Analysis Tutorial Prospectus

Melanie L Salas

**Title**

Investigating Heat Stress-Induced Disruption of the LCA5L, MYBL1, and MAGEB4 Genes and Their Pathways in Spermatogenesis Using Multi-Omics Data

**Research question(s)**

How will heat stress affect gene expression associated with gene regulation? Under heat stress, what is the role of protein aggregation and oxidative stress, and how does the loss of the key genes (LCA5L, MYBL1, and MAGEB4) amplify these effects?

**Objectives(s)**

This study will investigate how heat stress disrupts spermatogenesis through pathways of LCA5L, MYBL1, and MAGEB4, focusing on chromatin modifications, gene expression, and oxidative stress in germ cells. This will help identify the goal in molecular disruptions, regulation mechanisms of germ cell survival, and fertility preservation strategies.

**Approach**

To analyze differences in gene expression, chromatin accessibility, and enrichment in RNA-Seq and ATAC-Seq data, we will use DESeq2 for differential gene expression analysis. R will be employed to perform additional tasks, such as integrating multi-omics data and visualizing the impacts of heat stress on germ cell health. Moreover, statistical analyses in R will be used to assess oxidative stress and protein aggregation in heat-stressed knockout mice

**Selected references**

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