## Data Visualiation with R Exercises With Plots

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

## Filtering and Selecting

1. Use filter to find out how many genes have an adjusted p-value less than 0.05.

```
filter(results, adjp < 0.05) %>%
  nrow()
```

2. Find out which gene has the smallest p-value by sorting the data using arrange.

```
arrange(results, adjp) %>%
  select(., GeneID, Name, adjp) %>%
  head(1)
```

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.

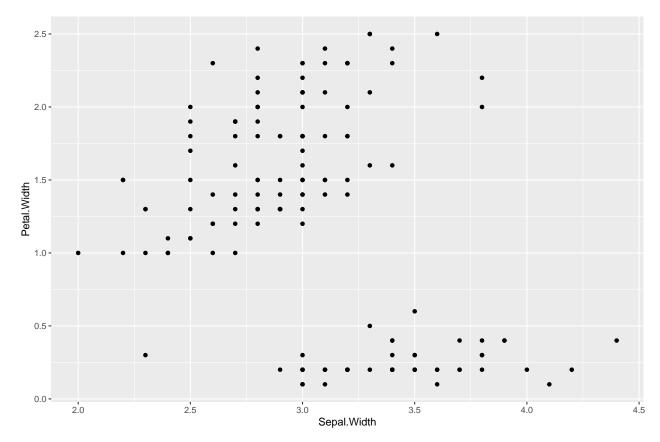
```
normalised_counts <-
select(results, GeneID, Name, contains('normalised_count'))</pre>
```

5. Make the new data.frame data tidy using pivot longer.

## **Plotting**

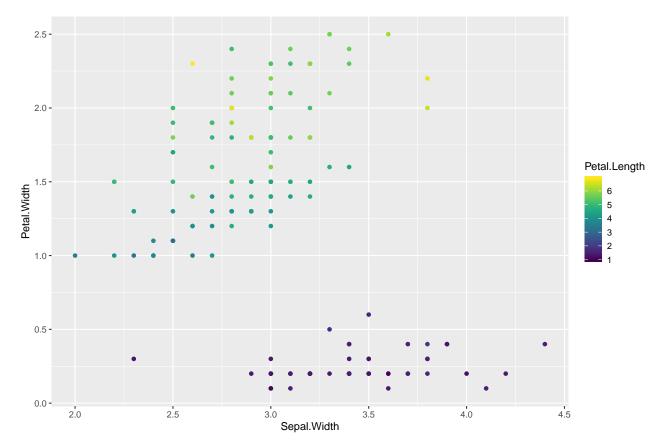
1. Using the iris dataset make a plot of Petal.Width (y) against Sepal.Width (x).

```
ggplot(data = iris) +
geom_point(aes(x = Sepal.Width, y = Petal.Width))
```



 $2. \ \ Now colour the points by Petal. Length and use the viridis colour scale using \verb|scale_colour_viridis_c|.$ 

```
ggplot(data = iris, aes(x = Sepal.Width, y = Petal.Width)) +
  geom_point(aes(colour = Petal.Length)) +
  scale_colour_viridis_c()
```



 $3. \ \ Change\ the\ colours\ to\ use\ with\ \verb|scale_fill_manual|.$ 

```
ggplot(data = iris, aes(x = Sepal.Width, y = Petal.Width)) +
  geom_point(aes(fill = Species), shape = 22, size = 3) +
  scale_fill_manual(values = c('firebrick2', 'steelblue3', 'orange'))
```

