

# Cell Localization and Identification (CLI) Toolbox manual

The CLI MATLAB toolbox finds the components (cell somas or axons and dendrites) in each measurement unit of each input .mesc file. Input files should be scanned on the same scene and transformed into the same coordinate system (with e.g. our NonRigid4Reso toolbox). If a component shows activity in any of the measurement units, CLI represents it in all other measurement units, too. The boundaries of the ROIs found are saved into .mescroi files and the fluorescent signals (in dF/F version) are saved in the curve format of MES (.gorobj).

Note that your computer needs to have more RAM than the size of t-stack in the measurement units you want to process.

## Installation

### 1 Prerequisites

The following components are required to successfully run the CLI toolbox.

#### 1.1 Required/optional MATLAB toolboxes

The following MATLAB toolboxes are needed for running the algorithm of [Eftychios Pnevmatikakis](#):

- Statistics and Machine Learning Toolbox
- Image Processing Toolbox

Depending on the settings, the following toolboxes may also be required:

- Signal Processing Toolbox (recommended but not required)
- Parallel Computing Toolbox (recommended for large datasets but not required)
- Optimization Toolbox (not required)

The minimum required MATLAB version is R2015a.

#### 1.2 Required other software

- The CVX library which can be downloaded from <http://cvxr.com/cvx/download/> After unpacking CVX, open MATLAB and run cvx\_setup from inside the CVX directory to properly install and add CVX to the MATLAB path.

For further releases you may need the following packages:

- SPGL1 package from <https://github.com/mpf/spgl1> (for solving constrained\_foopsi using SPGL1)

- Bayesian spike inference package from [https://github.com/epnev/continuous\\_time\\_ca\\_sampler](https://github.com/epnev/continuous_time_ca_sampler) (for using the “MCMC” deconvolution method)
- For more information, see [https://github.com/epnev/ca\\_source\\_extraction](https://github.com/epnev/ca_source_extraction)

### 1.3. Relation to other software

- CLI saves fluorescent curves into curve format of the MES application (“gorobj”). MES (at least version 5.3311) must be installed into the folder C:\MES\MES5\_released. A lite version of MES can be downloaded from <http://femtonics.eu/software/sw-download>

## 2 Installation

For installation, you simply need to open the toolbox file (CLI.mltbx) in the Open menu point of MATLAB, and then a popup window appears where you simply need to click on Install.

For detailed information, see the section on managing toolboxes in the MATLAB documentation.

## 3 Usage

After the CLI toolbox is installed, it can be started by typing `cli` in the MATLAB command prompt.

Required input fields:

Input fields:

- **filenames** The files to be processed. They must be scanned on the same scene and transformed into the same coordinate system.
- **K** The number of components to be found.
- **tau** Half of the average component diameter (in pixels).
- **edgepixelnum** The number of pixels to ignore on the image edges (artificial margin to exclude motion correction artefacts).
- **frames2drop** The number of frames to be dropped from the beginning of the t-stack (the first few frames are sometimes biased).
- **interaction** When switched to Supervised, components can be manually added or removed.
- **Advanced parameters** Parameters for fine tuning the algorithm.

## 4 Saved output data

For each measurement unit of each session, the following data are stored:

1. average image of the unit (avgimage)
2. .mescroi file for the ROIs found in the measurement unit
3. ROIs in raster format (rasterROI)
4. ROI descriptor with the following fields (ROI\_DESC)
  - a. centroid
  - b. coordinates of contour of the ROIs (coords)
  - c. bounding box of the ROI (bbox)
  - d. fluorescent curves – raw or dF/F version (fluor\_curve\_raw and fluor\_curve\_dFpF)
  - e. rank of activity (positive integer for ROIs found by the algorithm and -1 for copied ROIs) (act\_rank)
  - f. number of cluster (cluster\_id)