

BioNumerics Tutorial:

Installation and setup of the *Spa typing plugin*

1 Introduction

The *Spa typing plugin* offers extra functionality to BioNumerics to do Spa typing for *Staphylococcus aureus*. Sequences in the database can be screened for known spa repeats and types downloaded from the SpaServer, data can be submitted to the SpaServer via a synchronization process, and entries can be clustered based on the spa types. In this tutorial the installation of the *Spa typing plugin* in a new database is covered.

2 Creating a new database

To illustrate the installation and setup of the *Spa typing plugin*, we will start by creating a new, empty database.

1. Double-click on the BioNumerics icon () on the desktop.
2. In the *BioNumerics Startup* window, press the  button to enter the *New database wizard*.
3. Enter a database name, e.g. “Staphylococcus aureus”.
4. Click <*Next*> and then <*Finish*>.

A new dialog box pops up, asking whether to create a new relational database for data storage or to use an existing one.

5. Leave the default option *Create new* enabled and press <*Next*>.

The next dialog asks which database engine should be used for storing data.

6. Select the default option and press <*Finish*>.

The *Plugins* dialog box pops up which allows you to install additional functionality.

7. Press <*Proceed*> to start BioNumerics.

The *Main* window opens with an empty database.

3 Installing the Spa-Typing plugin

1. The *Plugins* dialog box is called from the *Main* window by selecting *File* > *Install / remove plugins...* (.
2. Select the *Spa typing plugin* from the list in the *Applications* tab (Figure 1) and press the <*Activate*> button.

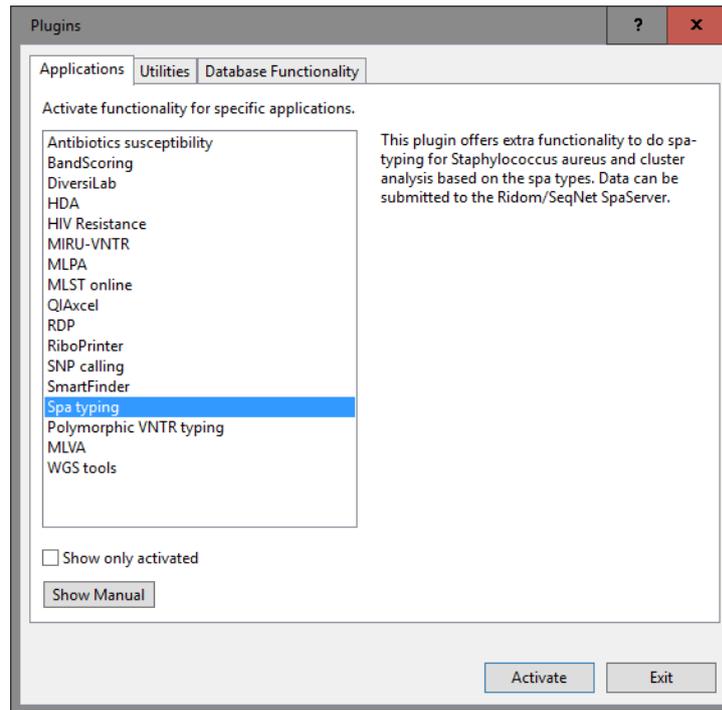


Figure 1: Install a plugin in the database.

The next dialog asks to confirm the installation of the *Spa typing plugin*. Installation of the plugin requires administrator privileges on the relational database.

3. Press **<OK>** twice to confirm the installation.

BioNumerics checks if the Character data module is present in the BioNumerics configuration.

- If the Character data module is present in the BioNumerics configuration, the repeat succession information will be stored in a character type experiment *and* in an information field. The repeat information stored in the associated character type will be used when using the matching and clustering tools.
- If the Character data module is *not* present in the current BioNumerics configuration, the repeat succession will only be stored in an information field. Information fields can only contain up to 80 characters, so long repeat successions may be truncated when stored in an information field. BioNumerics will warn you for this by displaying a message upon installation of the plugin.

The *Spa typing settings* dialog box pops up (see Figure 2).

4. For this exercise, leave all settings unaltered and press **<OK>**.

BioNumerics imports the types and repeats from the Ridom/Seqnet SpaServer.

5. When the *Spa typing plugin* is successfully installed, a confirmation message pops up. Press **<OK>**.
6. Press **<Exit>** to close the *Plugins* dialog box.

4 The Main window after installation of the plugin

The *Spa typing plugin* installs itself in a menu of the BioNumerics software (see Figure 3).

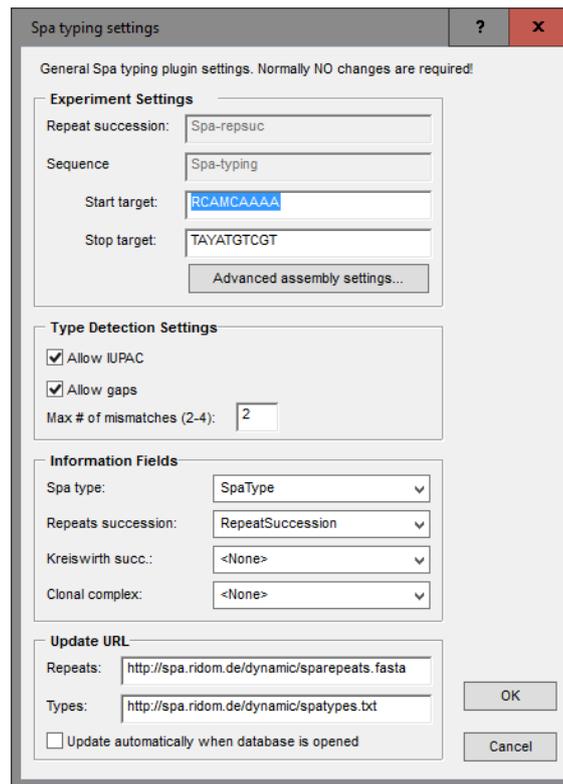


Figure 2: Spa typing settings.

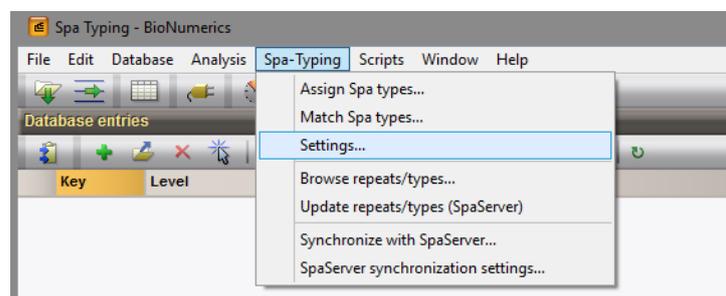


Figure 3: The Spa-Typing menu-items.

In the *Main* window, some initialization has been done to the database with the installation of the *Spa Typing* plugin:

- The information fields specified in the *Information fields* panel of the *Spa typing settings* dialog box are present in the *Database entries* panel.
- The *Experiment types* panel lists the experiment types. BioNumerics has automatically created a sequence type called **Spa-typing**. If the Character data module is present in the BioNumerics configuration, a character type called **Spa-repsuc** is created upon installation of the plugin.

1. To call the *Spa typing settings* dialog box again from the *Main* window, select *Spa-Typing* > *Settings*. Press <OK> to close the dialog.

The lists of Spa repeats and Spa types, downloaded from the SpaServer, can be queried by the user.

2. Select *Spa-Typing* > *Browse repeats/types* in the *Main* window.

3. Select *repeats/types* in the *Repeats/Types* panel (see Figure 4) and press the *<Find>* button to look for a repeat/type.

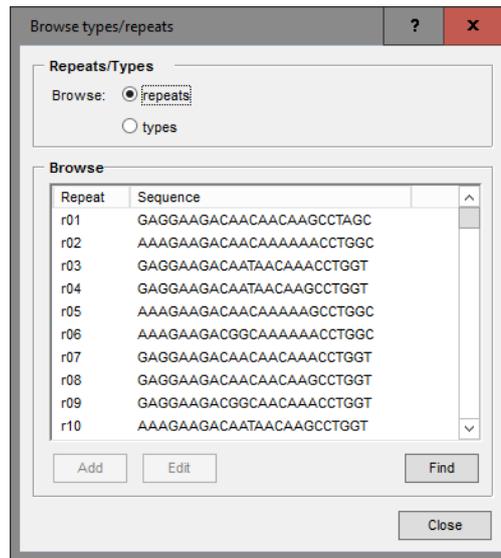


Figure 4: Search for repeats or types.

4. Close the dialog with the *<Close>* button.
5. The list of known repeats and types can be updated with the command *Spa-Typing > Update repeats/types (SpaServer)*.



You can perform analyses without being connected to the internet, but you will be unable to update the list of known repeats and types.