ChRO-seq: a new lens for interpreting genome sequence

I will introduce ChRO-seq, a new molecular tool to map the location of RNA polymerase, and a suite of machine learning tools designed to identify functional regions of the genome using ChRO-seq data. I will show how ChRO-seq is useful to identify causal DNA sequence variants that drive evolutionary changes in adaptive immunity in humans. Finally, I will use ChRO-seq to identify transcription factors that contribute to inter-tumor heterogeneity in cancer, using brain tumors as an example.

Dr. Charles Danko, PhD
Assistant Professor of Epigenetics
Baker Institute for Animal health

Host: Dr. Bluma Lesch, PhD
Assistant Professor
YSM Department of Genetics

Tuesday, October 22, 2019
11:30am - 12:30pm

The Anlyan Center – N107

The Genetics Calendar of Events can be viewed on-line at
https://medicine.yale.edu/genetics/events/seminars.aspx