**Week 3 LCQB**

This week, I improved my size reduction algorithm based on some visualization results and on some phylogenic trees comparison metrics that i adapted to fit our case. I managed to ensure that my simplified trees displayed accurate information, even though it displays less information than the complete tree.

I was challenged by Frederic and his team to go even further in the size reduction. This is why I’m developing a new solution to prune further my simplified lineage trees. This solution is based on the Treemer method, that I adapted to our problem. It is able to drastically reduce the number of nodes displayed on the tree, without altering the information concerning the most abundant clonotypes. However, I’m currently facing visualization issues, that I’m not yet able to understand and explain. The metrics I’ve developed are giving me perfect results, but this is not coherent with what I’m seeing on the visualization web interface. I’ve noticed that between two different kinds of visualization, the results were not coherent aswell.

I think my next challenges are to overcome this visualization issue, in order to evaluate my advanced pruning algorithm. If the results are satisfying, I will have to make sure my code is actually understandable by the team, so it can be implemented in the existing solution. I would also like to challenge my algorithms on more test sets, perhaps with more clonotypes.