Resource Sharing Plan:

Software

The proposed project will develop statistical and computational approaches to be made available for broader use as open source R software packages. These packages will be made freely downloadable through publically accessible online repositories such as GitHub and BioConductor thereby enabling other groups to apply these methods to other single-cell studies. Mailing lists, issue reporting, wiki documentation, and other infrastructure will be set up to connect and assist researchers applying these methods in their investigations.

My advisor, Dr. Peter Kharchenko and I, have excellent track records in delivering computational tools to the scientific community, including software for inferring spatial localization of gene sets (Fan *et al*, manuscript in review), pathway and gene set overdispersion analysis (Fan *et al*, manuscript in review), single-cell differential expression analysis (Kharchenko *et al,* Nature Methods 2014), analysis of ChIP-seq data (Kharchenko *et al,* Nature Biotechnol. 2008), analysis of repetitive elements (Day *et al,* Genome Biol. 2010), and identification of transposable element insertions (Lee E *et al,* Science 2012).

Publications

All results generated in this project will be published in peer-reviewed journals and will be made available to the scientific community. In such publications, as well as in related presentations or press releases, we will fully acknowledge the support provided by NIH in conducting this work.