Seminar/Talk

Inferring the structure of large empirical fitness landscapes

David McCandlish

Cold Spring Harbour Laboratory

Host: Nick Barton

Simple models for the relationship between genotype and phenotype can often be restated in terms of an assumption about how the effects of mutations change when they occur on different genetic backgrounds. For example, additive models correspond to the assumption that the effect of a mutation is independent of genetic background, and pairwise interaction models allow the effects of a mutation to change between genetic backgrounds but assume that the epistatic coefficient between any pair of mutations is background-independent. What constraints on the global geometry of the genotype-phenotype relationship do these assumptions impose, and what should we do when these assumptions are violated? Here I will discuss new statistical methods for predicting how the effects of mutations change across genetic backgrounds. By relaxing the assumption of strict global background-independence of mutational effects to an assumption of approximate local background-independence, we can construct models that behave similarly in many ways to these simple models but which can capture more complex and realistic global geometries for the genotype-phenotype relationship. I will illustrate these ideas with applications to pre-mRNA splicing and the evolution of karyotypic abnormalities in human cancer.

Wednesday, February 1, 2023 12:30pm - 01:30pm
Online Event ()

This invitation is valid as a ticket for the ISTA Shuttle from and to Heiligenstadt Station. Please find a schedule of the ISTA Shuttle on our webpage: https://ista.ac.at/en/campus/how-to-get-here/ The ISTA Shuttle bus is marked ISTA Shuttle (#142) and has the Institute Logo printed on the side.

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