

# A Framework for Parameter Estimation and Model Selection From Experimental Data in Systems Biology Using Approximate Bayesian Computation

Juliane Liepe, Paul Kirk, Sarah Filippi, Tina Toni, Chris P. Barnes, Michael P.H. Stumpf

## EXAMPLE INSTALLATION ON UBUNTU

This is an example of how to install Python and all dependencies required to follow this protocol on an Ubuntu (12.04.2LT2) computer. The general instructions for any Linux or Mac OS X platform can be found in the *'README.txt'* file and in the manual, both of which are included in the *ABC-SysBio* package.

Before installing *ABC-SysBio* we need to install Python and the following packages:

- Numpy
- Scipy
- Matplotlib
- libSBML

The Ubuntu distribution already includes Python. To check this, type in the terminal:

*which python*

This should result in:

*/usr/bin/python*

Now install Numpy. Download Numpy from:  
<http://sourceforge.net/projects/numpy/files/>  
and unzip the file. In the terminal go to the Numpy directory and type:

*python setup.py install*

Next we install Scipy. Download Scipy from:  
<http://sourceforge.net/projects/scipy/files/>  
and unzip it. In the terminal go to the Scipy directory and type:

*python setup.py build*  
*python setup.py install*

We now install Matplotlib. Download Matplotlib from:  
<http://sourceforge.net/projects/matplotlib/files/>  
and unzip it. In the terminal go to the Matplotlib directory and type:

```
python setup.py build  
python setup.py install
```

We now need to install Swig, which is necessary for libSBML. On the Ubuntu computer go to *Software center* and search for 'swig'. In the results list choose 'swig - generate scripting interfaces to C/C++ code' and click on 'install'. Alternatively download Swig from <http://sourceforge.net/projects/swig/files/> and unzip it. In the terminal go to the Swig directory and type:

```
./configure  
make  
sudo make install
```

Furthermore we need to install xml2, which is also required for libSBML. Again go to the [Software center](#) and search for 'xml2'. Select 'xml2 - Convert between XML, HTML, CSV and a line-oriented format' and click on 'install'

Finally we install libSBML. Download libSBML from:  
<http://sourceforge.net/projects/sbml/files/libsbml/>  
and unzip it. In the terminal go to the libSBML directory and type:

```
./configure --with-python --with-swig  
make  
sudo make install
```

To check that all python libraries have been successfully installed, start python in the terminal and try to import Numpy, Scipy, Matplotlib and libSBML:

```
Python 2.7.3 (default, Apr 10 2013, 06:20:15)  
[GCC 4.6.3] on linux2  
Type "help", "copyright", "credits" or "license" for more information.  
>>>  
>>> import numpy  
>>>  
>>> import scipy  
>>>  
>>> import matplotlib  
>>>  
>>> import libsbml  
>>>
```

Assuming that the previous steps were completed successfully, we can now install *ABC-SysBio*. Download the *ABC-SysBio* package from: <http://sourceforge.net/projects/abc-sysbio/files/> and unzip it. Open a terminal and type:

```
cd abc-sysbio-2.07  
python setup.py install
```

This places the *ABC-SysBio* package into

```
<dir>/lib/python2.7.3/site-packages/
```

and writes the scripts

```
<dir>/bin/abc-sysbio-sbml-sum  
<dir>/bin/run-abc-sysbio
```

Then type the command

```
run-abc-sysbio -h
```

This will display a list of options for the *ABC-SysBio* package and you are ready to run the examples.

### **EXAMPLE INSTALLATION ON MAC OSX 10.8 (Mountain Lion)**

This is an example of how to install all of the dependencies required to follow this protocol on a Mac running OSX 10.8. It assumes that you have the default Python installed and that you have the latest version of Xcode and the command line tools.

Before installing *ABC-SysBio* we need to install the following Python packages:

- Numpy
- Scipy
- Matplotlib
- libSBML

Luckily the first three can be obtained easily by installing the Scipy Superpack: <http://fonnesbeck.github.io/ScipySuperpack/>

To obtain a compatible version of libSBML it is best to install libSBML from source. Download libSBML from:

```
http://sourceforge.net/projects/sbml/files/libsbml/
```

and unzip it. In the terminal go to the libSBML directory and type:

```
./configure --with-python=/usr/ --prefix=/usr/ --enable-m64
```

```
make  
sudo make install  
sudo cp -r /usr/lib/python2.7/site-packages/* /Library/Python/2.7/site-  
packages/
```

Assuming that the previous steps were completed successfully, we can now install *ABC-SysBio*. Download the *ABC-SysBio* package from:  
<http://sourceforge.net/projects/abc-sysbio/files/>  
and unzip it. Open a terminal and type:

```
cd abc-sysbio-2.07  
sudo python setup.py install
```

This places the *ABC-SysBio* package into

```
/Library/Python/2.7/site-packages/
```

and writes the scripts

```
/usr/bin/abc-sysbio-sbml-sum  
/usr/bin/run-abc-sysbio
```

Then type the command

```
run-abc-sysbio -h
```

This will display a list of options and you are ready to run the examples.