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Hello Sir/Ma'am,

I am writing this letter with great enthusiasm as I am interested in the Computational or Bioinformatics Research/Staff Scientist position in your group. I have a broad background in computational and quantitative biology with specific training and expertise in genomics, chromatin biology and machine learning. I am currently completing my postdoctoral studies with **Prof. Martin Aryee and Prof. Alexander Meissner**, where my focus is to understand the dynamics of gene regulation using single-cell genomics.

My long-term research interests are understanding the dynamics of gene regulation and how alterations in gene expression contribute to different diseases using high throughput sequencing datasets, including RNA-seq (bulk and single-cell), ChIP-seq, ATAC-seq (bulk and single-cell) and CRISPR based assays (CRISPRi, CRISPRa and dual assays), long read sequencing data and integration of these datasets. In addition, I develop tools & approaches for genomic data analysis and apply machine learning algorithms to understand inter and intra-sample variations in the datasets. My academic training and research experience have given me an excellent background in multiple disciplines, including computational biology, molecular biology, and genetics. I have extensive experience generating and testing hypotheses by modeling publicly available datasets, including TCGA, CCLE, GTex, Gene Expression Omnibus and DepMap.

Following my master's studies in Computational Biology at the Carnegie Mellon University, Pittsburgh PA, I pursued my interest in computational biology and began my research focusing on two major themes for my doctoral thesis under the mentorship of **Prof. Zhandong Liu, Prof. Huda Zoghbi and Prof. Kunal Rai** at Baylor College of Medicine and MD Anderson Cancer Center, Houston, Texas. First, I used **integrative genomics and systems biology methods to analyze large-scale multi-omics sequencing data**. These approaches were applied to identify novel gene regulatory networks (Litvak et al. 2012, Pohodich et al. 2018, Kochat*, Raman* et al. 2021), novel epigenomic enhancer subtypes in colorectal cancer (Orouji*, Raman*, Singh* et al. 2021) and decode the role of TRIM28/KRAB repressors modulating heterochromatin and CpG methylation in pluripotent stem cells (Oleksiewicz*, Gładych *, Raman* et al. 2017). Second, I have **contributed to developing statistical methods/approaches in identifying the latent variables**, also known as batch effects (Yi*, Raman* et al. 2018) and sources of spurious results such as failure to measure baseline variability in RNA-seq datasets (Raman*, Pohodich* et al. 2018, Raman et al. 2021). For my postdoctoral training, I continue to build on my previous training in transcriptional regulation by moving into multi-omic single-cell assays (Gu*, Raman* et al. 2021; Shareef et al. 2021) and further understand the role of DNA methylation in the development

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and diseases.

I have strong written and verbal communication skills and have collaborated with scientists and non-scientists of diverse backgrounds. In addition, I am a strong team player, which is evident through various academic projects I have worked on and successfully published. I have attached my two-page resume, academic curriculum vitae and anticipate an opportunity to meet and discuss the position.

Sincerely,
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* denotes for co-first authorship or authors contributed equally to the manuscript.