HYRS Weekly Report – Week 3

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This week in HYRS, I completed differential gene expression analysis for my project and performed downstream analysis using various pathways in Enrichr, using the KEGG and Gene Ontology pathways to analyze and interpret the data. STRINGdb was used to construct PPI networks for both males and females. I researched the top significant genes present in both males and females using the NCBI database to find their functions, and other diseases/pathways they could be linked to. I started working on my final scientific poster as well and discussed what my lab shadow could potentially look like.