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Inference of selection in the adaptive immune system YUVAL ELHANATI, CURTIS CALLAN, Joseph Henry Laboratories, Princeton University, Princeton, THIERRY MORA, Laboratoire de physique statistique, CNRS and Ecole normale superieure, Paris, France, ALEXANDRA WALCZAK, Laboratoire de physique theorique,, CNRS and Ecole normale superieure, Paris, France — The adaptive immune system can recognize many threats by maintaining a large diversity of immune cells with different membrane receptors. This receptor diversity is based on initial random sequence generation, using a recombination mechanism, followed by functional selection stages via interactions with self and foreign peptides. These selection processes shape the initially random receptor ensemble into a functional repertoire that can bind many foreign pathogens. We analyzed high throughput data of human receptor sequences to infer the selection pressures on particular elements of the receptors using maximum likelihood methods. We can quantify the global and site-specific selection pressures and disentangle selection on amino acids from biases in the generated repertoire. We find correlations between generation and initial selection of receptors, and a significant reduction of diversity during selection, suggesting natural evolution of the generating mechanisms.

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