

COMPUTATIONAL RESEARCH in BOSTON and BEYOND SEMINAR

Predicting the effect of mutations with generative models of evolutionary sequences

ADAM RIESSELMAN
Harvard University

ABSTRACT:

Modern genome sequencing and synthesis can acquire and generate tremendous molecular diversity in a day, but our ability to navigate and interpret the exponentially large space of potential biological sequences remains limited. Central to this challenge is the lack of a priori knowledge about epistasis, i.e. non-additive interactions between positions in a molecule or genome. I will describe how generative models fit to evolutionary sequences can be used to help explain these factors. I will then discuss two classes of generative models, discrete undirected graphical models and neural-network powered latent variable models, which can reveal the three dimensional structures and mutational landscapes of proteins and RNA solely from evolutionary information.

FRIDAY, MAY 4, 2018
12:00 PM – 1:00 PM
Building 32, Room 124
(STATA)

Pizza and beverages will be provided.

<http://math.mit.edu/crib/>