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`.