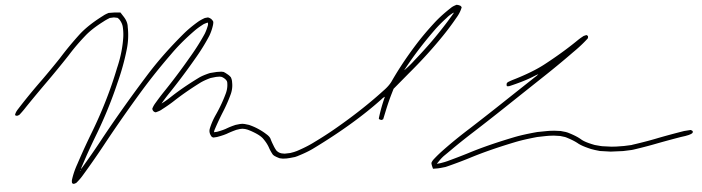
November 13, 2018

Dear Loyal,

I am delighted to be joining the team of co-PIs including yourself, Drs. Hicks, Fertig, Greene, Hampton, and Patro, proposing to work on statistical and algorithmic method development and software implementations for single-cell datasets generated by the HCA. I pledge to commit 10% effort and supervise the full time graduate research of a Biostatistics PhD student from UNC-Chapel Hill in working on this project.

As you know, I am an Assistant Professor of Biostatistics and Genetics at UNC-Chapel Hill, and am a leading developer of statistical software for RNA-seq analysis in the Bioconductor Project, including the DESeq2, apeglm, tximport, and tximeta packages. I have collaborated with Dr. Rob Patro on bias-aware estimation of transcript abundance from RNA-seq in the Salmon and Sailfish software and estimation of uncertainty during transcript quantification since 2015. We are currently developing a number of software projects in parallel, including tximeta and a set of modular packages for the propagation of uncertainty from quantification for bulk RNA-seq to downstream statistical inference and visualization methods. I am also well versed in the statistical methods and papers by Dr. Hicks on the topic of single-cell RNA-seq, some of which were developed while we were both postdoctoral fellows in the same lab of Dr. Rafael Irizarry at Dana-Farber Cancer Institute, and the high dimensional matrix factorization approaches of Dr. Fertig, which we have discussed in depth at a recent Bioconductor conference in Toronto. I am therefore well positioned to collaborate on the statistical and software goals in this proposal, and look forward to collaborating with you, Drs. Greene and Hampton as well. I am excited to work with the co-PIs on this proposal to disseminate versioned reference cell type catalogs through widely used frameworks for genomic data analysis including R/Bioconductor and Python.

Sincerely,



Michael Love

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