21/05/17-21/05/21

Meeting with Hatem; he proposed that I should add housekeeping genes and tissue specific genes.

Read recount2 documentation to understand how to implement the different methods; add\_metadata (useful for brain tissue only), add\_predictions

Read about RSE; counts are per base, and they are in the assays class, to get the reads count I need to apply read\_counts method.

Searched fo how to open the data with R on the computer.

Explored the data and the R packages; mainly performed some tests to see how the things are organized.

Searched for GTEx attributes dictionary and looked at some attributes.