EDAT Documentation v.1

**Background**

**Objectives**

* The overall objective of the project was to create an app using R-Shiny in order to allow a person to explore gene expression data without extensive computational knowledge and rigor. The app will incorporate two dimensionality reduction algorithms, PCA and t-SNE, to help aid in data visualization. The user then may further visualize the data by selecting only specific genes, time points, and donors they wish to visualize.
* In order to accomplish this, some processing is needed to convert the raw fold change data into a usable format. Currently the program only accepts pre-processed gene expression data using the ration of change over the original expression level, but we hope to have the program process raw data in the future. Once the data has been processed, the user is able to subset the data using the UI which calls the subset() function in the program which extracts only the selected data. See the image in results for more information.
* In regards to the PCA performed by the program, we are using the prcomp() function which accepts the scale and center parameters which will soon be modifiable by the user. The variance of each dimension is also computer with the PCA and is displayed in a corresponding scree plot.
* For the t-SNE performed we are using the function Rtsne() which is part of the RTsne package. We will implement the function such that the user can adjust the dimension, initial\_dimension, perplexity, pca, and max\_iter parameters.

**Results**

[IMAGE OF SIDEPANEL SUBSETTING SECTION]

[EXPLANATION OF IMAGE]

[IMAGE OF PCA]

[EXPLANATION OF IMAGE]

[IMAGE OF SCREE]

[EXPLANATION OF IMAGE]

[IMAGE OF TSNE]

[EXPLANATION]

[DIFFICULTIES AND IMPROVEMENTS]

* Ui
* Labels hover
* Optimization
* Parameter selection

**Conclusion**

[NEW IDEAS AND WORK REMAINING]

**Usage**

With Processed Data:

With Raw Data: