21/05/31 to 21/06/04

* Training to the prevention of occupational risks in research laboratory.
* Meeting with Iva where we discussed mainly the histone variants mutations.
* Calculated the different possibilities of raw counts (Paired end & rounded, paired end & not rounded, not paired end and rounded, not paired end and not rounded). I will be using the paired end, rounded version.
* Selected the GTEx & TCGA attributes, available on GitHub: <https://github.com/Ala-Eddine-BOUDEMIA/Chromatin-Dynamics/tree/main/Data>
* Plotted some attributes, the code and images are also available on GitHub.
* Read and watched videos about edgeR filtering and normalization (TMM) as well as the other normalization methods (RPKM, FPKM, TPM).

21/06/07 to 21/06/11 goals

* Determine the number of counts per sample and per tissue.
* Plot the mean counts per sample and per tissue.
* Filter the genes using edgeR.
* Do some QC, following the DESeq2 documentation or EdgeR’s if there is any.
* Normalize the data using edgeR (TMM).
* Determine the number of counts per sample and per tissue.
* Plot the mean counts per sample and per tissue.
* Re-do QC.
* Start with the clustering.