Utilizing Graph-Guided Deep Neural Networks to Predict TCR – Antigen Binding Affinity

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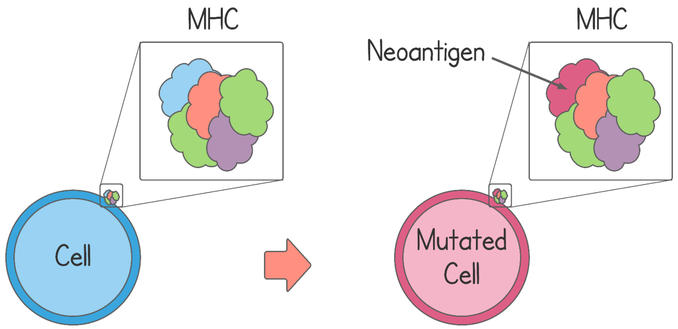
Question: Can we predict the binding affinity of a T cell receptor and antigen accurately?

Biological Background

- T cells investigate the major histocompatibility complex MHC of cells to find pathogens in the body.
- Cancer cells produce neoantigens which bind to their MHC for T cells to investigate
- A binding between an epitope on the antigen and the TCR starts an immune response in the body.
- However, cancer can evade immunosurveillance.



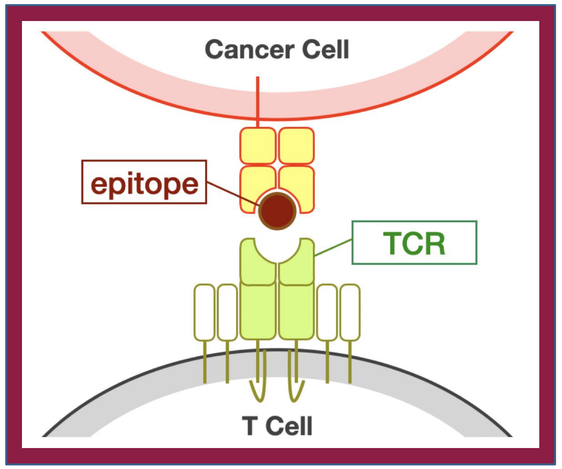
Mutations create neoantigens on a cell's MHC

Motivation

- Immunotherapy helps the immune system recognize tumors as pathogens to eliminate
- Treatments requires finding the T cell receptors (TCR) that will bind to tumor antigens.
- This can be time consuming and difficult
- A computational solution for predicting binding affinity can save time designing treatments

Convolutional Neural Networks

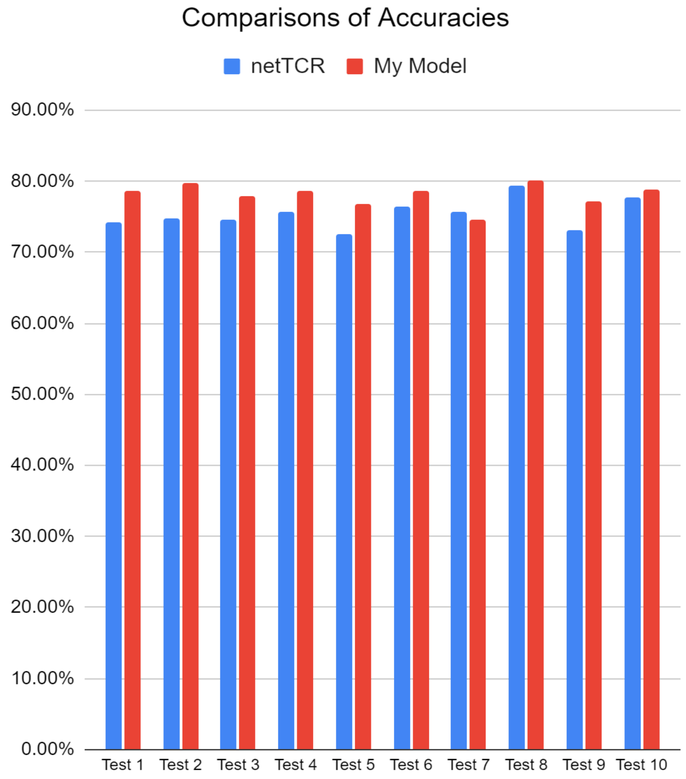
- Make use of the convolution, which can prevent overfitting and share information in the network.
- Can be used to make predictions outside of the training data, allowing us to find novel bindings.



Binding between a cancer cell and a T cell

Our Approach

- Use the amino acid sequence from the TCR and epitope as inputs to our computational model.
- Generate a large amount of negative input data utilizing mismatching from positive data
- Utilize a convolutional neural network to find a binding probability between a TCR and epitope



Proposed model accuracy vs netTCR

Current Results

- A paired t-test on our model's accuracy and netTCR's - a similar computational model - shows our model offers a statistically significant improvement in accuracy.
- We have performed downstream analysis on the physiochemical properties of the TCRs in hopes of improving accuracy in further research.

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