

How to install rxncon – OS X edition



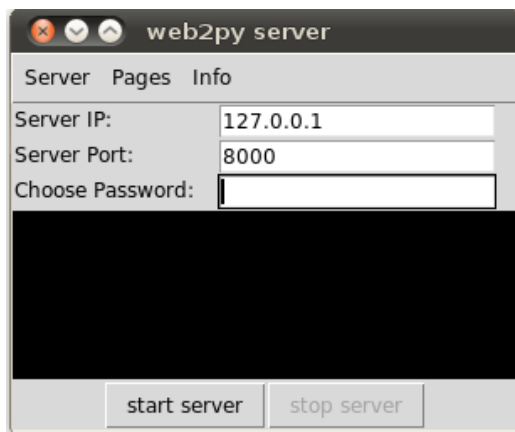
Installing rxncon on OS X \geq 10.5

- create a folder e.g. rxncon_osx
- Download rxncon here: http://www.rxncon.org/rxncon/plugin_release/download and save it on your computer in the created directory
- change to the respective directory and extract the file either on the Terminal with

```
tar -xzf rxncon_osx.tar.gz
```

or in the finder with double click on rxncon_osx.tar.gz

- You may now start rxncon double clicking on the web2py.app:
- The *web2py* window opens



- Choose a temporary password and click on "Start server"
- Your browser will automatically open and start the rxncon application
- As a first time user you will be asked to create a user-id

Additional programmes and configuration

To be able to use rxncon, make sure you have done the following things:

Install and Configure libSBML

- Download and install swig from <http://www.swig.org/> (the installation is tested with swig 2.0.2)
- Download libSBML source here: <http://sbml.org/Software/libSBML>

```
tar xzf your_libsbml.tar.gz
```
- Extract the files from the archive
- Change to your_libsbml_folder directory and create a 'build' folder with

```
cd your_libsbml_folder/  
mkdir build
```
- Run cmake-gui and set:

Where is the source code: `your_libsbml_folder/`

Where to build the binaries: `your_libsbml_folder/build/`

- Click on configure and choose *Unix Makefiles* as generator for the project
- Enable `WITH_PYTHON`
- Set `CMAKE_OSX_ARCHITECTURES=i386`
- Click again on configure
- Change to the command line and change in the `your_libsbml/`
- Change the cmake python variables with

```
-DPYTHON_EXECUTABLE=/usr/bin/python2.5
```

```
-DPYTHON_INCLUDE_DIR=/System/Library/Frameworks/Python.framework/  \\  
Versions/2.5/include/python2.5
```

```
-DPYTHON_LIBRARY=web2py.app/Contents/Frameworks/Python.framework/  \\  
Versions/2.5/Python\\
```

the command is

```
cmake -DPYTHON_EXECUTABLE= -DPYTHON_INCLUDE_DIR= -DPYTHON_LIBRARY= ./build
```

with the respective path

- If the configuration is done change in the build directory and do the following

```
cd build
```

```
make
```

```
make install
```

Now, libsbml is installed and you have to copy the compiled site-package to web2py Resources usually this is

```
cp -R /usr/local/lib/python2.5/site-packages rxncon_osx/web2py/  \\  
web2py.app/Contents/Resources/
```

If everything works without errors than libsbml is successfully installed and linked to your web2py version.

Install and Configure BioNetGen

- Download BioNetGen here: http://bionetgen.org/index.php/BioNetGen_Distributions

- Extract the files from the archive
- BioNetGen should be installed now
- Specify the BioNetGen path. You may try:

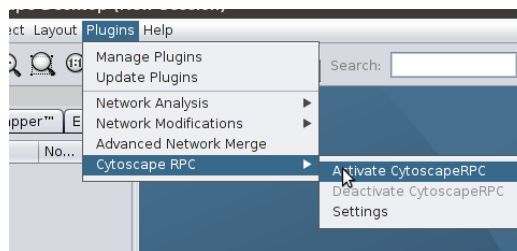
```
dpkg -S BNG2.pl
```

- Copy the line that ends with *BNG2.pl* and paste it into the field for the BNGL path (go to the *Configure* page at rxncon)
- Copy the default path for Perl and paste it into the specified field in the configuration menu

```
/usr/bin/perl
```

Install Cytoscape

- Download cytoscape here <http://www.cytoscape.org/download.html>
- Start Cytoscape
- Install the XMLRPC plugin by selecting: Plugins >Manage Plugins extgreater 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)



Configure the Biographer path

After starting rxncon go to the *Configure* page. Here you will find the point 'Set the location of biographer. Biographer Url:'. For visualization we recommend to use the biographer version provided by rxncon. To use this version you can copy and paste the following link into the field for the Biographer path

```
http://127.0.0.1:8000/biographer
```

If you want to use the online version of biographer copy and paste the following link into the field for the Biographer path

```
http://biographer.biologie.hu-berlin.de/
```

Python

- web2py brings his own python version which is python 2.5

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.