SMAP Quick Start Guide

# Installation

## Requirements

1. Matlab newer than 2014a, performance boost with 2015b. Toolboxes: Optimization, Image processing, Curve fitting, Statistics and Machine Learning. Optional (not currently used): Parallel Computing. A stand-alone version will be released, but will be limited in extensibility.
2. Mac or Windows
3. For GPU fitting: NVIDIA graphics card. CUDA driver (currently V5.0, but later upgrade to 7.0).

## Installation

1. Clone git depository:
   1. Contact Jonas to have your username added as a SMAP collaborator
   2. Use Terminal (MacOS) or Cmd (Win). Use cd to go to the target directory.
   3. Type: git clone <https://github.com/jries/SMAP>
2. In Matlab: run SMAP.m, if questioned, change folder

## Micromanager users

1. Save your images as single or multi-image Tiff stack, turn on “save metadata” in preferences
2. Edit ‘settings/CameraCalibration.xls according to templates (for Andor and photometrics camera).
   1. camId, port, preamp and readoutrate are used to determine the state of the camera. Based on this, the conversion abd offset are read out from the xls file. Also lines with 1 define the tags to search for Multiplier Gain and ROI.
   2. First column: 1: defines name of the tag. 2 defines string.
   3. Open a metadata.txt to find the corresponding tags for your cameras (e.g. SerialNumber and insert in the rows which start with 1, insert the strings in the rows with 2.
   4. You can also define the pixelsize (in nm) of your microscope

# Single-molecule localization

## Basic fitting

1. In the **Localize** Tab, **load images**: Select one image inside a directory containing all the tifs, or a tiff-stack.
2. If micromanger with a fitting CameraCalibration.xls was used and metadata.txt was found, the acquisition parameeters are automatically set. Otherwise you can either **load meatadata** from a previous experiment or manually **set Cam Parameters**.
3. You can specify a frame range which to fit. **Empty localizations** removes current localization data from the memory (recommended). Check **Online analysis** if you want to fit during the acquisition (then the maximum frame is ignored, and SMAP waits for new images).
4. In the **Peak Finder** Tab you can set the parameters for the initial guessing of single-molecule positions. Usually this is done on a background-corrected image. Use ToolTips (hover mouse over control) to get information about specific parameters.
5. By pressing **Preview** after selecting a frame with the slider next to it an image will open which will show the positions of the found localizations. Use this to optimize peak finding parameters. The preview mode determines which images are shown here.
6. You can determine a ROI in which the fitting is performed. First use either an elliptical or rectangular ROI in the popup menu. With **Fit in ROI** you can select a region in which to fit, with **Remove ROI** you can select a region which to exclude from the fit. You can define multiple ROIs. **Clear ROI** to fit everything.
7. In the Fitter Tab you set
   1. The size of the ROI in which the fitting is performed
   2. The fitter module and its parameters
   3. If to fit on the background corrected data (not recommended)
8. In the **Localizations** Tab you can switch on the rendering during the fitting and set the update time. In addition, you can do simple pre-filtering of the data. To set these parameters you can again use **Preview**. Found candidate positions are marked with a box, found localizations which pass the filters are marked by a circle.
9. Now you can fit the whole data by pressing **Localize**.
10. The fitted localizations are automatically saved in the base directory of the images with an extension ‘\_sml’.

## Batch processing

1. You can save your acquisition fit settings (previous paragraph) with the **Batch** button.
2. In the **Input Image** Tab open the **Batch processor**.
3. The batch file you just saved is already set as the main batch file. But you can replace it by another with **load main batchfile.** If **use for all** is checked, this will be used for all the fits, otherwise only for the datasets which are not imported to the batch processor with a batch file.
4. With **add** you can add a) further batch files, b) one single image from a stack or c) a multiple tiff stack. These appear in the list on the left.
5. You can multiple directories with **add directories**. These directories contain a) tiff images, b) further directories with Tiff images inside (here use the filter string below to specify which directories to load, and the **>#images** to set a lower limit for the number of images.
6. You can remove items from the list, but don’t empty it. With Batch process the fitting starts.

# Rendering

## Load localizations

1. In the **File** tab press **Load** and select a file containing localizations (‘\_sml.mat’, but also ‘.csv’).
2. The localizations are automatically grouped (i.e. localizations in adjacent frames stemming from one and the same fluorophore are combined into one localization), using the parameters below (maximum allowd displacement, maximum time in frames the molecule can be dark). Note that also the ungrouped localizations are always available. If you change the parameters, press **Group** to regroup.
3. After loading the **Render** tab is opened and an overview image is displayed. By clicking in the overview image or pressing **Reconstruct**, the superresolution image is calculated.
4. **Load** clears current data before loading. **Add** adds a file to the current localizations
5. After loading localizations, you can add single tiff images (diffraction limited markers) and associate them to a localization file.

## Modify the size and location of the image

1. by setting the pixelsize in the Format GUI (or use the mouse wheel to zoom in and out). Use pre-defined pixel sizes.
2. You can change the size of the image window.
3. You can move around the superresolution image by clicking on it, then the clicked point will be centered.
4. Right-click resets the view to display all localizations.
5. In **par** you can also specify a different size of the image in pixel and binning of pixels.
6. Here you can also quickly turn individual layers on and off.

## Set the appearance of the image

1. The parameters in the **Layer** tab determine how the image is rendered and which localizations are rendered.
2. You can define multiple layers (**+**) which are overlayed in the superresolution image.
3. The checkbox in the upper left corner determines if the layer is displayed.
4. Select the file and the channel(s) to display.
5. Select the renderer: Gauss, histogram, diffraction limited reconstruction or Other (external renderer). In case you have attached a Tiff image to the data, you can choose here to display it.
6. Select Color coding: Normal uses the value of the reconstructed image for coloring, but you can also color the image according to the z-coordinates or any other field (property) of the localizations.
7. Select the corresponding look-up table (LUT).
8. The values on c-range determine the range of the paramters used for coloring which are mapped onto the entire LUT. Use **remove out** to remove localizations outside the LUT, otherwise they will be displayed with the minimum or maximum color of the LUT.
9. You can select with the **group** checkbox if to display grouped or ungrouped localizations.
10. The button to the right determines how to contrast the image. Set **absolute** intensities, or the fraction of pixels to be not saturated (**quantile**). The quantile parameter can be between 0 and 1 (typically: 0.995) or a negative number Q (typically -3.5). Then the fraction 10^Q is not saturated.
11. With the remaining fields you can determine minimum and maximum values for filtering (see paragraph below).
12. The **par** button opens a dialog to set additional parameters: minimum size of the Gaussian image for reconstruction, the size of the reconstructed Gaussian in units of the localization precision.
13. Shift x,y shifts the image, this can be used to correct for shifts between images.
14. By pressing **default** with **shift** you can save the current settings. Pressing it without shift, loads the settings.

## Filtering of localizations

1. You can toggle between the overview image and the filter GUI by pressing **OV-filter**.
2. The upper Table lists all properties (fields) of the single molecule localizations together with their minimum, mean and maximum value. You can set minimum and maximum values. Importantly, you can select if to filter these on these fields with the checkbox.
3. Below, you see a histogram representation of a specific field. You can select the field by either pressing on a row in the table or on a button in a **Layer** corresponding to the specific field (locp, frame, PSF, locprec z, z)
4. You can switch the filter on and off and change the range with the sliders. If **Auto update** is checked, the image is directly rendered on the fly. If you check **range fix** and move the sliders, the difference between minimum and maximum slider is fixed to the value below **range fix**.

## ROIs

1. You can define a region of interest with the buttons in ROIs (Format GUI). These ROIs are used by various plugins. For Line-ROIs you can specify the thickness of the ROI. You can toggle redrawing of ROIs.

## Saving

1. In the **File** tab you can select what to save (localizations, settings, Tif images) and press **save**.
2. When saving localizations (as ‘\_sml.mat’ or ‘.csv’) you can check **only visible** to save only the localizations currently displayed.

# ROI Manager

The ROI manager allows for simple automated, semi-automated or manual selection of ROIs which can be then annotated, sorted and run through an evaluation pipeline. The results of this evaluation can then be statistically analyzed.

## Manually generating a list of ROIs

1. Tab **ROIs/Settings** click **show ROI manager**
2. You find fields in which the whole file, a part of the file (called cell) or a ROI are shown, as well as lists for the selected ROIs. The file list is linked to the file list of the **File** Tab and cannot be edited here.
3. You can define the pixelsize for reconstruction and the FoV for the cells and sites (regions around the ROIs), as well as the ROI size itself.
4. Check **rotate** to rotate sites and **draw boxes** to show the positions of the selected cells or sites.
5. By clicking on an item in a list in the **Roi manager** you can select and draw it.
6. For fast scrolling through sites, the reconstructions are saved. Therefore, if you change any parameters (e.g. size of the FoV, or render parameters in the **Layers**) you need to **redraw**. You can **redraw all** in the **ROI/Settings** Tab.
7. By left-clicking in the File image you can select a cell. Add it with the **+** button above the cell image to the list. You can move a cell by right-clicking in the cell image. The cell will be centered around that spot.
8. In the same way you can left-click in the cell image to define a site and add it with the **+** button, and move it by right-clicking in it.
9. You can rotate it by pressing **Angle** and drawing a line. The site is rotated so that the line is horizontal.

## Annotate ROis manually

1. In the tab **ROIs/Annotation** ROIs can be manually annotated. There are four lists to choose from. The items are defined in text files (look at ‘settings/parlistdefault.txt and modify accordingly). You can load your settings file with **<-load**.
2. Use left-arrow and right-arrow keys to go to the previous and next site, respectively
3. Annotate site by clicking on the lists. Keyboard shortcuts are: up-arrow and down-arrow to choose list entries and shift + left-arrow/right-arrow to go to the previous/next list.
4. You can draw additional lines (two buttons on the right) and annotate size and angle.
5. Add an additional comment if needed.

## Sorting of ROIs

1. In the tab **ROIs/Sort** you can sort the ROIs according to up to four criteria.
2. Define if you want to sort ascending or descending
3. Select the parameter which is used for sorting.
   1. Hierarchy: File, Cell, Site
   2. Statistics: Number of photons, PSF size etc…
   3. List: any of the lists
   4. Annotation: any of the lines (length)
   5. Evaluation: the results of any evaluator. You can choose it with the **select** button. Use the list to navigate through all results.
   6. Other: you can select any parameter saved with a ROI for sorting.
4. Sort with the **Sort** button.

## Evaluation

1. In the tab **ROIs/Evaluation** you can select several evaluation processors which evaluate each site and return results, which are then saved with the ROIs.
2. Select processors with **add module** and **remove**.
3. If a module is checked, it is used for evaluation.
4. Clicking on a module in the list opens its GUI on the right. You can adjust paramters here and run the evaluation with **preview** or by redrawing a ROI.
5. Re-evaluate all ROIs with the same settings with **redraw all** in the **ROIs/Settings** tab.

## Analyze evaluation results

1. In **ROIs/Analyze** you can find plugins to analyze results.

## Automatic segmentation

1. In **ROIs/Segment** you can find plugins to automatically segment files and store the result as ROIs.

# Useful plugins

1. Plugins are found in the Plugins menu. A selection of regularly used plugins can be found in the Analyze and the Process tab in subtabs (configurable).
2. Select a plugin, edit the parameters and press Process.
3. With **showresults** you can toggle the window with the output of the module on and off.
4. **Info** displays a description text of the module in the results window.

## Drift correction

*Process/drift/driftcorrection*

1. Drift correction based on the localizations, but works also very well in case fidutial markers are present (in that case render the image ungrouped).
2. Select paramters to render a large part of the image. Only the FoV of the superresolution image is used for drift correction.
3. Choose the number of time points to perform the drift correction on (typically 7-25, this algorithm rather corrects for drifts than for fast jumps or oscillations). The other parameters usually need not be optimized (use Tool Tips to understand what they mean).
4. Use **Reference is last frame** to drift correct the first of two consecutive measurements.
5. Press **Process**. With show results you can display the results of the procedure.
6. The drift-corrected localizations are automatically saved as ‘\_driftc\_sml.mat’ files.

## Localization statistics

*Analyze/measure/statistics*

1. Get single-molecule statistics
2. If **use Roi**  is checked, only the localizations in the current ROI /FoV are evaluated.
3. If **use layers/filters** is checked, each layer is evaluated individually, otherwise statistics for grouped and ungrouped data are shown.
4. With **plot overview** you can have all results in one figure (e.g. for saving) rather than in individual tabs.

## FRC resolution

*Analyze/measure/FRC resolution*

Calculates the FRC resolution according to: R. P. J. Nieuwenhuizen, K. A. Lidke, M. Bates, D. L. Puig, D. Grünwald, S. Stallinga, and B. Rieger, “Measuring image resolution in optical nanoscopy,” Nat Methods, vol. 10, no. 6, pp. 557–562, Apr. 2013.

## 3D viewer

*Analyze/sr3D/Viwer3D*

1. Define a linear ROI in the superresolution reconstruction.
2. Press **Process**, a side-view reconstruction is opened
3. You can **set pixelsize** manually, otherwise the current pixelsize of the reconstruction is used.
4. You can use the controls to translate, rotate or zoom. ‘0’ resets the view.
5. When the sideview window is selected you can use key shortcuts to translate, rotate (command / strg) or zoom (alt, this changes the size of the ROI). The direction is given by the arrows. The direction perpendicular to the screen can be accessed with the ‘.’ and ‘,’ keys.
6. Pressing ‘shift’ results in a smaller movement.
7. You can also manually move the ROI in the superresolution image.
8. With **use transparency** localizations closer to you partially block localizations in the background for a better 3D look.

## Calibrate Astigmatic PSF