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Dr. Loyal Goff  
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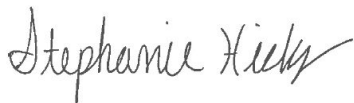
Dear Loyal,

I am writing to express my strong commitment in our continued collaboration for the *Chan Zuckerberg Initiative Seed Networks for the Human Cell Atlas*. Computational methods for the analysis of genomic data at the single-cell level is a major research focus in public health, in particular, in my department at the Johns Hopkins Bloomberg School of Public Health. Research stemming from your lab on finding latent space representations from high-dimensional single-cell genomics data, makes this pioneering and innovative proposed work extremely enticing to be a part of. The unique aspect of our approach is that we will not only develop fast search algorithms to search and to quantify differences between reference transcriptome maps (the Human Cell Atlas) and non-reference transcriptome maps in latent spaces, but we also will provide reference cell type catalogs for downstream users. Furthermore, we propose scalable software and training for the next generation of single cell data scientists to make the Human Cell Atlas and the computational methods stemming from this proposal accessible and easy to use.

To develop these computational methods in latent spaces, I am committed to working with our team at 15% effort to implement fast search algorithms in latent spaces (Aim 1) and to implement the methods developed into fast, scalable, and memory-efficient R/Bioconductor software packages (Aim 3). As you know, my research developing methods to remove systematic and technical biases from single-cell RNA-sequencing data has resulted in an NIH K99/R00 Pathway to Independence Award. In addition, I actively develop Bioconductor software, the pre-eminent resource of computational tools for integrative statistical analyses including single-cell analyses, using the R programming language. This work has resulted in an award from a separate *Chan Zuckerberg Institute Request For Applications* related to providing an interface between the Human Cell Atlas and Bioconductor. I am confident our team is well suited to complete the proposed work.

I am hereby stating my enthusiastic support and commitment to this project. I believe this will be a huge win for Human Cell Atlas community, not only in terms of the short-term resources generated, but also in the long-term knowledge derived from this work.

Sincerely,



Stephanie Hicks  
Assistant Professor of Biostatistics  
Johns Hopkins Bloomberg School of Public Health