Plotting Lines and Small Multiples with ggplot()

0. Load Everything


```
####
#00#
####
library(tidyverse)
library(knitr)
library(ggpmisc)
data("iris")
jaz <- read_csv("jaz_degs.csv")
```

---

1. Making Small Multiples with Facet Wrap

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a. Scatter Plot From 02/13/2023

This should look familiar.

```
####
#01#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))
```

Sepal Width vs. Sepal Length
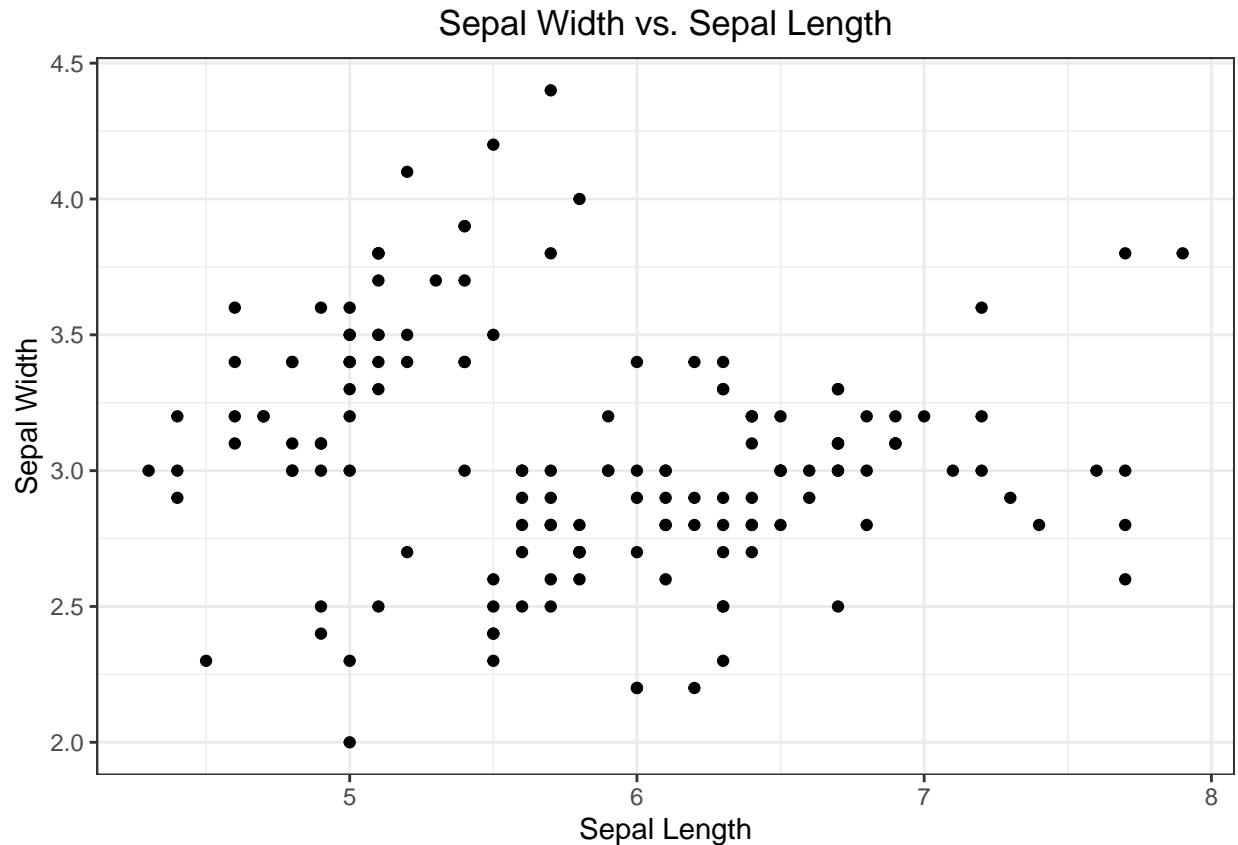
b. Facet Wrap by Species

Using the facet _wrap() function, we can make an individual plot for each level in a factor. For this plot, specifying "~Species" within facet_wrap() will make three individual plots: one for each species. Make sure to include "~".

```
####
#02#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5)) +
  facet_wrap(~Species)
```

Sepal Width vs. Sepal Length
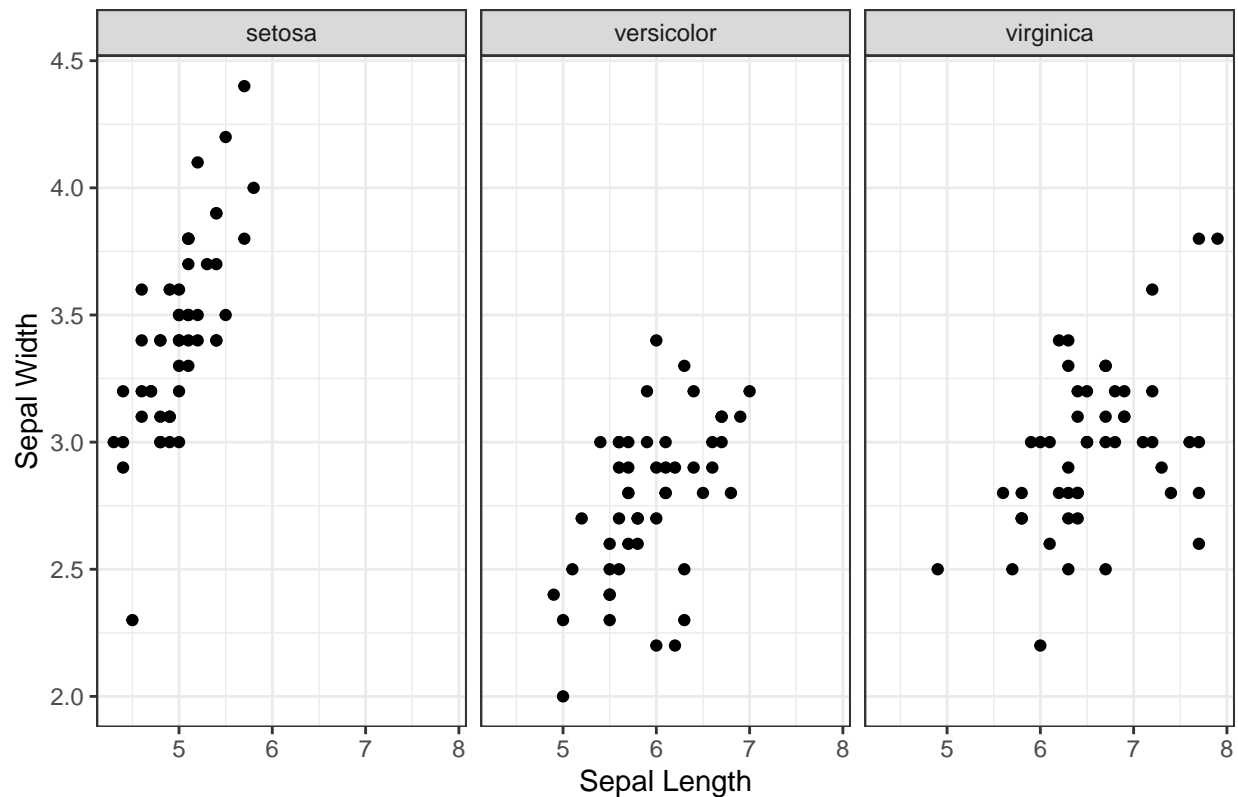
c. Free Scales in Facet Wrap

In plot 2b, the x and y axis scales are identical for all three plots. You can specify that each plot should get induvial x and y axis scales by specifying 'scales = "free" ' within facet_wrap().

```
####
#03#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5)) +
  facet_wrap(~Species,
             scales = "free")
```
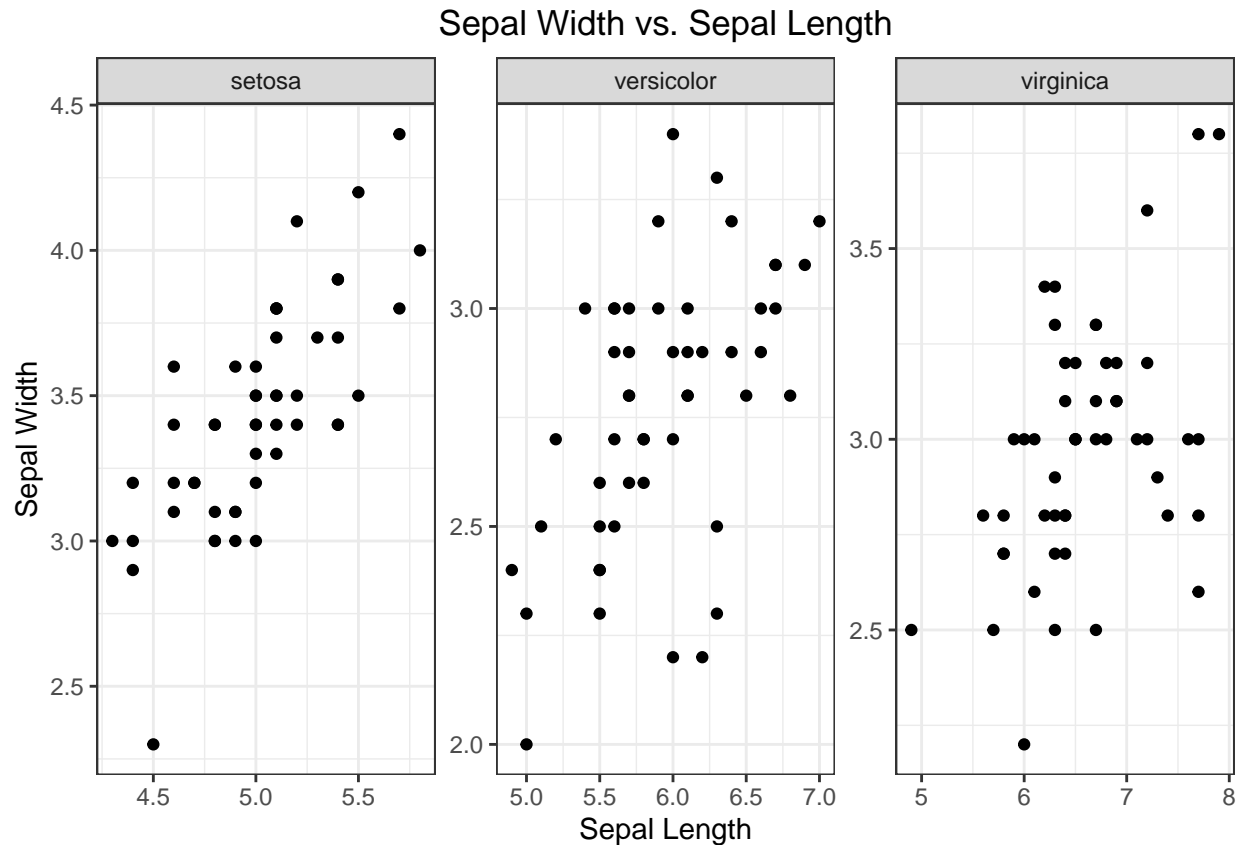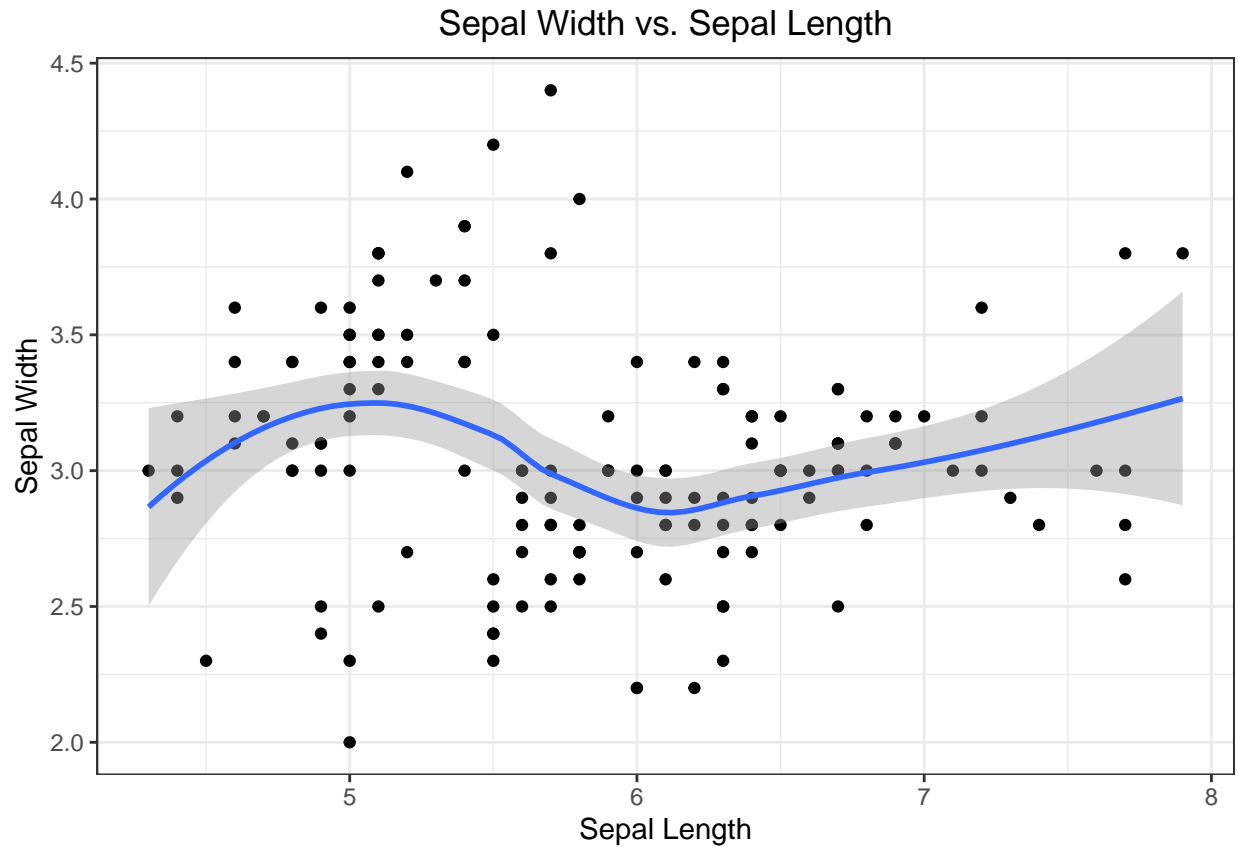
Sepal Width vs. Sepal Length

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2. Adding a Trend Line to a Scatterplot

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a. Using Default Method "loess"

Loess stands for Locally Estimated Scatterplot Smoothing. It's essentially a regression method that models "local" behavior very well.
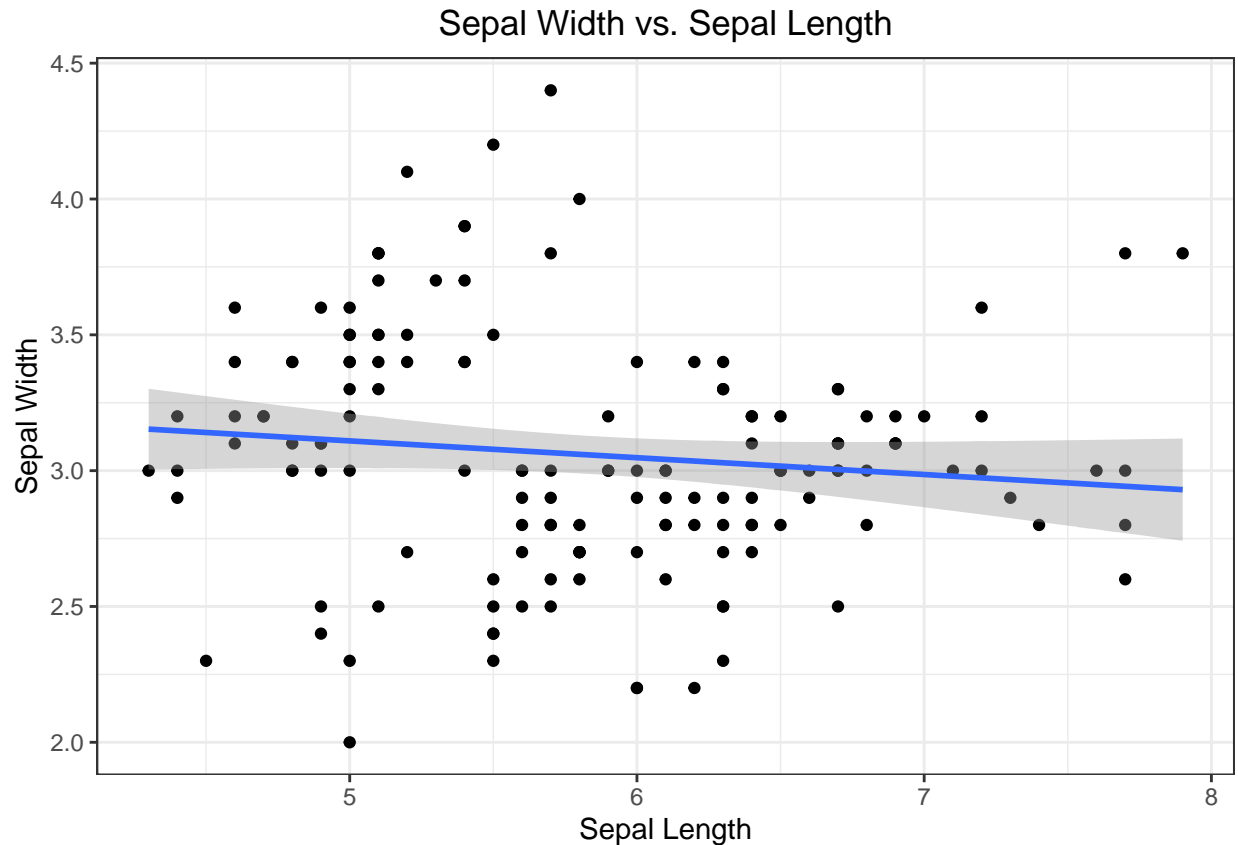
```r
####
#04#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  geom_smooth() +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))
```

Sepal Width vs. Sepal Length

b. Using Method "lm"

lm stands for Linear Model. Ordinary least squares regression is used to fit this line.

```
####
#05#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  geom_smooth(method = "lm") +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))
```

Sepal Width vs. Sepal Length

geom_smooth() has other methods beside "loess" and "lm" that may be worth checking out for you.

c. Plot R^2 for "lm" Line

It is sometimes helpful to calculate and plot an R^2 value which is the amount of variation in Y explained by X. R^2 will always be between 0 and 1. In this example, $R^2 = 0.01$ so 1% of variation in sepal width is explained by sepal length.

```
####
#06#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  geom_smooth(method = "lm") +
  stat_poly_eq(aes(label=after_stat(..rr.label..))) + #from ggpmisc package
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))
```
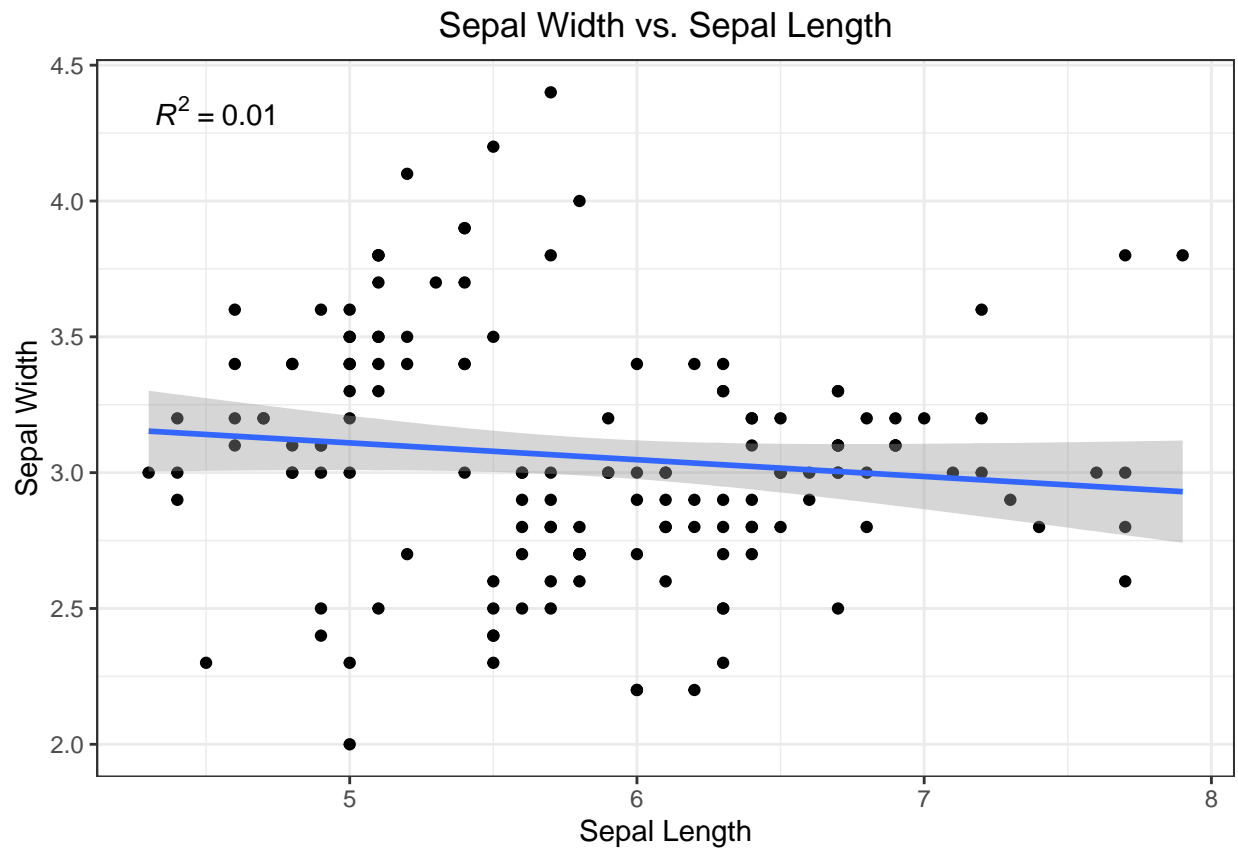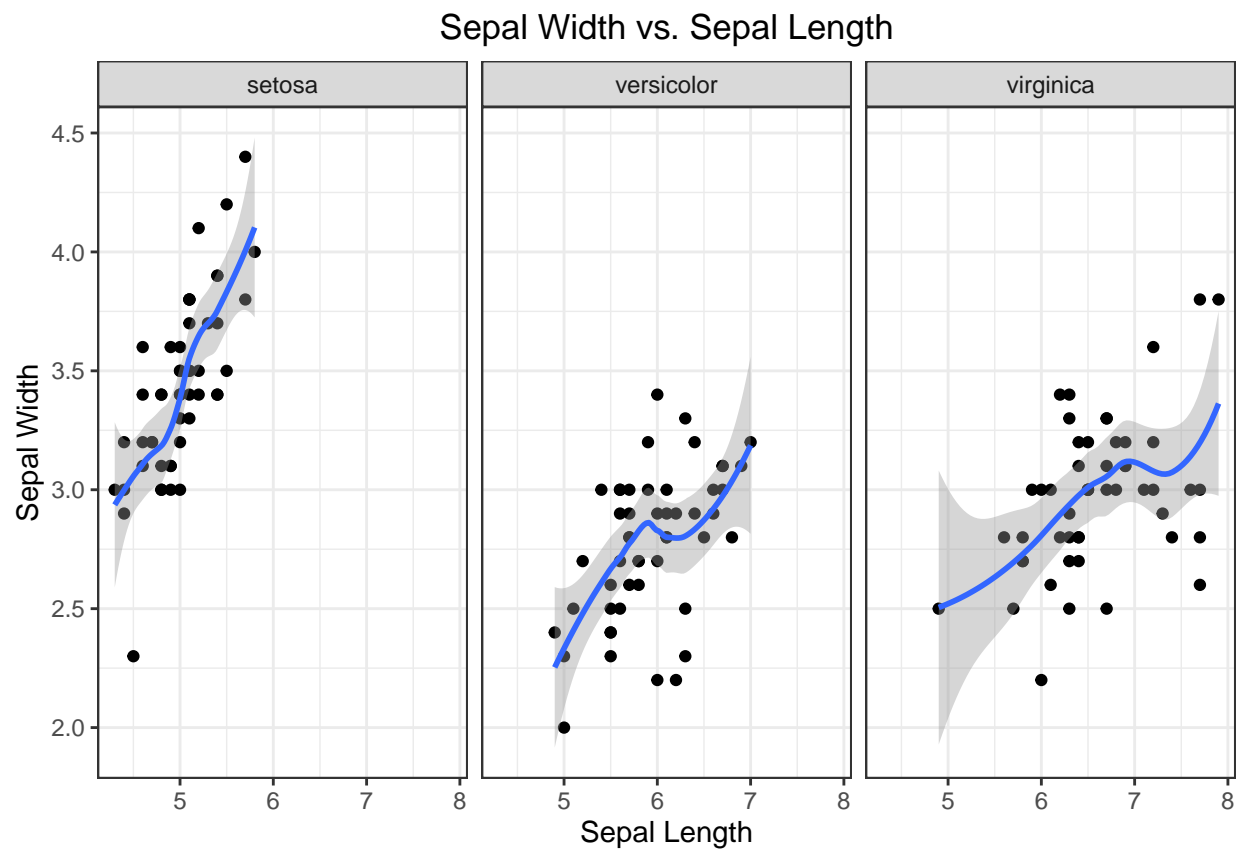
Sepal Width vs. Sepal Length
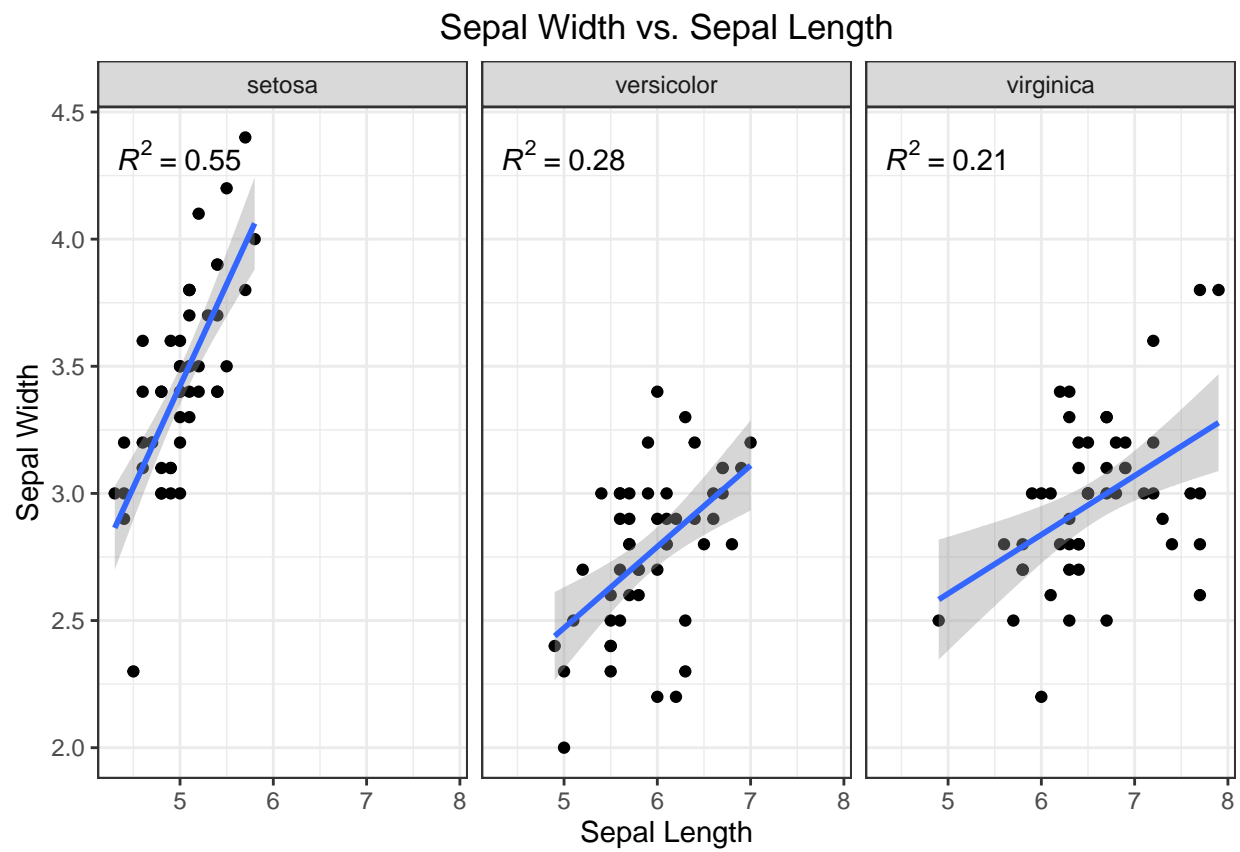
$R^2 = 0.01$

3. Try Out Small Multiples With Trend Lines

facet_wrap(~Species) and geom_smooth(method = "loess")

Sepal Width vs. Sepal Length

facet_wrap(~Species) and geom_smooth(method = "lm")

Sepal Width vs. Sepal Length

facet_wrap(~Species, scales = "free") and geom_smooth(method = "loess")

Sepal Width vs. Sepal Length

facet_wrap(~Species, scales = "free") and geom_smooth(method = "lm")

Sepal Width vs. Sepal Length

---
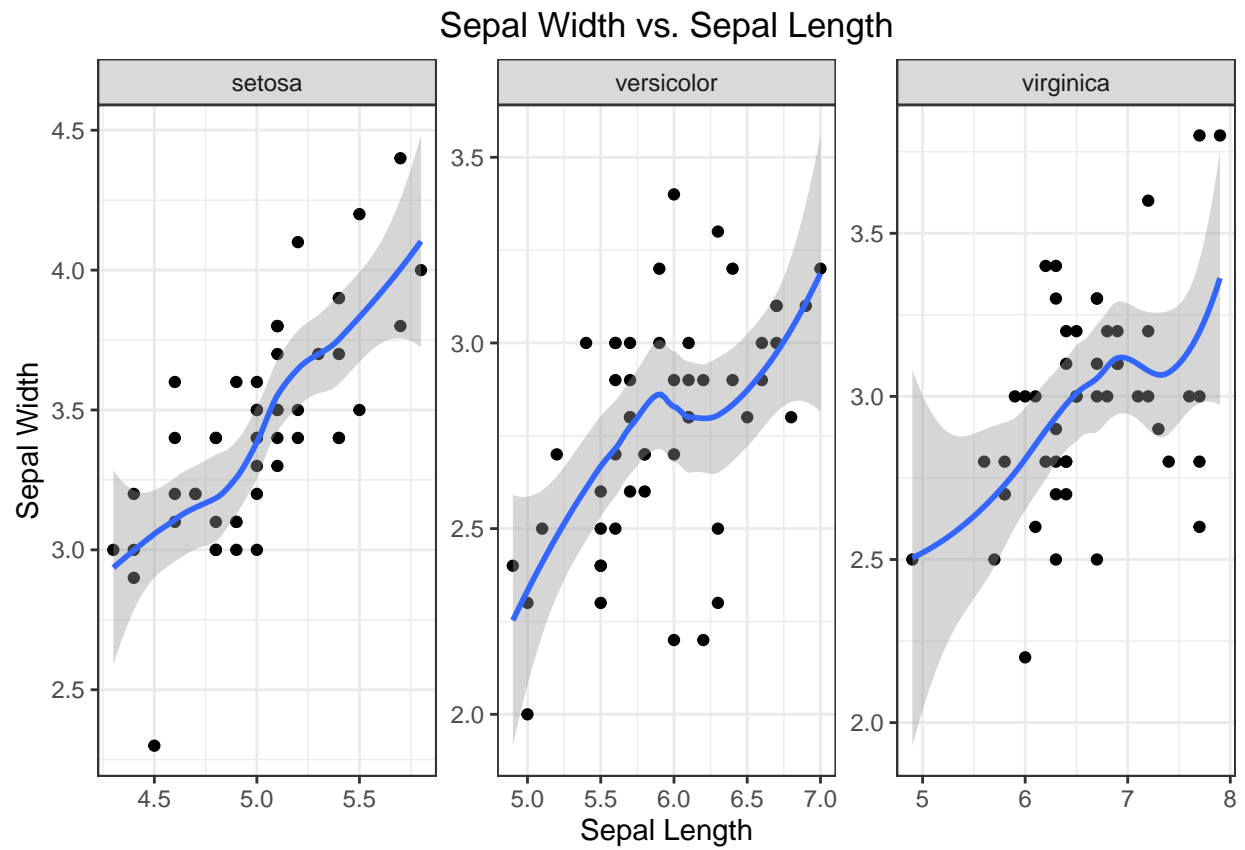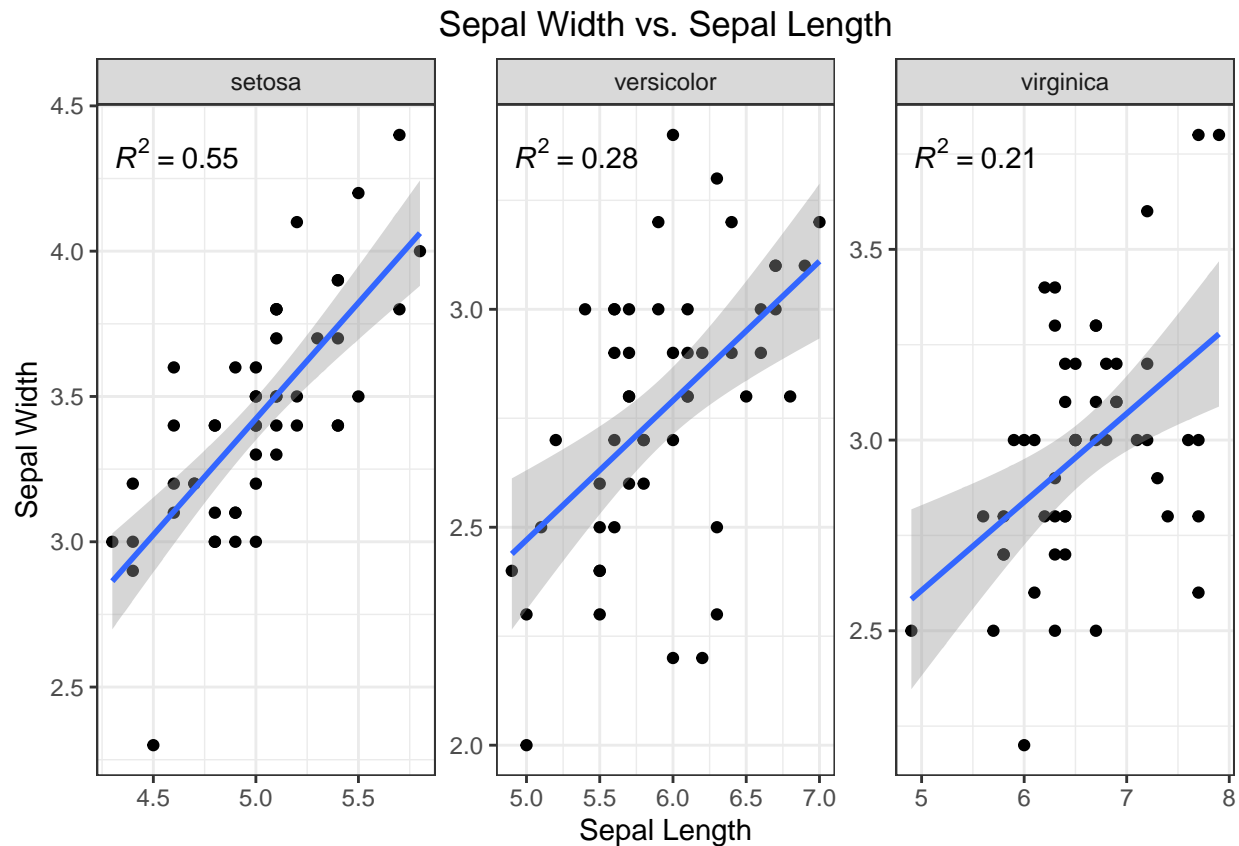
4. Time Course with JAZ Expression Data

This dataset is from Zander et. al., 2020. In this study, the phytohormone jasmonic acid (JA) was applied to Arabidopsis plants and their transcriptomic response over time was captured via mRNA sequencing and differential gene expression analysis.

I've taken a subset this data to include only JAZ genes which themselves are repressors of the JA pathway.

```
####
#11#
####
jaz %>%
  head(20)
```

```
## # A tibble: 20 x 11
##      ...1 Gene_ID     logFC logCPM    LR    PValue     FDR Sig   Time_~1 Symbol
##     <dbl> <chr>       <dbl>  <dbl> <dbl>     <dbl>   <dbl> <chr>   <dbl> <chr>
## 1       1 AT2G34600    2.74   2.76  31.5   2.04e-8 1.23e-5 Yes      0.25 JAZ7
```

```
## 2     2 AT1G19180  1.96    7.51  22.2      2.48e-6 7.85e-4 Yes      0.25 AtJAZ1
## 3     3 AT1G30135  4.35   -0.943 20.9      4.79e-6 1.21e-3 Yes      0.25 JAZ8
## 4     4 AT1G74950  1.17    6.28  11.8      5.89e-4 3.50e-2 Yes      0.25 JAZ2
## 5     5 AT1G17380  2.45    2.68  10.4      1.27e-3 5.44e-2 No       0.25 JAZ5
## 6     6 AT3G22275  2.17   -0.973  7.99     4.71e-3 1.23e-1 No       0.25 JAZ13
## 7     7 AT1G72450  1.10    4.97   6.69     9.71e-3 1.79e-1 No       0.25 JAZ6
## 8     8 AT1G48500 -0.374   2.29   1.08     3.00e-1 7.72e-1 No       0.25 AtJAZ4
## 9     9 AT3G43440 -0.0673  3.79   0.231    6.31e-1 9.25e-1 No       0.25 JAZ11
## 10   10 AT1G70700  0.166   6.40   0.196    6.58e-1 9.31e-1 No       0.25 JAZ9
## 11   11 AT5G20900 -0.0520  5.82   0.139    7.09e-1 9.44e-1 No       0.25 JAZ12
## 12   12 AT1G30135  5.01   -0.943 27.9      1.29e-7 2.83e-5 Yes      0.5  JAZ8
## 13   13 AT1G19180  2.15    7.51  26.3      2.89e-7 5.99e-5 Yes      0.5  AtJAZ1
## 14   14 AT2G34600  2.42    2.76  25.0      5.68e-7 1.08e-4 Yes      0.5  JAZ7
## 15   15 AT1G74950  1.71    6.28  24.2      8.61e-7 1.57e-4 Yes      0.5  JAZ2
## 16   16 AT1G72450  2.11    4.97  23.2      1.46e-6 2.47e-4 Yes      0.5  JAZ6
## 17   17 AT1G17380  2.63    2.68  11.8      6.03e-4 3.41e-2 Yes      0.5  JAZ5
## 18   18 AT3G22275  2.56   -0.973 11.6      6.63e-4 3.64e-2 Yes      0.5  JAZ13
## 19   19 AT1G70700  1.04    6.40   7.51     6.15e-3 1.80e-1 No       0.5  JAZ9
## 20   20 AT1G48500  0.421   2.29   1.40     2.36e-1 1.00e+0 No       0.5  AtJAZ4
## # ... with 1 more variable: primary <lgl>, and abbreviated variable name
## #   1: Time_hrs
```

Scatter Plot of JAZ Genes Overtime

We can see that our standard approach scatter plot approach is not very insightful.
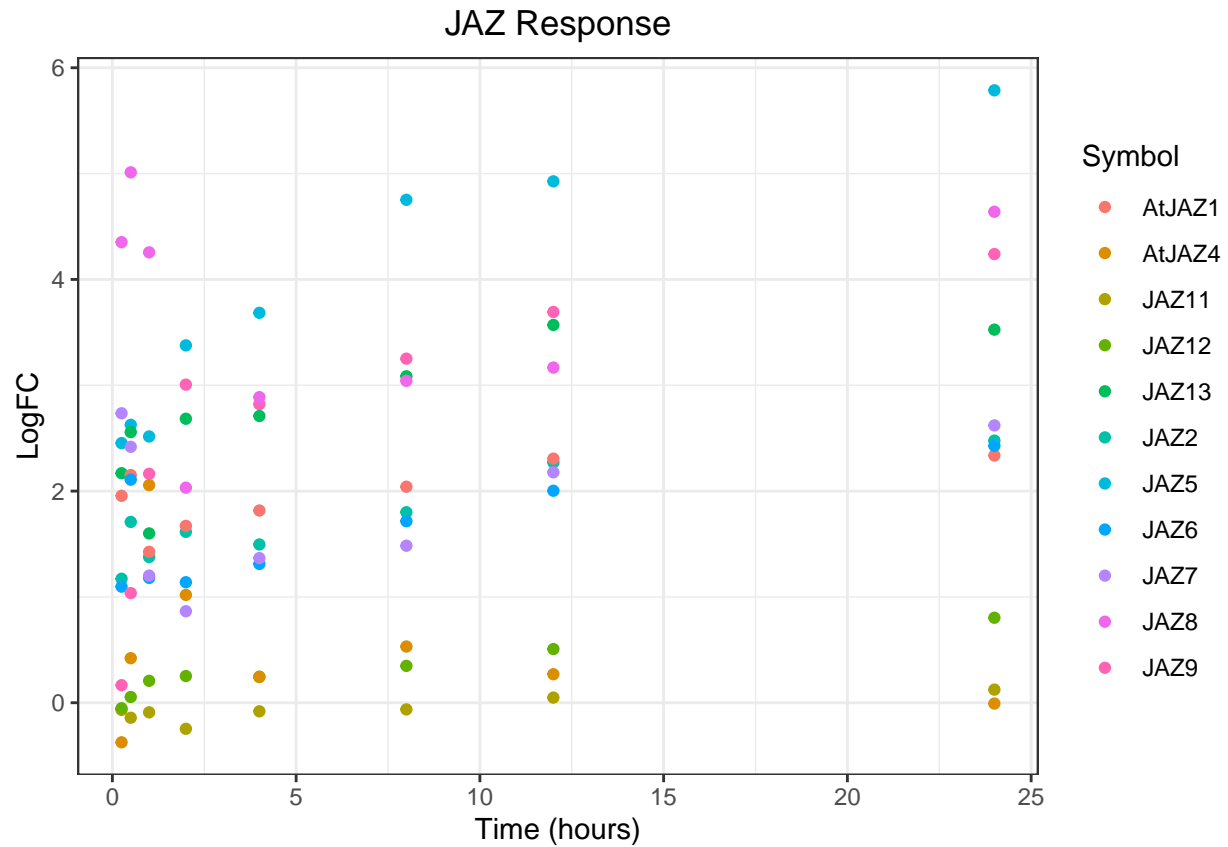
```r
####
#12#
####
jaz %>%
  ggplot(aes(x = Time_hrs, y = logFC)) +
  geom_point() +
  labs(x = "Time (hours)", y = "LogFC",
       title = "JAZ Response") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))
```
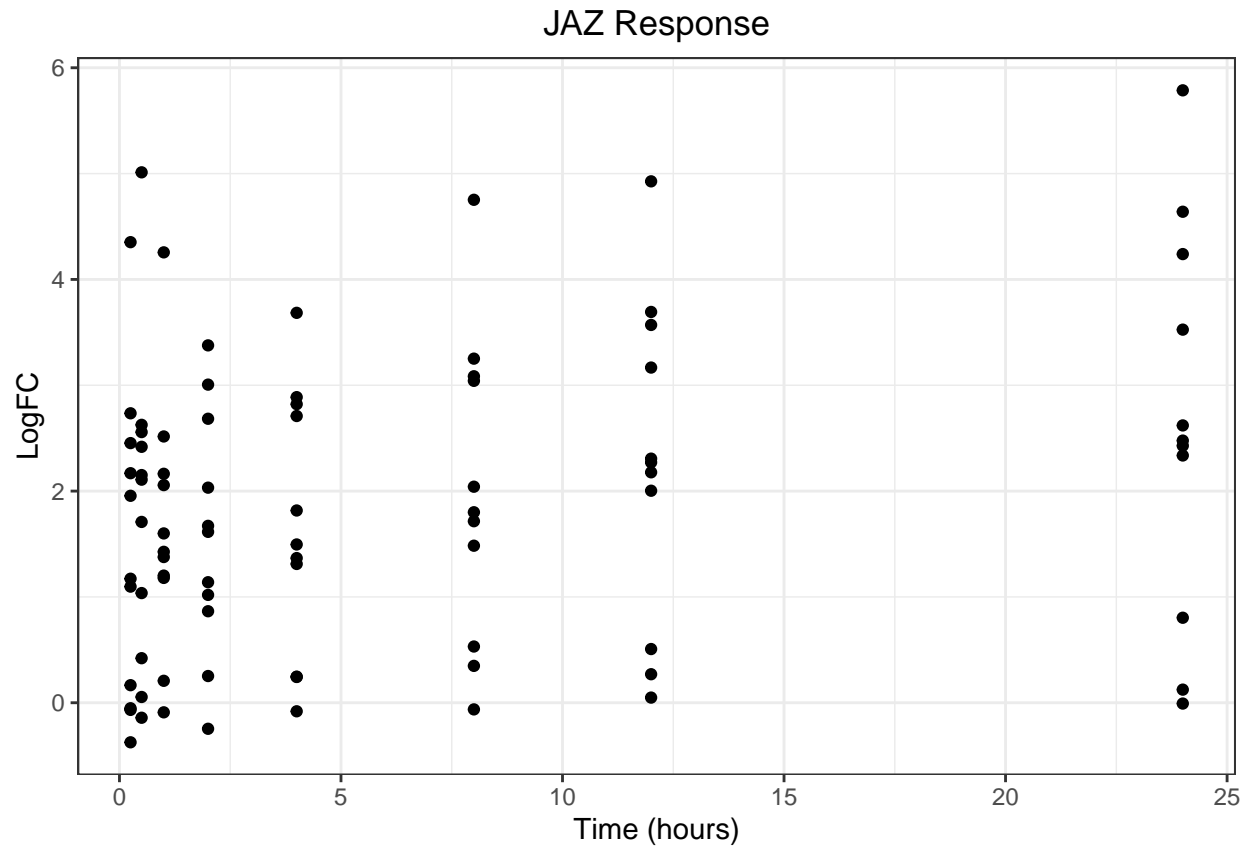
Scatter Plot and Color by Gene Symbol

Coloring by gene symbol is a little better but still not very insightful.

```
####
#13#
####
jaz %>%
  ggplot(aes(x = Time_hrs, y = logFC, color = Symbol)) +
  geom_point() +
  labs(x = "Time (hours)", y = "LogFC",
       title = "JAZ Response") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))
```

Add geom_line() to Connect Points by Symbol

```
####
#14#
####
jaz %>%
  ggplot(aes(x = Time_hrs, y = logFC, color = Symbol)) +
  geom_point() +
  geom_line() +
  labs(x = "Time (hours)", y = "LogFC",
       title = "JAZ Response") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))
```
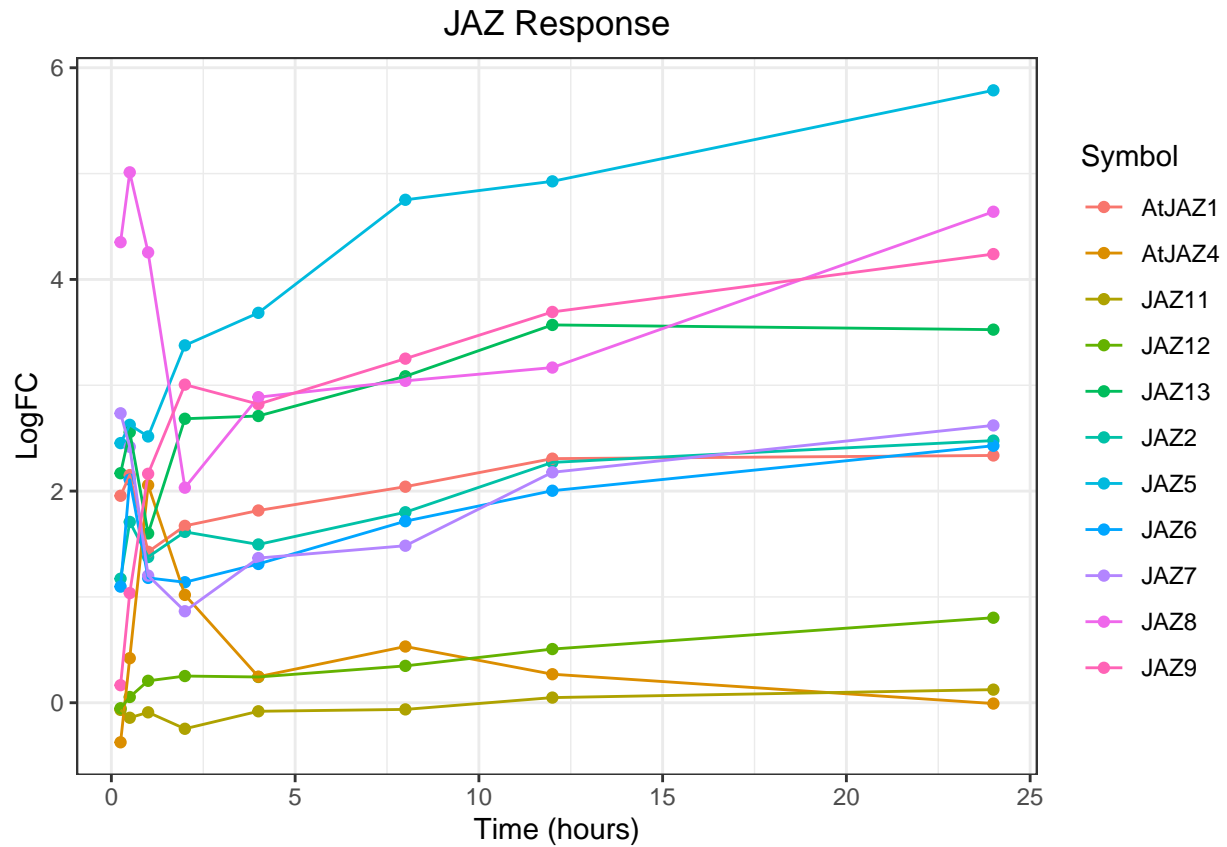
JAZ Response

Note that "color = Symbol" is required to generate the appropriate plot.

```
####
#15#
####
jaz %>%
  ggplot(aes(x = Time_hrs, y = logFC)) +
  geom_point() +
  geom_line() +
  labs(x = "Time (hours)", y = "LogFC",
       title = "JAZ Response") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))
```
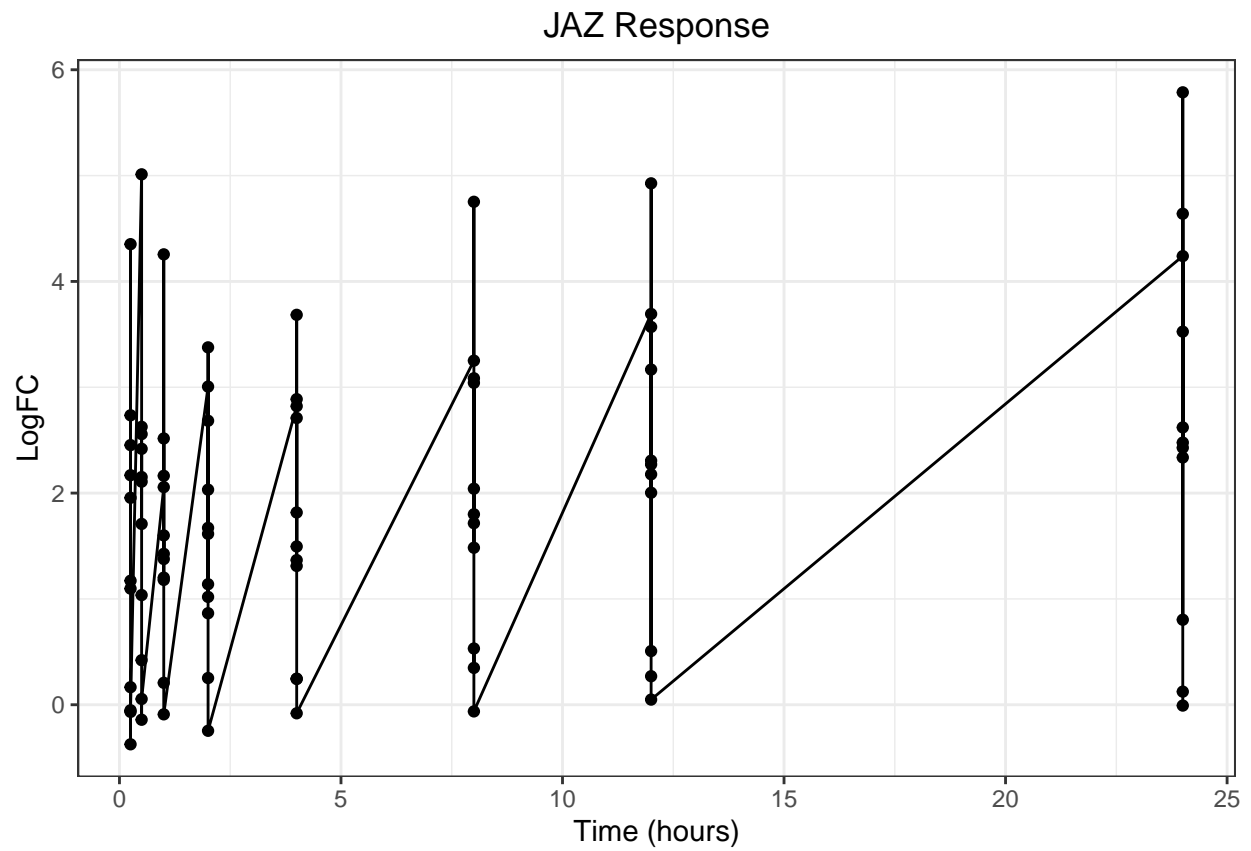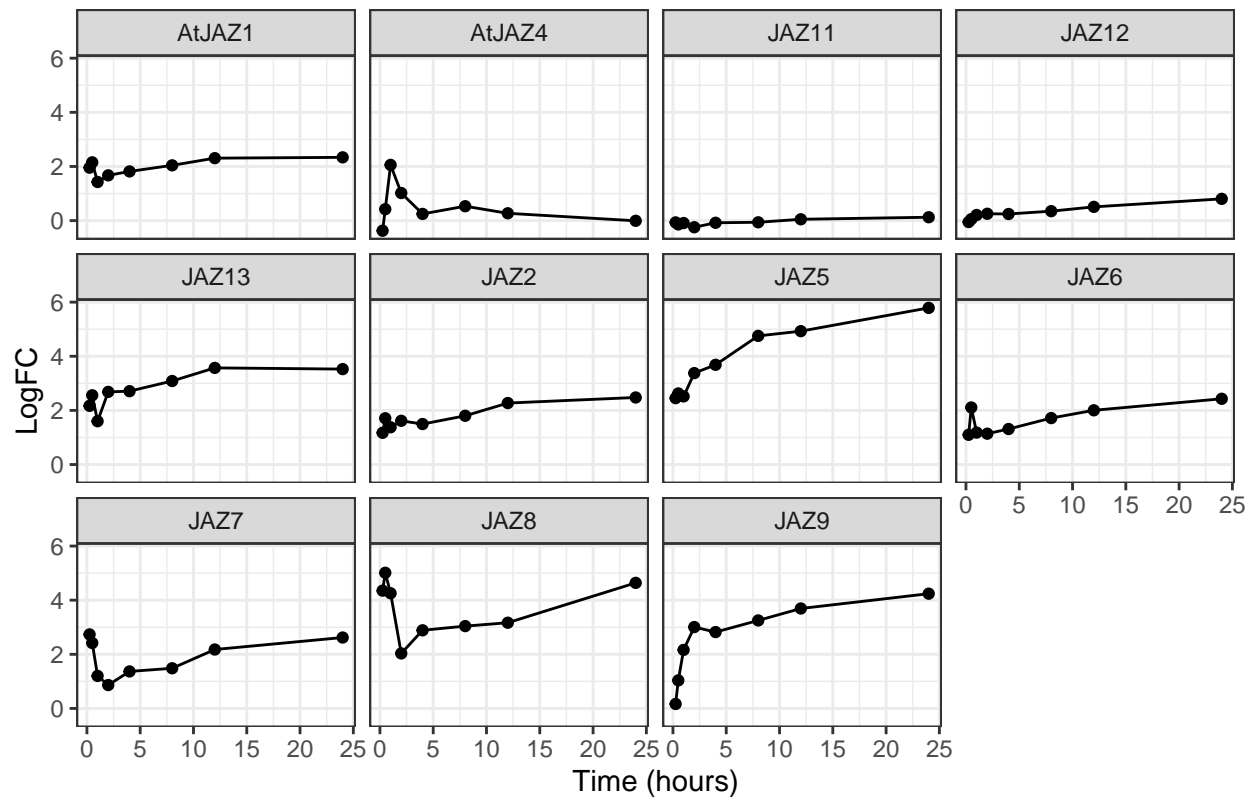
JAZ Response

5. Add Facet Wrap to JAZ Time Course

JAZ Response

JAZ Response
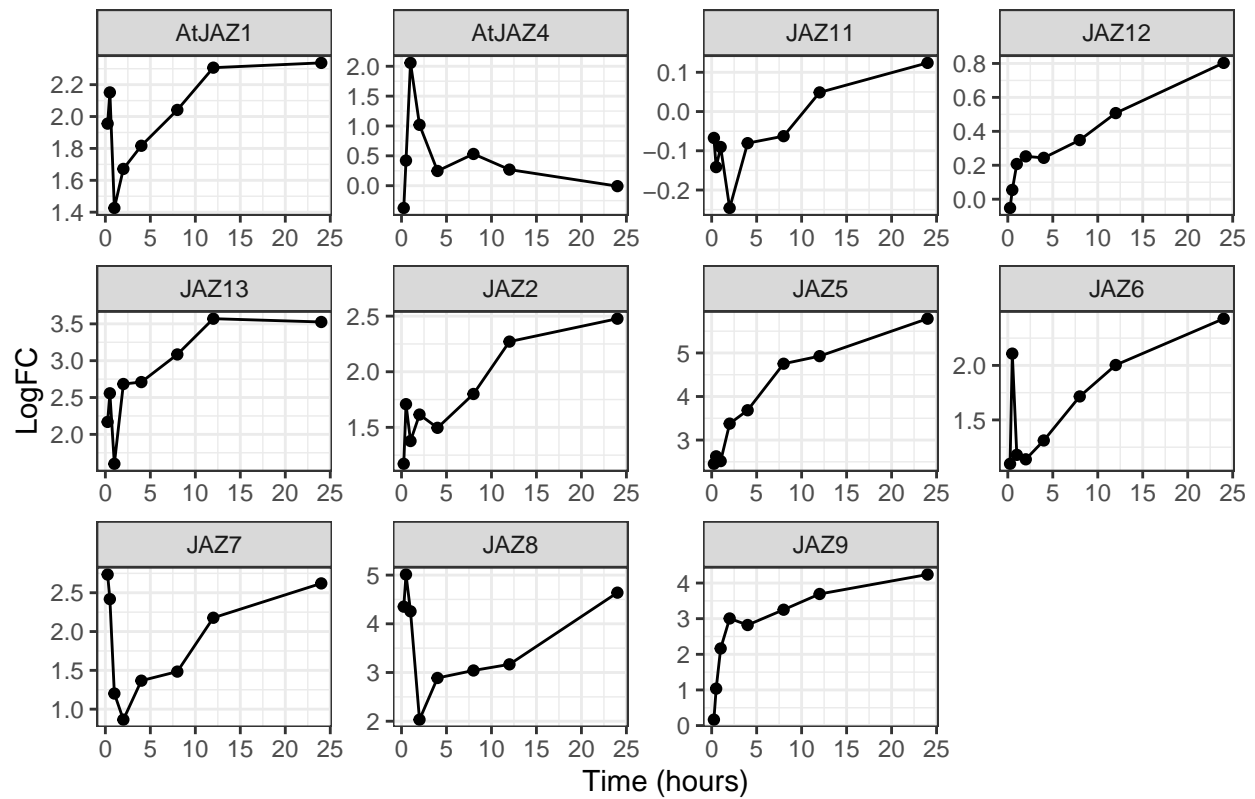
Appendix

```
####
#00#
####
library(tidyverse)
library(knitr)
library(ggpmisc)
data("iris")
jaz <- read_csv("jaz_degs.csv")

####
#01#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))
```

```
####
#02#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5)) +
  facet_wrap(~Species)

####
#03#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5)) +
  facet_wrap(~Species,
             scales = "free")

####
#04#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  geom_smooth() +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))

####
#05#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  geom_smooth(method = "lm") +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))

####
#06#
####
iris %>%
```

```r
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  geom_smooth(method = "lm") +
  stat_poly_eq(aes(label=after_stat(..rr.label..))) + #from ggpmisc package
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))

####
#07#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  geom_smooth() +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5)) +
  facet_wrap(~Species)

####
#08#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  geom_smooth(method = "lm") +
  stat_poly_eq(aes(label=after_stat(..rr.label..))) +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5)) +
  facet_wrap(~Species)

####
#09#
####
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  geom_smooth() +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5)) +
  facet_wrap(~Species,
             scales = "free")

####
#10#
####
```

```r
iris %>%
  ggplot(aes(x = Sepal.Length, y = Sepal.Width)) +
  geom_point() +
  geom_smooth(method = "lm") +
  stat_poly_eq(aes(label=after_stat(..rr.label..))) +
  labs(x = "Sepal Length", y = "Sepal Width",
       title = "Sepal Width vs. Sepal Length") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5)) +
  facet_wrap(~Species,
             scales = "free")

####
#11#
####
jaz %>%
  head(20)

####
#12#
####
jaz %>%
  ggplot(aes(x = Time_hrs, y = logFC)) +
  geom_point() +
  labs(x = "Time (hours)", y = "LogFC",
       title = "JAZ Response") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))

####
#13#
####
jaz %>%
  ggplot(aes(x = Time_hrs, y = logFC, color = Symbol)) +
  geom_point() +
  labs(x = "Time (hours)", y = "LogFC",
       title = "JAZ Response") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))

####
#14#
####
jaz %>%
  ggplot(aes(x = Time_hrs, y = logFC, color = Symbol)) +
  geom_point() +
  geom_line() +
  labs(x = "Time (hours)", y = "LogFC",
       title = "JAZ Response") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))

####
```

```
#15#
####
jaz %>%
  ggplot(aes(x = Time_hrs, y = logFC)) +
  geom_point() +
  geom_line() +
  labs(x = "Time (hours)", y = "LogFC",
       title = "JAZ Response") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))

####
#16#
####
jaz %>%
  ggplot(aes(x = Time_hrs, y = logFC)) +
  geom_point(aes()) +
  geom_line() +
  facet_wrap(~Symbol) +
  labs(x = "Time (hours)", y = "LogFC",
       title = "JAZ Response") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))

####
#17#
####
jaz %>%
  ggplot(aes(x = Time_hrs, y = logFC)) +
  geom_point() +
  geom_line() +
  facet_wrap(~Symbol,
             scales = "free") +
  labs(x = "Time (hours)", y = "LogFC",
       title = "JAZ Response") +
  theme_bw() +
  theme(plot.title = element_text(hjust = 0.5))
```