics Startup* window, double-click on the **DemoBase Connected** database to open it.
2. Select a single entry in the *Database entries* panel by holding the **Ctrl**-key and left-clicking on the entry. Alternatively, use the **space bar** to select a highlighted entry or click the ballot box next to the entry.

Selected entries are marked by a checked ballot box (see Figure 1) and can be unselected in the same way.

3. In order to select a group of entries, hold the **Shift**-key and click on another entry.

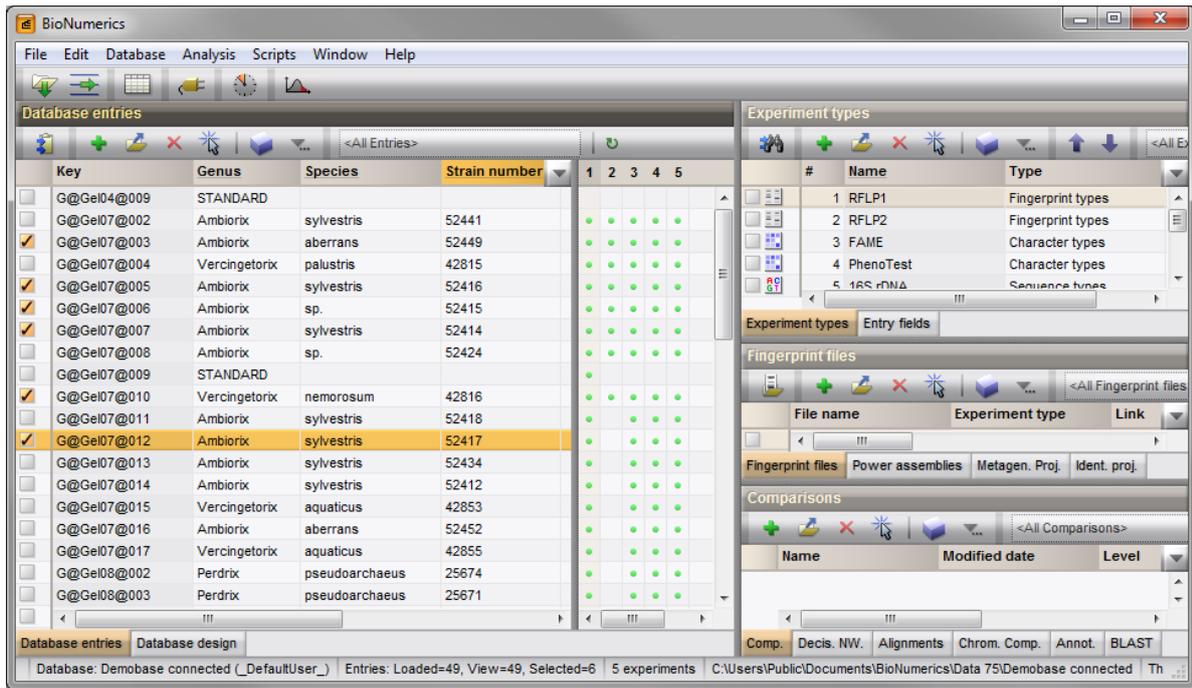


Figure 1: Selected entries are marked by a checked box.

A group of entries can be unselected the same way.

4. All entries can be selected at once with **Ctrl+A**.
5. Double-click on an entry to display its *Entry* window.
6. A single entry can also be selected or unselected from its *Entry* window using *Edit > Select / unselect this entry* ()
7. To invert the complete selection, i.e. to select all entries in the *Database entries* panel, except the currently selected ones, click on the *Database entries* panel to highlight this panel and use *Edit > Invert selection*.
8. To show only the selected entries, click on  in the toolbar and select *Selected Entries*.

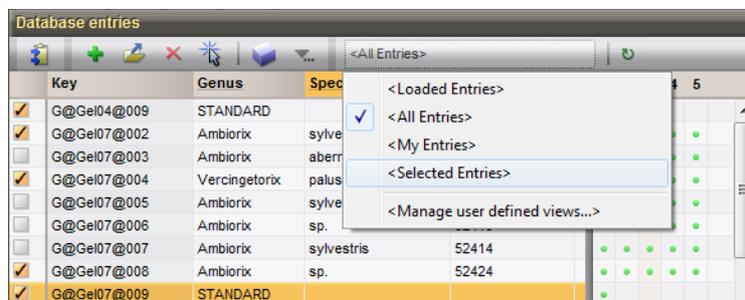


Figure 2: Display options in the *Database entries* panel.

9. To display all entries again, click on  in the toolbar and select *All Entries*.
10. Clear all selected entries with *Database > Entries > Unselect all entries (all levels)* (, F4).

4 Automatic search and select functions

To quickly find back entries in a long list, the *Find* dialog box is available in BioNumerics.

1. In the *BioNumerics Startup* window, double-click on the **DemoBase Connected** database to open it.
2. In the *Main* window, highlight the *Database entries* panel and select **Edit > Find object in list...** Alternatively, click on the  in the toolbar of the *Database entries* panel.

This calls the *Find* dialog box (see Figure 3). In the text box next to **Search for** you can type some text that will be searched for in all currently displayed information fields.

3. As an example, enter "s".

The display gets updated with those database entries that fulfill the search criteria (= "hits"). The number of hits is displayed as well (**Found**). When one or more hits are found, the column 'Hit column' displays the name of the information field in which the hit was found and the column 'Hit text' shows the matched string (see Figure 3).

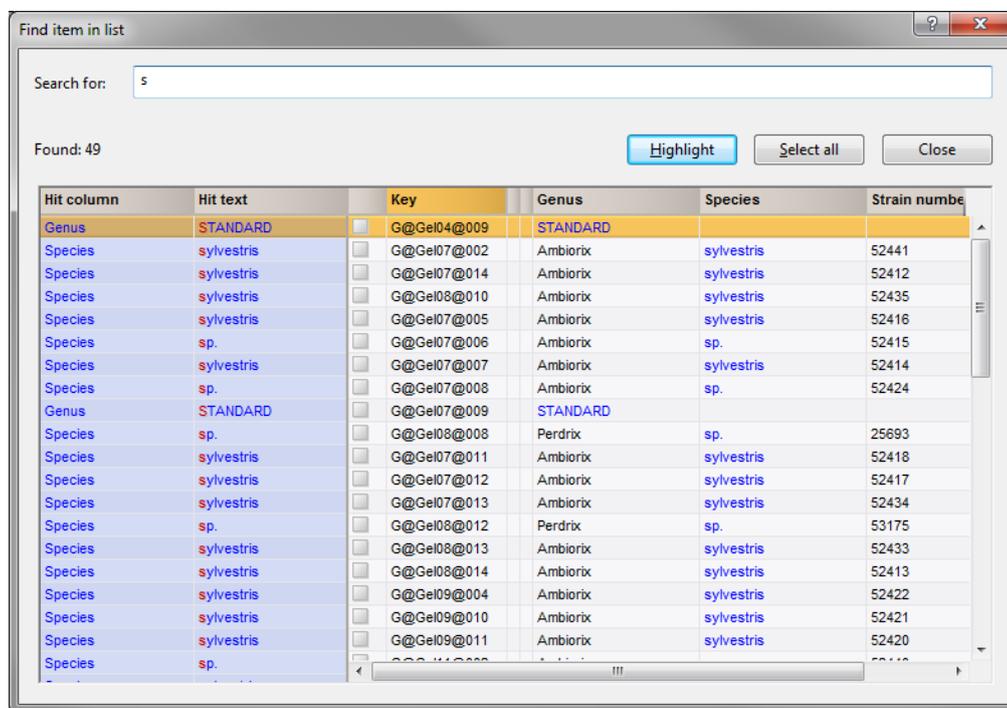


Figure 3: Find entries in list.

Further typing should narrow the search down:

4. As an example, enter "y" next to "s".

The display gets updated (see Figure 4).

5. Press the **<Select all>** button.

All database entries that fulfill the search criteria are selected in the database.

Entries can also be selected based on the presence/absence of an experiment:

6. Highlight an experiment type (for example **RFLP1**) in the *Experiment types* panel. Alternatively click on the experiment column in the *Experiment presence* panel.
7. Select **Database > Entries > Select entries with experiment (add)**.

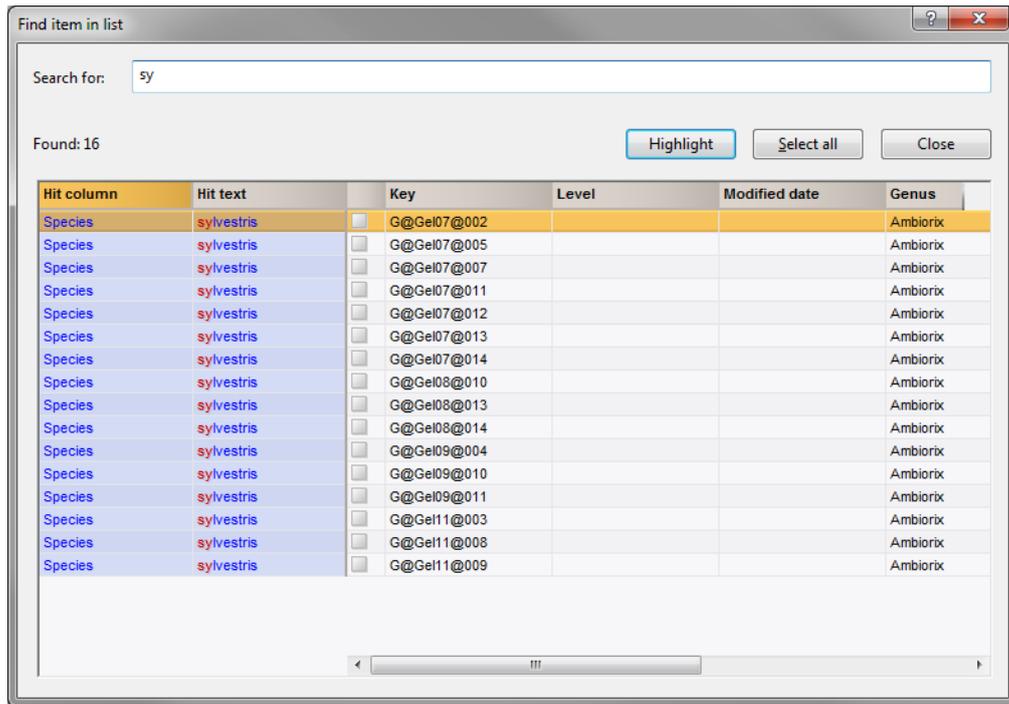


Figure 4: Find entries in list.

8. Alternatively, right-click on the experiment column number in the *Experiment presence* panel and select *Select entries with experiment (add)* (see Figure 5).

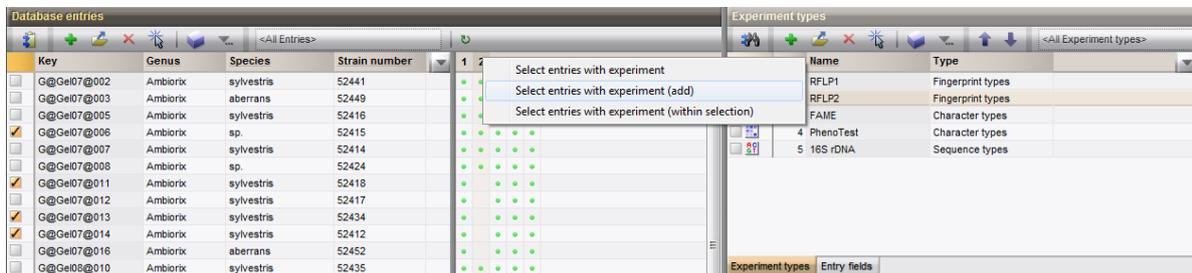


Figure 5: Select entries based on the presence/absence of an experiment.

All entries that have an experiment for the highlighted experiment type are added to the current selection.

5 Conclusion

Creating selections in BioNumerics as described in the two sections above are the basis of all analysis tools present in BioNumerics. More information about the analysis tools available in BioNumerics can be found in the analysis tutorials on our website.