**Cell Migration Analysis Platform (CMP)**

This program is designed to facilitate high-population single-cell migration analysis for non-programmers. It is useful for comparing the migration behavior of thousands of cells within various environments.

The analysis pipeline involves 5 stages:

a. Cell-Tracking and Migration Data Generation

b. Data Preprocessing (experiment reconstruction and grouping)

1. Data Filtering

2. Analysis

**Stage** **a**: A script runs automated tracking on batches of time-lapse microscopy video files using the TRACKMATE plugin within FIJI. TRACKMATE outputs cell centroid spatial and frame data in xml format.

**Stage** **b:** TRACKMATE output files are grouped to appropriate experiment directories. One experiment should contain all data files corresponding to all the video files for that experiment. Additionally, within each experiment directory there may be a **coordinates.txt** file and a **settings.txt file**. The coordinates file is used to combine migration data from multiple data files in order to reconstruct the full experiment. The settings file is used to specify various parameters specific to the experiment. All experiment directories should be contained in one parent directory. The parent directory is then loaded and saved into CMP for analysis.

**Stage 1**: Data filtering may be performed to select cells with specific qualities or within a specific spatiotemporal ranges for analysis.

**Stage 2**: CMP serves as a powerful library for performing custom analysis, and offers easy extensibility of track filters, measurement functions, and analysis scripting. Users not comfortable with programming have various “comprehensive” analysis scripts that can be performed with a single execution that will produce vast quantities of graphs and excel sheets reporting…

1. Spatiotemporal correlations to cell track measurements, including average movement speed, average velocity, migration persistence, and directionality.

2. Cell-track measurement binning and other-measurement correlations

3. Experiment summaries and cross-experiment comparisons

Stage 1 and 2 may be an iterative process, where preliminary analysis is performed before filtering and more analysis.

**Cell Track Attributes:**

**Cell Track Filter Functions:**

**Current Measurement Functions:**

**Directionality**: ( ) where “Cell vector” is the positional vector a cell has moved in one frame and “Field vector” is the vector defined as the direction of the gradient. The percent (decimal) of movement in the direction of increasing concentration within a chemical gradient.

**Migration** **persistence** (): The percent (decimal) of movement in one direction, as opposed to any direction

**Mean** **velocity** (): The average movement over the entire temporal range

**Mean migration speed** (): The average distance travelled per frame