Bacterial Gene Expression in Space, Time, and Numbers
(Kim, Golding)

The flow of genetic information in bacteria is typically perceived to take place in a homogenous, well-mixed environment. In this module, students will use genetic and environmental perturbations, single-cell and single-molecule imaging, and theoretical tools, to explore how perturbing the spatial organization of the RNA degradation machinery in *E. coli* affects stochastic gene expression.

The theme includes:

- Super-resolution imaging of RNase E in live cells, followed by image analysis to obtain the spatiotemporal dynamics of individual molecules.
- Simultaneous labeling of a single gene and the RNA molecules transcribed from it, in both live and fixed cells. The multi-color data will be analyzed to measure the transcriptional activity of an individual gene copy in the cell.
- Theoretical modeling of stochastic transcription in *E. coli*, using both solvable equations and stochastic simulations. Direct comparison of model predictions with the experimental data above will be used to estimate kinetic parameters (transcription initiation, elongation, and RNA degradation) and reveal how these parameters are modulated by spatial perturbation of the RNA degradation machinery.