Description

CSSTORM.m	containing the main analysis code.
MolEst_eps.m	containing the CVX optimization code.
MolKernel.m	containing the description of the PSF.
100_molecules.spe	test image corresponding to one frame from the simulation in this manuscript with 100 molecules randomly distributed in a 24 x 24 pixel area, corresponding to the left panel of Figure 1a.
100_molecules_cs_result.spe	CS analysis results of 100_molecules.spe, corresponding to the right panel of Figure 1a.
SpeHeader.class	SPE ImageJ plug-in with the frame number bug fixed.

Requirements

The code has been tested on MATLAB 2009 with CVX v1.21 installed. CVX is a free optimization software for MATLAB which can be downloaded from http://cvxr.com.

File format

The input data and output data uses the WinView SPE image format. Conversion of SPE format to and from other formats can be done easily in ImageJ after installing the SPE plug-in (http://rsbweb.nih.gov/ij/plugins/spe.html). Note that the SpeHeader.class provided by the original website contains a bug and needs to be replaced by the one included here (courtesy of Wenqin Wang, Harvard University).

Usage

```
CSSTORM (<input file>, <debug mode>, <eps>, <ADU>, <base line>)
```

`input file`	needs to have the .spe extension name. The result will be saved in a .spe file with "_cs" appended to the input file name.
`debug mode`	set to 1 to display a graphic window which shows the process of CS optimization. Otherwise, set it to 0.
`eps`	target (unweighted) reduced chi squared for the optimization. A value of 1.5 generally gives good results. For experimental data acquired by an EMCCD camera, a value of 2.1 should be used to account for the excess noise introduced by the camera gain.
`ADU`	the number of photons corresponding to one camera count.
`Base line`	the baseline offset of the camera.

Example

```
CSSTORM('100_molecules.spe', 0, 1.5, 1, 100)
```

This MATLAB command analyzes the supplied example image. The results will be saved in 100_molecules_cs.spe. If the program runs correctly, it should be the same as 100_molecules_cs_result.spe.

Notes

For compressed sensing to run correctly, the PSF of the microscopy system needs to be specified in MolKernel.m, preferably in an analytical form as in the provided example. The PSF of the microscopy system can be determined as described in the supplementary methods.

If the input file contains multiple frames, which is the true case for analyzing experimental data, the result is also saved as a multi-frame image stack in one .spe file. Each frame of this stack corresponds to the compressed sensing analysis results of one frame in the input file. A STORM image can be generated by summing all the frames of the result image stack, e.g. in ImageJ.