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Model for TCR Analysis and its Application to TCR-Epitope Binding Prediction and TCR Clustering

T cell receptors (TCRs) play an important role in the adaptive immune system. The ability to accurately predict or characterize binding interactions between TCRs and target antigens, partly because of the vast diversity of TCRs and epitopes, is challenging. While there has been progress in the development of computational models dedicated to this, the question of how to specifically embed TCR sequences into numeric representations remains largely unexplored compared to protein sequences in general.

Researchers at Arizona State University developed a novel bidirectional amino acid embedding model designed explicitly for T cell receptor (TCR) amino acid sequences. This model is able to learn patterns of amino acid sequences and predict the next amino acid in a sequence. It is also able to complete TCR-related downstream tasks such as discriminating binding and non-binding TCR epitope pairs and clustering TCR sequences. It shows a significant amount of prediction improvement compared to current state of the art models, and reduces sample annotation cost.

This model will reduce the cost and time needed to narrow down a set of candidate TCR targets, thereby accelerating the development of personalized immunotherapy for vaccine development and cancer treatment.

Potential Applications

- Personalized immunotherapy
- Vaccine development
- Cancer therapeutics development

Benefits and Advantages

- Outperforms existing models for TCR-epitope binding prediction
- This model is “context aware” – it is able to predict the next amino acid in a sequence based on previously read sequences
- This model is trained without any explicit supervision, but interprets TCR sequences better
- Negates the need for complex deep neural network architectures
- Reduces annotation costs
- Able to complete TCR-related downstream tasks such as discriminating binding and non-binding TCR epitope pairs and clustering TCR sequences

For more information about this opportunity, please see

Zhang et al - eLife - 2023

For more information about the inventor(s) and their research, please see

Dr. Lee's departmental webpage