**Week 5 LCBQ**

This week, the challenge was to integrate my size reduction algorithms to the VicoD pipeline. This was mostly done by Lucile, I’ve just had to make my code understandable and to write a short document describing how each function was working. I helped her in correcting some bugs.

In the meantime, I started to think about ways to compare lineage trees coming from the same patient at different times. I’ll think more about this issue once I’ll have examples of the kind of results I can get from my experiments. I also thought a bit about the introduction of my internship report.

I also wrote algorithms that will work on fasta files and will remove the clonotypes that have a number of reads under a given threshold, either absolute or relative to the total number of reads.