Sambuca/Bioopti on Windows

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# Outline

* 1. Install Git
  2. Install Anaconda
  3. Install Python IDE (optional)
  4. Apply the fix for IPython Notebooks on CSIRO Windows machines
  5. Clone the code repositories (sambuca and bioopti)
  6. Create Anaconda environments
  7. Test the installation

# Install Git

<http://git-scm.com/download/win>

During the install, keep all the default options (safest).

For more info on using Git, see one of the many online Git tutorials. A good reference is <https://www.atlassian.com/git/tutorials/>

Scientific Computing also have a [Git Learning Station](https://wiki.csiro.au/display/ASC/7+Version+Control) that will help with learning the basic commands.

## Optional Git GUI

If you want a Windows GUI for working with Git, the best I have found is SourceTree:

<http://www.sourcetreeapp.com/>

# Install Anaconda

Download the installer from <https://store.continuum.io/cshop/anaconda/>

You want the full installer for Python 3. Select the 32 or 64 bit versions depending on your operating system.

Unless you have local admin rights, select the "Just Me" option during installation.

Read the [Anaconda Quickstart Guide](https://store.continuum.io/static/img/Anaconda-Quickstart.pdf)!

Also read [the conda documentation](http://conda.pydata.org/docs/intro.html). Conda is the primary tool for managing your Anaconda installation.

And the general Anaconda [documentation](http://docs.continuum.io/anaconda/index.html) perhaps.

After installation, it is a good idea to update the packages. Open a windows Command prompt and run these two commands:

conda update conda

conda update anaconda

## Optional - Python IDE

Anaconda comes with Spyder, a good IDE for Scientific Python. However, I prefer [PyCharm Community edition](https://www.jetbrains.com/pycharm/) as it has better support for the Python environments used in Sambuca and Bioopti.

If you have Visual Studio, then [Python Tools for Visual Studio](http://microsoft.github.io/PTVS/) can also be useful. I haven't tested its Python environment support.

The Sambuca and Bioopti source repositories do not (and should not) contain the project files for specific IDEs. However, importing existing code into a project is generally not difficult, although the process varies by IDE. Also, bioopti contains an ide\_run.py file in the top level directory. This file is not part of the bioopti package, but it can be used to run the application from an IDE. It is required as the entry points generated by pip during the bioopti install are not useable by the IDE.

# Fix for IPython/Jupyter Notebooks on CSIRO Windows Systems

If you have tried running IPython Notebooks on your CSIRO Windows PC, you may have noticed that it simply doesn't work. Instead the browser stops responding as soon as you launch a notebook. The problem is a port conflict between the VNC Server instance used for remote administration of Windows PCs and one of the libraries used by IPython Notebooks.

Until a fix works its way through the open source pipeline, the IM&T Desktops team have developed a workaround for this issue. Simply run the following script to change the VNC Server port on your PC:  
[\\ds.csiro.au\resources\Scripts\IPython-VNCport-fix\IPythonNotebookFix.bat](file:///\\ds.csiro.au\resources\Scripts\IPython-VNCport-fix\IPythonNotebookFix.bat)

This adjusts the port used by VNC Server so that it no longer conflicts with the IPython Notebook server.

You only need to run this script once. If you have already run it in the past, then running it again is still safe.

# Clone the Code Repositories

The required repositories are all contained in a project on CSIRO’s Bitbucket server: <https://bitbucket.csiro.au/projects/SAM>

Running Bioopti and Sambuca requires the [bioopti](https://bitbucket.csiro.au/projects/SAM/repos/bioopti/browse), [bioopti\_data](https://bitbucket.csiro.au/projects/SAM/repos/bioopti_data/browse), [sambuca](https://bitbucket.csiro.au/projects/SAM/repos/sambuca/browse), and [sambuca\_core](https://bitbucket.csiro.au/projects/SAM/repos/sambuca_core/browse) repositories.

There are two ways of cloning the repositories:

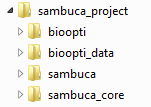
The easiest is to use SourceTree:

* 1. Install SourceTree if you haven't already done so.
  2. Point your browser at the required repository.
  3. Click the "…" button at the top left of the page, and select "Clone" from the list of options.
  4. Select the "Clone in SourceTree" button
  5. Follow the SourceTree wizards to complete the process.

To clone with the Git command line:

* 1. In Windows File Explorer, select the directory that you want to be the parent to the Sambuca code.
  2. Right click inside the directory and select "Git Bash Here" from the context menu.
  3. Point your browser at the required repository.
  4. Click the "…" button at the top left of the page, and select "Clone" from the list of options.
  5. Copy the HTTP URL to the clip board (control-c)
  6. At the Git command line, type "git clone " and then shift-insert to paste the repository URL into the command line.
  7. Press enter.

I suggest creating a work directory somewhere, and cloning both projects to that location. You should end up with something like this:



# Create Anaconda Environments

Python environments must be used for Sambuca and Bioopti. They cannot use the default Anaconda environment due to the requirement for some custom packages (to address issues in some Anaconda packages).

Note that some packages are installed with conda (the anaconda package installer), while other packages are installed with pip (the Python installer) because they are not available through conda.

* 1. Open a Windows Command prompt in your "sambuca" directory.
  2. Create a conda environment using the reqs-conda.txt file in the root sambuca directory:  
     conda create -n sambuca --file conda-reqs.txt
  3. Activate the environment:  
     activate sambuca
  4. Download and install matplotlib (to work around an issue in the Anaconda matplotlib package):
     1. Download these to your python-working directory:
        1. [matplotlib](http://www.lfd.uci.edu/~gohlke/pythonlibs/#matplotlib). Choose either 1.4.3-cp34-none-win32 for 32 bit windows, or the amd64 version for 64 bit windows.
        2. [pillow](http://www.lfd.uci.edu/~gohlke/pythonlibs/#pil). Again, choose the most recent version in either 32 or 64 bit mode to suit your installation.
     2. In the windows prompt, with the sambuca environment activated, change to the directory where the whl files are downloaded. Then install them with pip:  
        pip install Pillow-2.8.1-cp34-none-win\_amd64.whl  
        pip install matplotlib-1.4.3-cp34-none-win\_amd64.whl
  5. Install the sambuca and bioopti projects in development mode:
     1. Change to the sambuca directory, then:  
        pip install -e.[dev,test]  
        python setup.py develop
     2. Repeat those two commands for bioopti. The first command uses pip to install the remaining packages that were not installed with conda, while the second installs the sambuca and bioopti packages in develop mode, which means that any changes to the source are immediately reflected in the installed package seen by other Python code.
  6. The pytest-sugar package gives nice test output on Linux, but on Windows it makes the test output almost unreadable. You might want to uninstall it:  
     pip uninstall pytest-sugar

# Test your Installation

Try the following commands in a windows command prompt.

|  |  |
| --- | --- |
| Command | Expected result |
| activate sambuca | Activates the conda environment |
| bioopti | Runs bioopti GUI |
| pylint --output-format=text ./sambuca | Runs pylint on the Sambuca code. Assumes you are in the top sambuca directory. Note you might need to change the pylint settings in |
| make html | Generate html documentation |
| py.test | Runs unit tests |