

ECL 290

Reconstructing complex population histories with gene flow

Synopsis: The rapid increase in genomic data has revealed reticulate evolution across the tree of life, even in large multicellular eukaryotes. “Hybridization” or the exchange of genetic material between distinct lineages plays a more important role in evolution than previously recognized, both facilitating and impeding the generation of novel adaptations. However, gene flow can also distort or obscure the relationships among lineages, making the reconstruction of population histories much more challenging. Advances in sequencing technology as well as computational tools and resources have enabled us to better characterize both the extent and timing of admixture events over the course of evolutionary history.

In this 2-unit course, we will use the primary literature to explore genomic approaches that enable molecular ecologists to reconstruct complex histories of divergent lineages that include gene flow. We will spend the first part reviewing the conceptual basis, strengths, and limitations of different methodological approaches (e.g. tree-based, LD-based, ancestry block-based, coalescent-based). For the second part, we will discuss the application of these methods in recently published case studies with an emphasis on connecting approaches to specific evolutionary questions that can be applied across a variety of systems. Participants will be responsible for providing a short presentation to synthesize several papers and lead a group discussion.

Dates: Thursdays January 6—March 17, 2022

Meeting time: Thursdays 1:10 –3:00 pm, Location: 1105 VM3B

Instructor: Ben Sacks

Units: 2

ECL 290 CRN: 20999

(Same course: PHR 243 CRN = 36967)