

Speaker: Stephanie Hicks, Johns Hopkins

Date: Wednesday, February 23, 2022

Time: 11:30 AM to 1:00 PM

Host: Bonnie Berger

Title: Scalable statistical methods and software for single-cell data science

Abstract: Single-cell RNA-Seq (scRNA-seq) is the most widely used high-throughput technology to measure genome-wide gene expression at the single-cell level. However, single-cell data present unique challenges that have required the development of specialized methods and software infrastructure to successfully derive biological insights. Compared to bulk RNA-seq, there is an increased scale of the number of observations (or cells) that are measured and there is increased sparsity of the data, or fraction of observed zeros. Furthermore, as single-cell technologies mature, the increasing complexity and volume of data require fundamental changes in data access, management, and infrastructure alongside specialized methods to facilitate scalable analyses. I will discuss some challenges in the analysis of scRNA-seq data and present some solutions that we have made towards addressing these challenges.