## Seminar/Talk

# Butterfly speciation - what can we learn from model based genome scans?

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Host: Nick Barton

Genome scans for outliers of divergence are generally based on one dimensional summary statistics, such as F_st or d_xy and have become a mainstay of speciation research. Such scans suffer from a number of well known limitations. Most fundamentally, they do not allow to connect sequence variation to the population level processes. Interpretations of outlier scans are verbal and ignore the large variation inherent in the coalescent. I will describe a general likelihood framework for model based scans that allows to quantify heterogeneity in effective gene flow and population size along the genome. I will illustrate the insights that can be gained from this decomposition of the genomic landscapes of speciation through an analysis of whole genome data in two European sister species of Scarce Swallowtail butterfly.

**Wednesday, December 11, 2019 12:30pm - 01:30pm**
I22 Lakeside View (I22.01)

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