



BIONUMERICS®

version 8 - PLUGINS



iTOL integration plugin

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NOTES

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- Velvet for Windows, source code can be downloaded from <https://www.bionumerics.com/download/open-source>
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- Fastp version 0.22.0, <https://github.com/OpenGene/fastp>

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Chapter 1

Starting and setting up BIONUMERICS

1.1 Introduction

The *Interactive Tree Of Life* or iTOL [1] is a popular online tool for tree visualization and annotation. A publicly accessible instance of this software is available on <https://itol.embl.de/> (see Figure 1.1).

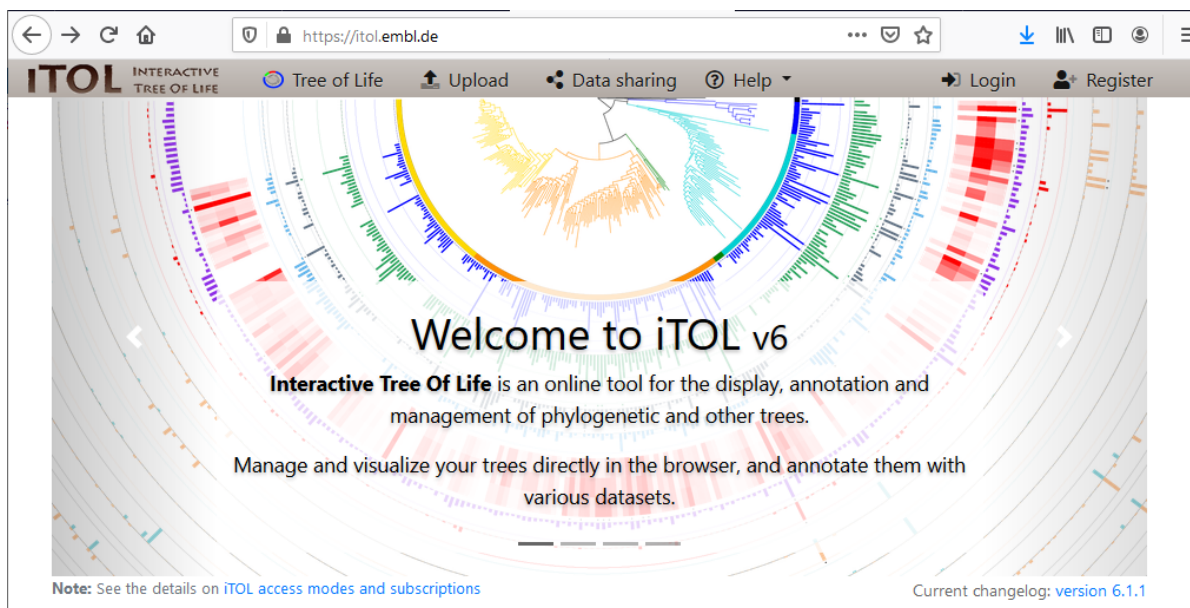


Figure 1.1: The iTOL home page on <https://itol.embl.de/>.

The *iTOL integration plugin* in BIONUMERICS allows you to upload dendrograms and meta data from your BIONUMERICS database to the iTOL server.

1.2 Prerequisites

In order to benefit from the features in the *iTOL integration plugin*, you need an iTOL account with an active subscription and an API key generated.

- 2.1 First log in to your iTOL account or create an account on https://itol.embl.de/itol_account.cgi following the instructions outlined on this page.

iTOL requires an active subscription to upload trees, i.e. free access will not work. For more information on iTOL accounts, see <https://itol.embl.de/infoReg.cgi>.

2.2 Check if you have an active subscription on the iTOL account information page <https://itol.embl.de/userInfo.cgi>. If not, purchase your subscription keys and activate your subscription according to the instructions that came with the keys.

Finally, you need to generate an API key which the *iTOL integration plugin* (or other software) uses to identify itself against the iTOL API.

2.3 On the iTOL account information page, press the "Create API key" button.

Your API key is shown on the same page (see Figure 1.2).

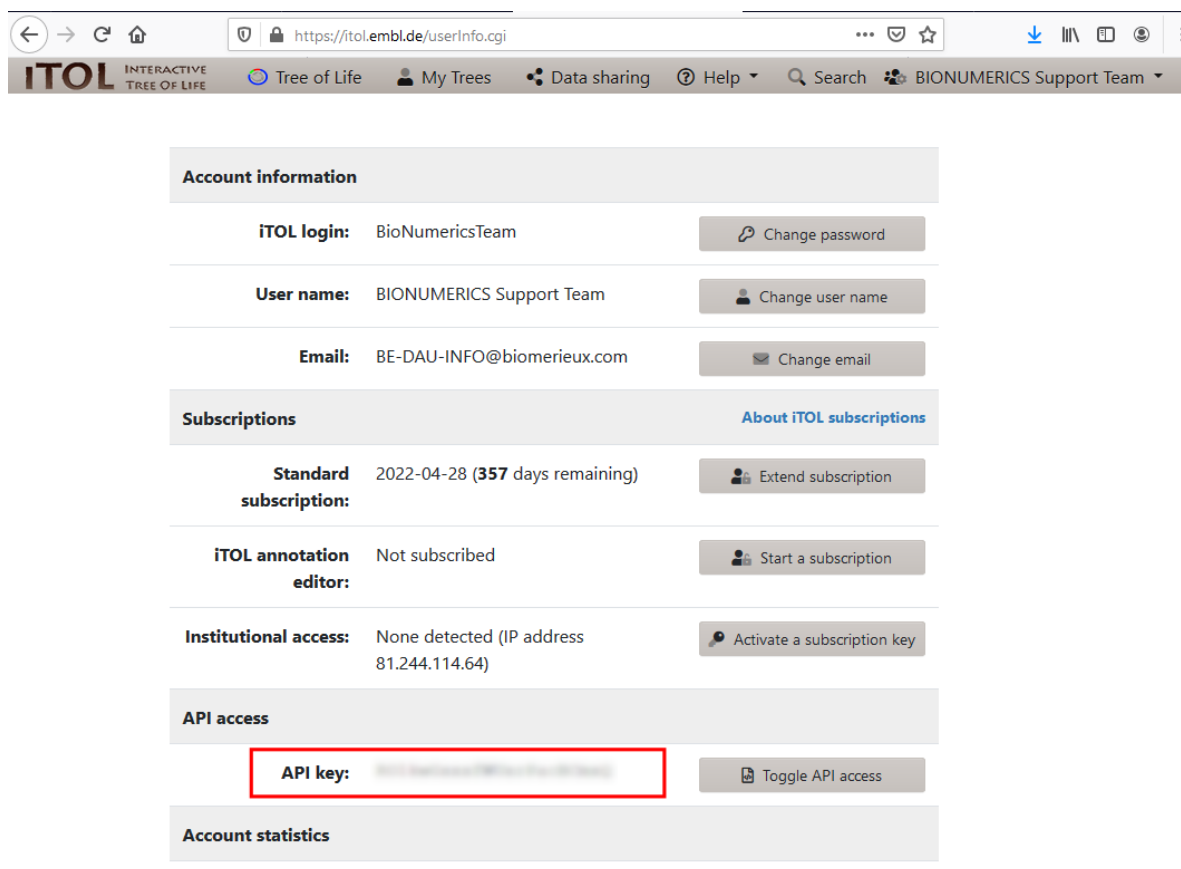



Figure 1.2: The iTOL account information page with the API key indicated.

This API key should be copied and pasted in the *iTOL settings* dialog box during installation of the *iTOL integration plugin* (see 1.4).

Optionally, a dedicated project can be generated to which trees generated in your BIONUMERICS database are added. A default project called "Sample project" is always generated.

1.3 Startup program

Make sure the latest version of BIONUMERICS is installed (<https://www.bionumerics.com/download/software>). The installation manual can be downloaded from <https://www.bionumerics.com/download/manuals>.

When BIONUMERICS is launched from the Windows start panel or when the BIONUMERICS shortcut () on your computer's desktop is double-clicked, the **Startup program** is run. This program shows the *BIONUMERICS Startup* window (see Figure 1.3).

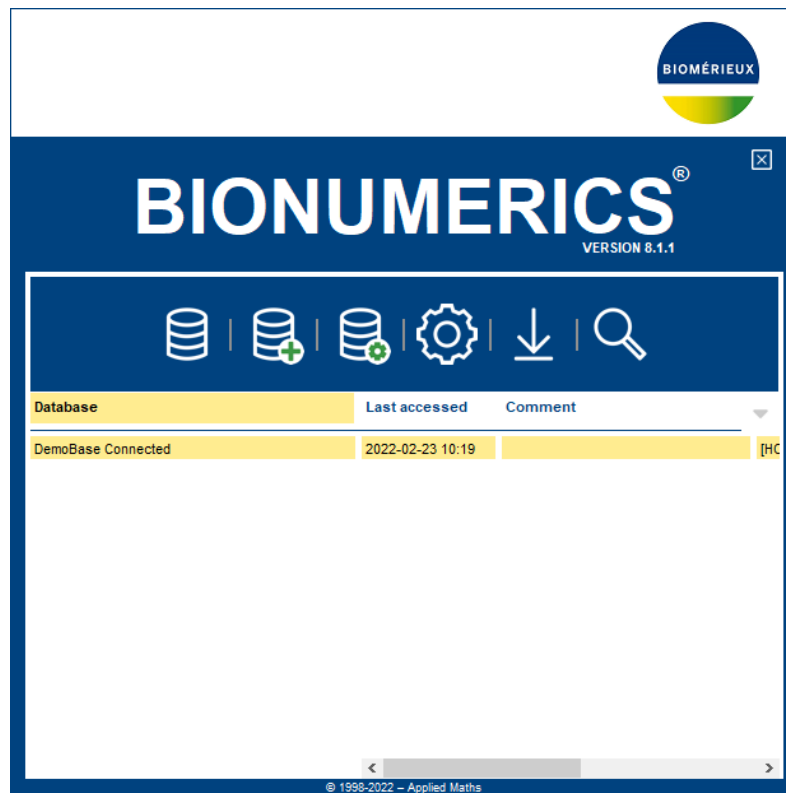





Figure 1.3: The *BIONUMERICS Startup* window.

A new BIONUMERICS database is created from the Startup program by pressing the  button.

An existing database is opened in BIONUMERICS with  or by simply double-clicking on a database name in the list.

1.4 Installing the iTOL integration plugin

The *Plugins and Scripts* dialog box can be called from the *Main* window by selecting **File > Install / remove plugins...** () (see Figure 1.4).

When a particular plugin is selected from the list of plugins, a short description appears in the right panel.

A selected plugin can be installed with the **<Install>** button. The software will ask for confirmation before installation. Some plugins are only supported in specific BIONUMERICS configurations. If the plugin is not supported by your BIONUMERICS configuration, it cannot be installed and an error message will be generated.

Once a plugin is installed, it is marked with a green V-sign. It can be removed again with the **<Uninstall>** button.

If the selected plugin is documented, pressing **<Show Manual>** will open its manual in the *Help* window.

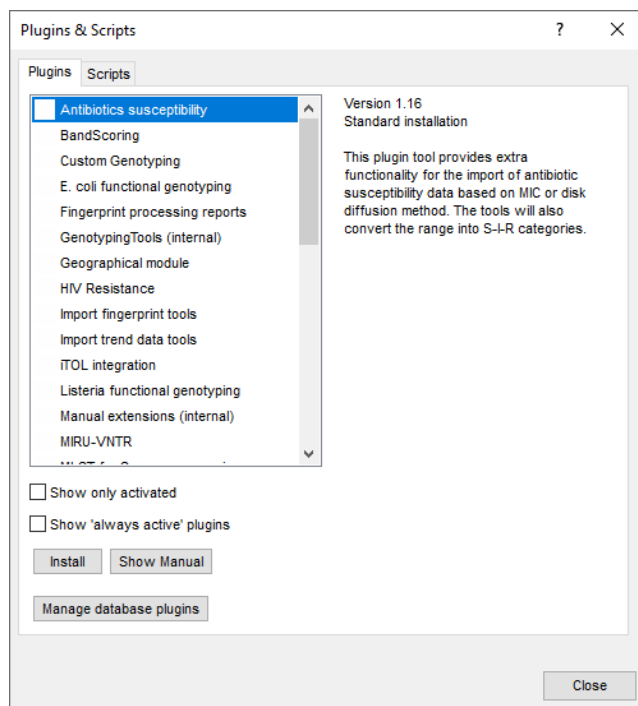


Figure 1.4: The *Plugins and Scripts* dialog box.

Proceed as follows to install the *iTOL integration plugin*, starting from the *Plugins and Scripts* dialog box:

4.1 Select the *iTOL integration plugin* in the list and press the **<Install>** button.

4.2 Confirm the installation of the plugin and press **<OK>**.

The *iTOL settings* dialog box pops up (see Figure 1.5).

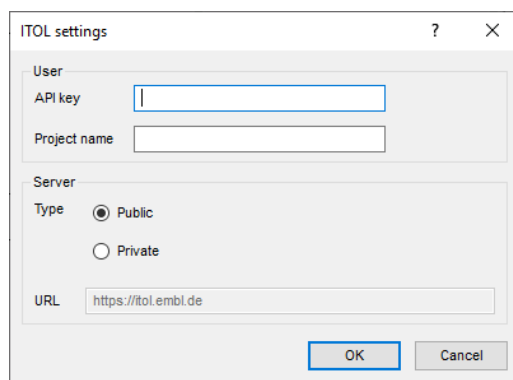


Figure 1.5: The *iTOL settings* dialog box.

In the **API key** text box, an API key as generated on the iTOL account information page should be entered (see 1.2).

Project name corresponds to the name of the iTOL project under which the exported trees will be listed.

By default, the plugin integrates with the **Public** iTOL server from EMBL (<https://itol.embl.de/>), which will be applicable for most users. If desired, a **Private** iTOL server can be used after

entering the corresponding **URL**.

4.3 Enter **API key** and **Project name** and press <**OK**> to close the *iTOL settings* dialog box.

A message appears to indicate that the *iTOL integration plugin* is installed, with the recommendation to restart the database.

4.4 Press <**OK**> to close the message.

Once the plugin is successfully installed, it is marked with a green V-sign in the *Plugins and Scripts* dialog box.

4.5 Press <**Close**> to close the *Plugins and Scripts* dialog box.

4.6 Close and reopen the database to activate the features of the *iTOL integration plugin*.

The *iTOL integration plugin* adds items to the menu of the *Comparison* window.

Chapter 2

Exporting trees to iTOL

2.1 Background

Most dendrograms or trees in BIONUMERICS are calculated in the *Comparison* window. In addition, several other windows offer the option to export dendrograms to the *Comparison* window. Any tree in the *Comparison* window, regardless the dataset it was calculated on, can be exported to iTOL with the *iTOL integration plugin*. For maximum flexibility, the iTOL website is opened with the system's default web browser.

iTOL > Upload to iTOL... launches the main functionality offered by the plugin. It works according to the WYSIWYG (What You See Is What You Get) principle, meaning that – within the limits of what can be visualized in iTOL – whatever is shown in the *Comparison* window, will be included in the export. In summary, following data is exported:

- The dendrogram currently displayed in the *Dendrogram* panel.
- Any experiment data currently visualized in the *Experiment data* panel. All experiment types will be interpreted as characters and can be visualized in iTOL as heat maps. Note that sequences longer than 4,000 bases will not be exported, as they cannot be displayed in iTOL anyways.
- The entry information displayed in the *Information fields* panel.
- When defined, comparison groups (see ??), with their group labels and group colors.
- The similarity matrix as shown in *Similarities* panel.

The tree is uploaded under its **Dendrogram name**, as provided in the *Page 2* wizard page of the *Similarity coefficient* wizard (see ??). The uploaded tree can be further annotated and customized in iTOL and exported in different formats. For a description of this functionality, we refer to the iTOL help pages.



The uploaded tree can only be saved in your project when you are logged in with your iTOL account.

iTOL > Open iTOL... is essentially just a shortcut to open the iTOL website in the default browser. This can be useful e.g. to check beforehand if you are logged in with your iTOL account or to open any saved trees created earlier.

iTOL > Settings... opens the settings as discussed in 1.4. Once a correct **API key** is entered, it is unlikely that this field needs to be edited. However, the **Project name** needs to be altered if the tree should be saved under a different project.

Bibliography

- [1] Ivica Letunic and Peer Bork. Interactive tree of life (itol) v5: an online tool for phylogenetic tree display and annotation. *Nucleic Acids Research*, 04 2021. gkab301.

