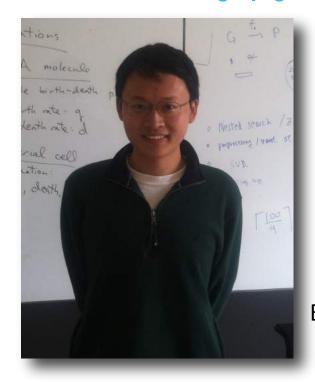




"Understanding Epigenomic Drivers of Human Diseases"



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Abstract:

New genomic technologies generate unprecedented data on the inner workings of cells. To harness this data to understand and diagnose human diseases, we need to tackle several challenges (opportunities) in machine learning.

In this talk, I will describe my research combining computational tools with high-throughput experiments to probe epigenomic regulations of cellular function. I will discuss a new method to identify changes in the epigenome across human populations that are associated with disease. We validated the method on DNA methylation experiments and applied it to rheumatoid arthritis, breast and colon cancer data to identify novel epigenetic biomarkers. In the second part of the talk, I will discuss ongoing work and new directions in contrastive learning and intelligent designs for synthetic biology.

Host: Fritz Roth