THEME 1: EVOLUTION OF CHEMOTAXIS

A predictive understanding of evolutionary dynamics is a central goal of quantitative biology. In this theme we use bacterial motility as a model system for understanding evolutionary dynamics at the population and single-cell level. We study evolution in the presence of a trade-off, and how individuality (cell-to-cell variability) evolves under selection. Bacterial populations exploit motility through a process called chemotaxis to respond to spatial and temporal gradients of nutrients and toxins in their environment. The mechanistic basis of chemotaxis is well understood in several model bacterial species. In this theme, we investigate the evolution of bacterial motility and chemotaxis. Using experimental evolution, stochastic simulations, single-cell tracking, genetic engineering and precise measurements of chemotactic responses in single-cells we study how selection for faster population-level migration is driven by genetic and phenotypic evolution at the single-cell level. Phenotypic measurements will determine how swimming speed and growth rate as well as cell-to-cell variability differ between ancestral and evolved strains. Genetic engineering will be used to study the genetic basis of the observed evolution and stochastic simulations will be used to gain insight into the selection process.

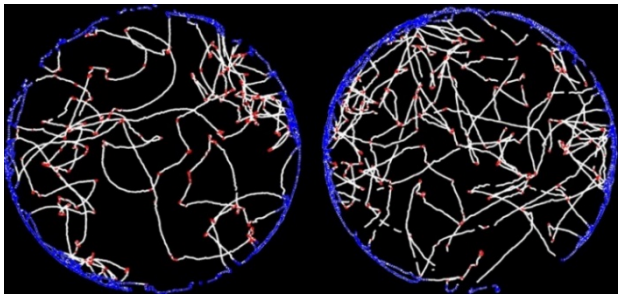
Students will participate in the following 4 modules:

MODULE 1: EXPERIMENTAL EVOLUTION OF BACTERIAL MIGRATION

Part 1: High-throughput single-cell tracking

Laboratory: Seppe Kuehn (UIUC Physics)

Students will track single *Escherichia coli* cells in an unstimulated environment using a high-throughput microfluidic technique. Measurements will determine how the selection process alters single-cell run-tumble statistics and swimming speed. Students will learn the fundamentals of microfluidics, image analysis, automated particle tracking, microscopy and data analysis with Matlab.



Kuehn Lab (unpublished)

Part 2: Manipulating genes: precision genetic engineering in *E. coli*

Laboratory: Tom Kuhlman (UIUC Physics)

Whole genome sequencing reveals the genetic basis of the evolution of bacterial motility. To pinpoint the effect of mutations on the phenotype we will use genome editing techniques to re-engineer mutations identified as a result of evolutionary selection. The method permits the precise integration of defined mutations into an ancestral genetic background to quantitatively assess the phenotypic effects of the mutation. Techniques include PCR, gel electrophoresis, genetic transformation and the interpretation of whole genome sequencing data.

MODULE 2: MEASURING CHEMOTACTIC RESPONSES IN SINGLE CELLS

Laboratory: Yann Chemla (UIUC Physics)

To determine how selection changes the response of single-cells to spatially defined chemical gradients, students will perform single-cell chemotactic response measurements using an optical trapping-based 'bacterial-treadmill' assay. Techniques include optical trapping and data analysis with Matlab.

MODULE 3: EVOLVING IN SILICO: STOCHASTIC SIMULATIONS OF EXPERIMENTAL EVOLUTION

Theory: Nigel Goldenfeld (UIUC Physics)

The selection for faster migration occurs at the population level. While direct measurements of single-cell swimming behaviors over the course of tens or hundreds of generations is not possible, stochastic simulations permit us to interrogate the evolutionary process at the single-cell level. We will use these simulations to study how the rate of evolution depends on mutation rate and environmental structure.