

## FlowRec

**Name of software:** *FlowRec* – software for reconstruction of the intracellular flows

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**Description:** The software allows us to compute the vector field of intracellular movements from *bright-field time-lapse microscopy raw image* series primarily. The basis of the method is detection of speeded-up robust features (SURF) and assembling them into trajectories. Two components of motion – direct and Brownian – are separated by an original method based on minimum covariance estimation. The Brownian component gives a spatially resolved diffusion coefficient. The directed component yields a velocity field, and, after fitting the vorticity equation, estimation of the spatially distributed viscosity.

**Requirements:** MATLAB2019b or future release, Computer Vision Toolbox, Image Processing Toolbox, Optimization Toolbox, non-mandatory: Instrument Control Toolbox (used for better progress reporting).

**Input parameters** (see *Osteoblast.m* and *Hepatocyte.m* as examples):

- Bayer – configuration of the camera Bayer filter, can be 'grayscale' for already pre-treated images
- pxsiz – size of pixel projected on a field, in nm
- wsize – flow reconstruction window, now deprecated
- met – metric threshold for detection of the SURF features, can be in [1..+inf), default 100
- alive – limit (in frames) for keeping the track which is not observed in computer memory, default is 1, better not to change
- mlen – the minimal length (in time domain, in frames) of the track which we save, default 12
- delay – period of image acquisition, in ms
- reduce – factor by which we reduce the image resolution, better to keep it  $\geq 3$ , default 4
- input – folder with the input images
- workdir – folder for intermediate and final results, can occupy a few GB of space

**How to use it:** See the examples *Osteoblast.m* and *Hepatocyte.m*. In the first run, the software will ask you to annotate a few images manually (can be configured, see 3<sup>rd</sup> argument of *SqueeshyMask* in the examples), and then it automatically interpolate the contour.

**Output:** *vispro.mat*, will be stored in the *workdir* folder after finishing of the process. For content see the examples.

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