Data Visualiation with R Exercises

Load the example dataset (example2.tsv) using read\_tsv.

library(tidyverse)  
results <- read\_tsv('example2.tsv',  
 col\_types = cols(Chr = 'c', Strand = 'c'))

## Filtering and Selecting

1. Use filter to find out how many genes have an adjusted p-value less than 0.05.
2. Find out which gene has the smallest p-value by sorting the data using arrange.
3. Make a new column in the data that is -log10 of the adjusted p-value column. You can use the log10() function to calculate this.
4. Make a new data.frame that contains the GeneID, Name and all the normalised count columns.
5. Make the new data.frame data tidy using pivot\_longer.

## Plotting

1. Using the iris dataset make a plot of Petal.Width (y) against Sepal.Width (x).
2. Now colour the points by Petal.Length and use the viridis colour scale using scale\_colour\_viridis\_c.
3. Change the colouring to Species, choose a hollow shape (one of 21-25) and pick 3 colours to use with scale\_fill\_manual.