**The folder CellSegmentationEdgeDynamics contains functions and scripts to:**

1. Segment cells, i.e. distinguish cells as objects form the background. This will result in a “mask”, i.e. a binary
2. Track cell movement, so that the same cells can be identified in subsequent frames
3. Parameterize the cell edge, this will result in n peripheral windows.
4. Relate peripheral windows of subsequent frames and determine cell edge velocity.
5. Measure fluorescence activity in cell peripheral windows.

The analysis will follow these steps:

Preparation:

The analysis pipeline expects

**Step 1:** Generate background reference images. This is to estimate the shape of the background.

**GenerateReferenceBackgroundImages.m**

**Step 2:** Determine the alignment parameters between channels: This is necessary as images in different channels are sometimes slightly shifted in x-y relative to each other.

**AlignmentParameters.m**

**Step 3:** Image segmentation. Generates masks to determine the cell outlines.

**OptimizeSegmentation.m**