Diary – Variant to Gene Mapping analysis (since 20/10/2023)

**20/10/2023**

Updates scripts for GTEx colocalisation. Worked on the 004\_concat\_results.R

Created a .xlsx file in the src/report/Variant\_to\_Gene\_Tables.xlsx; for tables on V2G analysis. Put a table with colocalisation data: locus, tissue, N\_gene\_sign/N\_gene\_tot

I still have to modify files for eQTLGen colocalisation; still to obtain GTExV8 files for Colon\_Transverse and Colon\_Sigmoid

Did colocalisation for ‘Stomach’ and ‘Small\_Intestine\_Terminal\_Ileum’ **\***

**23/10/2023**

We have OK for using U-BIOPRED eQTL data with genotyped data.

We have OK for using UBC Lung eQTL data.

There was an error in the script to run colocalisation with GTExV8. So I had to run colocalisation again for ‘Stomach’ and ‘Small\_Intestine\_Terminal\_Ileum’ **\***

After discussion with team, I do colocalisation only if the eQTL data for the tissue-gene-credset region contains significant association, aka pvalue <= 5x10-6. 🡪 Updated 003\_run\_coloc\_susie\_GTEx.R to integrate this step.