Installing OMERO.searcher Local Client version 1.3 in MacOSX

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The instructions described in this document explain how to install the prerequisites in MacOSX 10.8.* If you have successfully installed CellOrganizer for Python in your Mac, then skip to Section II.

I. Prepare your computer to install the prerequisites

Before we start installing the prerequisites for OMERO.searcher we need to make sure you have all the necessary libraries and compilers to install them.

1. **Install XCode**. You can install XCode in the Mac App Store by clicking <u>here</u> or visit the App Store. For more information about XCode click <u>https://developer.apple.com/xcode/</u>.

If you have Xcode already installed, make sure that it is up to date by using Software Update.

2. **Install Command line Tools for XCode.** Install them by running Xcode > Preferences > Downloads.



Check that the installation was successful by opening a terminal window and typing

\$ which gcc
/usr/bin/gcc

You should see an ouput similar to the one above.

3. **Install MacPorts**. This is a package manager that helps installing many GNU packages compiled for Mac. In terminal type

\$ which port
/opt/local/bin/port

If you get an output similar to the one above, then you have MacPorts. If MacPorts is installed, check that it is up to date by running these commands in terminal

```
$ sudo port selfupdate
$ sudo port upgrade outdated
```

The first command will update MacPorts definition and the second one will upgrade outdated packages.

WARNING: These two commands might take some time to run.

If you do not have MacPorts installed, then get it from http://www.macports.org/.

4. **Make account in Enthought using an academic email account ending in .edu.** You can create a account in Canopy Express or at <u>https://www.enthought.com/accounts/register/</u>. It is important to use your university email so you will get free access to the "Package Manager".

After you create your account, sign-in and navigate to Products > Enthought Canopy > Academic License to request the license



5. Install Enthought. It is Python distribution with a GUI, integrated code editor and IPython

console that comes with numpy+scipy+matplotlib+PIL+ipython.

Before installing the software we need to make sure that bash is our default shell. In terminal type



If /bin/bash is not the output of the command, e.g. /bin/tcsh, then bash is not your default shell. To change your shell the bash, simply type

\$ chsh -s /bin/bash

And follow the instructions.

Now, get Canopy Express from <u>https://www.enthought.com/products/epd/free/</u>. Be sure to download the copy that is consistent with your architecture, that is 32 or 64 bit.

WARNING: The first time you run Enthought be sure to click the use of Canopy as a default Python environment.



If you do not wish to start using Canopy at this point, you can access the software from the Applications folder or Launchpad.



6. Sign-in. After you click "Start using Canopy", login with the account created in step 4.

7. **Install pip**. Before we install pip lets verify that easy_install was successfully installed. In terminal type

```
$ which easy_install
/Users/icaoberg/Library/Enthought/Canopy 32bit/User/bin/easy install
```

You should see an output similar to the one above. Since easy_install points to Enthought, type in terminal

```
$ sudo easy install pip
```

After installing pip, verify that pip points to the right location by typing in terminal

```
$ which pip
/Users/icaoberg/Library/Enthought/Canopy 32bit/User/bin/pip
```

8. Restart your computer.

II. Install the Dependencies

You will need a terminal for all the next steps.

1. **Install libFreeImage**. Before we install this package lets verify that MacPorts was successfully installed. In terminal type

```
$ which port
/opt/local/bin/port
```

Since MacPorts was found, lets install libfreeimage by typing in terminal

\$ sudo port install freeimage

WARNING: Installing packages using MacPorts can be painfully slow. You might spend about an hour installing just this package.

2. **Install mahotas**. Before we install this package lets verify that Enthought was successfully installed and linked to terminal. In terminal type

```
$ which pip
/Users/icaoberg/Library/Enthought/Canopy 32bit/User/bin/pip
```

You should see something similar to the above. *Hint*: the change in prompt to Canopy 32bit is an indication it worked as well. In terminal type

\$ sudo pip install mahotas==0.6.6

To test that mahotas was successfully install type in terminal

```
$ which ipython
/Users/icaoberg/Library/Enthought/Canopy 32bit/User/bin/ipython
```

this will verify ipython is pointing to the right distribution. Then in terminal start ipython

```
$ ipython
Python 2.7.3 | 32-bit | (default, Mar 25 2013, 15:42:04)
Type "copyright", "credits" or "license" for more information.
IPython 1.0.dev -- An enhanced Interactive Python.
? -> Introduction and overview of IPython's features.
%quickref -> Quick reference.
help -> Python's own help system.
object? -> Details about 'object', use 'object??' for extra
details.
In [1]: import mahotas
In [2]: mahotas.__version__
Out[2]: '0.6.6'
```

3. **Install PySLIC**. Now that mahotas is available, we can read images and process them. We need to install pyslic to calculate features on images. Since we verified pip and ipython are working in the previous step we don't need to do it again. In terminal type

```
$ curl -o pyslic_0.6.1.1.zip
http://developers.compbio.cs.cmu.edu/python/pyslic_0.6.1.1.zip
$ unzip pyslic_0.6.1.1.zip
$ cd PySLIC-0.6.1.1
$ sudo python setup.py install
$ cd ..
```

To verify it install successfully

```
In [1]: import pyslic
```

Now we can calculate features on images.

COMMENT: This version of pyslic is not dependent on milk. That is why we are downloading a copy from developers rather than installing using pip.

5. **Install ImageMagick.** We need to use the convert tool for converting between image file formats. To install it type in terminal,

\$ sudo port install imagemagick

WARNING: This command will take some time to run.

To verify that the tool ImageMagick has been installed successfully, in terminal type

```
$ which convert
/opt/local/bin/convert
```

6. **Install the python packages required for this software using Enthought's package manager**. Open Canopy Express and sign in using your account. Then go to the "Package Manager".

COMMENT: It is easier to install these dependencies using Enthought than to use pip or easy_install. We need to install hdf5.

But first, before installing any packages, let's update the existing ones.



The screenshot above shows the package manager. Click "Install all Updates" to upgrade all the packages.

00	Package Manager – Canopy		
Q h5py)	CANOPY	Ivan Cao-Berg Need help? <u>Ask experts</u>
 Available Packages Installed Packages Updates 0 History 	FF h5py 2.1.3 Python interface to the HDF library		
115 packages available. 1 ma	tches	Install	all Canopy packages

After all the packages are updated just type h5py in the search box and click "Install".

III. Downloading and Installing OMERO.searcher

Visit the Murphy lab website to download the latest version of OMERO.searcher

http://murphylab.web.cmu.edu/software/searcher/

As of this publication, version 1.3 is the latest stable version of the local client. If you want to get and install the client from terminal; you can type

```
$ curl -o omero.searcher.client-v1.3.tgz
http://murphylab.web.cmu.edu/software/searcher/omero.searcher.client-
v1.3.tgz
$ tar -xf omero.searcher.client-v1.3.tgz
$ cd omero.searcher.client-v1.3
```

If you have followed all the instructions, then you are ready to use the local client.

IV. Running a Test

To verify that the local client is working properly, run one of the tests included with the client. In terminal type

\$ bash ./tests/test HPA slf34.sh OMERO.searcher Local Client version 1.3 /opt/local/lib/libfreeimage ['proteinatlas.org'] Checking for new stable version... Version is up to date. Loading content database(s) (this may take a while)... Loading content database for featureset slf34, server proteinatlas.org No list of available content databases found at http://proteinatlas.org/searcher/ Using local copy of content database, which is same as latest version, also available on murphylab.web.cmu.edu Checking protein and DNA image lists 1 images found scale from query images is 0.08 scale/s from database is 0.08 rankSearchSet using dscale: 0.08 Calculating features for query set from local images Using supplied feature calculation function: calc slf34 at scale: 0.08 there are 173 features calculated search set has 1 images Ranking images rankSearchSet using dscale: 0.16 Calculating features for query set from local images Using supplied feature calculation function: calc slf34 at scale: 0.16 there are 173 features calculated search set has 1 images Ranking images rankSearchSet using dscale: 0.32 Calculating features for query set from local images Using supplied feature calculation function: calc slf34 at scale: 0.32 there are 173 features calculated search set has 1 images Ranking images rankSearchSet using dscale: 0.64 Calculating features for query set from local images Using supplied feature calculation function: calc slf34 at scale: 0.64

there are 173 features calculated search set has 1 images Ranking images rankSearchSet using dscale: 1.28 Calculating features for query set from local images Using supplied feature calculation function: calc_slf34 at scale: 1.28 there are 173 features calculated search set has 1 images Ranking images Making HTML results file

You will notice some files have been created in your directory

\$ ls		
HPA_11-H9-2_2.html	proteinatlas.org-slf34-v3.pkl	scripts
images	proteinatlas.org_version tests	
<pre>murphylab.web.cmu.edu_vers</pre>	ion pyslic	version
omero.searcher.py	ricerca	

Essentially, a content-database (proteinatlas.org-slf34-v3.pkl) and a report (HPA_11-H9-2_2.html). If you open the HTML file in a web-browser you should see something similar to the next screenshot.

	O.searcher results	×							H.
← → C 🗋 file	e:///Users/icaober	g/Desktop/omero.se	archer.client-v1	.3/HPA_11-H9-2	_2.html			S 🚽 🔮	k =
🕏 Spotify Web Player	🗠 CellOrganizer	OMERO.searcher	🥱 OMERO.web	My Pogoplug	Bookmark This	9 🧕 OMERO Jenkins		» 🚞 Other	Bookmark
OMERO.	.searchei	r results							
		images/proteinat images/proteinat	las/11_H9_2_g las/11_H9_2_b	reen.bmp lue.bmp					
Query Image(s)									
Content Database		['proteinatlas.org	slf34-v2.pkl']						
Original Scale		0.08							
Comparison Scale/	/s	[0.08, 0.16, 0.32	2,0.64,1.28]						
Feature Set		slf34							
Number to Retriev	ve	10							
Results									
0.0	8	0.16		0	<u>52</u>	0.64		1.28	
Thumbna	il Image Data	Thumbnail	Image Data	Thumbna	ail Image Data	Thumbnail	Image Data	Thumbnail	Image Data
	Info	100	Info		Info		Info		Info
		200	Info	្តីទ	Info		Info	2.2	
	Into	1 . As		300		(3).0.0		· ·	Info