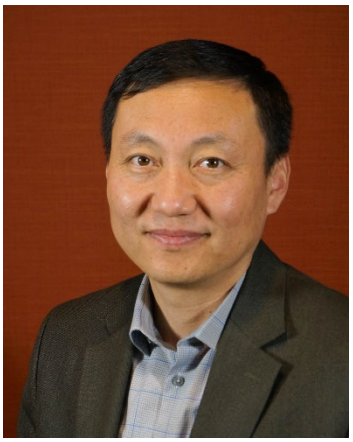
Yale SCHOOL OF MEDICINE
GENETICS DEPARTMENT SEMINAR SERIES

# Decrypting the Noncoding Genome with Single Cell Epigenomics

A large number of sequence variants have been linked to complex traits and disease through genome-wide association studies, but deciphering their biological function is still challenging because most of them reside in noncoding DNA, where functional annotation is still lacking. A growing list of studies has shown that noncoding risk variants may contribute to human disease by perturbing the transcriptional regulatory sequences. However, it is still unclear whether this mechanism generally applies to the tens of thousands of risk variants identified to date. Efforts to address this question have been hampered by a lack of tools and maps to explore the transcriptional regulatory sequences in the genome especially in complex tissues. Here, I will present our recent progress in the mapping and of transcriptional regulatory sequences in the human and mouse genomes, with the use single cell epigenomic techniques. I will also discuss the development of highly predictive models for assessing the impact of sequence variants on DNA binding of transcription factors.



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**Host: Dr. Siyuan Wang, PhD**
Assistant Professor
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## Tuesday, September 8, 2020

11:30am - 12:30pm

**via Zoom**

https://zoom.us/j/91858028355?pwd=b2VhWlB3RU5rMlpsVmlyRHB0NElPZz09
**pw: 7852649**

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