

Seminar 2017

Modeling and understanding complex sequence-function relationships



David M. McCandlish
Assistant Professor
Simons Center for Quantitative Biology
Cold Spring Harbor Laboratory

Advances in high-throughput genetics now allow the effects of thousands of mutations to be measured simultaneously. How can we understand the complex patterns of genetic interaction revealed by these assays? I will showcase several computational tools to address this problem with applications to protein stability and function, transcription factor binding sites, RNA folding, and molecular evolution.

Friday September 15, 2017

2:30 PM Laufer Center 101

Host: Tom MacCarthy

Refreshments: Hub 110 after seminar

