# N.O.P.E.

# Neural net Optimized for Predicting Epitopes

Louise Huuki and Adam Karami

Antibodies are proteins that allow the immune system to recognize foreign proteins, known as antigens, within the body. The tip of an antibody is variable and functions like a key, only able to bind to a certain region of an antigen known as the epitope. As both regions are highly variable, finding antibody-antigen matches is currently in an expensive wet lab experiment. The ability to predict which region of a protein is likely to act as epitope to any antibody could narrow down the number of possible pairings and be very beneficial to an antibody research workflow. Predicting epitope location may also help with determination of what functions of the target may be inhibited by antibody binding.

To aid in this prediction we developed a neural net to annotate each amino acid with the likelihood that it is epitope. The input in the neural net is a representation of the structure of the protein around a single amino acid, the other amino acids and empty space. We considered biological knowledge when defining the radius around an amino acid and representing amino acids in a numerically. The data used to train the algorithm was around 500 predicted protein structures, broken down in to amino acids, and corresponding epitope annotation gathered from experimentation.

Results?