Neural Networks for Antibody Design

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Antibodies are key components of the immune system, playing a crucial role in targeting harmful foreign agents. Currently, efforts are underway to develop antibodies for treating diseases, including amyloid-β (Alzheimer's disease), influenza, HIV, and SARS-CoV-2. A fundamental characteristic of antibodies is their binding strength to specific targets, which is the result of intricate physicochemical and structural determinants. However, our limited understanding of such determinants hinders our ability to rationally design optimised antibodies for research and therapeutic purposes. Computational methods can serve as a valuable tool to predict antibody binding strength in tandem with experimental assays, thereby refining design strategies and leading to time and resource savings.

My PhD project consists of the development of ANTIPASTI, a Neural Network that predicts antibody binding strength from experimental measurements of their atomic coordinates and types. ANTIPASTI takes into account structural, energetic and global correlational relationships, and thus achieves state-of-the-art predictive accuracy on published experimental data. Furthermore, ANTIPASTI is interpretable, since the model can be used to find the antibody regions that are most relevant for binding strength, revealing that both structural contacts and long-range correlations play an important role in its determination.

ANTIPASTI's ability to extract meaningful information from structural data holds promise for advancing our understanding of the structural and physicochemical determinants of antibody behaviour. Its impact spans antibody engineering and therapeutic development, making it relevant to a broad audience of computational biologists, structural biologists, immunologists, bioengineers, and clinicians.