Abstract:
New technologies allow us to understand many biological processes at the molecular level but require principled machine learning methods to capture the underlying dynamics of the cell populations. In this talk, I present two projects. In the first project, we design a dynamic graphical model to jointly analyze different types of genomic aberrations from multi-location/multi-time biopsies of metastatic breast cancer. The model allows us to accurately characterize genomic aberrations and understand oncogenic processes from next-generation sequencing data at a significantly larger scale. In the second project, we propose a dimensionality reduction approach to recover intrinsic biological structure from single cell Hi-C contact maps. With mouse ES cells, our dimensionality reduction approach successfully recovers the intrinsic cell-cycle manifold, and shows its robustness in terms of the number of contacts.

Bio:
Dr. Jie Liu received his Ph.D. in computer science from the University of Wisconsin-Madison. He is currently a Moore/Sloan Data Science Postdoctoral Fellow in the Genome Sciences Department and eScience Institute at the University of Washington. His research interests are machine learning and its applications in biomedical informatics.