**Week 1 LCQB**

During this first week, I got to discover the analysis part of our research project. Thanks to the reading of a few articles, I understood the necessity of lineage tree to describe efficiently the BCR diversity, and I am starting to understand how to grow such trees aswell. The main difficulty of this analysis is that, in contrast with usual phylogenetic tree, our observations aren’t limited to the tree’s leaves. Some DNA sequence characterize internal nodes of the tree, therefore we can not always use the existing tools to build our trees. The first part of my work here is to understand how we could simplify complex lineage trees, in order to be read more easily by clinicians. I’ve been given an article to read, which gave me the keys to understanding what is at stake in the reduction of the size of a tree. I understood quite quickly that the few existing algorithms would, at best, have to be adapted to our case. Indeed they are not able to take into account the fact that we are observing internal nodes. The next steps of our work would be to design an algorithm which could simplify our trees, and to find at least one metric that could mesure if the resulting tree is close enough to the initial one, to be sure we do not skew the results read by the clinicians.