

Respective Contributions:

Project proposal:

I entered the lab of Dr. Peter Kharchenko with a great interest on applying computational approaches to analyze single cell data. Dr. Kharchenko, along with my collaborators in Dr. Catherine Wu's lab, have proposed several different research directions for me that were based on training potential, interest, importance to the field, and feasibility for completion during my time in graduate school. After careful reading and assessment of available datasets and resources, I chose to design and pursue a research plan to develop statistical methods and computational tools to study subclonal evolution in chronic lymphocytic leukemia, which is the topic of this research proposal.

Dr. Kharchenko has been a very supportive and attentive mentor who has provided me with extensive training and expertise in statistical analysis, method benchmarking, method validation, software development, software documentation, computational parallelization, and various programming languages such as R and C++. He encouraged me to write this proposal. I completed background research and preliminary analyses with input from Dr. Kharchenko and Dr. Wu. I designed the structure and aims of this proposal. I also wrote this research proposal and designed all figures.

Additionally, Dr. George Church, Dr. Lili Wang, and Dr. Nils Gehlenborg provided comments and feedback on this proposal.

I am submitting this research proposal with Dr. Kharchenko, Dr. Church, and Dr. Wu's review and approval.

Data Sources:

Through collaboration with Dr. Catherine Wu's group at the Dana-Farber Cancer Research Institute, we were able to obtain the single cell RNA-seq and previous bulk whole exome-seq datasets that will be used in this project. I have met with Dr. Wu to discuss the datasets and will be able to contact her in the future if specific questions about these data arise while carrying out the proposed project.