Assignment 2 Report – CGS4144

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**Density of Per-Gene Median Expression (log2)**: The plot shows the density distribution of the median gene expression values. The data was calculated from gene expression values across multiple samples in the dataset.

**Key Observations:**

* Peak near Zero Expression:

There is a significant spike in the distribution near 0 on the log2 scale, indicating that a large portion of the genes have low to very low median expression across the samples. This could represent genes that are either not expressed or have very low expression in the studied conditions.

* Secondary Peak around 1-2 (log2 scale):

A smaller peak appears around log2 values of 1-2, indicating a subset of genes with moderate expression levels.

* Long Tail of High Expression:

suggests that a smaller fraction of genes exhibit high levels of expression, with a gradual decrease as the expression levels increase.

A screen shot of a grid

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**Heatmap (significant differentially expressed genes)**: The plot demonstrates the correlation between male and female differentially expressed genes in the set

**Key Observations:**

* The red areas in the top left and bottom right quadrants of the heatmap represent the genes with the highest cross correlation between male and female samples.

A graph with red and blue dots

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**PCA Plot (female vs male expression of low grade glioma):** This plot shows the principle components from a PCA decomposition of the set, and color codes them based on sex.

**Key Observations:**

* Inverse correlation: seeing as many of the datapoints are directionally opposite through the origin, it is likely that there is some sort of inverse correlation between the two groups. Additionally, it looks like each subgroup has some correlation with it’s other members based on the grouping relative to origin.

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**Volcano Plot (gene differential expression):** Shows gene expression differences between diff expr. Set.

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A graph with a green line and a line

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**GO Enrichment Dot Plot** This plot shows the number of genes involved in each process from the set. The larger the dot, the more genes are involved with the corresponding y axis process set. The warmth of each dot represents statistical significance from a p value adjustment, with warmer p values representing more significant gene clusters.

**Key Observations:**

* Antigen Receptor Gene Clusters Prominent

From this plot, we can see that many of the genes involved in immune response and antigen receptor pathways show significance relative to the presence of low-grade gliomas in our population. Furthermore, they have the highest gene ratio, furthering this hypothesis by indicating that their gene clusters are more dense.

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**KEGG Enrichment Dot Plot:** This plot shows the frequency of genes involved in each of the processes outlined on the y axis. The larger the dots, the more genes from the set are involved in the expression. Red dots are more likely to be significant. The x axis represents the ratio of genes in an expression cluster to genes in the entire set.

**Key Observations:**

* Th1 and Th2 Cell Differentiation: It could potentially be significant that these Th1 and Th2 regulatory genes have correlation with sample low grade gliomas. Th1 is important in modulating anti-tumor activity in humans.

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**t-SNE Plot – Gene Expression Data:** The plot shows the density and correlation of similarities between genes. The female genes (coded with purple) seem to trend slightly more clustered, but both groups do have defined boundaries.

**Key Observations:**

* Potential Negative Correlation

Based on the angles of the female and male data points and clustering, it seems like there are defined differences between the two, and that they may have a negative correlation across the two subsets.

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**UMAP Plot – Gene Expression Data:** The plot also shows the density and correlation of similarities between genes using the UMAP paradigm. The female genes (coded with purple) seem to trend slightly more clustered, but both groups do have defined boundaries. While we hoped the UMAP would give us a more defined clustering, it seems relatively similar with many of the same features.

**Key Observations:**

* Potential Negative Correlation

Similarly to the t-SNE plot, the UMAP plot suggests that there could be a negative correlation across the two subsets.