

# BiophysTO Lunchtime Talks

## Dr. Alan Moses

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### Stochastic models for the evolution of quantitative molecular traits

Quantitative models of sequence-specific transcription factors recognizing their DNA binding sites is a well-studied biophysics problem. Under certain biophysical assumptions, the binding of transcription factors can be predicted based on the DNA sequence. We have been extending this framework to model the evolution of transcription factor binding, by considering the binding of transcription factors to regulatory DNA as a quantitative molecular trait. We first consider a model of transcription factor binding in the absence of selection, and find that it violates the assumptions of the classical Brownian motion model used as the neutral model for quantitative traits. We show that in the absence of selection, quantitative molecular traits evolve under a (directional) mutational force, which we model using a simple Langevin equation, leading to an OU process. Using this model as the null hypothesis, we formulate a likelihood ratio test and apply it to detect selection on sequences bound by transcription factors in genomic data. Because our approach does not rely on detecting conservation in sequence alignments, it should be able to detect stabilizing selection, which is hypothesized to explain the evolution of regulatory DNA.

*Host: Dr. Anton Zilman*

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Sponsors: UTM-Chemical and Physical Sciences/VP Research/Vice-Dean Graduate  
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Thursday, October 15 – 12:00 pm, noon  
Davenport Room, Chemistry Building  
(and via streaming to Davis Building 4001 UTM)