**16/09/22**

**15:00**

Currently looking and trying to understand a dataset which represents gene expression in Alzheimer’s cases. To be more specific, clones of induced pluripotent stem cells (IpSC) with a presenilin 2 mutation. The columns are slightly confusing. The headers indicate RNA mutations, which can also be found on NCBI. Table

Description automatically generated

It is not yet clear to me what the numbers indicate in each row. I’m aiming to understand within the next hour, before the end of this lecture.

**15:14**

It seems that the numerical values represent “MAS 5.0”, according to the NCBI pages. There’s not much information about MAS 5.0 on the page itself, so I’ll search further.

**15:20**

MAS5 Appears to be an algorithm to calculate gene expression. It’s still not clear to me what the proportions are of the greatly varying values.

**15:22**

After quickly skimming through abstracts of some studies, it seems that the algorithm has a high false-positive rate.

15:23

According to bmcbioinformatics, the values are transcript concentrations.

**15:27**

The algorithm belongs to an organization named Affymetrix.

**15:35**

The ID\_Ref column also indicates Affymetrix probe ID names, not the genes themselves.