Research Introduction

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Introduction

We are looking to model the extremely abundant and diverse T cell receptor-beta repertoire through a DNA recombination algorithm. Research in the past has discovered a link between T cell repertoire diversity and immunity to infection. It has been shown that diversity in TCRs(T cell receptors) within the T cell repertoire is significant in creating enhanced immunity to pathogens.[1] Creating such a diverse repertoire of TCRs stems from the process known as V(D)J Recombination, which is shown to have profound effects on the immune response as linked to the diversity of TCRs. Sub-optimal recombination activity has been revealed to cause partial immune defects.[2] My research builds on the already created parallel computing process that utilizes multiple GPUs to more efficiently and effectively run the V(D)J Recombination algorithm and model the diverse TCR repertoire. I will attempt to correlate the most frequently generated recombination pathways that occur during V(D)J recombination to the appearance of the final sequences. By identifying such correlations, we can point to specific pathways that are frequently used and investigate further into their importance in the immune response. This research can enable immunologists to identify gene sequences that play an important role in diseases such as cancer.

References

[1] S. Turner, N. Gruta, K. Kedzierska, P. Thomas, and P. Doherty, "Functional Implications of T Cell Receptor Diversity," Current Opinion Immunology, vol. 21, no. 3, pp. 286-290, 2009.

[2] A. Berland, J. Rosain, S. Kaltenbach et al., "PROMIDISα: A T-cell receptor α signature associated with immunodeficiencies caused by V(D)J recombination defects," J Allergy Clin Immunol, vol. 143, no. 1, pp. 325-334, 2019