SuperResAlignL V2.0

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These source codes are distributed as accompanying codes for the article "Deformed Alignment of Super-Resolution Images for Semi-flexible Structures in 3D" by Shi *et al* at Bo Huang group. The main code is SuperResAlignL.m. There are 9 inputs for this function to give you the most freedom to tweak parameters. SuperResAlignL(file, imsize, zoomfactor, pixelsize, photonpercount, usfac, angrange, angstep, n\_iteration). The output is the aligned molecule list in a txt file. Three other outputs are optional. The description of the input and output is commented in the codes.

**Demo**

The package include four demos which are the data used in our paper “Deformed Alignment of Super-Resolution Images for Semi-flexible Structures in 3D”. The input of Demo1 is a molecule list of ciliary transition zones used in our paper, Figure 1. The input of Demo2-4 are molecule lists of simulated ring structures in Figure 2. You can test run the codes with the Demo 1 using following command lines in Matlab:

Deform\_robust(‘2-Cep164-647-cntrl\_0001\_list\_cluster1\_20150414\_30\_s’);

[sumim,regi,allIm] = SuperResAlignL('2-Cep164-647-cntrl\_0001\_list\_cluster1\_20150414\_30\_s\_tran\_redu\_robust,5,50, 175, 0.41,100,90,3,10);

If everything goes as it should, you would receive the same results as in the output subfolders. The aligned image will also display in Matlab for a quick check when the calculation finishes.  The command window records are also included with the demos so that you have an idea what to see and how long to wait (usually < 20 min).

**Error Codes**

1. If it shows an error after displaying “Generating image array ...”. It is most likely because the imsize you set is too small to include all the coordinates.