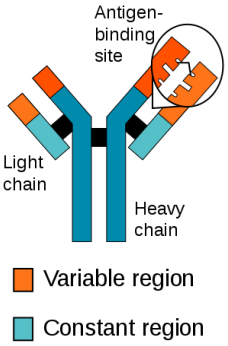
Week 1 report

After this week's readings, I was asked to write a reflection note answering some questions. Some of the answers were easy to find within the pages I have read and some I had to 'google'.

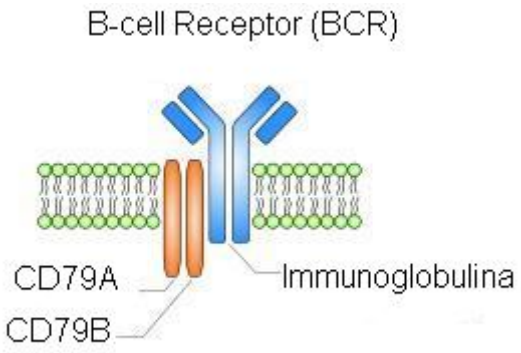
First, we start with **Protein Structure**: It is basically the amino acid composition of the protein chains and the 3D conformation of their Atoms. There are many levels of this:

1. The primary structure is just the sequence of the amino acids, they are bound by Peptide Bounds.
2. The Secondary structure is the folding of the primary chains into 2 types of regular structures that are alpha-helixes and Beta-sheets. These structures are held together by Hydrogen Bounds.
3. The tertiary structure represents the 3D form of the protein molecule, the secondary structures fold and form a globular structure. This is driven by many interactions including ionic bonding, hydrogen bonding, disulfide bonds, and hydrophobic interactions.
4. Quaternary structure is the aggregation of 2 or more subunits. This structure is held by non-covalent interactions.

Second **IgG structure**: The IgG immunoglobulin molecule consists of four polypeptide chains, composed of two identical γ heavy (H) chains and two identical κ or λ light (L) chains. Each IgG has 2 antigen-binding sites. Also, we recognize 2 different regions in the IgG: The constant region and the Variable region (which responsible for Antigen recognition).



BCR: The B cell receptor (BCR) is a transmembrane protein on the surface of a B cell. It has the same structure as the immunoglobulin (antibody). The BCR transmits activatory signals into the B cell following its recognition of its specific antigen.



Pre-B cells which come after ProB cells (synthesis of an intracytoplasmic μ heavy chain) plays a critical role in the allelic exclusion by inducing a decrease in the expression of the RAG genes which stops the recombination of the heavy chain genes and then the RAG genes are re-expressed to carry out the VJ rearrangements of the light chain genes.

Receptor editing is a process that occurs during the maturation of B cells, at the stage of immature B cells (right after pre B cells). During maturation in the bone marrow, B cells are tested for interaction with self-antigens, which is called negative selection. They can avoid apoptosis by modifying the sequence of light chain V and J genes so that it has a different specificity and may not recognize self-antigens anymore.

B cell repertoire: all the specificities of B lymphocytes at a given moment in an individual's life. The B lymphocyte repertoire of an individual comprises several million B lymphocytes distinguished by the specificity of their immunoglobulin. The generation of these millions of different immunoglobulins cannot be explained by the general rules of conventional genetics as the human genome has only 30,000 genes. Therefore it is very interesting to look at the strategy behind the generation of these repertoires and also to study its diversity on an individual and a population level to help us understand our immune system and our “immune history” in order to predict our responses to different diseases, viruses, vaccines, ...etc.

A clone is (in this context) is a group of identical B cells that all react to the same antigen.

Species richness is a measure of the total number of species in a community. However, complete inventories of all species present at a certain location is an almost unattainable goal in practical applications.

Shannon-Wiener diversity index: It assumes that individuals are randomly sampled from a very large community and that all species are represented in the sample. It is used by ecologists

when a system contains too many individuals for each to be identified and examined. A small sample is used; the index is the ratio of the number of species to their importance values within a trophic level or community.

Simpson's index expresses the probability that any two individuals drawn at random from an infinitely large community belong to the same species. This index is used for large sampled communities.

The Gini index measures the inequality among values of a frequency distribution. A Gini coefficient of zero expresses perfect equality, where all values are the same. A Gini coefficient of one (or 100%) expresses maximal inequality among values.

Chao1 is a method for estimating the number of species in a community. The Chao richness estimator was developed by Anne Chao and is based on the concept that rare species infer the most information about the number of missing species. Because the Chao richness estimator gives more weight to the low abundance species

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I could not get my head around the Berger Parker index and the Inverse Simpson index. Also I would need more explanation to understand all these indices and their importance in our project's context.
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