

Transition Counting Quickstart

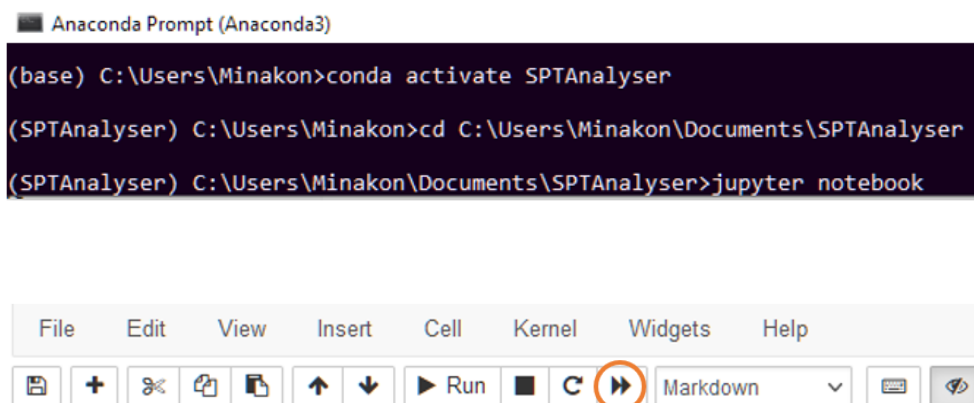
This manual concisely guides through the process of installing SPTAnalyser and applying transition counting to the test dataset. Please read “Manual_Tracking_Routine” if more information is required.

Installation

```
conda create --name SPTAnalyser
conda activate SPTAnalyser
conda install pip pywin32
pip install jupyterlab
pip install SPTAnalyser-XXX-py3-none-any.whl
pip install jupyter_contrib_nbextensions
jupyter notebook
```

Run the analysis

In the Anaconda Prompt, activate the environment, change the directory to the transition counting jupyter notebook (transitionCounts.ipynb), and open the notebook. A browser will open with the notebook. Initialize the notebook by clicking on the double arrow symbol. The notebook contains further instructions on how to run the analysis.



Test dataset

The dataset contains the following files of 60 HeLa cells marked with non-activating Fab ligand (more data is available at [BioStudies](#)). Required input files for transition counting are *.tracked.csv files from swift for the trajectory and segment information and *.h5 files from trackStatistics to extract diffusion state information of the segments. The analysis matches *.h5 and *.tracked.csv files, based on matching file names.

- *.csv file = localization file from ThunderSTORM
- *-protocol.txt = information file with ThunderSTORM parameters
- *_tracked.csv file = tracked file from swift
- *.tracked.meta.json = information file with swift parameters
- *.h5 = SPTAnalyser file from trackStatistics