

Population Dynamics Virtual Seminar



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17.09.21 - 14:30 GMT, 15:30 CET

Dynamics, Feedback, and Transient Antibiotic Resistance in Single Cells

Cell-to-cell heterogeneity in gene expression and growth can have critical functional consequences, such as determining whether individual bacteria survive or die following antibiotic exposure.

In this talk, I will describe experiments using single-cell time-lapse microscopy to measure gene expression and growth in *Escherichia coli*, focusing on genes related to stress response. In support of this, I will describe our recent advances in automated image processing of time-lapse microscopy images using a deep learning model (DeLTA). Once trained, this algorithm requires minimal input from the user and can rapidly segment, track, and reconstruct lineages for bacteria growing in microfluidic chips and on two dimensional surfaces.

Suggested Readings: J. B. Lugagne, H. Lin, M. J. Dunlop. - *DeLTA: Automated Cell Segmentation, Tracking, and Lineage Reconstruction using Deep Learning*. - PLOS Computational Biology,
<https://doi.org/10.1371/journal.pcbi.1007673>, 2020.
<https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1007673>

O.M. O'Connor, R. N. Alnahhas, J-B. Lugagne, M. J. Dunlop - DeLTA 2.0: A deep learning pipeline for quantifying single-cell spatial and temporal dynamics -
<https://doi.org/10.1101/2021.08.10.455795>
<https://www.biorxiv.org/content/10.1101/2021.08.10.455795v1>