

Project 1a: Evolution of overlapping binding sites

Consider the following scenario: A gene needs to be turned on under some condition and off under different conditions. This is implemented with a binding site for an activator and an overlapping binding site for a repressor, so that either one or the other can be bound, but not both at the same time. Develop a model for the evolution of such overlapping sites.

Project 1b: Coexistence in fitness landscapes

Construct a fitness landscape in which two quasispecies coexist. Can you make the less fit quasispecies dominant in the population? You could also try to construct a concrete example with transcription factor binding sites.

Project 1c: Fixation in growing populations

Study mutations and their fixation in a growing rather than constant population.

Project 1d: Evolution of antibiotic resistance

Use the experimentally determined fitness landscape of Weinreich et al. to simulate the evolution of antibiotic resistance and to study paths of evolution in that landscape. N.B.: Here fitness is not given by the growth rate directly.

Presentation opportunity: Predicting evolution

Predicting the evolution of rapidly evolving seasonal viruses is of interest for preparing the health system for the next waves of infection. An example is the adaptation of the influenza vaccine to the predicted mixture of virus strains. Several groups have developed methods to improve that prediction based on statistics of observed sequences:

- M. Luksza, M. Lässig. A predictive fitness models for influenza. Nature 507, 57-61 (2014)
- R. Neher et al. Prediction, dynamics, and visualization of antigenic phenotypes of seasonal influenza viruses. PNAS 113, E1701-E1709 (2016)

If someone (or a group) is interested, prepare a short presentation to explain the key ideas to the class. If you are interested, let me know.