Single cells (DeLTA)

Scripts

- convert_nd2.py (Python)
- run_delta.py (Python)
- SLURM_job_submission.sh (bash)
- SLURM_array_job_submission.ch (bash)
- run_delta_array_job.py (Python)
- analyse_delta_results.py (Python)
- tree_plot.R (R)
- process_results.R (R)
- compare_tracking_results.py (Python)

Example

- The example consists of a short time-lapse movie with two channels (phase contrast and fluorescence)

Pre-Processing

For the subsequent steps, images must be converted into individual TIFF files, separated by time-step as well as channels. The images must be named according to the following pattern `Name_[position number]_C[channel number]_T[time-point].tif`. The `convert_nd2.py` script can be used to automatically convert Nikon Image Files (.nd2) into the correct format. **Usage**:

```
python convert_nd2.py path/to/ND2/file.nd2
```

Segmentation and Tracking

The segmentation and tracking of individual cells is done by the DeLTA2.0 pipeline. Detailed instructions on installation and usage can be found in the documentation. The `run_delta.py` script is a short example on how to run the pipeline. The pipeline can also be run in Google Colab for testing or on ScienceCluster for faster speeds. The provided `SLURM` scripts can be used to submit jobs on ScienceCluster. More detailed instructions can be found in the `README_SC_DeLTA_setup.md` file and the ScienceCluster documentation.

Analysis and Measurements

analyse_delta_results.py: Convert cell data from DeLTAs .pkl file into CSV format and calculates additional metrics.

tree_plot.R: Used to plot a lineage tree based on the tracking data from DeLTA

compare_tracking_results.py: Can be used to check how accurate DeLTA tracks individual cells and divisions by comparing it to manually tracked

positions. A more detailed description of the analysis can be found in the `README_test_DeLTA_tracking.md` file.

Further analysis steps can also be found in the supplement of the related paper **Space and epigenetic inheritance determine inter-individual differences in siderophore gene expression in bacterial colonies**