

## Integrative Methods and Practical Challenges for Single-cell Multi-omics



**Abstract:** Fast-developing single-cell multi-omic technologies enable the measurement of multiple modalities, such as DNA methylation, chromatin accessibility, RNA expression, protein abundance, gene perturbation, and spatial information, from the same cell. Single-cell multi-omics provides a more comprehensive exploration and identification of cell characteristics, while also presenting challenges in developing computational methods and tools for integrative analyses. In this review, we provide an overview of the integrative methods and summarize the existing tools that developed to target the integrative study for a variety of single-cell multi-omic data. The various functionalities and practical challenges in using the available tools in the public domain are explored through several case studies. Finally, we identify remaining challenges and future trends in single-cell multi-omics modeling and analyses.

**About the Speaker:** With a Ph.D. degree in computational science and 12 years' research experience in bioinformatics, I view myself as a well-trained bioinformatics researcher and computational modeler of biological systems. Through independent investigation and collaborative studies with numerous biologists, I have developed a strong and long-term interest in (1) understanding of how functional machinery encoded in a genome/metagenome; (2) elucidation of the metabolic systems and their regulatory mechanisms in a cell; and (3) development of enabling computational techniques in support of the above scientific studies. My technical strength is in big-data mining & modeling with the advent of high-throughput Omics technologies. During the past few years, I have gained substantial experience in developing and applying advanced software techniques / web databases in carrying out my own bioinformatics research, with an emphasis in single-cell RNA-Seq and ChIP-Seq data modeling and analyses. As of now, I have received research grants from the NIH, NSF, and OSU as an independent investigator (PI) or a co-PI. I have published 95 research papers in leading bioinformatics journals such as Nucleic Acids Research, Bioinformatics, PLoS Computational Biology, and Briefings in Bioinformatics.

**Qin Ma, PhD**

**Friday, February 21<sup>st</sup>, 11:00am-12:00pm**

**105 BRT**