Data Analysis & Visualization Portfolio

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Ciernia Lab Projects

Ciernia Lab (Djavad Mowafaghian Centre for Brain Health, UBC)

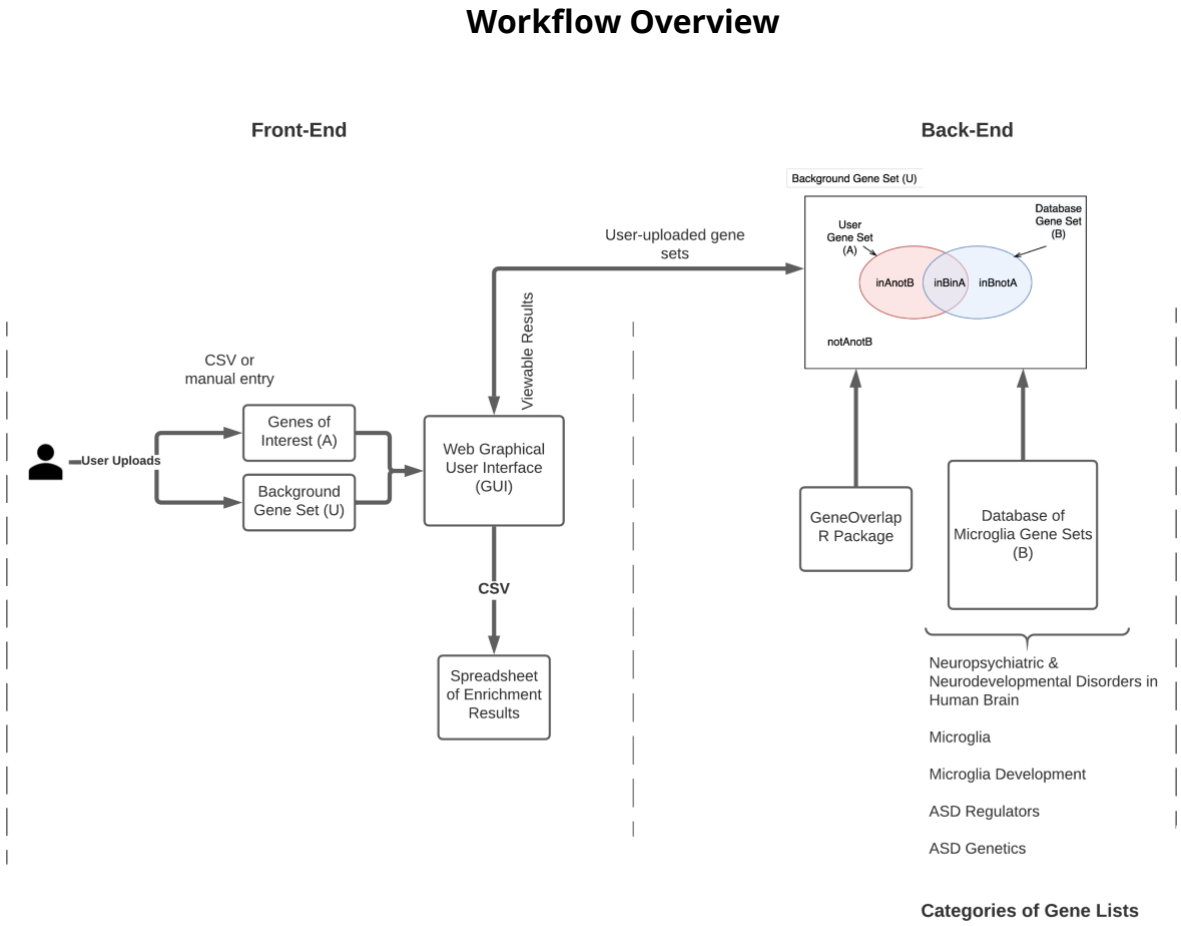
Period of Involvement: September 2019 - Present

Organization Link: https://ciernialab.med.ubc.ca/

Microglia Enrichment Calculator Project

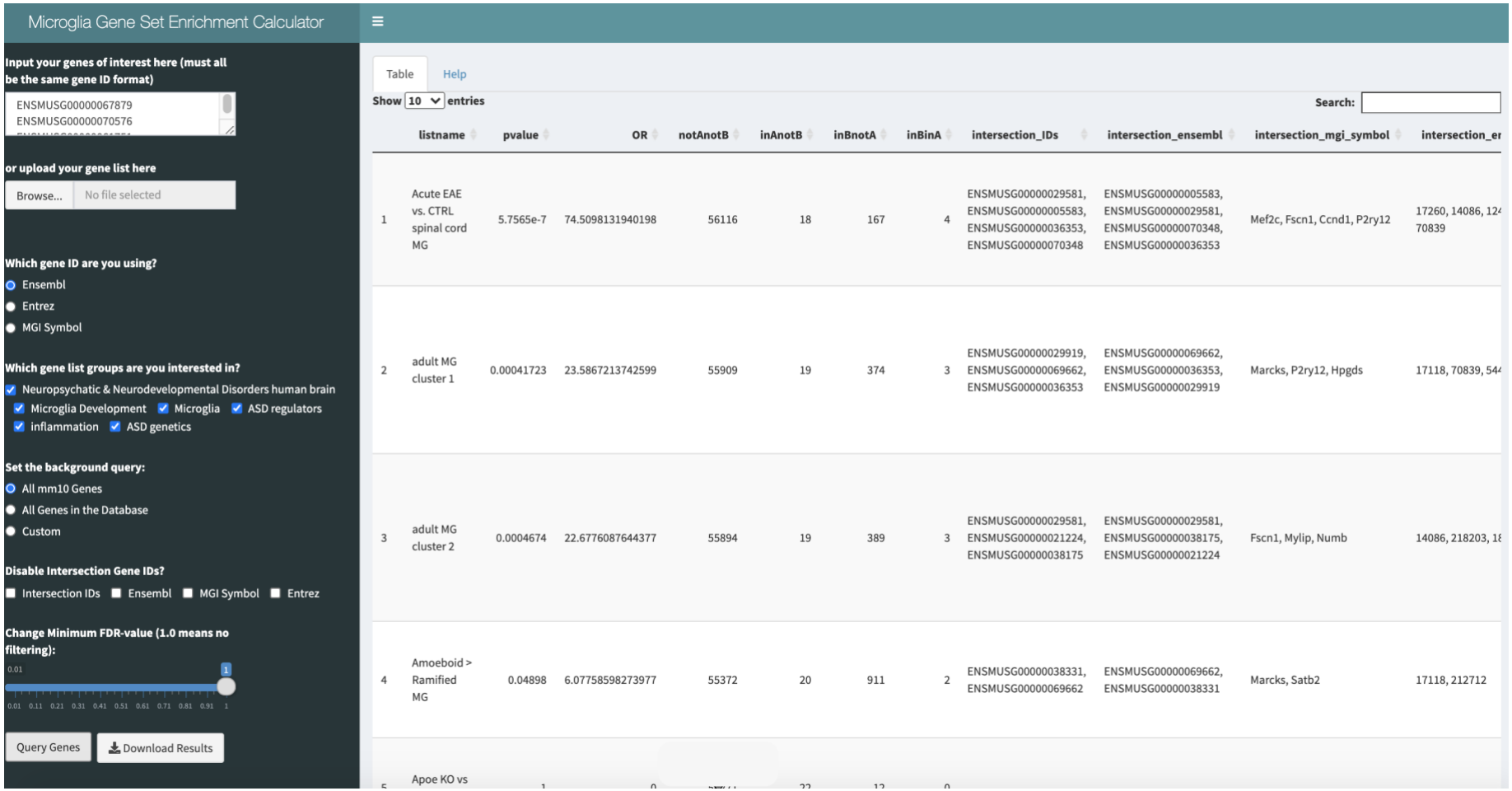
An interactive dashboard developed to allow non-technical lab members to perform basic statistical analysis. Outputs results to an interactive table.

Built using the Shiny package and the GeneOverlap package in R, and hosted on shinyapps.io.



You can access the app at: https://ciernialab.shinyapps.io/MGEnrichmentApp/
GitHub repository with more details can be found at: https://github.com/ciernialab/MGEnrichmentApp

Screenshot of Dashboard:

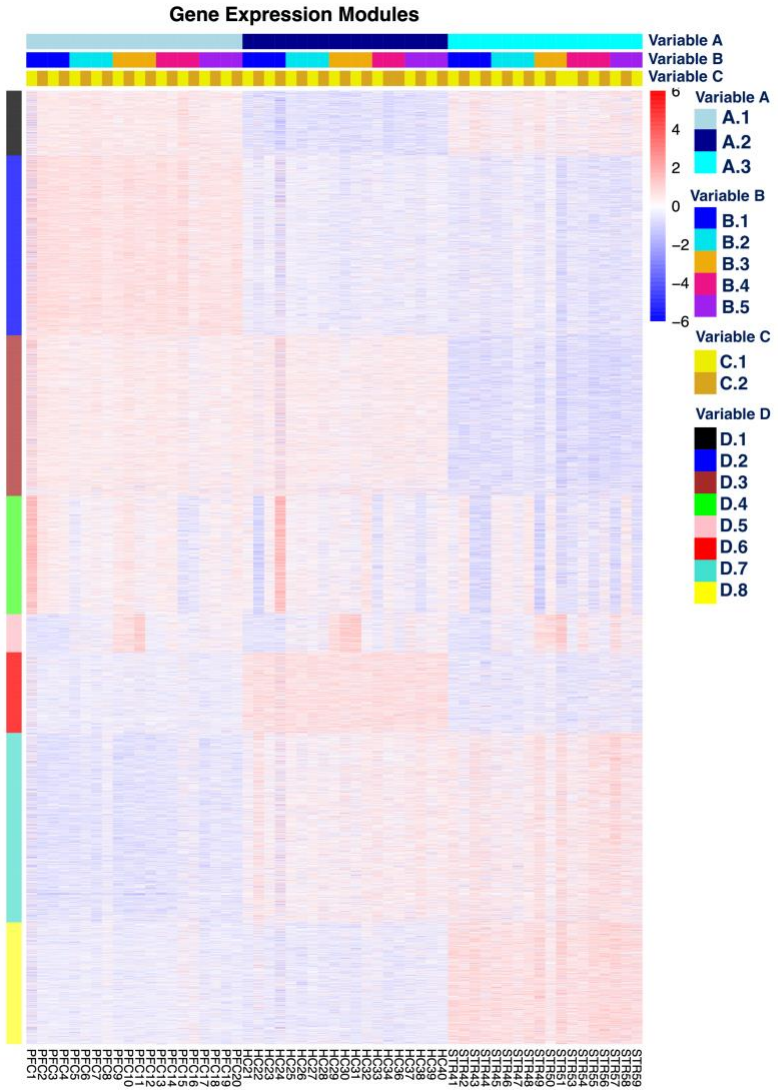


You can access the app at: https://ciernialab.shinyapps.io/MGEnrichmentApp/
GitHub repository with more details can be found at: https://github.com/ciernialab/MGEnrichmentApp

Gene Expression Project

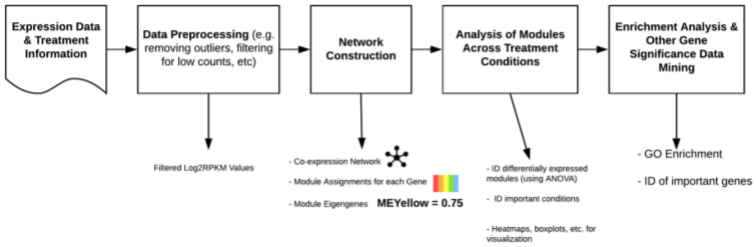
A data analysis project I worked on as a bioinformatics research assistant in the Ciernia Lab.

This heatmap figure on the right was the key visual I made, representing changes in gene expression of a certain category (module) of genes across different samples and variable conditions. Each column is a sample, and each row is a different gene.



Made using the [WGCNA] package in R.

Workflow Overview:



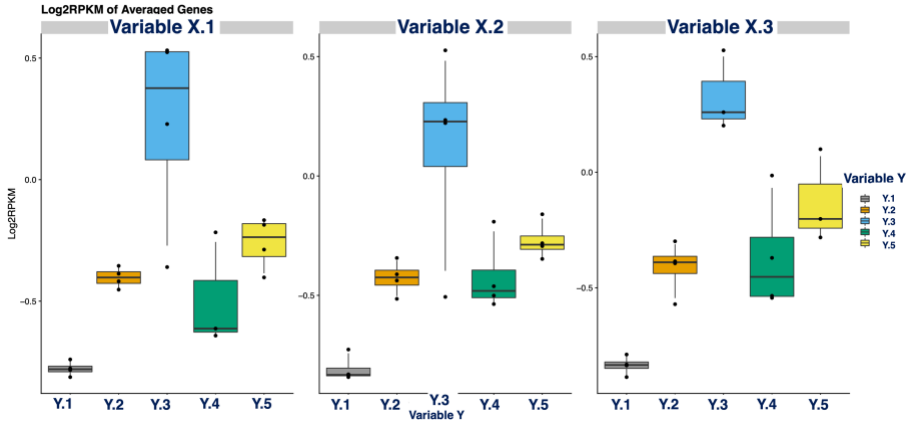
Side note: I know the heatmap is very busy, and the figure we actually used was a smaller, more concise version of this, which I can't show since the data is currently unpublished.

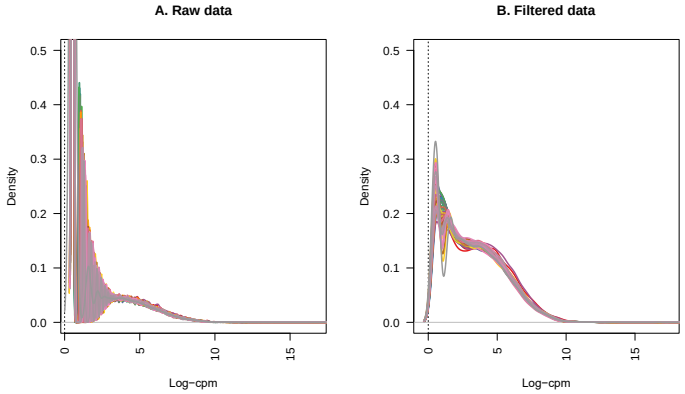
GitHub repository with more details about the analysis and background of the project can be found at: https://github.com/justinjao/Gene_Expression_Project

Some other visualizations I made in the intermediate steps of the analysis:

Boxplots showing changes in gene expression values in differerent conditions.

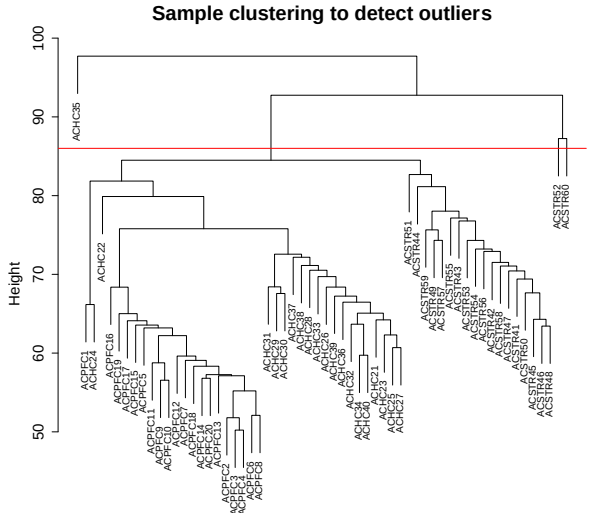
Made using ggplot2 package in R.





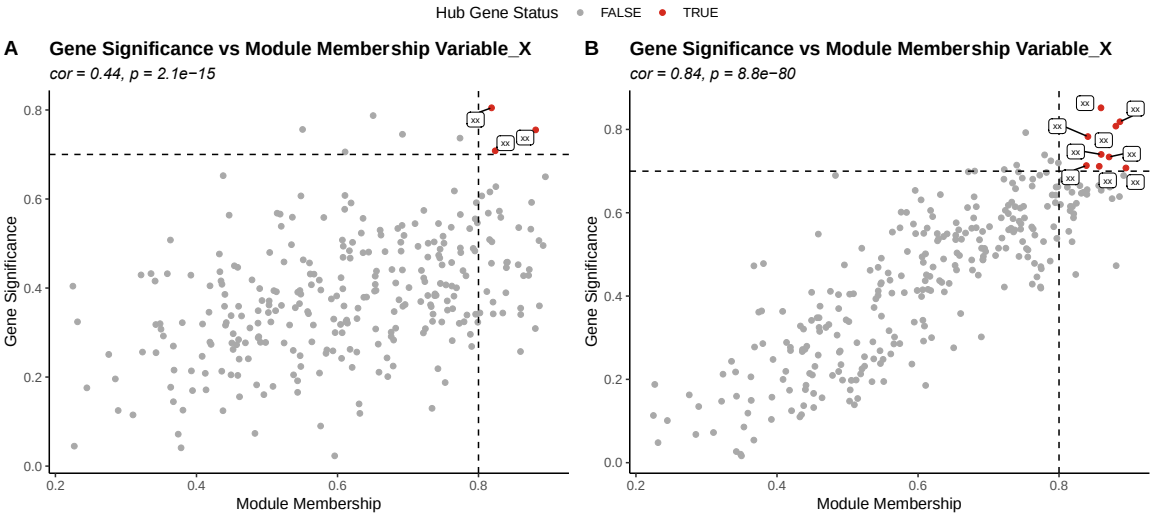
Expression values before and after filtering

Both made using WGCNA package in R.



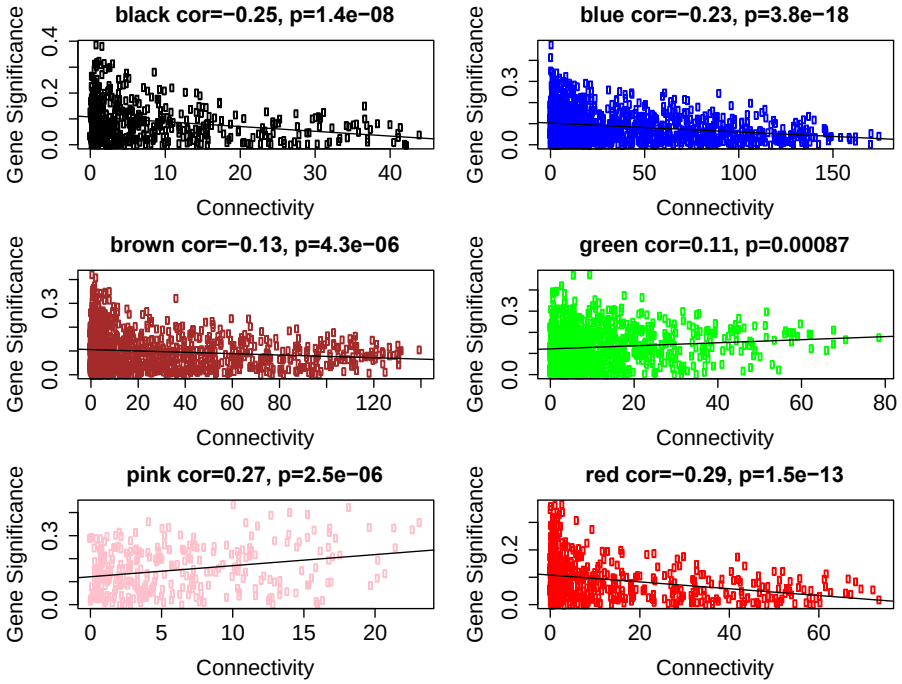
Hierarchical clustering to visually inspect samples for outliers

GitHub repository with more details about the analysis and background of the project can be found at: https://github.com/justinjao/Gene_Expression_Project



Scatterplot with cut-offs at dotted line to select for highly relevant genes (gene labels censored as xx).

Made using ggplot2 package in R.



Gene significance vs connectivity plots to determine relevance of different modules identified.

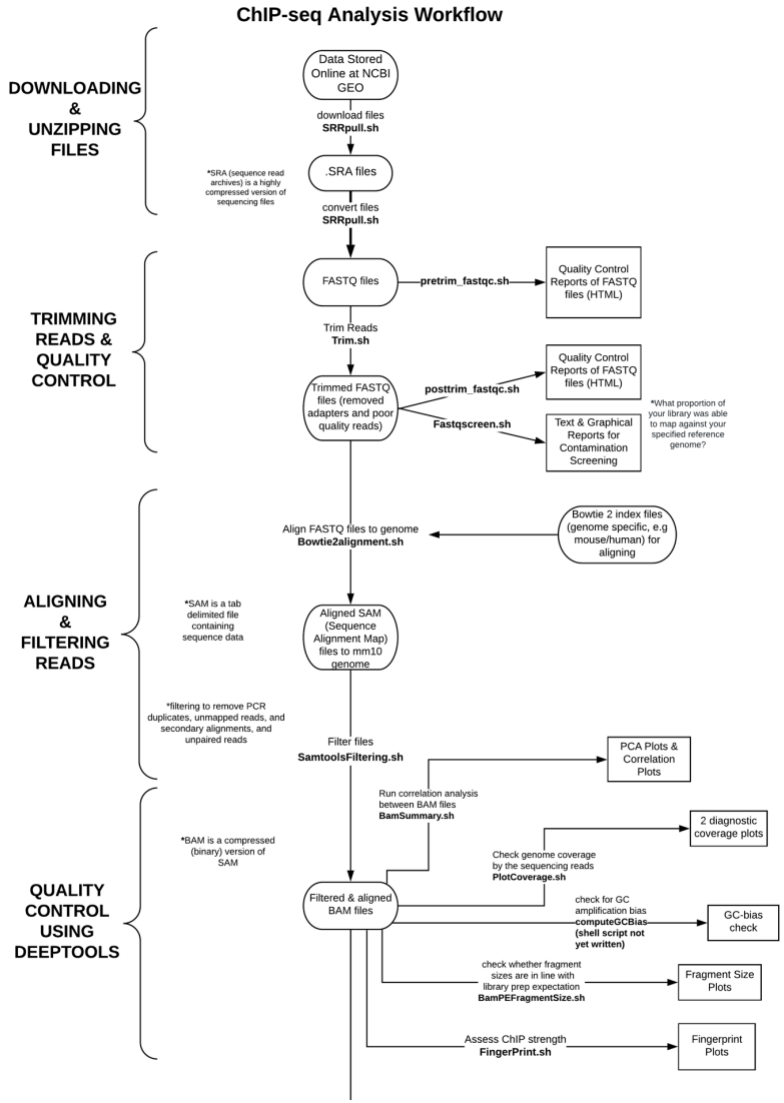
Made using the WGCNA package in R.

GitHub repository with more details about the analysis and background of the project can be found at: https://github.com/justinjao/Gene_Expression_Project

ChIP-seq Workflow Diagram

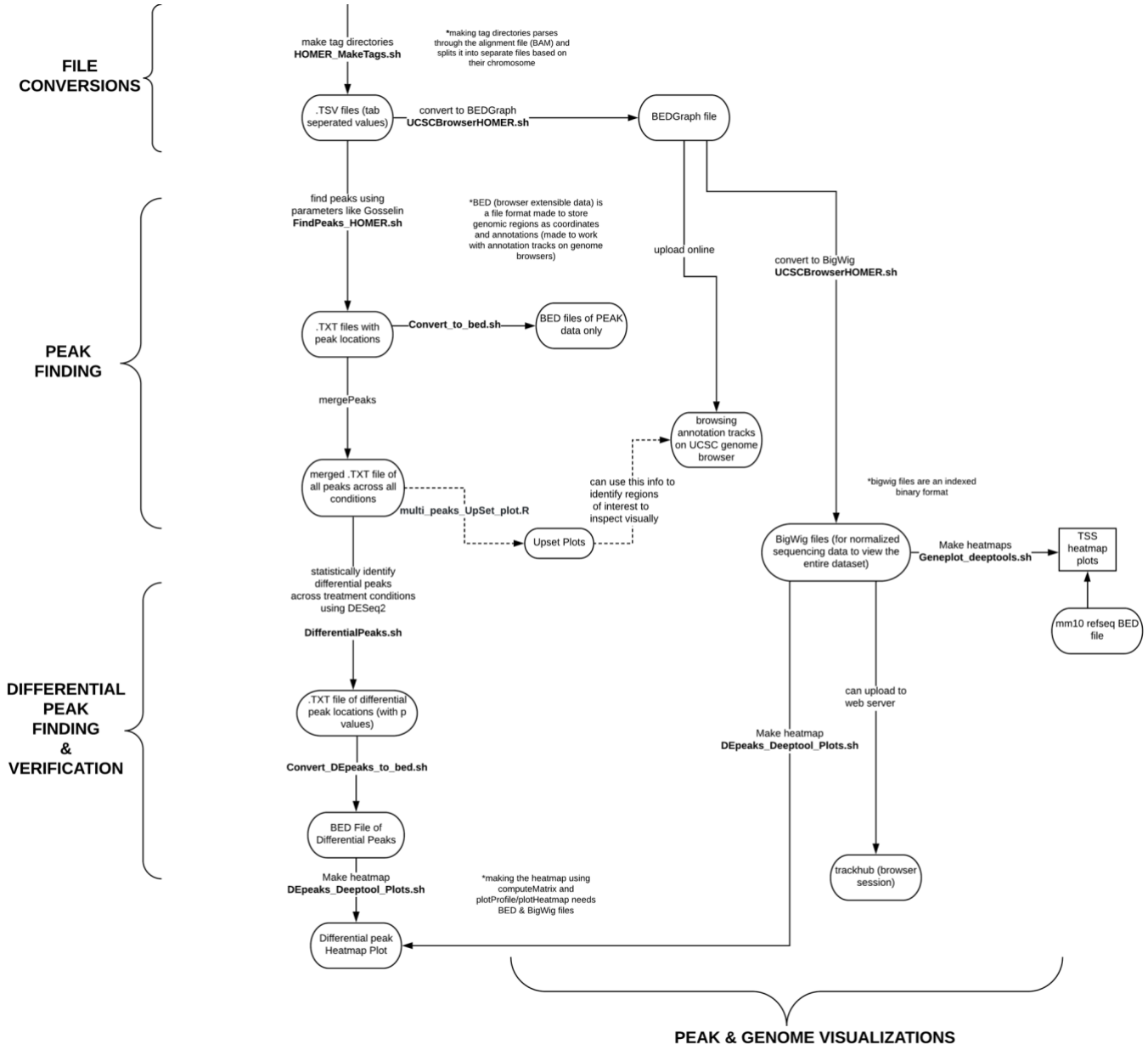
Because of the pandemic, our lab had to temporarily shutdown, and so a lot of members started exploring more computational projects.

One such analysis is called Chromatin-Immunoprecipitation sequencing analysis (ChIP-seq). To help members of my lab learn the data analysis pipeline (such as what scripts to run, and what each step of the analysis was doing), I made this flowchart.



GitHub repository with more details about the analysis and background of the project can be found at: https://github.com/ciernialab/Alder-ChIPseq-Tutorial

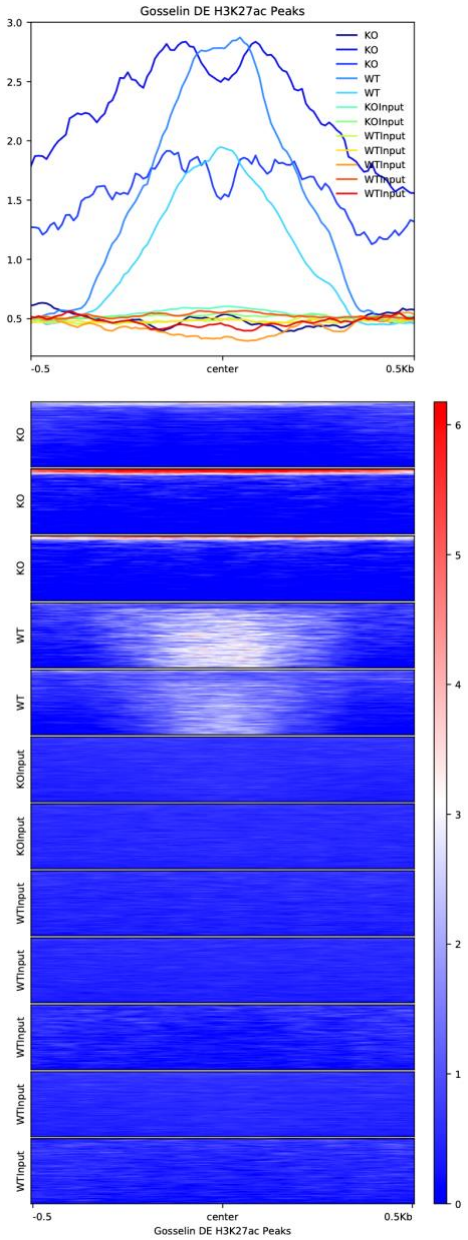
Part 2 of the flowchart:



GitHub repository with more details about the analysis and background of the project can be found at: https://github.com/ciernialab/Alder-ChIPseq-Tutorial

Peak-finding (one of the figures that can be generated from ChIP-seq).

Made using HOMER software.



GitHub repository with more details about the analysis and background of the project can be found at: https://github.com/ciernialab/Alder-ChIPseq-Tutorial

BC Cancer Projects

BC Cancer Agency

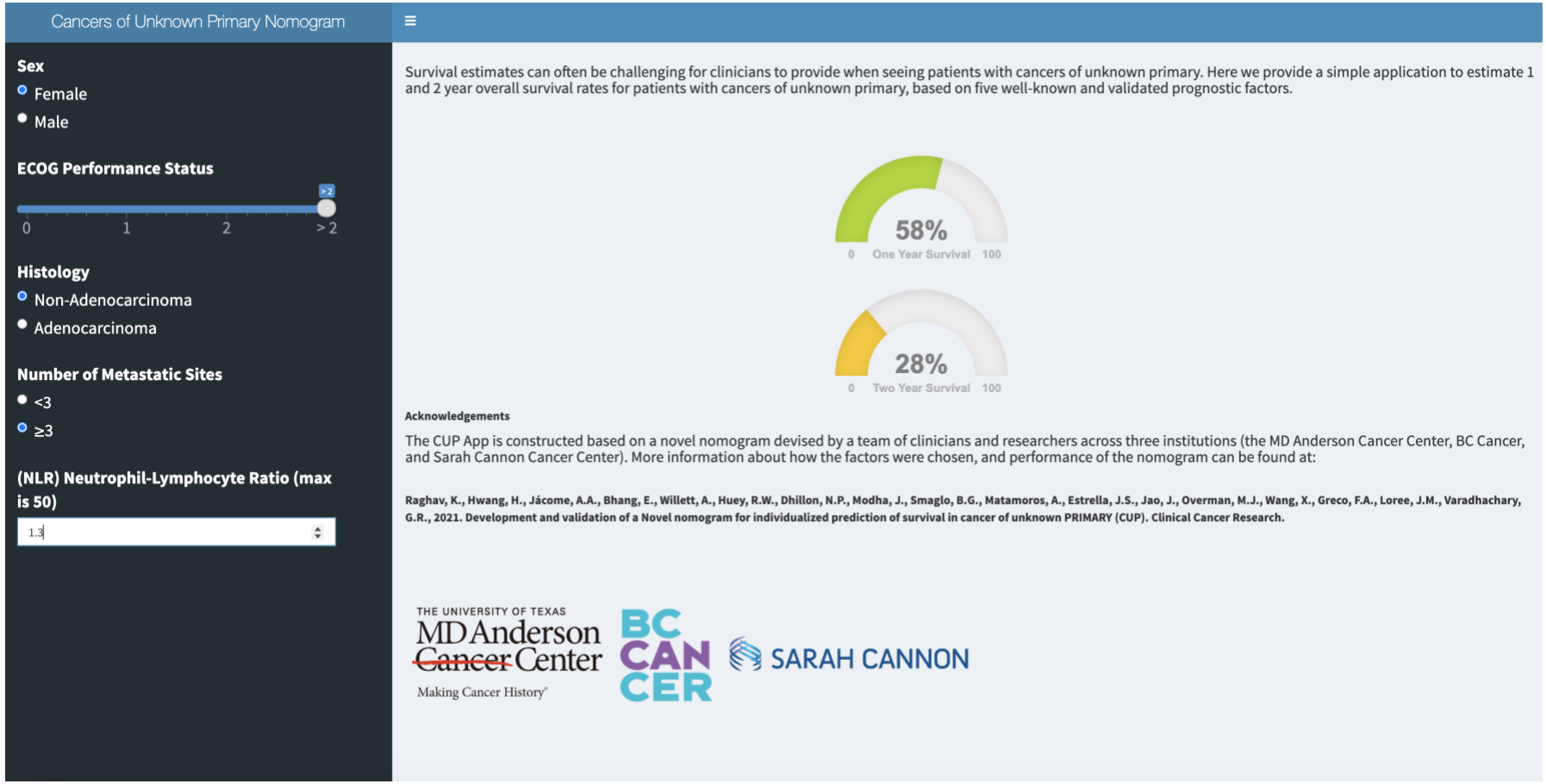
Period of Involvement: January 2019 – September 2019, July 2020 – September 2020

Organization Link: http://www.bccancer.bc.ca/

Cancer of Unknown Primary Nomogram

An interactive dashboard I built using the Shiny package in R, in the summer of 2020.

The tool was devised to allow real-time use in the clinic for assisting oncologists with assessing 1 and 2 year survival rate from cancers of unknown primary.

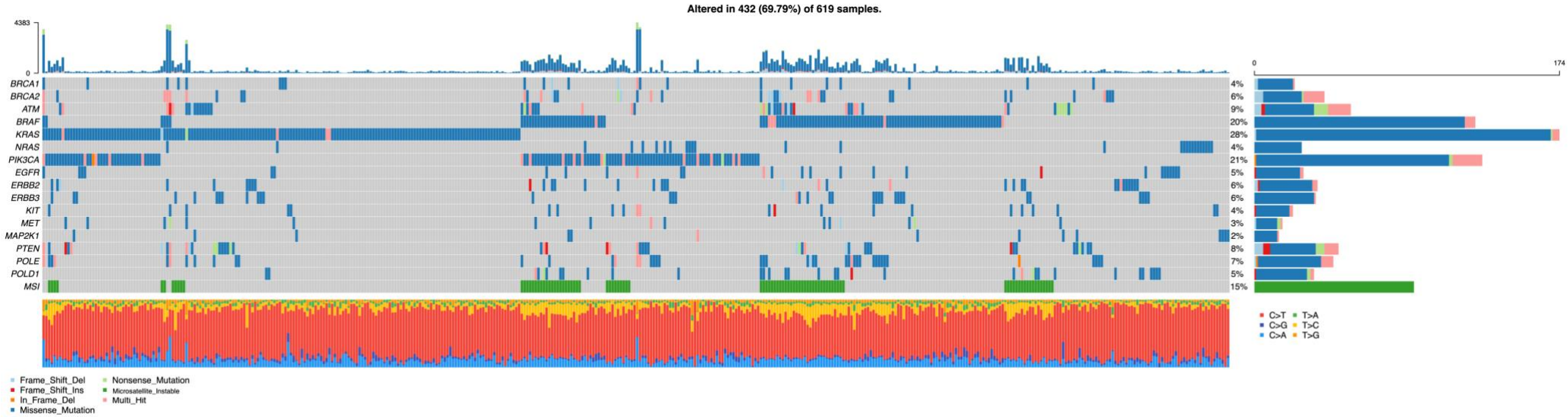


GitHub repository with the code can be found here: https://github.com/justinjao/CUP_Nomogram_App
Publication about how the nomogram was devised can be found at: http://doi.org/10.1158/1078-0432.CCR-20-4117

BRCA Analysis Visualizations

A project I worked on during my time as a clinical research assistant in 2018. I was looking at gene expression profiles of colorectal cancer patients with a certain type (BRCA1/2) of mutation. The project is currently on hiatus, but I still managed to explore a new tool for visualizing gene information, and made some neat graphics which I wanted to share!

An oncoplot, which shows the mutation profile of our cohort of patients, with annotations for the types of mutation, and what the mutation was, and how the gene was mutated.

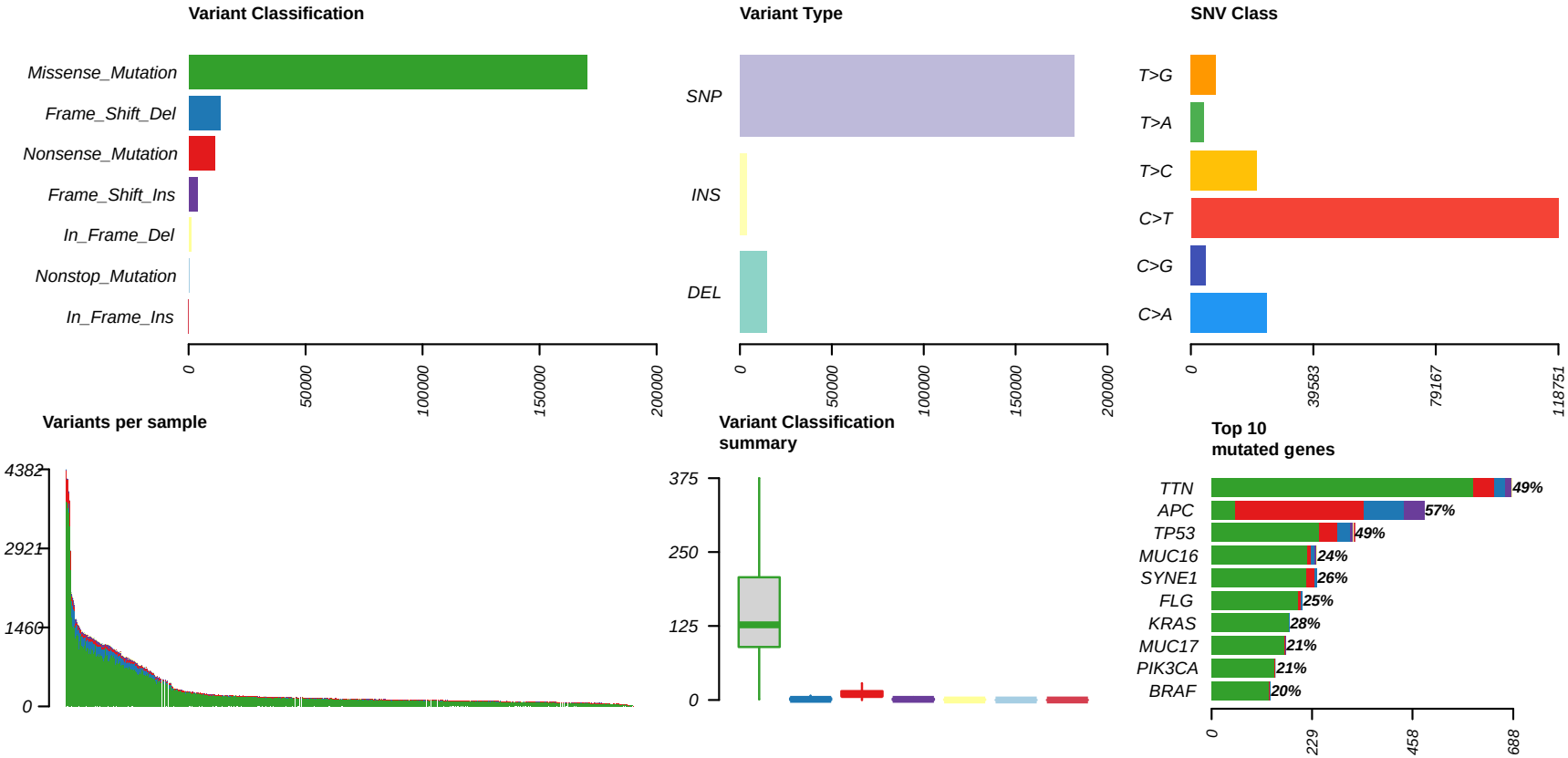


Made using the maftools package in R.

Side note: I know this figure is busy and hard to interpret. If I were to actually prep it for usage, I would certainly make it more concise and easier to draw insights from.

No links available for this project.

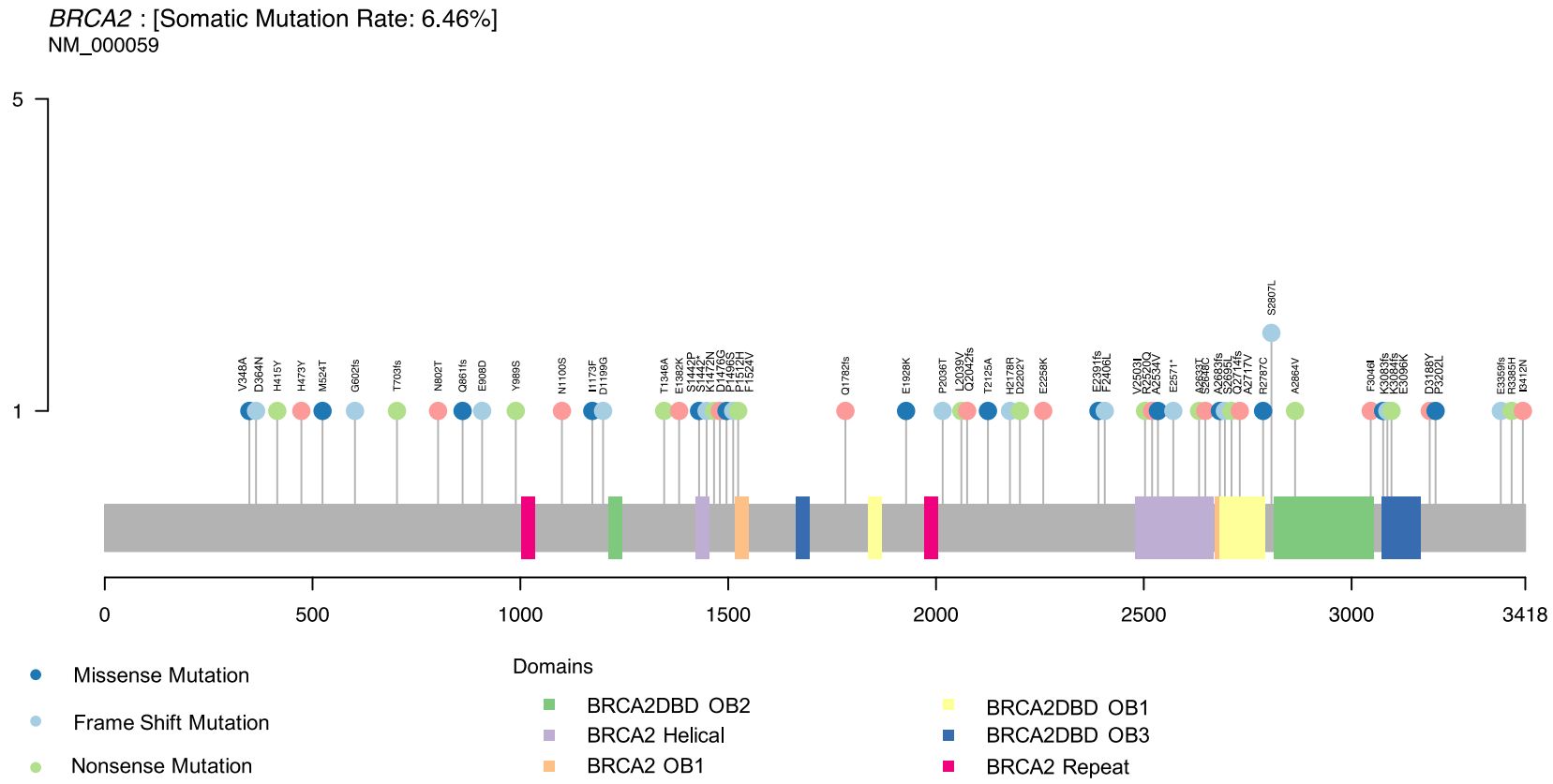
Some further summary visualizations of the data, exploring the mutation profiles of the patients.



Made with the maftools package in R.

No links available for this project.

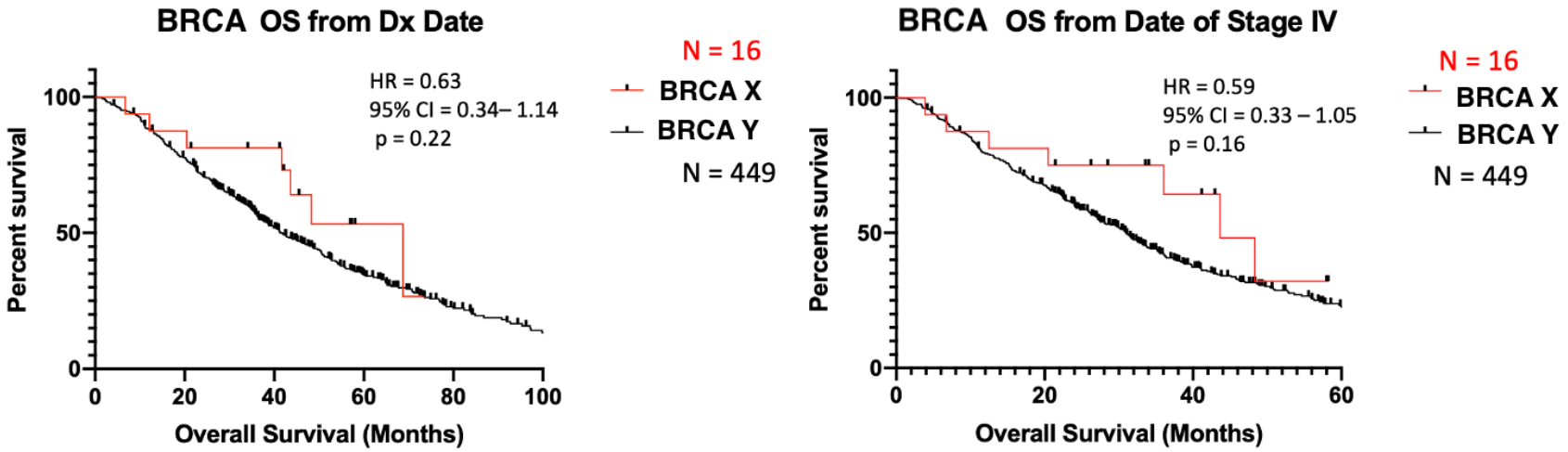
A lolliplot (i.e. lollipop) plot, representing the mutations in the cohort and where they're located on the gene itself.



Made using the maftools package in R.

No links available for this project.

A survival plot (Kaplan Meier curve), visualizing the overall survival of the cohort based on their mutation status.



Made using [Prism GraphPad] software.

No links available for this project.

Genome Institute of Singapore Projects

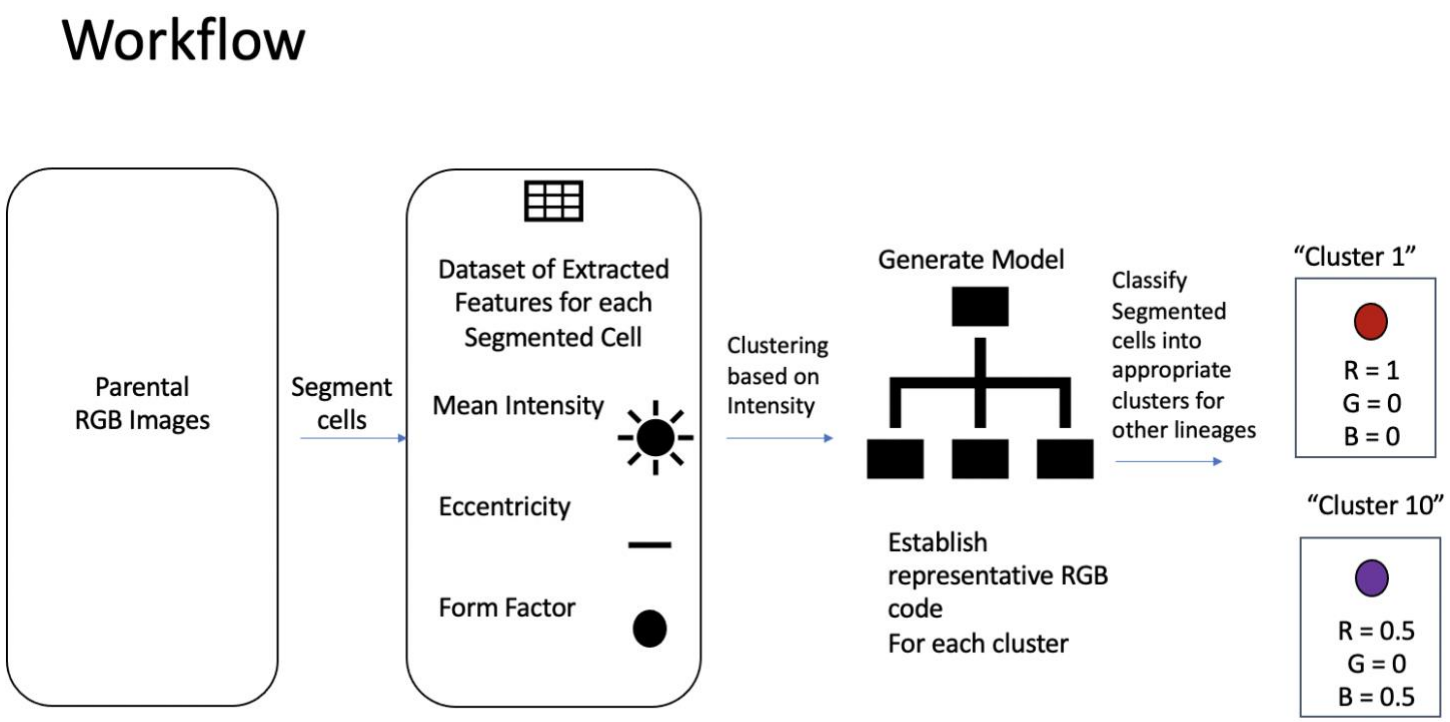
Genome Institute of Singapore (Centre for High Throughput Phenomics)

Period of Involvement: June 2018 – December 2018

Organization Link: https://www.chip-phenomics.org/

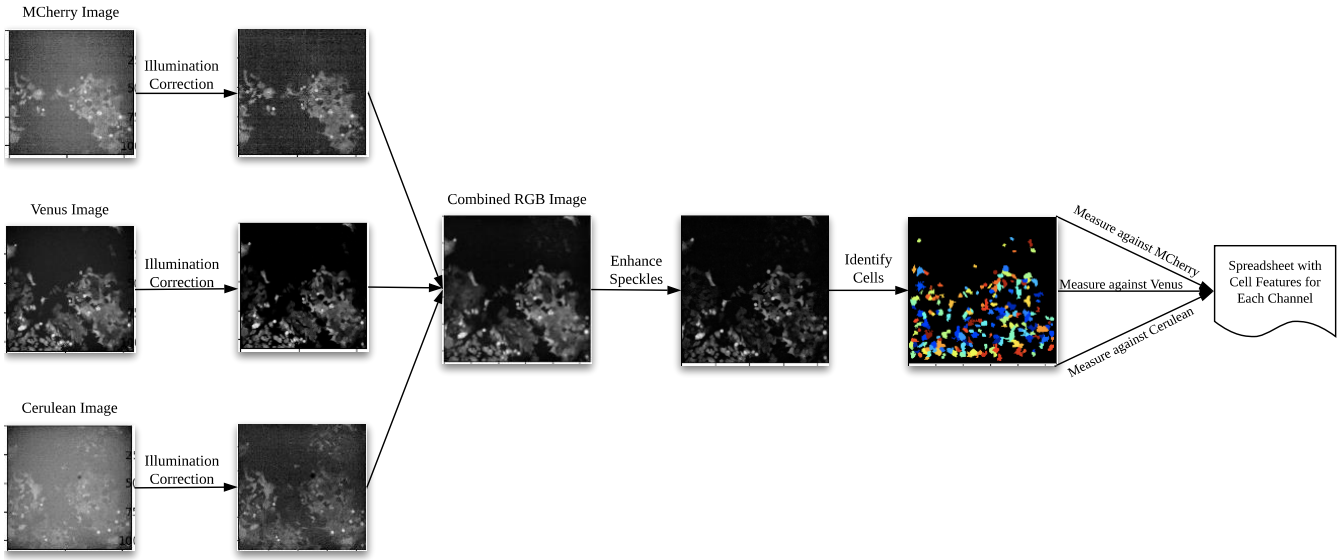
RGB Analysis Project

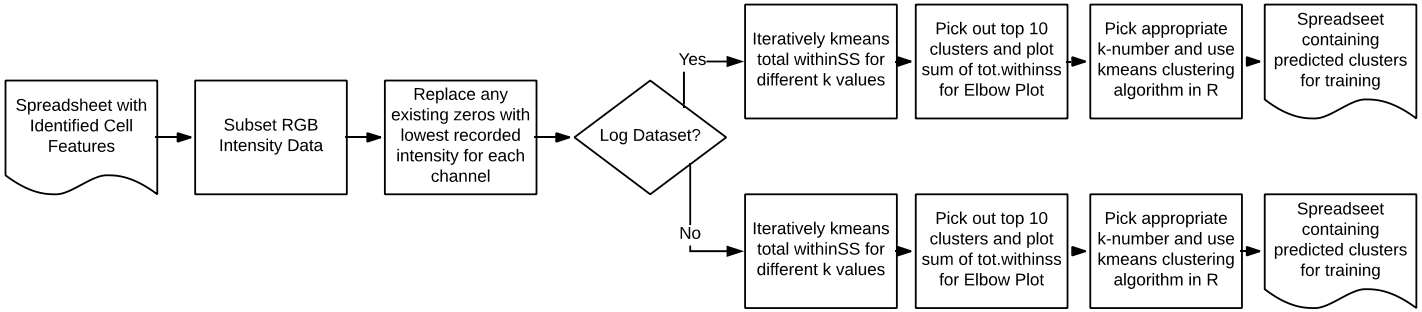
The first real analysis project I worked on. We were tracking changes in population dynamics of colorectal cancer cells as they evolved, and I used image data (fluorescence intensity in red, green and blue light channels) to accomplish this. I first performed image segmentation to extract image features. Then, I used k-means clustering to group the cells based on their colour profile, and random forest classification to match the colour profile of cancer cells as they evolved, to determine how the cell populations changed.



No links available for this project.

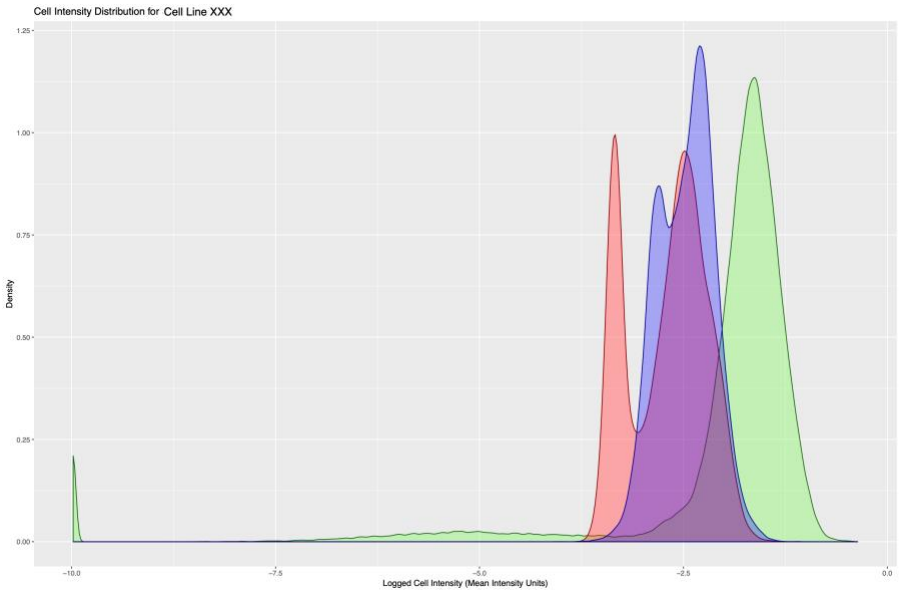
Image segmentation was performed using [CellProfiler](#) software.





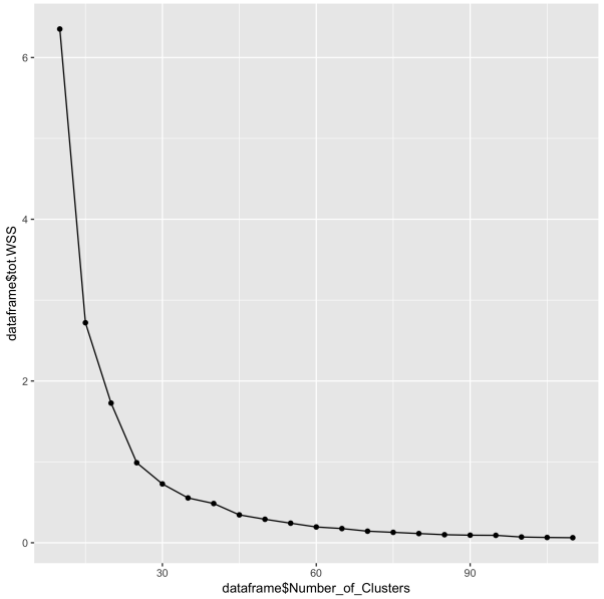
Data pre-processing steps

No links available for this project.



Plots to visualize initial colour distributions of cancer cells.

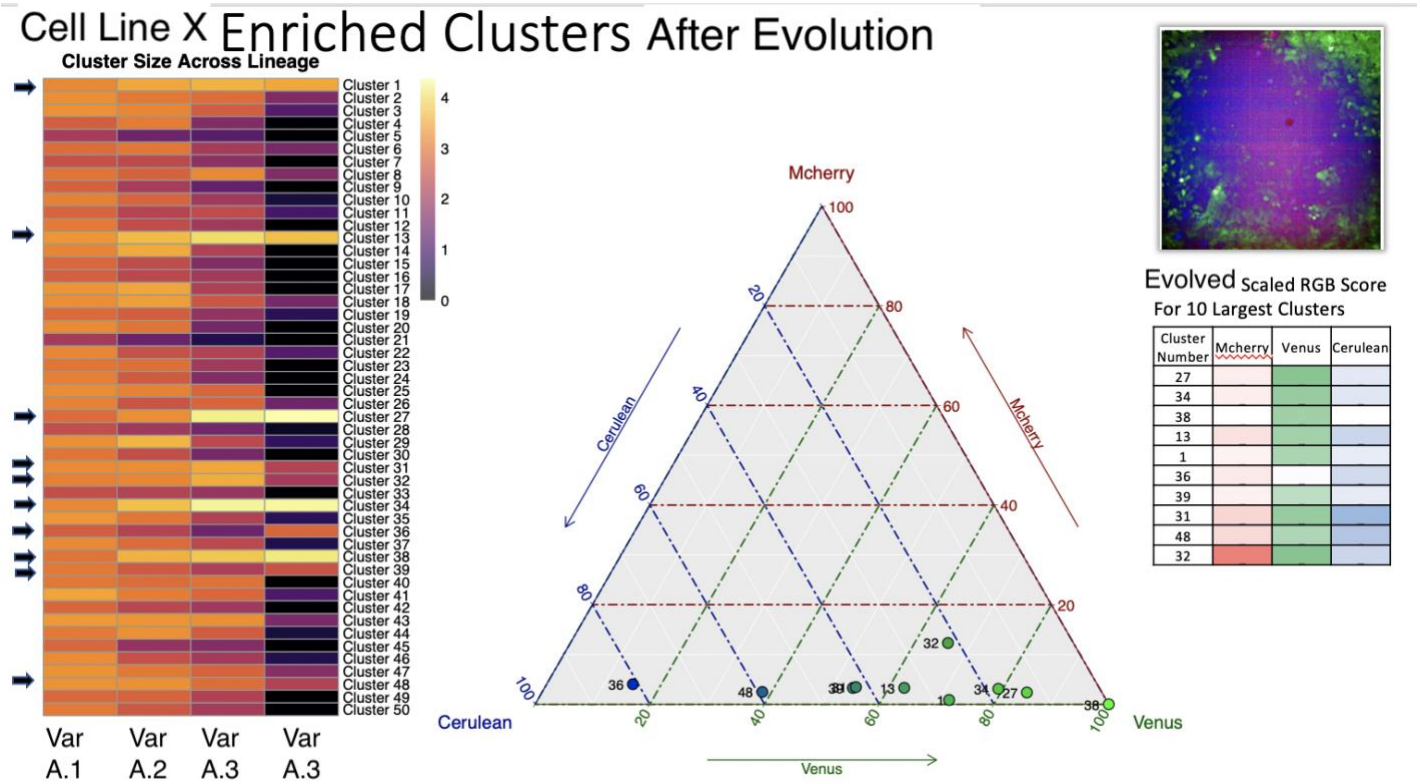
Made using ggplot2 package in R.



Elbow-plot used to determine appropriate number of clusters to use for k-means clustering.

Made using ggplot2 package in R.

No links available for this project.



Heatmap showing changes in clusters of cell populations as cancer cells evolve (left to right).

Made using pheatmap package in R.

Evolved Scaled RGB Score For 10 Largest Clusters

Cluster Number	Mcherry	Venus	Cerulean
27			
34			
38			
13			
1			
36			
39			
31			
48			
32			

← Sample image

← table showing scaled colour distribution

A ternary plot used to visualize the colour distribution of the clusters generated.

Made using ggtern package in R.

No links available for this project.