**Week 2 LCQB**

This week, I started to design algorithms, that are supposed to simplify the lineage trees given by clonalTree, to help biologists to understand them. The challenge here is to erase some nodes that aren’t valuable to understand the diversity of the BCR lineage, without altering the global structure of the tree. For the first step of this size reduction, I’ve chosen to delete nodes that were not very abundant and that had no children. This is supposed to reduce the « comb effect », which makes trees hard to be read. In case this reduction is not enough, or if it does not gives satisfying results, it can be completed or replaced by an algorithm based on the treemer method, which would delete the sequences that are the closest in terms of distance.

The first step algorithm is already giving results, which are to be analysed in order to determine if they are relevant to the initial problem. Therefore, I aim to analyse these results this week. To do so, I need to find a metric that allows me to know if a tree is similar to another one. This has to be my top one priority. If I find one, I’d be able to evaluate my algorithms and improve them. I’m kind of blind without it, since the visual aspect of the tree is not enough to evaluate if the size reduction is correct.