



Yale SCHOOL OF MEDICINE

GENETICS DEPARTMENT SEMINAR SERIES

Decrypting the Noncoding Genome

Unmasking the Role of Gene Regulation in Complex Traits and Disease

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 an incomplete understanding of the transcriptional regulatory sequences in the genome. Here, I will present our recent progress in the mapping and functional characterization of transcriptional regulatory sequences in the human and mouse genomes. I will discuss the development of highly predictive models for assessing the impact of sequence variants on DNA binding of transcription factors. I will also describe how mapping the long-range chromatin interactions allows us to infer the target genes of noncoding risk variants in Alzheimer's disease and other common diseases.



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Host: Dr. Siyuan Wang, PhD

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Tuesday, March 3, 2020

11:30am - 12:30pm

The Anlyan Center – N107