

Self-supervised learning of cell dynamics

Lab: computational bioimaging and bioinformatics, ENS

Location: ENS Paris, 45 rue d'Ulm, 75005 Paris

Contacts: Auguste Genovesio (auguste.genovesio@ens.psl.eu), Lisa Bedin (lbedin@bio.ens.psl.eu)

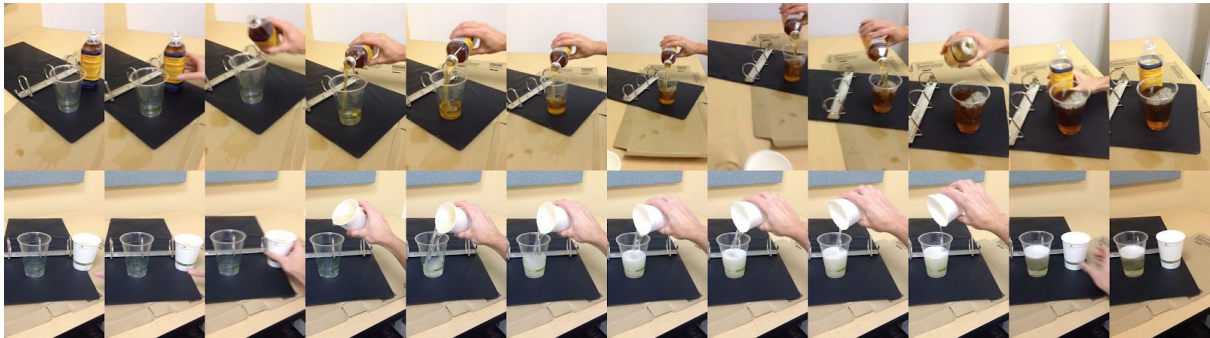


Fig a. Self-supervised learning of temporal features [1] allows for synchronizing natural videos without the need of temporal labels.



Fig b. These methods cannot be directly applied to cellular video microscopy, since cellular morphological features are a consequence of both temporal biological events such as cell entering mitosis (red circle) and random events such as overlapping of cells (blue square).

Background

Approaches to learn deep dynamical features from videos without the need of temporal labels has significantly improved [1]. However, while these methods perform well on detecting semantic cues in natural videos, they cannot yet discriminate semantic from non-semantic variability in cellular microscopy image sequences. Our lab has developed automated image analysis methods for extracting hand-crafted dynamical features from videos of cell divisions [2]. Yet this kind of method doesn't leverage the sequential information and is biased toward a few number of features: shape, size, number of cells. We would like to develop self-supervised methods leveraging sequential data for the extraction of non-biased cellular dynamical features.

This project

The goal of the project is to develop a self-supervised model to learn deep representations of videos of cellular processes. The trainee will have to 1) explore strategies for extracting cellular dynamic features in a context of deforming and overlapping cell soft-bodies, 2) evaluate the models both on real microscopy image sequences and on generated synthetic videos of cell divisions.

The candidate:

The candidate should know Python and preferably have some experience with PyTorch or Tensorflow for deep learning.

Bibliography

[1] Dwibedi et al, Temporal Cycle-Consistency Learning, in CVPR, 2019

[2] Li et al, Detection and tracking of overlapping cell nuclei for large scale mitosis analyses, in BCM Bioinformatics 2016