

SMALL-LABS User Guide

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Last updated: March 13, 2018

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*****If you obtained this code (and thus User Guide) from a source other than the Biteen Lab GitHub please visit <https://github.com/BiteenMatlab/SMALL-LABS> to obtain the latest version of the code.**

Note: Currently copying and pasting commands from this .pdf doesn't always work reliably, instead it's usually better to type the code directly.

1 Introduction

SMALL-LABS is an algorithm which allows single molecules to be localized even in the presence of a spatially arbitrarily complex, temporally low frequency background. Because the background subtracted is the true background (minimizing or eliminating subtraction of molecule images) the localization and intensity measurement of the molecule is extremely accurate. This document is a detailed guide for users on how to use the provided code. **See the Quick Start Guide for a quick introduction to the using this code.**

This code runs in Matlab (currently tested in versions 2014a through 2017b) and currently takes input movie data as .mat files or TIFF stacks with adaptability to other image types (TIFF stacks are read using *TIFF-Stack* to read the TIFFs and write a new movie as a .mat, see the note at the end of this section on how to install this package). If your data is in another format, the easiest thing to do would be to convert it to a .mat file (preferred) or TIFF stack (otherwise you can add other formats to the function *Movie2mat.m* as described in the function). Conversion to TIFF stack can be accomplished using a variety of programs including ImageJ's Bio-Formats plugin.

The function *SMALLLABS_main.m* is the wrapper for the rest of the code, it performs all of the steps in the SMALL-LABS algorithm in the correct order. Simply run *SMALLLABS_main.m* in the Matlab workspace by specifying the directory containing your movies, specifying the three required parameters, and any optional parameters. The various steps can also all be done independently using *SMALLLABS_main.m* by setting the appropriate action parameters. Furthermore, *SMALLLABS_main.m* can be used to do localization without background subtraction if desired.

1.1 Workflow

The basic (default) workflow (doing full background subtraction) in SMALL-LABS is:

0. Convert the movie file to .mat if it's a different format, using *Movie2mat.m*

1. Average (or median) subtraction (make the avgsub movie) using *AVG-SUB_movs.m*
 - ⇒ Subtracting this background removes the low-frequency background
2. Molecule detection (guess molecule locations) in the avgsub movie, using *Guessing.m*
3. Identify frames before and after each guess in which there isn't another guess nearby, using *Mol_off_frames.m*
 - ⇒ This process gives an *off_frames* list for each guess
4. For each guess, time-average (or median) a small area around the guess using the *off_frames* list, using *Subtract_then_fit.m*
 - ⇒ This average is the True Background
5. Subtract the True Background, and fit the background-subtracted image, using *Subtract_then_fit.m*

Additional optional steps currently included in the SMALL-LABS package

1. Track the fit results
2. Make a View-Fits movie showing the fitting results.

1.2 The Measurement results

Several files containing the results from the various steps will be written to the data directory. Most importantly, the fit results will be collected in a .mat file called *moviename_AccBGSUB_fits.mat* which contains the `fits` structure. Each individual guess will generate a row in the `fits` struct, the fields are:

<code>frame</code>	frame number of the fit
<code>row</code>	row coordinate of the fit
<code>col</code>	column coordinate of the fit
<code>widthr</code>	Gaussian standard deviation in the row dimension
<code>widthc</code>	Gaussian standard deviation in the column dimension
<code>ang</code>	angle of an asymmetric Gaussian fit
<code>offset</code>	intensity offset of the fit
<code>amp</code>	amplitude of the fit
<code>err</code>	error on the fit
<code>sum</code>	sum of pixel intensities in ROI around the fit
<code>goodfit</code>	Boolean of whether or not the fit is a goodfit
<code>states</code>	if <i>gpufit</i> was used, convergence flag

2 Using *SMALLLABS_main.m*

SMALLLABS_main.m is the wrapper function for the SMALL-LABS algorithm.

Note: that by setting 'bgsb' to false *SMALLLABS_main.m* will do fitting without doing background subtraction. Doing this obviates a lot of parameters, it doesn't matter what they're set to, importantly the required parameters of avgwin and moloffwin can be set to anything.

2.1 Inputs

SMALLLABS_main.m has four required inputs:

file_or_directory_name is the name of the directory where the movies will be selected OR the filename of a single movie OR a list of movies to be fit. If a directory is entered, then uigetfile will open and allow movie files (of any extension) to be selected. If the filename of a single movie is entered the SMALL-LABS will analyze that movie. If a list of movies is entered, then SMALL-LABS will sequentially analyzed the movies in that list. For a list of movies that file should be a .txt file with each full filename (e.g., directory\moviname.ext) on a separate line.

dfrlmsz is the size of a diffraction limited spot in pixels. It's the nominal diameter, NOT the FWHM or something similar. Must be an integer! Given the diffraction limit size of an imaging system d in pixels (d converted to pixels using the pixel size in the imaging plane) we find that a value for $dfrlmsz \approx 1.4d$ works well

$$d = \frac{\lambda}{2NA} \Rightarrow dfrlmsz \approx 1.4d$$

avgwin is the length of the temporal window (in frames) to be used for the average subtraction.

moloffwin is the length of the temporal window (in frames) to be checked to determine in which frames that molecule was off and are thus safe to subtract. Needs to be an even integer.

The inputs are entered with the order as shown below

```
>>SMALLLABS_main(file_or_directory_name, dfrlmsz,
avgwin, moloffwin, 'optional.parameter.name',
optional.parameter.value)
```

SMALLLABS_main.m also takes a number of optional parameters (a complete list can be found in Appendix A. Further details about the function of each optional parameter can be found in their corresponding section throughout this guide. All optional inputs are input as name-value pairs, for example setting to set 'bpthrsh' to 93, include 'bpthrsh', 93 in the function call to *SMALLLABS_main.m*. NOTE if you reference the default val-

ues in *SMALLLABS_main.m* that you only need the field name and not the name of the struct, e.g., `'offset',2500` NOT `'params.offset',2500`.

For example the function call

```
>>SMALLLABS_main('Test data and simulations', 7, 300,  
100, 'check_guesses', true)
```

opens the *Test data and simulations* directory to select movies there. `dfrlmsz=7`, `avgwin=300`, `moloffwin=100`, and the optional parameter `'check_guesses'` is set to `true`.

If no checking commands (for example `'check_guesses'`) were sent, *SMALLLABS_main.m* will automatically proceed through the entire calculation implementing the SMALL-LABS algorithm. After each step, the resultant data is saved in the data directory. A progress bar shows the overall progress for the current batch of movies and the displays what step is currently being run on which movie, this information is also logged (with timestamps) in the Matlab command window.

In general SMALL-LABS is a fairly fast an memory-efficient program. This is especially true if a CUDA enabled GPU is available and/or if Matlab's parallel computing toolbox is available. If you run into speed or memory problems, see Sec. 9 for strategies to overcome this.

3 Average Subtraction

This step is skipped if `'bgsub'` is set to `false`.

This step is skipped if `'makeAvgsub'` is set to `false`.

The first step in SMALL-LABS is approximate background subtraction by subtracting a moving temporal mean (or median). This is accomplished in *AVGSUB_movs.m*. The parameter `avgwin` is the length of the temporal window over which the mean (or median) is calculated. Because this step can be somewhat slow, first there is a check to determine if the `avgsub` movie has already been created. If so, then there's a further check to determine whether or not any of the parameters have changed. If they're identical, this step is skipped. To bypass this process, simply delete the `avgsub` movie from the directory.

The `avgsub` movie is saved in the data directory as the original movie file name, but with “_avgsub” appended.

3.1 Optional parameters

`'do_avg'`, is a Boolean parameter¹ Set to `true` to subtract the average, or set to `false` to subtract the median. The default is `true` (subtract the mean).

¹Boolean variables are either true or false. In Matlab they can be set using `true` or `false`, or 1 or 0.

'offset', this is a constant offset to be added to all pixels in the avgsub movie after the subtraction. This is to avoid negative pixels. Because the avgsub movie is only used for guessing, the absolute value of these pixels isn't very important and 'offset' should be large enough to avoid negative pixels. The default value is 1000.

3.2 Considerations

Choosing avgwin should balance the characteristic on time for the molecules and the characteristic timescale for background changes. avgwin should be much longer (at least approximately one order of magnitude is ideal) than the characteristic on time of the molecules to minimize the amount of the molecule intensity being subtracted and affecting the guessing. Conversely, avgwin should be smaller than the characteristic time of the low frequency background changes, so that over the course a window, the background is essentially constant.

You can check if you chose an appropriate avgwin value qualitatively by watching the avgsub movie (which is shown during the guess checking procedure): if you see that during part of a molecule's track it appears as a dark spot instead of a bright spot, then you know that you need to increase avgwin. Conversely, if you see that the background features appear and disappear instead of never being present, then you know that you need to reduce avgwin. If large portions of the movie look saturated, or if there were warnings printed to the command window about negative pixels, then you need to increase offset.

Setting 'do_avg' to false causes the median to be subtracted instead of the average. This is actually a more accurate way to calculate the background because the median is less sensitive to outliers (in this case molecules appearing). However, because calculating a median first requires sorting, it is slightly slower than calculating a mean, so if you have the extra time or computing power, using the median would be advantageous, but it will cause this step to take longer.

4 Guessing

This step is skipped if 'guessing' is set to false.

The next step in SMALL-LABS is molecule detection, called here guessing² This is the only step in which molecules are detected, and though there are a number of false positive checks later, there are no further false negative checks. So it is critical to ensure that as many molecules are detected as possible.

²Called guessing for two reasons, firstly, the molecule location is imprecisely measured as compared with later super-resolution fitting. Secondly, because the molecules haven't gone through a series of false positive checks yet to be sure that it is truly a molecule.

4.1 Optional parameters

'**bpthrsh**' is the main parameter to increase or decrease the sensitivity of the detection during guessing. '**bpthrsh**' sets the intensity threshold over which molecule shaped groups of pixels will be searched for. '**bpthrsh**' is the value of the percentile of intensities in the movie (or individual frame, see '**pctile_frame**' below) after the movie was spatially bandpassed to suppress pixel noise. Default is 95.



'**egdesz**' is the number of pixels around the edge of the frame to ignore. Default is `dfrlmsz`.

'**pctile_frame**' is a Boolean determining whether or not to calculate the intensity percentile for the threshold (using '**bpthrsh**') frame by frame, or using the entire movie. If set to `true` the percentile is calculated frame by frame, if set to `false` the entire movie is used. Default is `false`.

'**mask_fname**' is the filename of a mask to set the boundaries of where guessing will occur in frame. To not use a mask simply leave '**mask_fname**' empty (in Matlab empty is `[]`). If '**mask_fname**' is set `true` (or 1), then the program will look for a file in the same directory as the movie with “_PhaseMask” appended to the name of the movie. The mask is a .mat file which has a logical array (or at least where nonzero entries will be converted to 1s) called `PhaseMask` that is the same size as a frame in the current movie. Default is `[]`, no mask.

'**make_guessmovie**' is a Boolean determining whether or not to save a .avi movie showing the guess results to the data directory. If set to `true` the movie will be made and saved, if set to `false` this will be skipped. Default is `false`.

4.2 Checking the guessing

It is highly recommended that the guessing parameters are checked for every new movie analyzed (or at least one or several representative movies in a batch of movies). To do this, set '**checkGuesses**' to `true`. This causes *Guessing.m* to pause in the Matlab debugger once guessing has finished for the first frame. A figure appears showing those results, as shown in Fig. 1. Look through the movie frames to check the guessing. This is accomplished either by pressing the *Continue* button  in the editor tab, or entering `dbcont` in the command window. When ready to stop checking the guesses, stop the debugger, either by pressing the *Quit Debugging* button  or entering `dbquit` in the command window.

If satisfied with guessing rate, then simply rerun SMALL-LABS with '**checkGuesses**' set to `false`. If not satisfied, change the relevant parameter and rerun SMALL-LABS with '**checkGuesses**' still set to `true`.

In SMALL-LABS it's best to over-guess (include more false-positives) slightly. The reason for this is that there are a series of false-

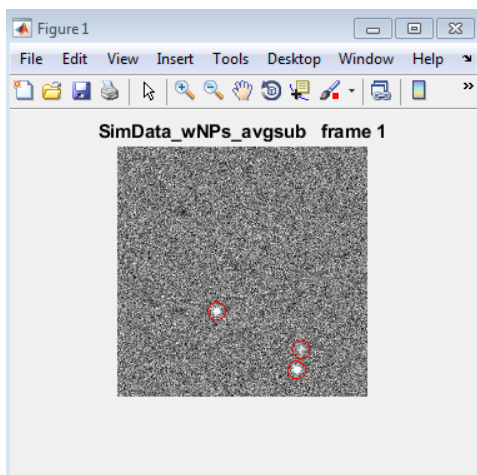


Figure 1: Guessing results as shown in the check guess procedure.

positive checks that occur later, but no further chance to reduce the false-negative rate, so it's best to get it as low as possible here. Furthermore, the accuracy of the true background removal in SMALL-LABS depends on not including images of the molecules in the foreground. So if the false-negative rate is too high images of molecules will be included in the background and reduce the accuracy of the subtraction.

The easiest way to change the guessing rate is by increasing or decreasing `'bpthrsh'`. To increase the detection rate, lower `'bpthrsh'`, and to decrease the detection rate increase `'bpthrsh'`.

If you see that the guessing missing a lot of molecules and reducing the threshold isn't helping discriminate molecules from pixels, then consider changing `dfrlmsz`.

If you're having a hard time determining if guessing is going well or not, try making saving a movie by setting `'make_guessmovie'` to `true`. This enables you to inspect the movie more closely than with the simple frame viewer in SMALL-LABS. I recommend using ImageJ to view the .avi movie, which allows easy navigation through the frames and easy scaling of the grayscale.

4.3 Considerations

For SMALL-LABS it is best to have a *slightly* high false-positive rate in guessing for the reasons discussed above. If the false-positive rate gets too high though, then it will obviously take more time to analyze the all of those guesses. Therefore it is important to balance accuracy here with speed by setting a reasonable false-positive rate, in practice a false-positive rate $\approx 10 - 25\%$ is probably a good target.

If the movie being analyzed has large variations (in molecule density, brightness, background, etc.) over the course of the movie, then it's probably best to guess frame by frame, by setting `'pctile_frame'` to `true`. If the variations are small though, it's likely more robust to use the entire movie to calculate the percentile.

5 Constructing the off-frames list

This step is skipped if `'bgsb'` is set to `false`.

This step is skipped if `'makeOffFrames'` is set to `false`.

The next step in SMALL-LABS is determining the off-frames list for each detected molecule. This is accomplished in *Mol_off_frames.m*. For each detection a local off-frames list is constructed; this list enumerates all frames in which no molecule was detected in the local region around the molecule. A local region is defined as a square around the detection with edge size $2 \times \text{dfrlmsz} + 1$ (in pixels). The off-frames list is only constructed for a temporal window around the detection. The length of this temporal window is set by `moloffwin`. There are no optional parameters for this step.

5.1 Considerations

A warning will print to the command window if a detection has fewer than 5% off frames in its `moloffwin`. If you get this warning at all, or especially for many molecules, you should consider increasing `moloffwin`.

The same discussion about choosing the length of `avgwin` applies to choosing `moloffwin`. Briefly, it should be as long as possible, without including low frequency changes in the background. Basically, the characteristic on/off time of the molecules should be small compared with `moloffwin`, but the characteristic time for the background to change should be large compared with `moloffwin`.

6 Subtracting and Fitting

This step is skipped if `'fitting'` is set to `false`.

The subtraction of the true background and PSF fitting are accomplished in the same step in SMALL-LABS, in the *Subtract_then_fit.m* function. If `'bgsb'` is set to `false`, then subtraction is skipped and just fitting is done. The subtraction calculates the mean (or median) of the off-frames (as determined in *Mol_off_frames.m*) in a local region around the guess. The local region is the same $2 \times \text{dfrlmsz} + 1$ (in pixels) square around the guess as was used in *Mol_off_frames.m*.

After fitting, a number of false-positive checks are done. The results of these false-positive checks determine whether or not the fit is a *goodfit* and should be used for further analyses.

For background subtraction ('*bgsb*' set to `true`) fit results are saved in a .mat file in the data directory called *movienam*_AccBGSUB_fits.mat, where *movienam* is the name of the movie being analyzed. If background subtraction is not being used, then the file is called *movienam*_fits.mat.

6.1 Optional parameters

'MLE_fit' is a Boolean determining whether or not to use MLE (maximum likelihood estimation) fitting or to use least-squares fitting. If set to `true` MLE fitting will be used, if set to `false` least-squares fitting will be used. Default is `false`. ***Currently using MLE fit on a GPU is not functioning, this will be fixed as soon as possible.

'stdtol' is one of the goodfit (false-positive) parameters. *stdtol* is the tolerance on the width (standard deviation of the fitted 2D Gaussian). See Sec. 6.3 for a more detailed discussion on the goodfit parameters. Default is 1.5.

'maxerr' is second changeable goodfit parameter. It is the maximum error on the fit, defined using normalized residuals. Default is 0.10.

'do_avgsub' is a Boolean determining whether or not to subtract the mean or the median of the off-frames. If set to `true` the mean will be subtracted, if set to `false` the median will be subtracted. Default is `true`.

'which_gaussian' is a flag determining which Gaussian function to fit to. Set to 1 to use a symmetric 2D Gaussian, set to 2 to use a fixed angle asymmetric 2D Gaussian, set to 3 to use a freely rotating asymmetric 2D Gaussian. See Sec. 6.2 for more details. Default is 1, the symmetric 2D Gaussian.

'fit_ang' is the angle (in radians) to which the fixed angle asymmetric 2D Gaussian will be fit. Default is 0.

'usegpu' is a Boolean determining whether or not to use a CUDA enabled GPU for the fitting if one is available. If set to `true` the GPU will be used, if set to `false` the GPU will not be used. Default is `true`.

6.2 Gaussian fit parameters

There are currently three options for the functional form of PSF to fit to. NOTE: because all of the math is here is done on images (arrays) in Matlab, the coordinate system is rows and columns, *r* & *c*, as opposed to something potentially confusing like *x* & *y*. See the document included in this package titled *Image Coordinates in Matlab and ImageJ.pdf* for more details.

The first functional form is the symmetric 2D Gaussian

$$\mathbf{1} \quad A \exp \left(-\frac{(r - r_0)^2 + (c - c_0)^2}{2\sigma^2} \right) + B$$

the fit results are:

```

row    = r0
col    = c0
widthr = σ
widthc = σ
ang    = 0 (meaningless in this context)
offset = B
amp    = A

```

The second functional form is the fixed angle symmetric 2D Gaussian, where the angle $\theta = ang$.

$$\mathbf{2} \quad A \exp \left(-\frac{((r - r_0) \cos \theta - (c - c_0) \sin \theta)^2}{2\sigma_r^2} + \frac{((r - r_0) \sin \theta + (c - c_0) \cos \theta)^2}{2\sigma_c^2} \right) + B$$

the fit results are:

```

row    = r0
col    = c0
widthr = σr
widthc = σc
ang    = θ = ang (not a fit parameter here)
offset = B
amp    = A

```

The third functional form is the same as #2 except that now the angle θ is an additional fit parameter.

Finally, the `sum` isn't a fit parameter, but rather is the sum of all pixel intensities in the background subtracted image of the molecule (the local area in the $2 \times df_{rlmsz} + 1$ square).

6.3 Goodfit (false positive) checks

SMALL-LABS does a number of a goodfit checks to keep the false positive rate low. The two non-customizable checks are

1. Checking the the fit coordinates (`row` & `col`), the amplitude `amp`, or the sum `sum` are all positive. If any are negative, then it's a bad fit.
2. Checking that the amplitude is less than the sum (`amp < sum`). If it's larger then it's a bad fit.

The two customizable goodfit checks are

1. Check the width of the Gaussian fit, defined by the standard deviation σ , as compared to an expected width. For a given nominal diffraction limit size `dfrlmsz`, the expected width, σ_E , is $\sigma_E = \text{dfrlmsz} / (2\sqrt{2\log 5})$. A goodfit is a width that satisfies the condition $(\sigma_E / \text{stdtol}) \leq \sigma \leq (\sigma_E \times \text{stdtol})$. For an asymmetric Gaussian $\sigma = (\sigma_r + \sigma_c) / 2$.
2. Check the error on the fit. The error is defined as a psuedo R^2 value. For a fitted function F of a dataset D , we calculate this psuedo R^2 as

$$R^2 = 1 - \frac{\sum (D - F)^2}{\sum (D - \langle D \rangle)^2}$$

If $R^2 \geq \text{maxerr}$ then it's a goodfit.

The best way to determine if the goodfit checks are accurately discriminating between false positives and true positives is to watch the ViewFits movie, as described in Sec. 8. If they seem too stringent or too lenient, change them and remake the ViewFits movie to check again. The easiest way to do this is to use the provided function *Change_GoodFits.m* which allows a fit's goodfit status to be reevaluated with new goodfit parameters *without* having to re-fit the movie, and thus can proceed much faster. Similarly, one doesn't need to make the entire ViewFits movie, instead setting `'write_mov'` to `false` puts the ViewFits function into debug mode which allows you to inspect a small number of frames carefully, and not have to wait for the entire movie to be made.

7 Tracking

This step is skipped if `'tracking'` is set to `false`.

After fitting, SMALL-LABS calls a single-particle tracking algorithm using the Hungarian method. The tracks are saved to the fits .mat file in the `tracks` variable. To aid in intensity measurements SMALL-LABS also creates a track filter logical vector for all guesses called `trk_flg` which indicated if a molecule was sucesfully organized into a track AND the particular detection was not the first or last frame of the track. This is to avoid including molecules which turned on or off partway through a frame, and thus will have their intensity reduced. A true indicated that the detection passed the track filter, and a false that it did not.

7.1 Optional Inputs

Tracking in SMALL-LABS uses the function *Track_3D2.m* (written by David Rowland), further details about the meaning of the track parameters can be found in that function.

'**savetracks**' is a Boolean determining whether to save the output of *Track_3D2.m* directly in its own .mat file. The `tracks` & `trk_fit` variables will still be saved to the fits .mat file. Set to `true` to additionally save the raw output from *Track_3D2.m*, and set to `false` not to. Default is `false`.

The next inputs are the tracking parameters, these are inputted to SMALL-LABS as a single vector. I'll only give a cursory explanation of these parameters here, see *Track_3D2.m* for more details. The default values are [0.01,200,0.5,3,3,1,0]

minimum merit

`trackparams(1)=0.01`

Integration time (ms)

`trackparams(2)=200`

gamma

`trackparams(3)=0.5`

maximum step size

`trackparams(4)=3`

minimum track length

`trackparams(5)=3`

speed estimation window halfsize

`trackparams(6)=1`

time delay between consecutive frames (ms)

`trackparams(7)=0`

8 The ViewFits movie

This step is skipped if 'makeViewFits**' is set to `false`.**

Lastly, SMALL-LABS makes a ViewFits movie to show the results of detection, fitting, and tracking. This is an especially useful tool as humans are excellent at looking at most single-molecule movies and determining whether the program incorrectly identified some feature as molecules (false-positives) or missed a lot of molecules (false-negatives). The ViewFits movie is saved in the data directory as *moviename_ViewFits.avi*.

8.1 Optional Inputs

'**orig_movie**' is a Boolean determining whether or not to use the original movie, or to use the avgsub movie. Set to `true` to use the original movie, and set to `false` to use the avgsub movie. Default is `true`.

'**circ_D**' is the diameter (in pixels) of the circles shown in ViewFits movie to indicate molecule positions. Default is `dfrlmsz`

'**linewidth**' is the linewidth of the circles. Default is 1.

'**write_mov**' is a Boolean determining whether or not to make the entire ViewFits movie and write it to the data directory, or to go into debug mode

and allow the user to click through frames and inspect them there. Set to `true` make the entire movie and save it, and set to `false` to enter debug mode. Default is `true`.

'`autoscale.on`' is a Boolean determining whether or not to set the grayscale frame-by-frame or use a single grayscale for the entire movie. If using the entire movie 100 equally spaced frames are taken from the movie to set the grayscale. Set to `true` set the grayscale frame-by-frame, and set to `false` to use one for the entire movie. Default is `false`.

'`trackingVF`' is a Boolean determining whether or not to use the “standard” ViewFits format showing guesses, fits, and the track filter, OR to show only color coded tracks. Set to `true` to make the tracking ViewFits movie, and set to `false` to make the “standard” ViewFits movie. Default is `false`.

8.2 ViewFits color scheme

For the “standard” ViewFits a green circle indicated a goodfit, a red circle indicates a guess that didn’t pass the goodfit checks, and a pink circle indicates a molecule that passed the track filter. An example frame of a ViewFits movie is shown in Fig. 2

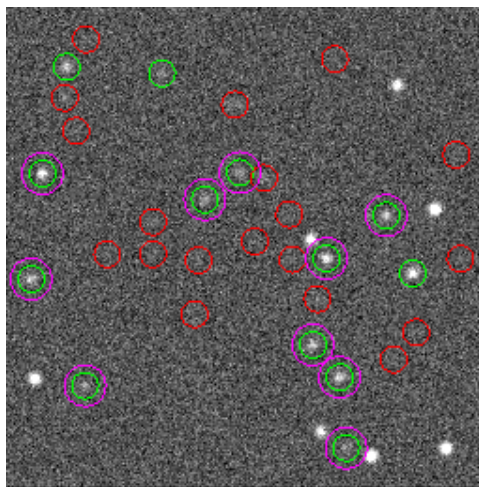


Figure 2: ViewFits frame. Note: this movie had several molecule shaped objects in the background, those aren’t missed molecules but actually the background.

For the tracking ViewFits movie, the circles only indicate molecules which were successfully organized into tracks. Colors indicate unique tracks. For simplicity there are only five unique colors that are simply cycled through. An example frame (same movie and frame number as in Fig. 2) of a tracking ViewFits movie is shown in Fig. 3. Note: Two molecules in the same frame will never be organized into the same track, so when, as is the case in Fig.

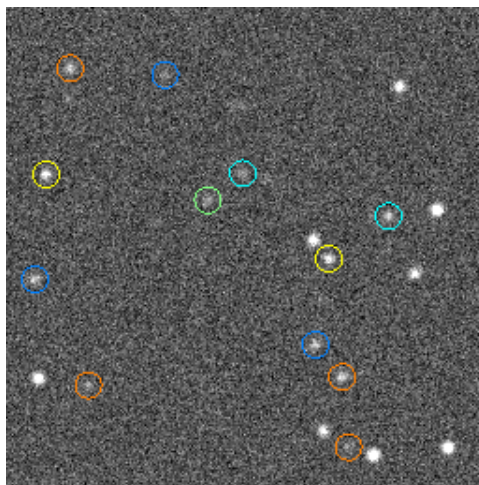


Figure 3: Tracking ViewFits frame. Note: this movie had several molecule shaped objects in the background, those aren't missed molecules but actually the background.

3 there are multiple molecules in one frame with the same color they are indeed in different tracks.

9 Speed and Memory Troubleshooting

SMALL-LABS is generally a fairly fast and memory efficient program, however a number of steps can be taken to make it faster or more memory efficient if that is needed.

Use smaller movies. Obviously using smaller movies will require less memory and time to analyze them. You can use the provided program *ROI_picker.m* to pick a smaller region of interest (ROI) within your original movies. If you consistently run out of memory in SMALL-LABS you have to either increase the memory of your computer or analyze the movie as several smaller movies.

Analyze fewer molecules. Every molecule guessed has to be analyzed, this includes creating an off-frames list, subtracting the True Background, and fitting, thus increasing the number of guessed molecules adds a lot more computations which need to be performed. If you reduce the number of guesses, this can greatly reduce the time to run the program. You can accomplish this by increasing `bpthrsh`, but be careful not to increase it so much that you miss molecules. You can also increase `egdesz` to skip fitting molecules near the edge of the frame (which may not be meaningful). Finally using least squares fitting is much faster than MLE fitting, setting `'MLE_fit'` to `false` accomplishes this.

Dont make a ViewFits movie. The optional step to make a ViewFits movie is fairly slow. If analyzing a batch of movies it's recommended to do all of the analysis first and then separately make ViewFits movies only for a few representative movies.

Use parallel computing. If you don't have the Parallel Computing Toolbox for Matlab, installing it allows SMALL-LABS to parallelize some steps. Additionally, running SMALL-LABS on a computer with a CUDA enabled GPU will allow the fitting step to proceed much faster.

10 Additional Programs Provided

In this package there are a number of additional programs provided which are not needed for the main operation of SMALL-LABS. The following are short descriptions of these programs; for additional details see the comments at the beginning of each program.

Change_GoodFits.m is a function which can be run after fitting to change the goodfit parameters (`maxerr` and `stdtol`) and also change `dfirlmsz` and consequently which fits are considered goodfits. This is much faster because it allows you to experiment with these parameters without having to fit the movie again.

ROI_picker.m is a function which allows you to pick an ROI in a series of movies and write a new TIFF stack movie of just that ROI³. This is helpful because it allows you to reduce the size of the movies being analyzed which will decrease how long it takes to analyze them.

stack.tiffs.m is a function which converts a folder of individual TIFF images into a single TIFF stack. By using *TIFFStack* and *saveastiff* it is fairly fast.

WriteListOfMovies.m gives an example of how to write such a list of movies using Matlab to be analyzed as a batch in SMALL-LABS. The beginning section of that script takes advantage of a specific naming convention for the movies (each is named `mov_xxxx.mat`), which likely won't be useful to your data, but it can be a good starting point for writing your own script.

In the Test data and simulations directory, there two programs for generating and working with simulated data:

SimulateDataPoisson.m is a simple script to simulate single-molecule data with various backgrounds. It generates data with Poissonian noise.

Check_Fitting_Simulated.m is a script which can be used to check how accurately simulated data was fit.

³At the time of writing it still saves the data as a TIFF stack, but will likely be soon updated to save `.mat` files instead.

11 The modularity of this code

SMALL-LABS is written as modular code. It was designed so that different parts of the code can be easily modified or even completely replaced. Throughout the code we've tried to copiously comment and, in particular, explain the inputs and outputs of the various steps and functions. This should help make any modifications or replacements simpler to implement.

In particular, I anticipate users may wish to utilize a specific guessing (detection) method or specific fitting method. For example if a non-Gaussian PSF is desired then the provided fitting functions won't be helpful and the guessing algorithm may not work. By simply modifying those two steps SMALL-LABS should still function and accurately subtract the local background.

To modify the guessing step, the simplest approach would be to replace the entire guessing function. The function should output the guesses in the same format as the provided function, which is as a .mat file using the same naming convention, and with an array called guesses that has columns 1. frame #, 2. row position (pixels), 3. column position (pixels).

To modify the fitting step, the simplest approach would be to add another if statement in the fitting section in *Subtract_then_fit.m*. In this new section fit the same array as in the other sections, called dataset. Then enter the fit results into the fits structure using the column definitions described in the introduction of this guide. Note that the goodfit checks will likely need to be modified to be appropriate for the new fitting method.

A List of all optional parameters

All optional inputs are input as name-value pairs, for example to set 'bpthrsh' to 93 include 'bpthrsh', 93 in the function call to *SMALLLABS_main.m*. This is a complete list of all the optional parameters and their default values, a duplicate list is in the comments in the beginning of *SMALLLABS_main.m*.

SMALL-LABS prints to the command window for every step it takes. If you want to disable this feature, edit *SMALLLABS_main.m* and change the line `verbose=true` (immediately preceding the `%%Parameter Defaults` section) to `verbose=false`.

A.1 Actions

Do background subtraction

```
'bgsub' = true
```

Make the average subtracted movie

```
'makeAvgsub' = true
```

Do guessing

```

'guessing'= true
Check the guesses
'checkGuesses'= false
Make the off frames list
'makeOffFrames'= true
Do fitting
'fitting'= true
Do tracking
'tracking'= true
Make the ViewFits movie
'makeViewFits'= true

```

A.2 AVGSUB parameters

Subtract the temporal average? otherwise use median

```

'do_avg'= true
AVGSUB offset
'offset'= 1000

```

A.3 Guessing parameters

the threshold percentile of the bandpassed movie

```

'bpthrsh'= 95
how many pixels to ignore around the edge of the frame
'egdesz'= dfrlmsz
compare brightnesses in each frame? otherwise use entire movie
'pctile.frame'= false
use a mask for guessing? Enter it's filename or set to true to look for .mat
file w/ "_PhaseMask" appended to movie name
'mask.fname'= []
make a movie (.avi) of the guesses to check parameters
'make_guesssmovie'= false

```

A.4 Fitting parameters

do MLE fitting? If not least squares fitting will be used

```

'MLE.fit'= false
Goodfit parameters. See Subtract_then_fit.m for the details
'stdtol'= 1.5
'maxerr'= 0.10
subtract the mean of off frames? If not use median
'do_avgsub'= true
Which Gaussian function to fit to when using LSQ fitting? 1. symmetric,

```

2. fixed angle asymmetric, 3. free angle asymmetric

`'which.gaussian' = 1`

the angle to fit to for a fixed angle Gaussian

`'fit_ang' = 0`

use a GPU if one is available?

`'usegpu' = true`

A.5 Tracking parameters

save the separate tracks .mat file?

`'savetracks' = false`

`'trackparams'` needs to be entered as a whole vector, the default is `[0.01,200,0.5,3,3,1,0]`

minimum merit

`trackparams(1)=0.01`

Integration time (ms)

`trackparams(2)=200`

gamma

`trackparams(3)=0.5`

maximum step size

`trackparams(4)=3`

minimum track length

`trackparams(5)=3`

speed estimation window halfsize

`trackparams(6)=1`

time delay between consecutive frames (ms)

`trackparams(7)=0`

A.6 ViewFits parameters

use the original movie? if not, use the avgsub movie

`'orig.movie' = true`

diameter of the circles showing the fits

`'circ.D' = dfirmsz`

linewidth of the circles

`'linewidth' = 1`

write a .avi movie showing the fits. If not, goes to debug mode

`'write.mov' = true`

autoscale frame by frame?

`'autoscale.on' = false`

use the tracking viewfits instead

`'trackingVF' = false`

B The goodframe list

SMALL-LABS has a built-in functionality to ignore specific frames. This is accomplished using the `goodframe` vector, which is a logical vector whose length is equal to the number of frames in the movie (giving a one-to-one correspondence between each frame in the movie and an element in `goodframe`). Unless given a `goodframe` list SMALL-LABS assumes all frames are to be used.

To input a `goodframe` list, simply save the `goodframe` vector to the `.mat` file containing the movie (`mov` array). The `goodframe` vector needs to be a logical vector, meaning either logical type variable or all of it's elements must be convertible to logical (0 & 1, etc.).

C Coordinate System

SMALL-LABS runs entirely in Matlab, and as such the coordinate system used is the most meaningful for Matlab arrays. Instead of returning x & y positions in some arbitrary coordinate system, SMALL-LABS uses, and returns, coordinates in row and column position using Matlab conventions for rows and columns and the origin. Throughout most of the program, the row and column numbers (integers) are tracked. The fitting step, which provides sub-pixel information, returns a non-integer row and column position. For example, fitting a guess at $(r, c) = (41, 153)$ may yield a position of $(r, c) = (42.0597, 153.9108)$.

For a more detailed tutorial on the coordinate system in Matlab and how it relates to the “normal” convention used in a Cartesian coordinate system, and also the coordinate system used in ImageJ (a free commonly used image viewer and analysis program), see the pdf included in this repository titled *Image Coordinates in Matlab and ImageJ.pdf*.

D Example movie list file

To send a list of movies to SMALL-LABS enter the `.txt` file containing the list as the first input `file_or_directory_name`. The `.txt` file should have the full filename (e.g., `directory\movienamename.ext`) for each movie on a separate line. For example to analyze the following list of movies

```
list_file.txt
E:\Microscope Data\2_29_18\mov_001.mat
E:\Microscope Data\2_29_18\mov_002.mat
E:\Microscope Data\2_29_18\mov_003.mat
E:\Microscope Data\2_29_18\mov_005.mat
E:\Microscope Data\2_29_18\mov_008.mat
E:\Microscope Data\2_29_18\mov_013.mat
```

```
E:\Microscope Data\2_29_18\mov_021.mat  
E:\Microscope Data\2_29_18\mov_034.mat  
E:\Microscope Data\2_29_18\mov_055.mat  
E:\Microscope Data\2_29_18\mov_089.mat  
E:\Microscope Data\2_29_18\mov_144.mat
```

simply enter

```
>>SMALLLABS_main('list_file.txt', 7, 300, 100,)
```

The optional script *WriteListOfMovies.m* gives an example of how to write such a list of movies using Matlab. The beginning section of that script takes advantage of a specific naming convention for the movies (each is named mov_xxxx.mat), which likely won't be useful to your data, but it can be a good starting point for writing your own script.