**Recoil velocities in wild type and mutants**

Requirements

- Install **Fiji/ImageJ** (this pipeline was tested using ImageJ 1.51h, Java 1.8.0\_66 (64bit), website: <http://imagej.nih.gov/ij>)

- Install **Matlab** (this pipeline was tested using 2018b Matlab version

1. Input data and architecture of the input

Input data is apical and basal ablation done in the same pupa in the central region.

Each folder corresponds to an animal: Pupa1 (Pupa2, … or Pupa(n)).

Folders contain movies corresponding to the apical and the basal ablations: ‘Apical.czi’, ‘Basal.czi’

1. Quantification of the recoils

In Fiji, run ‘QuantificationBasalApicalRecoil.ijm’.

Indicate the path ‘Data\Test\_RecoilQuantification’. In this folder, 2 examples of data are shown (Pupa1 is 15hAPF and Pupa2 is 23hAPF).

‘QuantificationBasalApicalRecoil.ijm’ will assist the user in measuring recoil velocities in the movies, save the drawn ROIs and the measured velocities.

Note that when the program has already been run, it will reuse the saved ROIs and will not ask the user to draw them again. If you want to define new ROIs, please erase the one that have been saved.

1. Plot the data

In Matlab, open ‘PlotRecoilVelocities.m’ and add ‘Function’ folder to Matlab path.

In the code, indicate the path ‘Data’ (contains ‘Values’ folder). ‘Data\Values’ folder contain the quantifications made with ‘QuantificationBasalApicalRecoil.ijm’ for the whole dataset (wild type and mutant conditions).