

An Improved Second-Generation Pipeline for IgOme Profiling

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Production of antibodies by B-cells is an essential component of the immune response in humans. Profiling the antibody repertoire for various biological conditions provides a powerful means for biomedical applications, including diagnostics and vaccine development. The combination of random peptide phage display libraries with high-throughput sequencing (Deep Panning) has been previously proven to be effective for characterizing monoclonal antibodies.

I present a modified version of the currently available pipeline for analysis of Deep Panning data. The modifications improve performance, reproducibility, and utility compared to the originally developed pipeline. The modified pipeline is validated using the original mAb Deep Panning experiment from the published paper. Based on the original study, I highlight the importance of the read parsing step in computational analysis of Deep Panning data. Effects of the read parsing on the following inference from Deep Panning data are considered.