

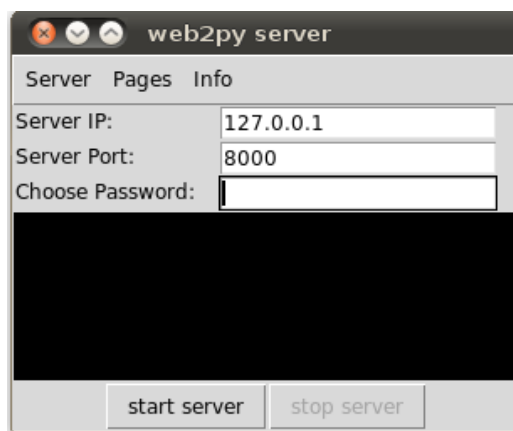
How to install rxncon – Windows edition



Installing rxncon on Windows

Here, you find guidance for the installation of rxncon. First things first:

- Download rxncon here: http://www.rxncon.org/rxncon/plugin_release/download and save it on your computer
- Extract the files from the archive. You need a programme to do that. (You can download the programme *7zip* for instance)
- Go to the *web2py* directory
- Double-click on the rxncon.bat file
- The *web2py* window should open



- Choose a temporary password and push "Start server" (The password will only be valid for this session)
- Your browser will automatically open and start the rxncon application
- If you are a first time user, create your user-id. While working in the browser, your work will be done and saved locally.

Additional programmes and configuration

Before you can start using rxncon you have to make some local configurations in the *Configure* menu at the rxncon website.

Install BioNetGen

- Download and install BioNetGen (you find BioNetGen here http://bionetgen.org/index.php/BioNetGen_Distributions#Source_Code_Distribution)
- Specify the BioNetGen path: Open the BioNetGen folder, click into the location field and copy it. Paste the path into the BioNetGen field in the *Configure* menu. Add \BNG2.pl
- Specify the Perl path. You may try

`C:\Perl64\bin\perl.exe`

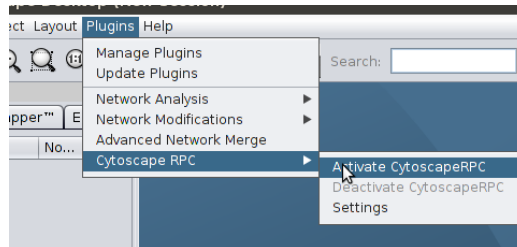
In case Perl is saved somewhere else, employ the find-tool in windows and search for Perl. Copy and paste the path to the path field for Perl.

- In case Perl is not installed, you may download it here: <http://www.perl.org/get.html>
- Save your changes

Install Cytoscape

- Download Cytoscape here <http://www.cytoscape.org/download.html>
- Start Cytoscape
- Install the XMLRPC plugin by selecting: Plugins > Manage Plugins > Available for Install > Communication/Scripting > CytoscapeRPC 1.2

- Start the XMLRPC plugin by selecting: Plugins > Cytoscape RPC > Activate CytoscapeRPC > OK (default options are fine; XML-RPC, Port 9000)



Specify the Biographer path

- Copy and paste the following link into the field for the Biographer path
<http://biographer.biologie.hu-berlin.de/>

Python

- You should use a Python version ≥ 2.5
- You may check the version you are using by starting Python (the version number will be shown in the Python shell)

Updating rxncon

- If there is a new version of rxncon available use the *Update* link in the header menu. (A restart of rxncon might be required.)
- The update process will download a web2py application package (*.w2p) and overwrite your current web2py application. All your data will still be available and ready to use with the new rxncon version.
- Some updates may require web2py to be updated. You can update the web2py server by going to <http://127.0.0.1:8000/admin/default/site> and using the *Update now* button.

First test

The installation and configuration is now finished. You may now test the example provided on the rxncon website. By clicking on *Simple example.xls* you will upload a small network. It is the Sho1 branch of the HOG pathway in the yeast *S. cerevisiae*. You can now choose the visualization format by pushing the Graph button. Try SBGN-PD. A new tab should open where you can edit the layout of the network.