

Installation on Windows

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3:17 PM

1. Create your top-level "sambuca_project" directory
2. Download and install Git from <http://git-scm.com/download/win>
3. Download and install WinPython from <http://winpython.github.io/>
 - a. **You must choose Python 3.4. Python 3.5 appears to have a bug in the pip installer that can prevent correct installation of the Sambuca and Bioopti packages.**
4. Install PyCharm Community Edition from <https://www.jetbrains.com/pycharm/>
5. Apply the IMT fix for Python Notebooks on CSIRO computers:
[\\ds.csiro.au\resources\Scripts\IPython-VNCport-fix\IPythonNotebookFix.bat](https://ds.csiro.au/resources/Scripts/IPython-VNCport-fix/IPythonNotebookFix.bat)
6. Clone the code repositories from: <https://bitbucket.csiro.au/projects/SAM>
7. Install the Python projects in develop mode in the order sambuca_core, sambuca, bioopti.
Follow the instructions in the video to launch a WinPython command shell, then the key command lines for each project are:
 - a. `python setup.py develop`
 - b. `pip install -e.[dev,test]`
8. Test the installation by running the unit tests from the command line:
 - a. `cd sambuca_core`
 - b. `py.test`
 - c. You will see that the output looks a bit mangled. This is from the pytest-sugar package that works nicely on Linux but mangles the test output on Windows. As a one-time step, uninstall this package with this command in the WinPython command shell:
 - i. `pip uninstall pytest-sugar`
9. Configure PyCharm.
 - a. Open sambuca_project directory as a PyCharm project
 - b. Configure the project to use the WinPython interpreter
 - c. Wait for PyCharm to finish crunching it's way through all your Python installations. It does this so that IDE features like autocomplete and inline help work correctly, but it can slow PyCharm down when it first encounters a Python installation.
 - d. Edit project configurations:
 - i. project unit tests for sambuca_core, sambuca, and bioopti
 - ii. composite all-tests
 - iii. bioopti runner