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Research Methods Tutorial Final

May 9th 2025

For this tutorial, I will be showing you how I was able to discover the disruption of Heat Stressed being induced in pathways in such genes as LCA5L, MYBL1, and MAGEB4 while using Multi-Omics Data, R, and some ChatGPT for information that was not found. Within this research, I wanted to investigate the following key points: “How will heat stress affect gene expression associated with gene expression? How are chromatin structures adjusted in response to heat stress? 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? The reason for this study is that investigating these key factors will help us identify the goal of what molecular disruptions are occurring, as well as the regulation of mechanisms of germ cell survival and fertility preservation strategies. To analyze transcriptomics and the changes in chromatin under heat stress. RNA-seq and ATAC-Seq data from testicular tissue of Wild type and knockout mice, specifically LCA5L, MYBL1, MAGEB4 is going to be processed in R. All of this data will be made up from Chat gpt due to some results that I have from the genes is not fully processed and cannot be used in R. The differential gene expression will be assessed using DESeq2, which is an R package that is used to analyze RNA-seq data to identify the different genes being expressed. So, while chromatin is accessible, it will be analyzed in DESeq2, as it is being performed to analyze genomic data and even give us a visualization of what is happening in the impacts of heat stress on germ cell health, while additional statistical analyses will assess oxidative stress and protein aggregation in heat-stressed knockout mice.

References

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