

## BioNumerics Tutorial:

# Combined analysis of fingerprint data

## 1 Aim

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In BioNumerics it is possible to obtain a combined dendrogram from multiple experiments. In this tutorial you will learn how to create a dendrogram based on fingerprint data coming from two different experiments.

## 2 Preparing the database

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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 Creating a composite data set of fingerprint data

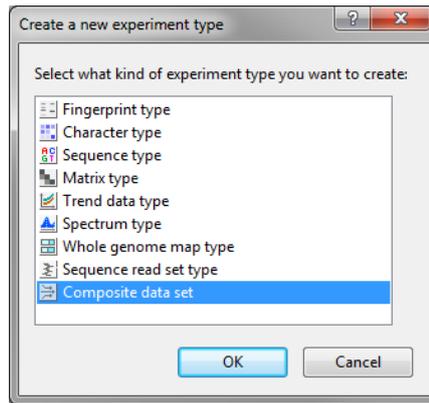
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A composite data set in BioNumerics is a "container" of experiment types, i.e. it holds data coming from one or several experiments. In a first step we need to define a *composite data set*, containing two fingerprint types as input.

1. In the *BioNumerics Startup* window, double-click on the **DemoBase Connected** database to open it.
2. In the *Main* window, click on  in the toolbar of the *Experiment types* panel and select **Composite data set** from the list.
3. Press **<OK>**, enter a name, for example "RFLP-combined" and press **<OK>**.

The *Experiment types* panel now lists the composite data type **RFLP-combined**.

4. Double-click on **RFLP-combined** in the *Experiment types* panel.



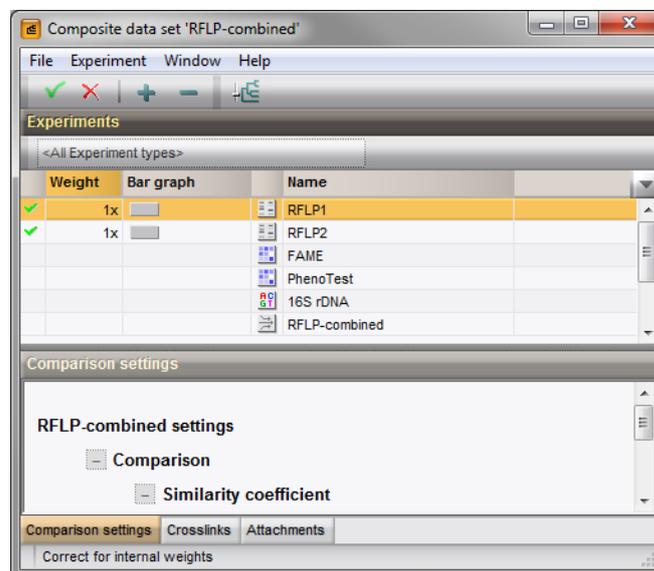
**Figure 1:** Create a new composite data set.

The *Composite data type* window is shown for **RFLP-combined**.

5. Click on **RFLP1** and select *Experiment* > *Include experiments* (✓).
6. Click on **RFLP2** and select *Experiment* > *Include experiments* (✓).

Both RFLP1 and RFLP2 are selected in the composite data set, and are marked with a green V-sign (see Figure 2).

The bar that appears in the 'Bar graph' column displays the weights assigned to each experiment type. Weights can be increased or decreased with *Experiment* > *Increase weight* (+) and *Experiment* > *Decrease weight* (-) respectively.



**Figure 2:** The Composite data set.

In order to treat the two fingerprint types on an objective basis, i.e. the number of bands in the compared patterns, the following is done:

7. Select *Experiment* > *Correct for internal weights*. The caption now shows "Correct for internal weights".
8. Close the *Composite data type* window with *File* > *Exit*.

9. In the *Database entries* panel of the *Main* window, select all entries except STANDARD: select **Ctrl+A** to select all entries and use the **Ctrl-** key to unselect the entries defined as STANDARD. Alternatively unselect the entries by unchecking the check boxes next to the entries.
10. Highlight the *Comparisons* panel in the *Main* window and select *Edit > Create new object...* (+) to create a new comparison for the selected entries.

## 4 Combined analysis of fingerprint data

### 4.1 Averaging the individual matrices

1. Select the experiment **RFLP-combined** in the *Experiments* panel.
2. Select *Clustering > Calculate > Cluster analysis (similarity matrix)...*

When selecting the option *Average from experiments*, the similarity matrices of the individual experiments (in this example **RFLP1** and **RFLP2**) are calculated first using the comparison settings defined for each individual experiment (double-click on the fingerprint type in the *Experiment types* panel and select *Settings > Comparison settings...* (ⓘ)) to access the settings). From these matrices, a combined matrix is calculated by averaging the values according to the defined weights.

3. Select *Average from experiments* and press <Next> and <Finish>.

The dendrogram is displayed in the *Dendrogram* panel (see Figure 3).

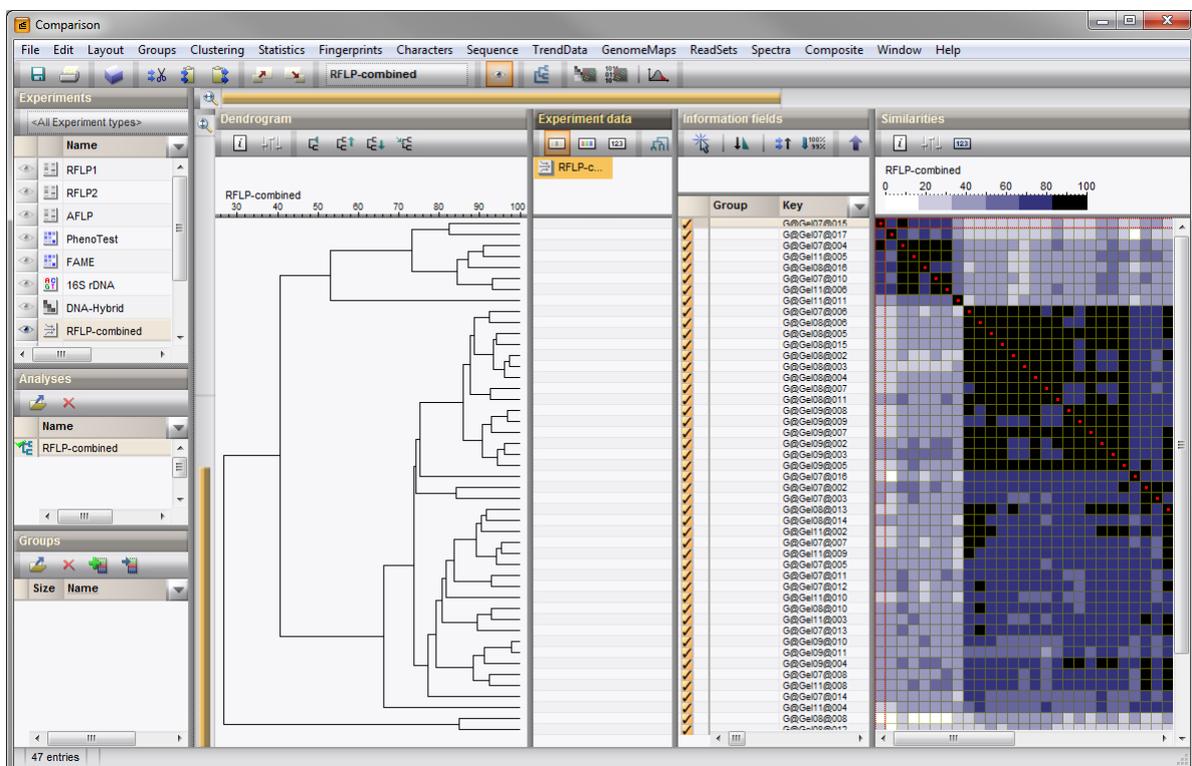


Figure 3: The *Comparison* window.

4. To view the settings used for the calculation of the individual matrices, select *Clustering > Show information* (ⓘ).

## 4.2 Creating a combined character matrix

In BioNumerics it is also possible to merge the characters (i.e. bandclasses in case of fingerprint data) from different experiments, and calculate a similarity matrix based on this merged character table, resulting in a combined dendrogram.

In order to combine fingerprints in one character table, we need to perform a bandmatching on each of the fingerprint type experiments (**RFLP1** and **RFLP2** in our example):

5. Select **RFLP1** in the *Experiments* panel and select *Fingerprints* > *Perform band matching...* (||||).
6. Select *Find classes on all entries* and press <OK>.
7. Select **RFLP2** in the *Experiments* panel and select *Fingerprints* > *Perform band matching...* (||||).
8. Select *Find classes on all entries* and press <OK>.
9. Click on the  next to the experiment name **RFLP-combined** in the *Experiments* panel to display the binary band matching table of RFLP1 and RFLP2 (see Figure 4).
10. Select *Clustering* > *Calculate* > *Cluster analysis (similarity matrix)...*

To calculate a similarity matrix based on the merged band matching table choose a coefficient under **Character data**. Binary coefficients measure the similarity based upon common and different bands; numerical coefficients use the band intensities for the calculation of the similarity.

11. Select a binary coefficient, e.g. *Dice* and press <Next> and <Finish>.

The resulting dendrogram is displayed in the *Dendrogram* panel (see Figure 4).

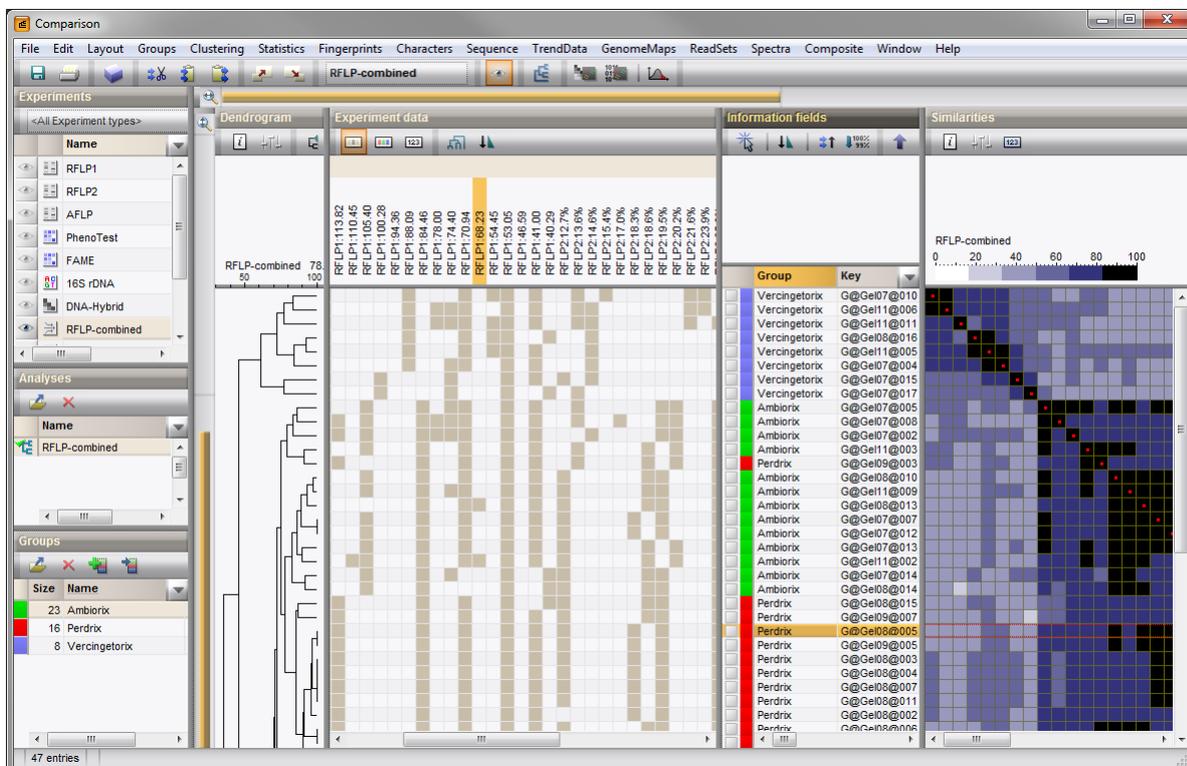


Figure 4: The Comparison window.