ROSE-3D Software README

This package is a supplementary software for the manuscript "Molecular-scale Isotropic 3D Super-Resolution Microscopy via Interference Localization". It contains the software for demonstration of ROSE-3D reconstruction. It also includes a script for calculating the Cramér-Rao Lower Bound (CRLB).

Reconstruction Demo

A demo dataset with 100 raw frames is provided in the folder **"data-100"**. To run the full reconstruction demo:

1. Navigate to the folder **"Reconstruction"**.
2. Add the folder **"lib"** to the MATLAB search path; this folder contains private functions required during reconstruction.
3. The folder **"RCC3D"** contains functions for RCC drift correlation, which will be called automatically during reconstruction.
4. To run the reconstruction, open and edit the script **run_Reconstruction.m**.
5. Finally, the reconstructed image is generated and saved as an image file.

The script will run automatically and display a summary report upon completion. Please note that, due to the small size of this demo dataset, the reconstruction will not produce a continuous image. A larger image dataset is available upon reasonable request to the authors.

CRLB Calculation Demo

To run the CRLB calculation demo:

1. Open the folder **"CRLB"**.
2. Run the script **run_z_vs_crlb.m**.

This script calculates the CRLB for centroid fitting and ROSE-3D localization, and compares their performance. The relevant parameters are defined at the beginning of the script and can be modified as needed.

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