Lama: The LocAlization Microscopy Analyzer Installing Lama

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Abstract

Program summary

program title: LAMA

version: 16.06

language: Python, Cython, C;

Operating system: Any with CPython distribution (e.g. Linux, MacOSX, Windows);

License: GPL3

nature of problem: comprises algorithms for post processing and data analysis for single molecule localization microscopy data sets

Scientific field

The *LocAlization Microscopy Analyzer* (LAMA) represents a graphical user interface that comprises several well established data post processing algorithms for *Single Molecule Localization Microscopy* (SMLM)

Availability and implementation

LAMA is written in python, cython, and c. It is published open source under GNU publishing license version 3 or later. The source code as well as pre-compiled versions for Microsoft Windows, Mac OS X are freely available from the lama web page http://users.uni-frankfurt.de/~malkusch/lama.html.

Keywords

Single Molecule Biophysics — Software — LAMA

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Contents

1. Introduction

This practical course covers the installation of the pre-compiled LAMA packages on Windows and OSX.

2. Download

LAMA can be obtained from our website for free(see figure 1: http://user.uni-frankfurt.de/~malkusch/lama.html). The latest version is announced at the upper left of the download section. Download the latest version for you operating system and follow the instructions within this tutorial.
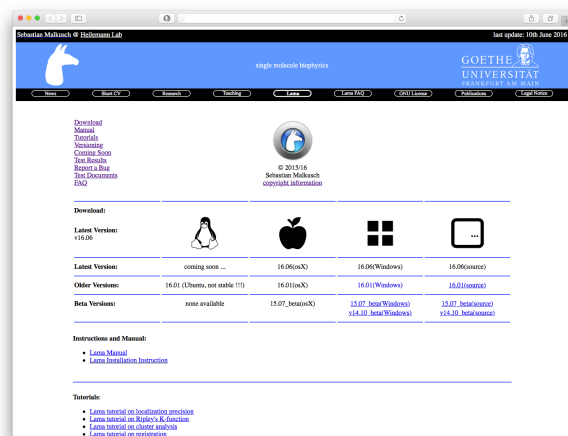

Figure 1. Lama hompage
The download section of the Lama hompage

3. Windows

If you have an outdated version of LAMA installed on your system, make sure you uninstall it, before upgrading to a current version. Installing the current version of LAMA on top of an outdated version may cause errors! After removing the outdated version, download the latest version form our webpage. Install it by double clicking on the downloaded .msi file. When launching LAMA, two windows will appear: The first is the LAMA terminal (see figure 2) that will give you information about the processing progress. It will also show an analysis finished successfully or it will show you error massages. The second is the graphical user interface (see figure 3), that allows you to use LAMA. For further information on how to use LAMA please refer to the manual or the other tutorials from our webpage.
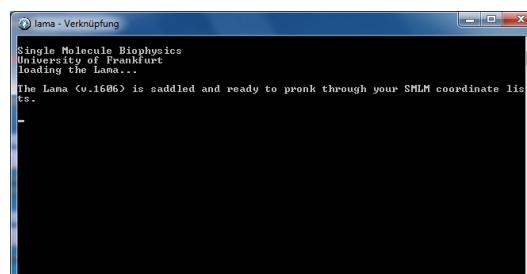

Figure 2. Lama gui
Lama terminal on Windows 7

Short installation guidance:

- uninstall any outdated version of LAMA installed on your system!

- download the pre-compiled .msi installer of the latest version from *Single Molecule Biophysics* (SMB) homepage

- execute the .msi installer
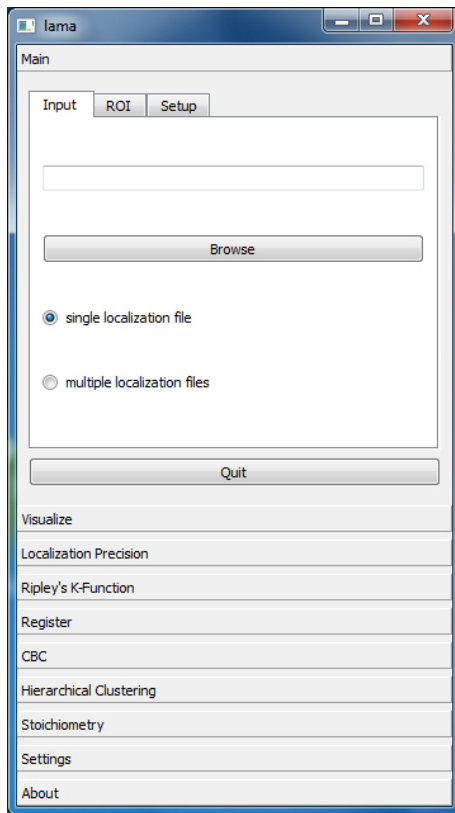
- start the programm by executing LAMA.exe

Figure 3. Lama GUI
Graphical user interface of lama on Windows 7

4. OSX

LAMA does not need an explicit installation on OSX. Just download the latest version form our webpage to a directory on your mac. Like the Windows version LAMA requires a terminal. Therefore, you will have to launch LAMA from terminal. By opening the the folder in your finder application and double clicking on the icon you will receive an error. Open the *terminal* app from *launchpad* and change to the directory you downloaded LAMA to by typing *cd folder-name* (see figure 4 line 1). Than type *cd Lama-16.06.app/Contents/MacOS/* and hit enter to change into the package folder (see figure 4 line 2). Launch the program by typing *./main* (see figure 5 line 1). When launching LAMA, a second windows will appear: The graphical user interface (see figure 6), that allows you to use LAMA. The LAMA terminal (see figure 5) will give you information about the processing progress. It will also show an analysis finished successfully or it will show you error massages. For further information on how to use LAMA please refer to the manual or the other tutorials from our webpage.
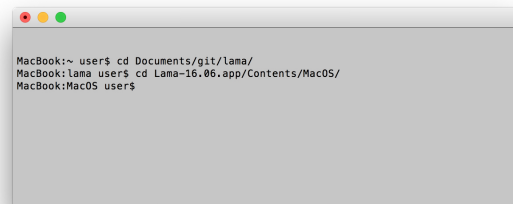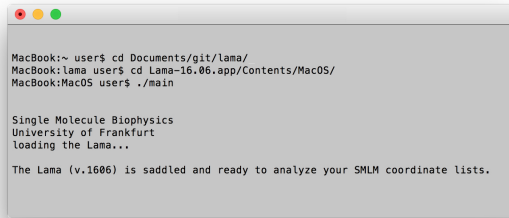

Figure 4. Terminal on OSX
The first line shows the change to the directory of the LAMA application, the second line shows how to navigate inside the application.

Figure 5. Launching Lama on OSX
The application is launched from within the .app directory by typing *./main*.

Short installation guidance:

- download the pre-compiled .app package from SMB homepage

- LAMA must be executed from terminal!

- start the terminal

- switch to the LAMA directory

- change directory by typing

  cd Lama-16.06.app/Contents/MacOS/

- start the program from the terminal by typing ./main
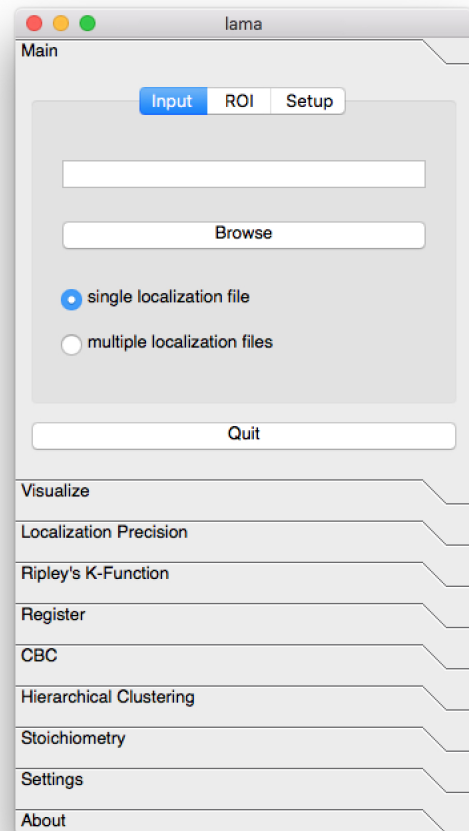

Figure 6. Lama GUI
Graphical user interface of lama on OSX

5. Ubuntu Linux

There are actually no stable pre-compiled packages of LAMA for Ubuntu available. Therefore, if you are using Linux, you will have to run the program via the python interpreter. Please refer to the next section *Installing LAMA from source*. We are currently working on a pre-compiled version for Ubuntu.

6. Installing LAMA from source code

The main program of LAMA is written in python. Therefore you will need to have python and some additional packages installed on your system. We tested LAMA successfully with python 2.7 and python 3.4.

For building LAMA from the source code you will need the following packages to be installed.

- Python v2.7.10 from `https://www.python.org`

- setuptools v17.11 from `https://pypi.python.org/pypi/setuptools`

- numpy v1.9.2+mkl from `http://www.numpy.org`

- pillow v2.9.0 from `https://pypi.python.org/pypi/Pillow/2.9.0`

- matplotlib v1.4.3 from `https://pypi.python.org/pypi/matplotlib/1.4.3`

- scipy v0.14.0 from `http://www.scipy.org`

- PyQt4 v4.11.4 from `https://pypi.python.org/pypi/PyQt4/4.11.4`

- cython from `https://pypi.python.org/pypi/Cython/0.23.1`

- a c++ compiler (gcc on Linux or clang on MacOSX or MS visual C++ compiler for Python 2.7)

In order to visualize images, you will need an image processing tool. We recommend one from the following list:

- ImageJ from `http://rsb.info.nih.gov/ij/`

- FIJI from `http://fiji.sc/Fiji`

- ICY from `http://icy.bioimageanalysis.org`

As LAMA is partly written in cython and c you will have to compile parts of the code. Therefore you will need to have a C++ compiler to be installed on your system (gcc on Linux, clang on MacOSX, or MS visual C++ compiler for Python 2.7 on Windows). In order to build LAMA from source code follow the instructions below:

- install all packages from the *Downloads* section on your system

- download the LAMA source code from the homepage

- extract the source code to a new folder

- start the terminal (or cmd on windows)

- go to the LAMA source code directory

- execute the respective make-xxx.yy file for your system

Appendices

Acronyms

ad   *analog-to-digital*

bcm   *binary cluster map*

CBC   *coordinate based colocalization*

CPU   *Central Processing Unit*

DBSCAN   *Density-Based Algorithm for Discovering Clusters in Large Spatial Databases with Noise*

EMCCD   *Electron Multiplying Charged Coupled Device*

FAS   *focal adhesion site*

FP   *fluorescent protein*

FRET   *Foerster Resonance Energy Transfer*

GNU   *GNU is Not Unix*

GPL   *GNU publishing license*

GUI   *graphical user interface*

HIV   *human immunodeficiency virus*

LAMA   *LocAlization Microscopy Analyzer*

LSE   *least-squares estimation*

lwm   *local weight matrix*

Malk   *Molecular Accuracy Localization Keep*

MCA   *Morphological Cluster Analysis*

MLE   *maximum likelihood estimation*

NeNA   *Nearest Neighbor in Adjacent frames*

OPTICS   *Ordering Points To Identify the Clustering Structure*

PALM   *photo activated localization microscopy*

pixel   *picture element*

ps   *photo-switchable*

PSF   *point spread function*

PSFs   *point spread functions*

rapidSTORM   *rapid yet accurate program implementing the direct stochastic optical reconstruction microscopy*

ROI   *region of interest*

SM   *single molecule*

SMB   *Single Molecule Biophysics*

SMLM   *single-molecule localization microscopy*

SNR   *signal to noise ratio*

STORM   *stochastic optical reconstruction microscopy*

References