



## Channing Methods Meeting

September 12 (Tuesday), 2023, 11AM (ET)

MCP 5<sup>th</sup>-floor large conference room

<https://us02web.zoom.us/j/579497999?pwd=cHNIWHMzWUJFUUVJTG1EeVJmY05aQT09>

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## Utility of recall-by-genotype approach for causal inference of drug target side-effects

Genetic variants associated with drug targets have been used as proxies to evaluate the potential side effects using Mendelian Randomisation (MR) approaches. However, a significant constraint in this approach is the necessity for large sample sizes to establish robust genetic proxies for both the drug targets and datasets containing the side effects to be evaluated. On the other hand, multi-omic datasets provide a wealth of information, enabling the simultaneous exploration of multiple potential side effects linked to drug targets. Nevertheless, these datasets often originate from relatively small sample sizes, rendering them less amenable to conventional MR analyses. In this presentation, I will focus on an innovative alternative approach called "recall-by-genotype." This approach offers a promising avenue for assessing potential side effects of drug targets using multi-omic data. By evaluating the utility of recall-by-genotype in this context, I aim to surmount the limitations associated with traditional MR and gain valuable insights into the diverse side effects of drug targets.

*Bio: Dr. Tinashe Chikowore is an Investigator within the Channing Division of Network Medicine and the Genetics Division at Brigham and Women's Hospital, as well as an Instructor of Medicine at Harvard Medical School. His research is centered on harnessing genetics, Omics technologies, and machine learning to delve into nutrition outcomes and complex diseases. Dr. Chikowore has earned recognition as a recipient of the esteemed Wellcome Trust International Training fellowship and the Charles Epstein Excellence in Human Genetics Award from the American Society of Human Genetics. He currently oversees the management of the Cardiovascular H3Africa Innovation Resource (CHAIR), which stands as the largest genomic resource dedicated to cardiovascular-related phenotypes in Africa.*

Hosted by Yang-Yu Liu