Overcoming the Limitations Posed by TCRβ Repertoire Modeling through In-Silico DNA Recombination Algorithm

Sreevatsa Nukala
The University of Arizona
snukala@email.arizona.edu

CONTENTS

I. 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 the 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 significance for the immune response. I will also create visualization tools to make correlation studies easier for the domain experts. I will extend the scalability analysis for the multi-GPU implementation and conduct execution time analysis with respect to number of GPUs ranging from 1 to 16. This research can enable immunologists to rapidly visualize and identify gene sequences that play an important role in immune response against diseases such as cancer.

REFERENCES

[1] S. J. Turner, N. L. L. Gruta], K. Kedzierska, P. G. Thomas, and P. C. Doherty, "Functional implications of t cell receptor diversity," *Current Opinion in Immunology*, vol. 21, no. 3, pp. 286 – 290, 2009, lymphocyte activation and effector functions / Vaccines. [Online]. Available: http://www.sciencedirect.com/science/article/pii/S095279150900082X

[2] A. Berland, J. Rosain, S. Kaltenbach, V. Allain, N. Mahlaoui, I. Melki, A. Fievet, C. Dubois d'Enghien, M. Ouachée-Chardin, L. Perrin, N. Auger, F. E. Cipe, A. Finocchi, F. Dogu, F. Suarez, D. Moshous, T. Leblanc, A. Belot, C. Fieschi, D. Boutboul, M. Malphettes, L. Galicier, E. Oksenhendler, S. Blanche, A. Fischer, P. Revy, D. Stoppa-Lyonnet, C. Picard, and J.-P. de Villartay, "Promidisα: A t-cell receptor α signature associated with immunodeficiencies caused by v(d)j recombination defects," *Journal of Allergy and Clinical Immunology*, vol. 143, no. 1, pp. 325–334.e2, Jan 2019. [Online]. Available: https://doi.org/10.1016/j.jaci.2018.05.028