

# COMPUTATIONAL RESEARCH in BOSTON and BEYOND SEMINAR

## Predicting the effect of mutations with generative models of evolutionary sequences

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### 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/>