Week 2

The B cell receptor (BCR) repertoire is highly diverse. This diversity is made essentially by somatic recombination of immunoglobulin genes and also by somatic hypermutation.

The lymphocyte repertoire of B and T cells is shaped throughout the life of an individual, as a response to environmental and pathogenic antigen. Therefore, the immune receptor clonal diversity and distribution can serve as a fingerprint of an individual's current immunological status can also be exploited for immunodiagnostic applications.

While immune repertoire sequencing datasets have increased from 10^3 to 10^6 sequencing reads per sample, it has still remained a challenge to extract specific fingerprints of entire repertoires. This is due to both biological and technological reasons, which make immune repertoire data are almost unique across individuals.

This challenge made scientists consider the use of sequence-independent quantifiers of clonal diversity. These diversity indices offer the possibility to correlate immune repertoire diversity to immunological status and allow comparisons across individuals.

The premise that immune repertoires accurately reflect immunological status serves as the basis for this, which means that maybe in the future it will enable early detection and diagnosis of disease/infection and provide more quantitative vaccine profiling and more other applications.

The main questions here are:

To what extent do diversity indices capture the immunological information in immune repertoire sequencing data?

How can diversity indices be used to quantitatively define and reveal immunological status?

What is are the proper tools/Pipelines at the moment that allows such studies and gives the best analysis? And what are the criteria to choose an appropriate one over another?

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There is an enormous diversity of B-cell receptors (BCRs, antibodies) and T-cell receptors (TCRs), theoretically approaching 10^13 and 10^18 protein sequences, respectively.

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