

Single-molecule tracking data – ReadMe File

Together with this file comes two directories, “slowSPT_data” and “spaSPT_data”, containing all the raw trajectory data for the single-molecule tracking experiments. For details of how the experiments were performed and acquisition parameters, please see the description in the methods section of the manuscript.

Each folder contains a series of CSV files. More specifically, all the trajectories from each single cell are provided in a single CSV file and replicates provided as additional CSV files. The name of the CSV file describes the experiment (slowSPT or spaSPT), the protein of interest (e.g. Halo-CycT1_WT) and the frame rate (e.g. 2 Hz or 95 Hz).

Each CSV file contains 5 columns:

1. “frame” refers to the frame of the movie in which the molecule was localized.
2. “t” refers to the time in units of seconds where the molecule was localized.
3. “trajectory” refers to the trajectory ID. For example, trajectory 3 may have four localizations. All localizations with the same trajectory ID form a single trajectory.
4. “x” refers to the x-coordinate of the localization in units of micrometers.
5. “y” refers to the y-coordinate of the localization in units of micrometers.

In the case of the spaSPT data, the CSV format is readable by Spot-On. Thus, you can directly upload the data to: <https://SpotOn.berkeley.edu/> and reproduce our analysis.