Gene network reconstruction using single cell transcriptomic data reveals key factors for autophagic process

Kyoung Jae Won(kyoung.won@bric.ku.dk)
U of Copenhagen

Abstract

Single-cell RNA sequencing (scRNA-seq) is a powerful tool to study heterogeneity and dynamic changes in cell populations. Data explosion fueled by technological development requires more efficient approach to process scRNA-seq data. Current algorithms for scRNA-seq data lack scalability, which can lead to exponential increase in processing time. To processes large-scale scRNA-seq data we propose a new approach called SHARP by applying ensemble random projection (RP). RP reduces the dimensionality of data by trading a controlled amount of error for faster processing time. RP approximately preserves cell-to-cell distances while achieving a substantial cost reduction for computing, a desired property in handling large-scale scRNAseq data. Ensembled average enhances modeling cell-to-cell distance by compensating errors of individual RP results. Applying SHARP to clustering using various scRNAseq datasets including 43,745 cells from murine kidneys, we found SHARP runs at least 40 times faster than previous algorithms while maintaining a better clustering performance.

Keywords: *SHARP: Single-Cell RNA-Seq Hyper-Fast and Accurate Processing via Ensemble Random Projection*

Biography

2005 Ph.D. in Electronics and Computer Science, University of Southampton, Southampton, UK
2006 - 2006 Postdoctoral Fellow, University of Copenhagen, Denmark
2007 – 2010 Postdoctoral Fellow, University of California, San Diego, Department of Chemistry & Biochemistry
2011 – 2018 Research Assistant Professor, University of Pennsylvania, Department of Genetics, School of Medicine
2018 - Associate Professor, University of Copenhagen, Denmark, BRIC