BRIGHAM AND WOMEN'S HOSPITAL
HARVARD MEDICAL SCHOOL

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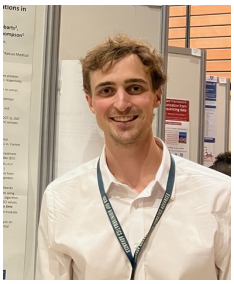
Department of Medicine
Channing Division of Network Medicine

Channing Methods Seminar

February 6 (Tuesday), 2024, 11AM (ET)

Remote seminar
https://us02web.zoom.us/j/579497999?pwd=cHNlWHMzWUlFUUVJTG1EeVJmY05aQT09
Meeting ID: 579 497 999
Passcode: 844168



Samuel Boyd
University of Kansas Medical Center

Multi-omic and network analyses after O-GlcNAc alteration identifies cellular processes which promote liver aneuploidy

Abstract: O-GlcNAc is a ubiquitous post-translational modification which affects intracellular proteins through two enzymes: OGT, which adds the molecule to a target protein; and OGA, which removes the modification. The fundamental challenge in understanding O-GlcNAcylation is that pharmacologic or genetic manipulation of O-GlcNAc leads to pleiotropic effects, impairing data interpretation. To address these challenges, we integrated multi-omic data –transcriptomic, proteomic, phospho-proteomic, and metabolomic– with molecular interaction networks. These integrated networks were analyzed using network diffusion algorithms to determine modules that were highly affected by O-GlcNAc perturbations. Through dry- and wet-lab approaches, we identified several pathways under direct control of O-GlcNAcylation that synergistically regulate cellular aneuploidy.

Bio: Sam Boyd is a PhD candidate in the Department of Biostatistics & Data Science at The University of Kansas Medical Center. His thesis centers on multimodal data integration using biological networks and algorithmic developments for optimal subnetwork identification. Sam strives to improve network models to be able to better reflect the complexity of real biological systems. He looks forward to defending his dissertation in April and to the next step in his professional journey.

Hosted by Arda Halu