

Heart and Brain Gene Analysis

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Introduction

For my project, I analyzed samples of genes from regions of the heart and brain using datasets from the GTEx Portal in R. I decided to focus on the heart and brain regions since these are, in my opinion, the most vital parts of the body. Disease risk in these areas can lead to death, and it is important that we catch a disease before it spreads and gets worse. Gene analysis is important because it helps us to understand how genes affect traits, health, and illness. It is crucial for discovering the genetic causes of diseases, enabling personalized therapy, and guiding medication development. Researchers can use gene expression and mutation analysis to forecast illness risk, adjust treatments, and identify new therapeutic targets. Beyond healthcare, DNA analysis contributes to breakthroughs in agriculture, environmental science, and basic biological research, making it an effective tool for improving both human life and our understanding of the natural world.

RNA Integrity Number (RIN) Analysis

The RNA Integrity Number (RIN) can assist in verifying the quality of RNA utilized in gene expression studies, which is critical for accurately analyzing how genes behave in healthy versus pathological situations. High-quality RNA (high RIN) produces more trustworthy data, allowing scientists to discover disease-related genes and pathways with greater confidence. By preventing RNA sample degradation, researchers can better detect early genetic changes linked with diseases, enhancing diagnostics, guiding drug development, and contributing to preventive methods such as identifying at-risk individuals before symptoms arise.

> 8.0: Indicates high-quality, intact RNA.

5.0 - 8.0: Suggests moderately degraded RNA.

< 5.0: Indicates degraded RNA, which may not be suitable for certain downstream applications.

Brain and Heart RIN Analysis

For the heart, there were two regions in this analysis, the atrial appendage and the left ventricle. Both regions averaged around 7.5 RIN for this sample, with the left ventricle region having a slightly higher average RIN but not too far. Both region's samples appear to have moderate to high RIN. There is one extremely low RIN outlier in the left ventricle region with a RIN below 4. This means that the patient's RNA tissue has been significantly degraded, and they may be at risk for diseases such as left ventricular hypertrophy. Refer to figure 1.1 in the appendix.

In the brain sample, there are also two regions, the cerebellum and the cortex. In contrast to the heart region, both brain regions had an average just below 7 RIN. Meaning their RNA is moderately degraded on average. Although, they had more outliers than the heart sample, seven in the cerebellum and three in the cortex to be exact. Also, the outliers had high RINs rather than low RINs, therefore, their RNA tissue is in practically perfect condition. Meaning there is less chance of brain disease for those patients. Refer to figure 1.2 in the appendix.

PCA Tissue Analysis

When I looked at the PCA for the heart and brain regions, I could see a clear separation of clusters, refer to figure 1.3 in the appendix. This tells me that these two tissue types are distinct, and there are some clusters that are closer together. The closer together the clusters are, the more biologically similar the tissue types are. In conclusion, the brain and heart tissues have unique gene expression patterns that are readily distinguished in the PCA. This shows that the principal components represent physiologically significant diversity, with tissue type playing a major role.

Conclusion

In conclusion, I learned a lot about the difference in heart and brain tissue expressions. I learned why gene analysis is important to help our future. Analyzing RIN helps determine the status of a patient's RNA, whether it is in good shape or degraded. Usually low RNA scores, below 5, are post-mortem samples because RNA quickly degrades after death. Heart tissue typically has higher and more stable RNA than brain tissue. If you are comparing gene expression between brain and heart, differences in RIN could bias your results, so it is important to check the RIN distribution across both tissue types. PCA tissue analysis shows us how the two types of tissue have significant diversity or similarity. In this example, I saw that brain and heart tissues are generally diverse from one another. Lastly, I learned that tissue type is the most important thing when analyzing different gene expressions.

Appendix

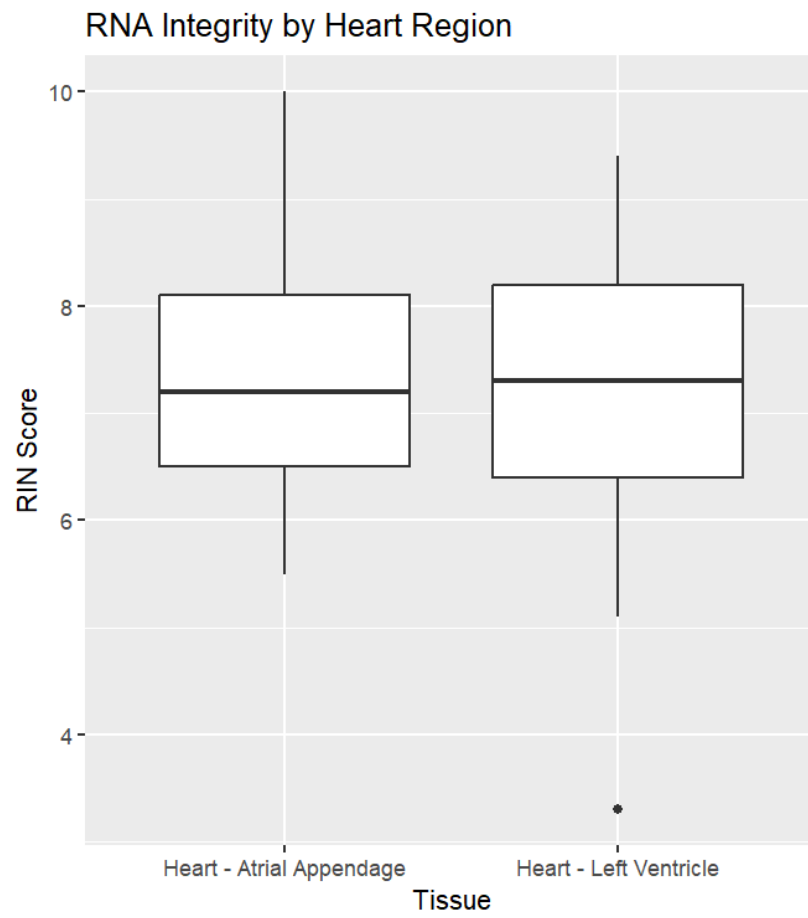


Figure 1.1

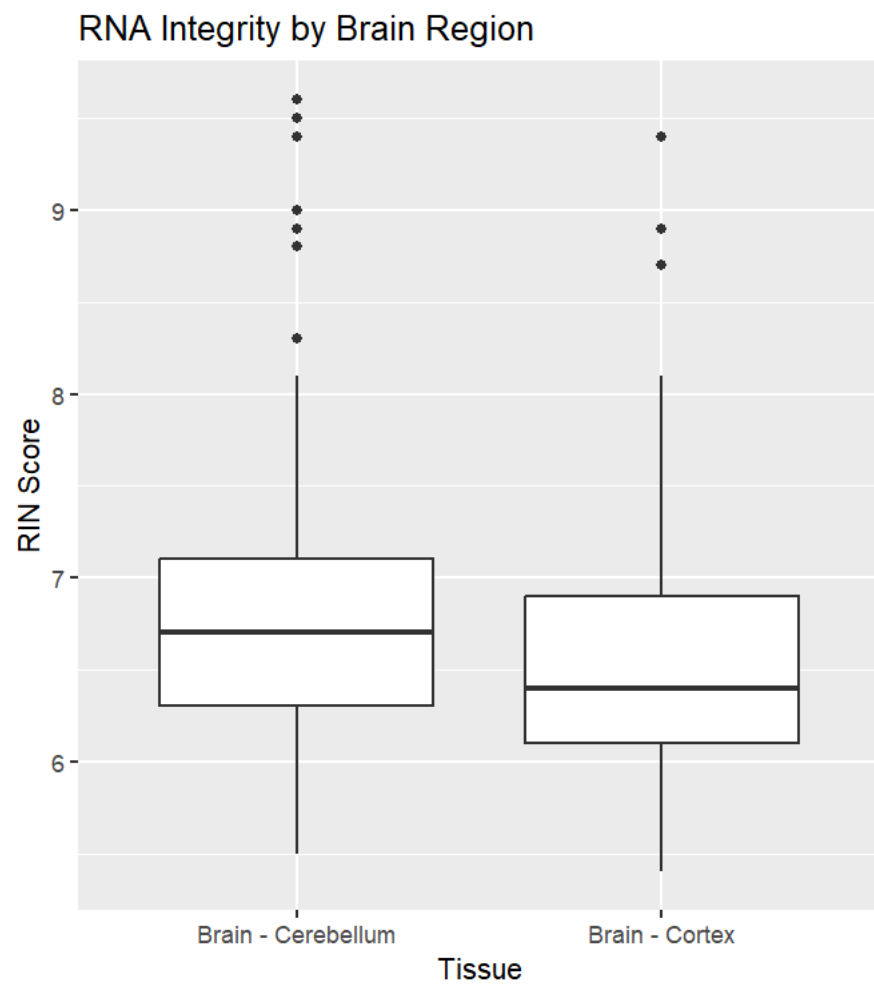


Figure 1.2

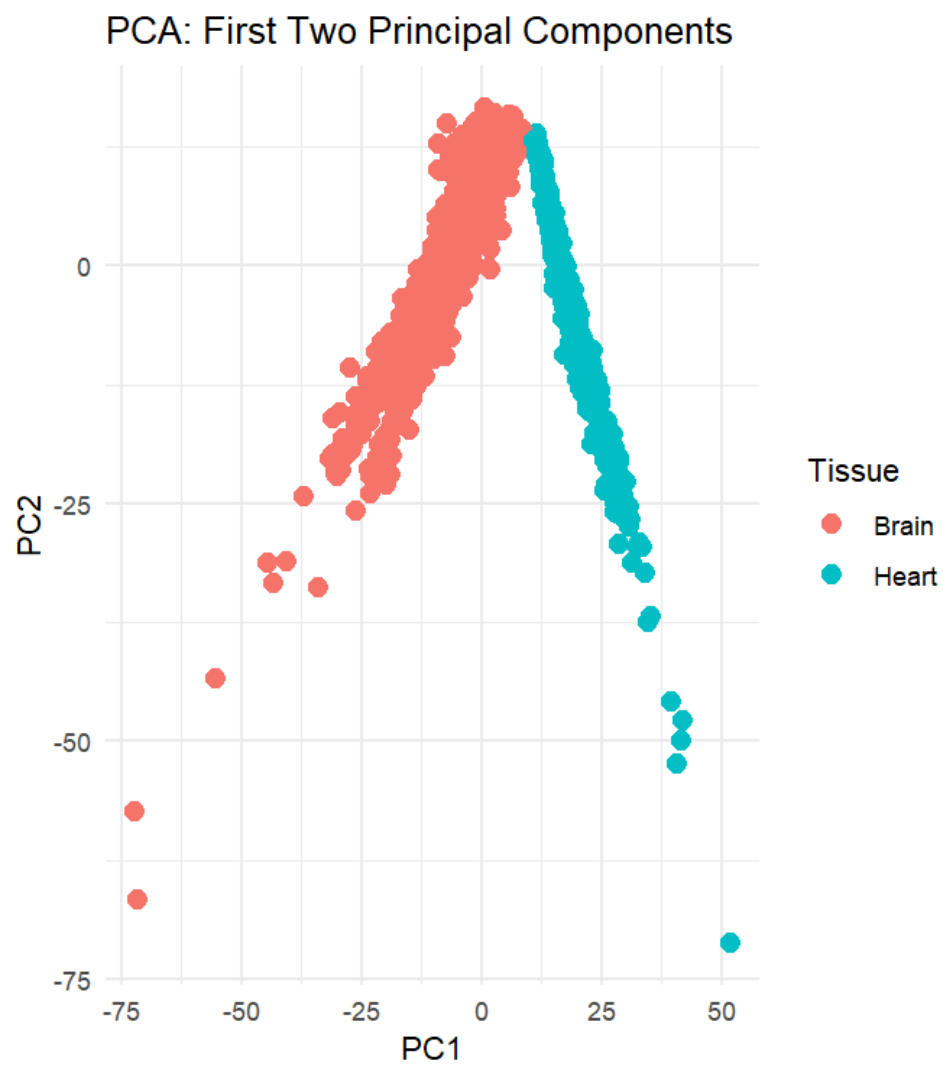


Figure 1.3