

Stats with geoms

INTERMEDIATE DATA VISUALIZATION WITH GGPLOT2



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ggplot2, course 2

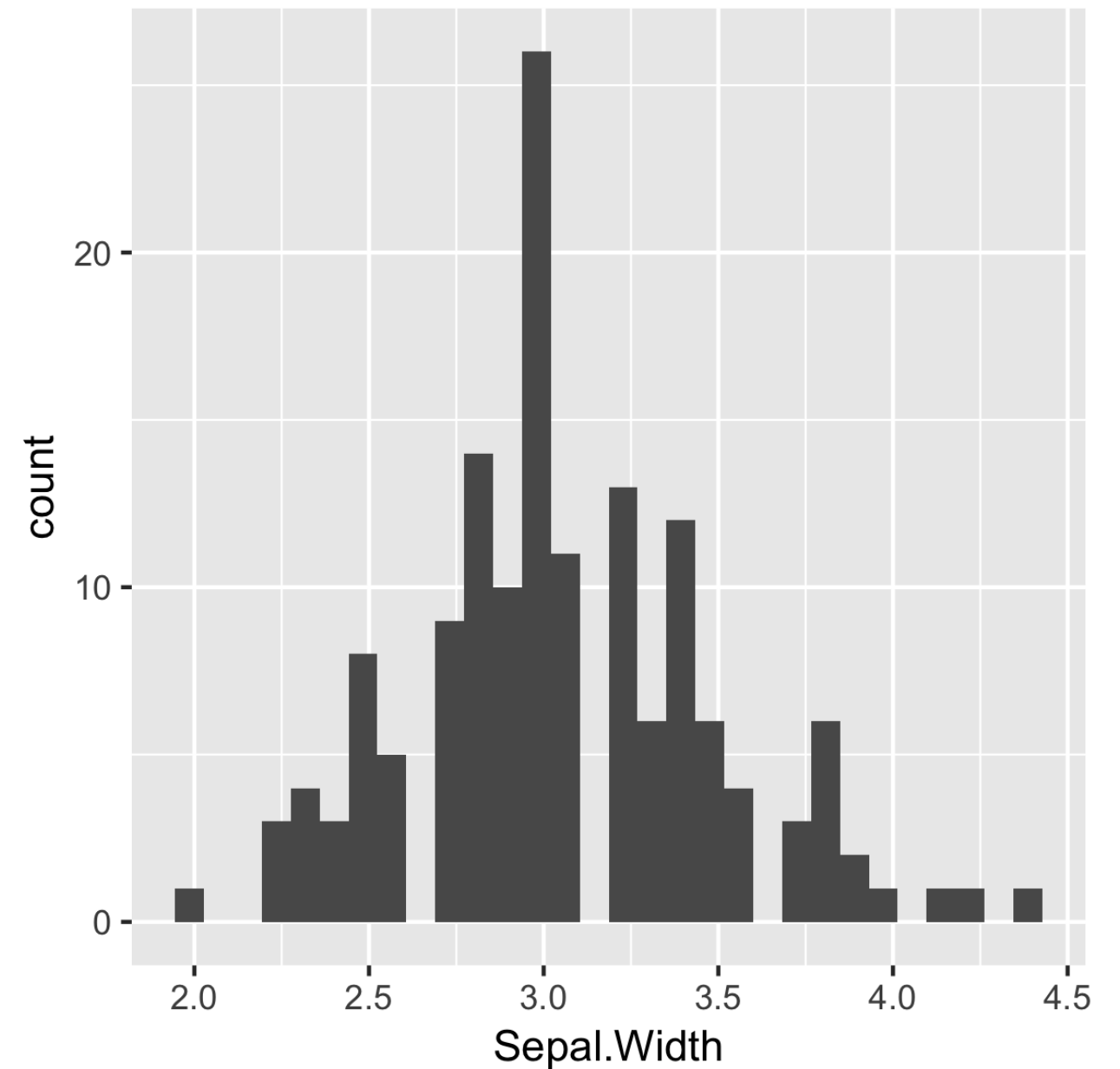
- Statistics
- Coordinates
- Facets
- Data Visualization Best Practices

Statistics layer

- Two categories of functions
 - Called from within a geom
 - Called independently
- `stats_`

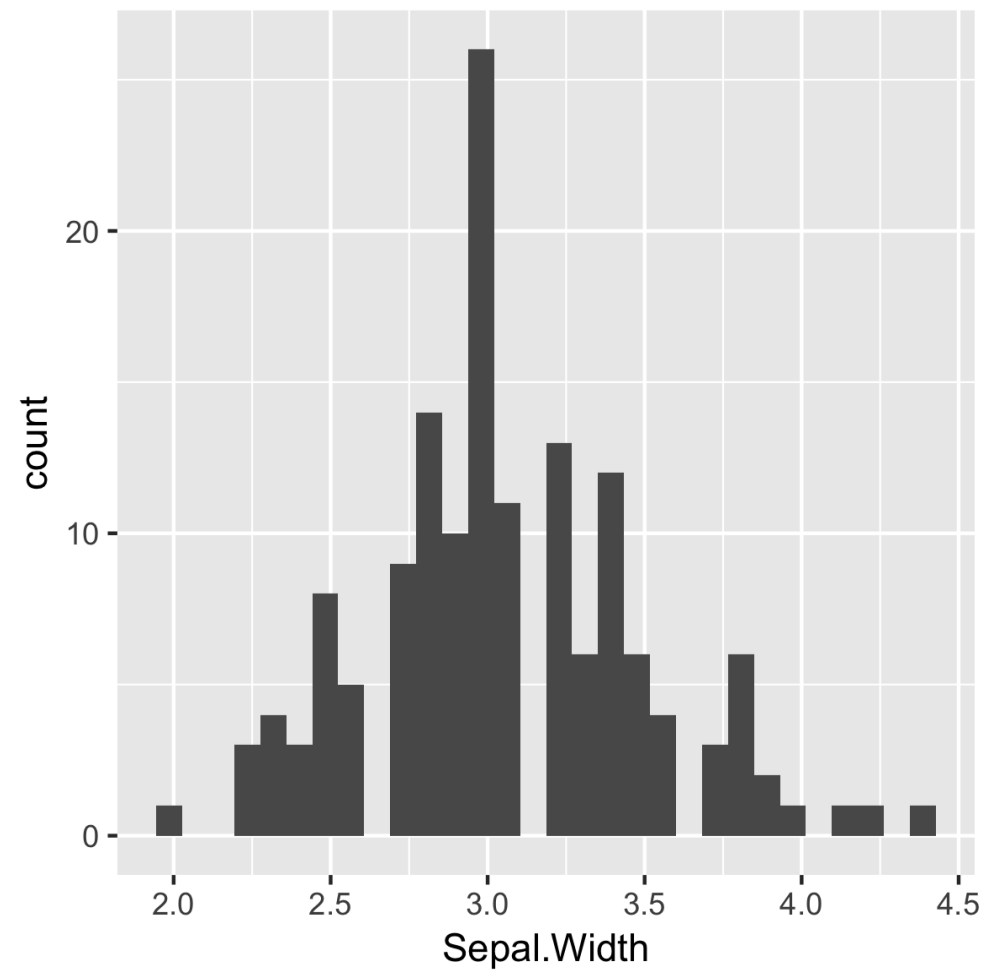
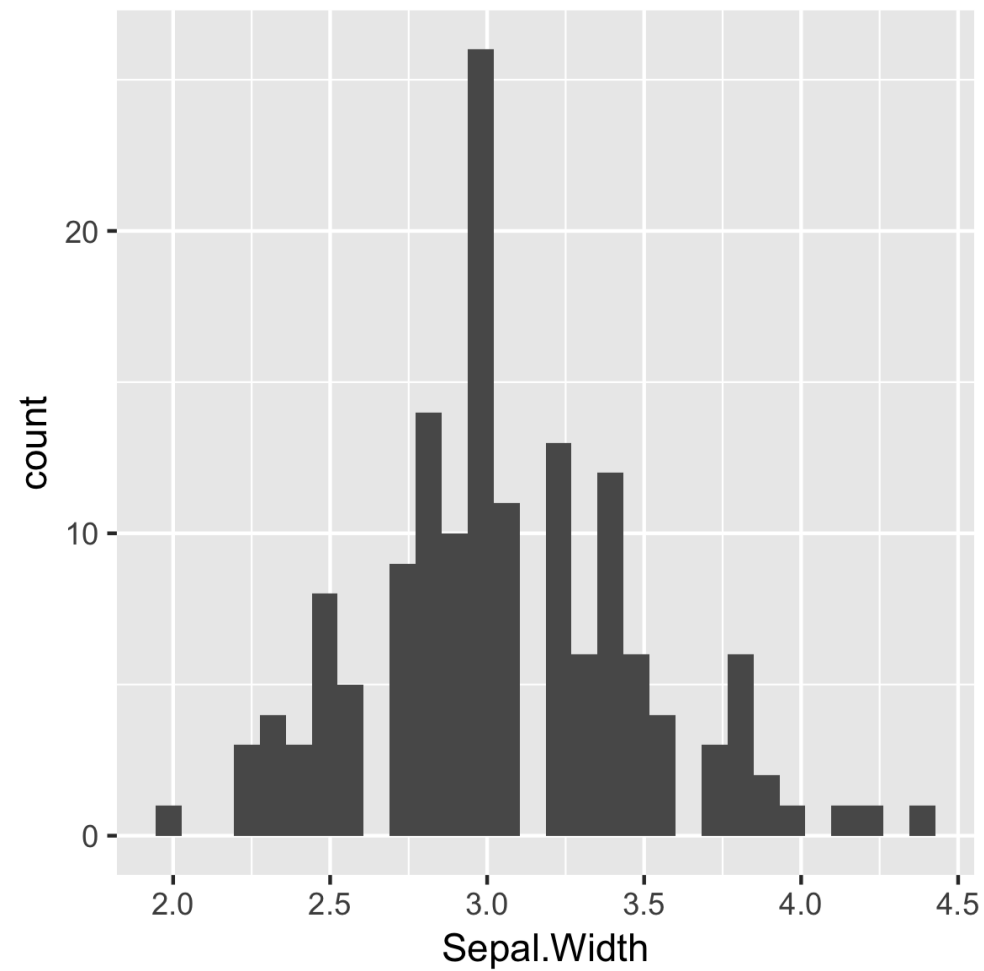
geom_ <-> stat_

```
p <- ggplot(iris, aes(x = Sepal.Width))  
p + geom_histogram()
```



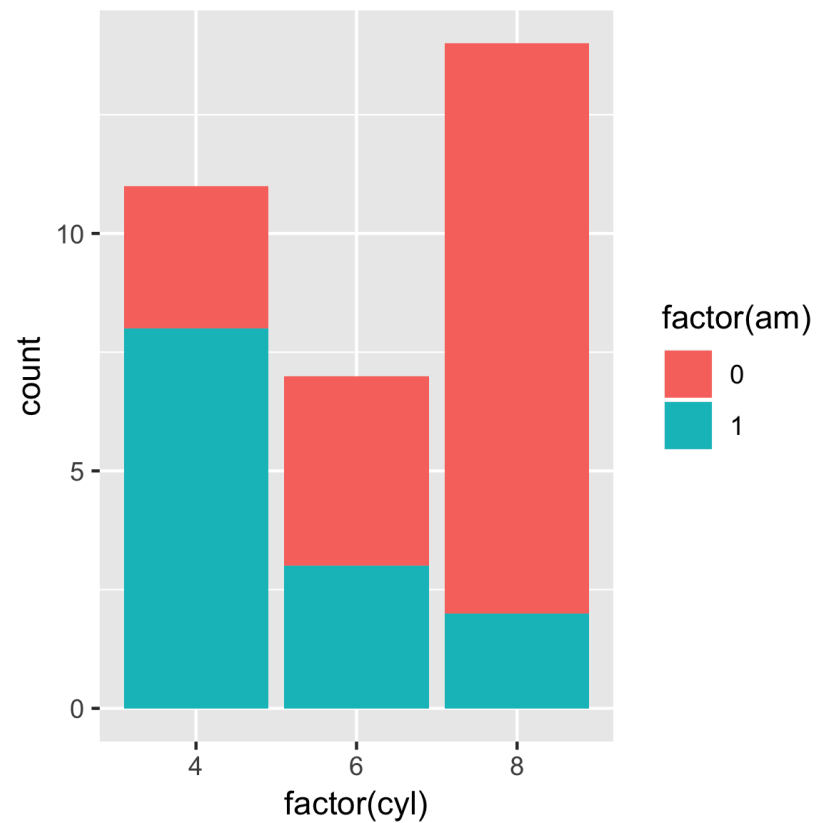
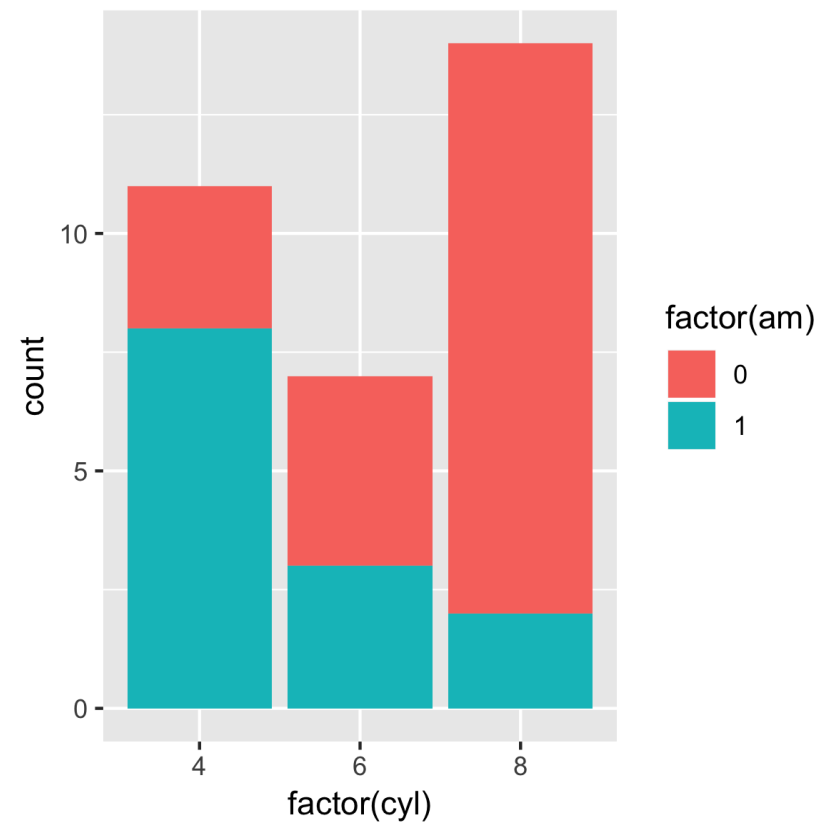
geom_ <-> stat_

```
p <- ggplot(iris, aes(x = Sepal.Width))  
p + geom_histogram()  
p + geom_bar()
```



geom_ <-> stat_

```
p <- ggplot(mtcars, aes(x = factor(cyl), fill = factor(am)))  
p + geom_bar()  
p + stat_count()
```



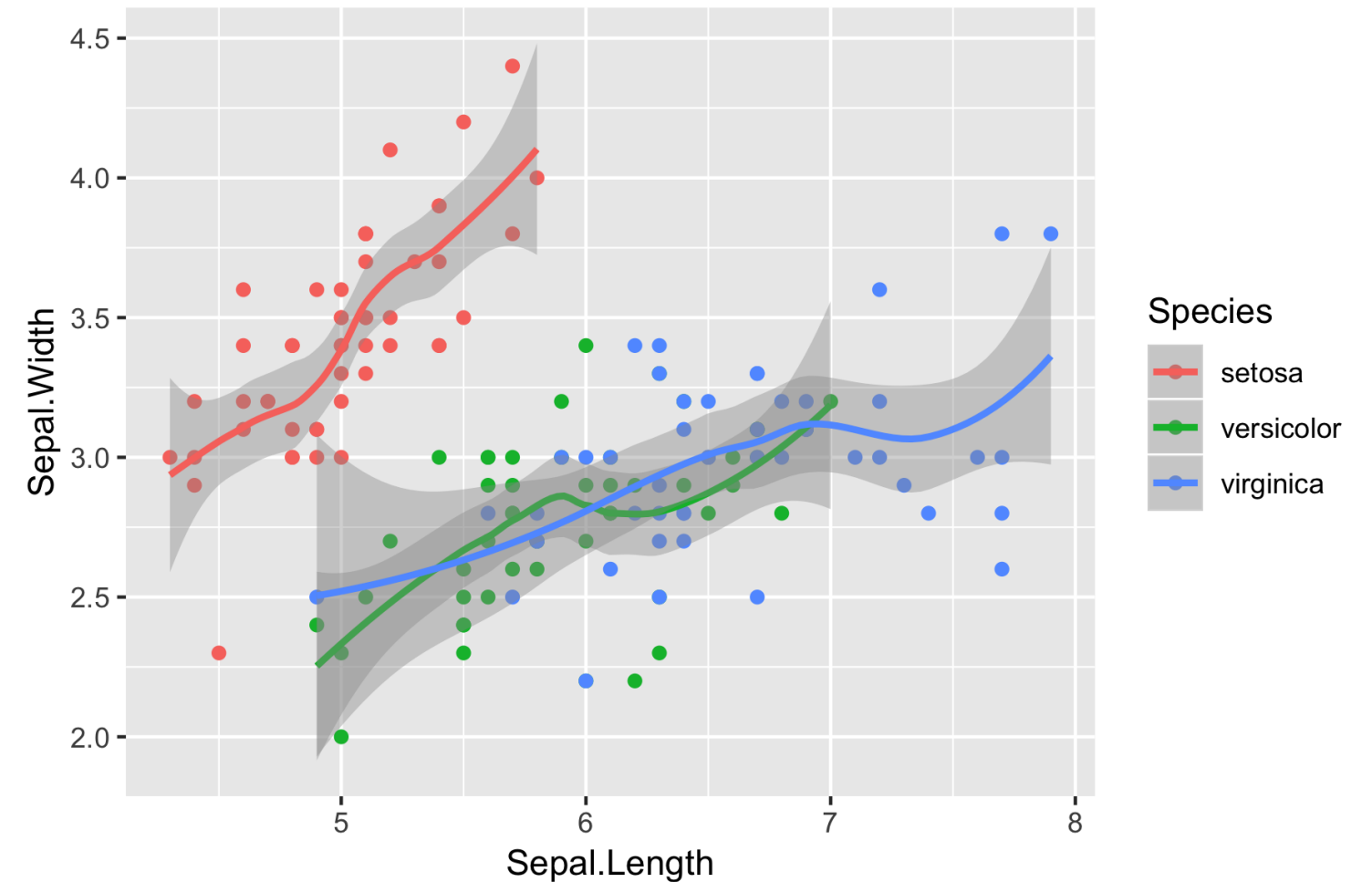
The geom_/stat_ connection

| stat_ | geom_ |
|--------------|------------------------------------|
| stat_bin() | geom_histogram() , geom_freqpoly() |
| stat_count() | geom_bar() |

stat_smooth()

```
ggplot(iris, aes(x = Sepal.Length,  
                 y = Sepal.Width,  
                 color = Species)) +  
  
  geom_point() +  
  geom_smooth()
```

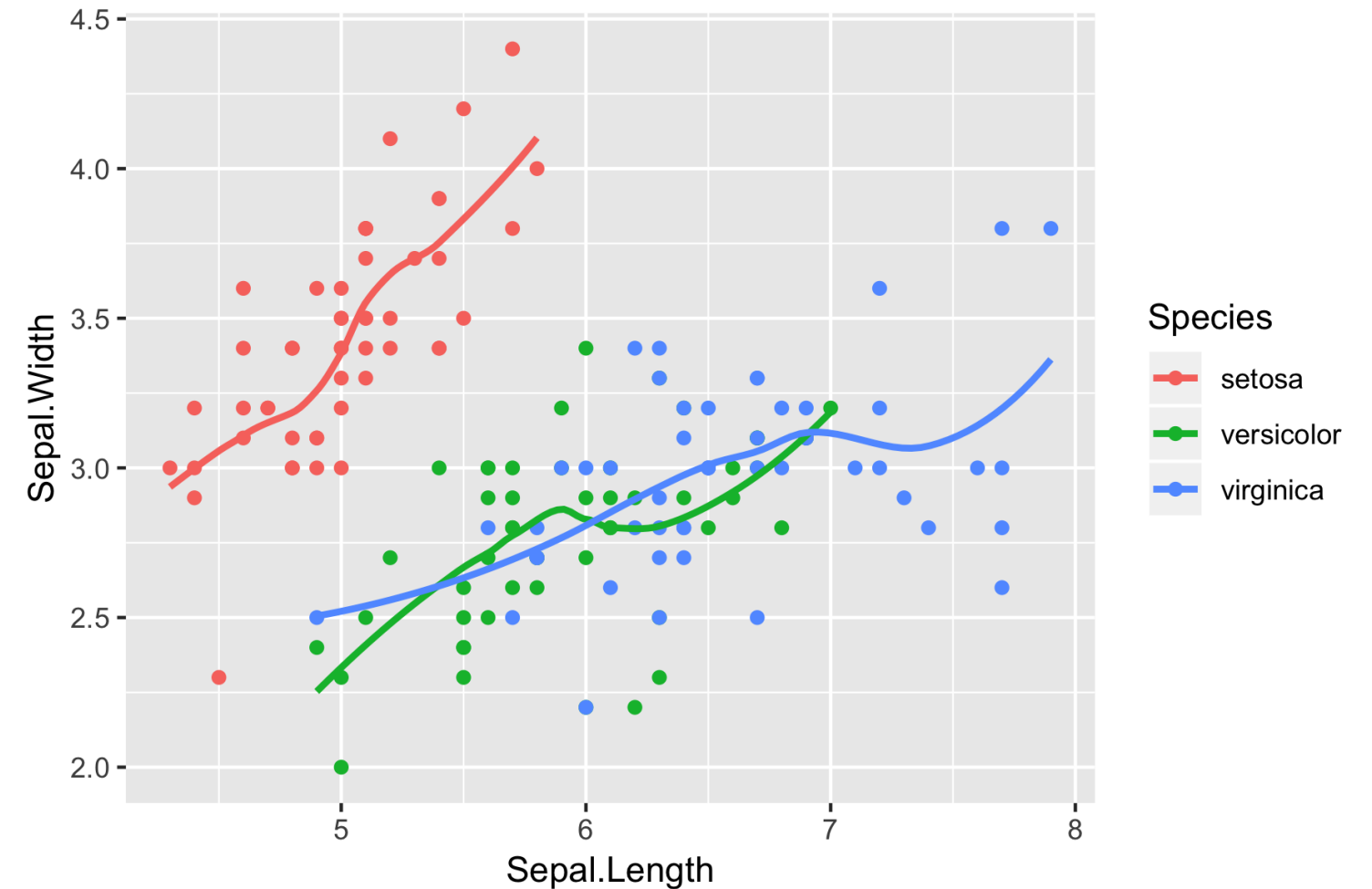
```
geom_smooth() using method = 'loess' and  
formula 'y ~ x'
```



stat_smooth(se = FALSE)

```
ggplot(iris, aes(x = Sepal.Length,  
                 y = Sepal.Width,  
                 color = Species)) +  
  
  geom_point() +  
  geom_smooth(se = FALSE)
```

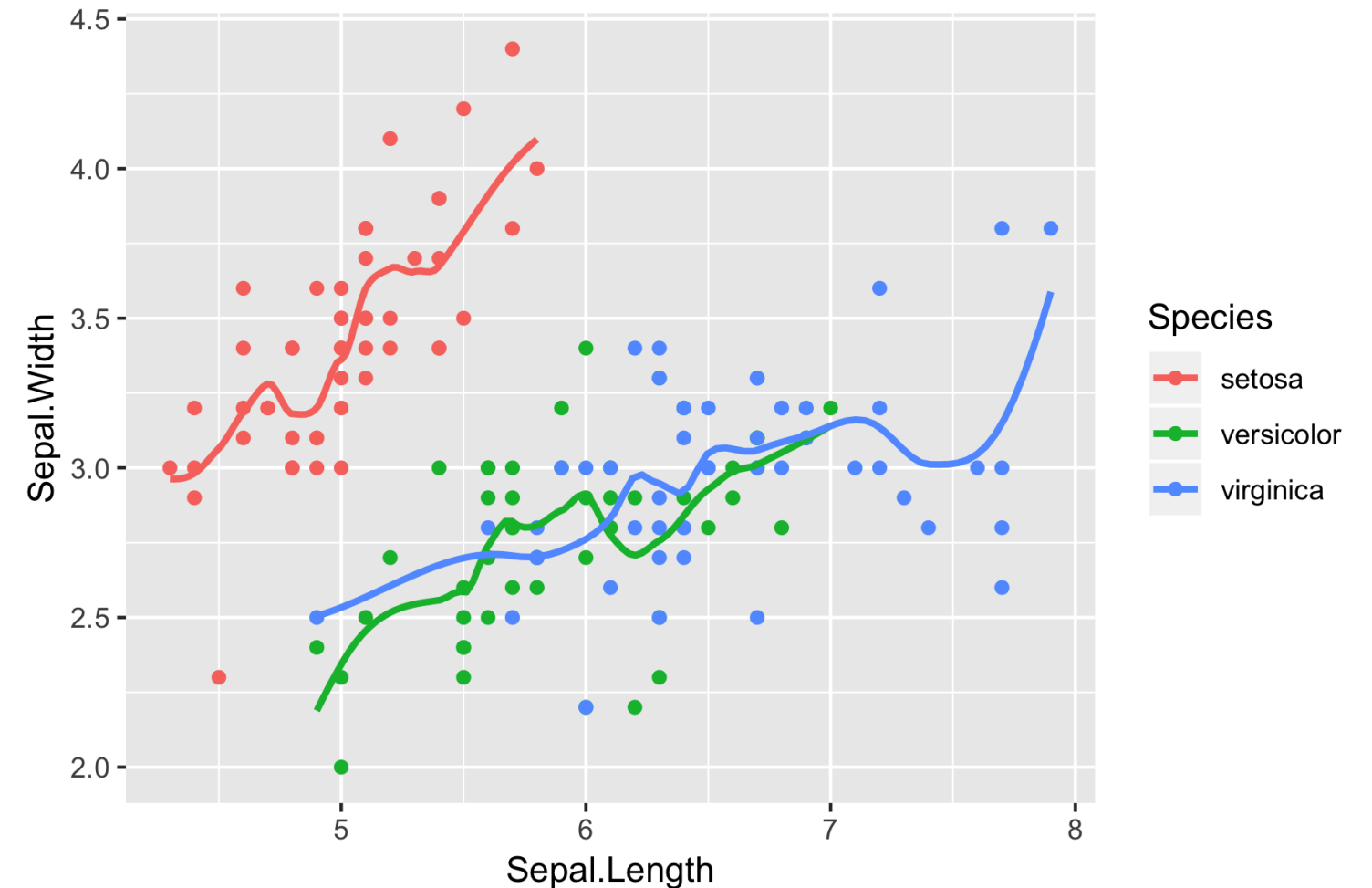
```
geom_smooth() using method = 'loess' and  
formula 'y ~ x'
```



geom_smooth(span = 0.4)

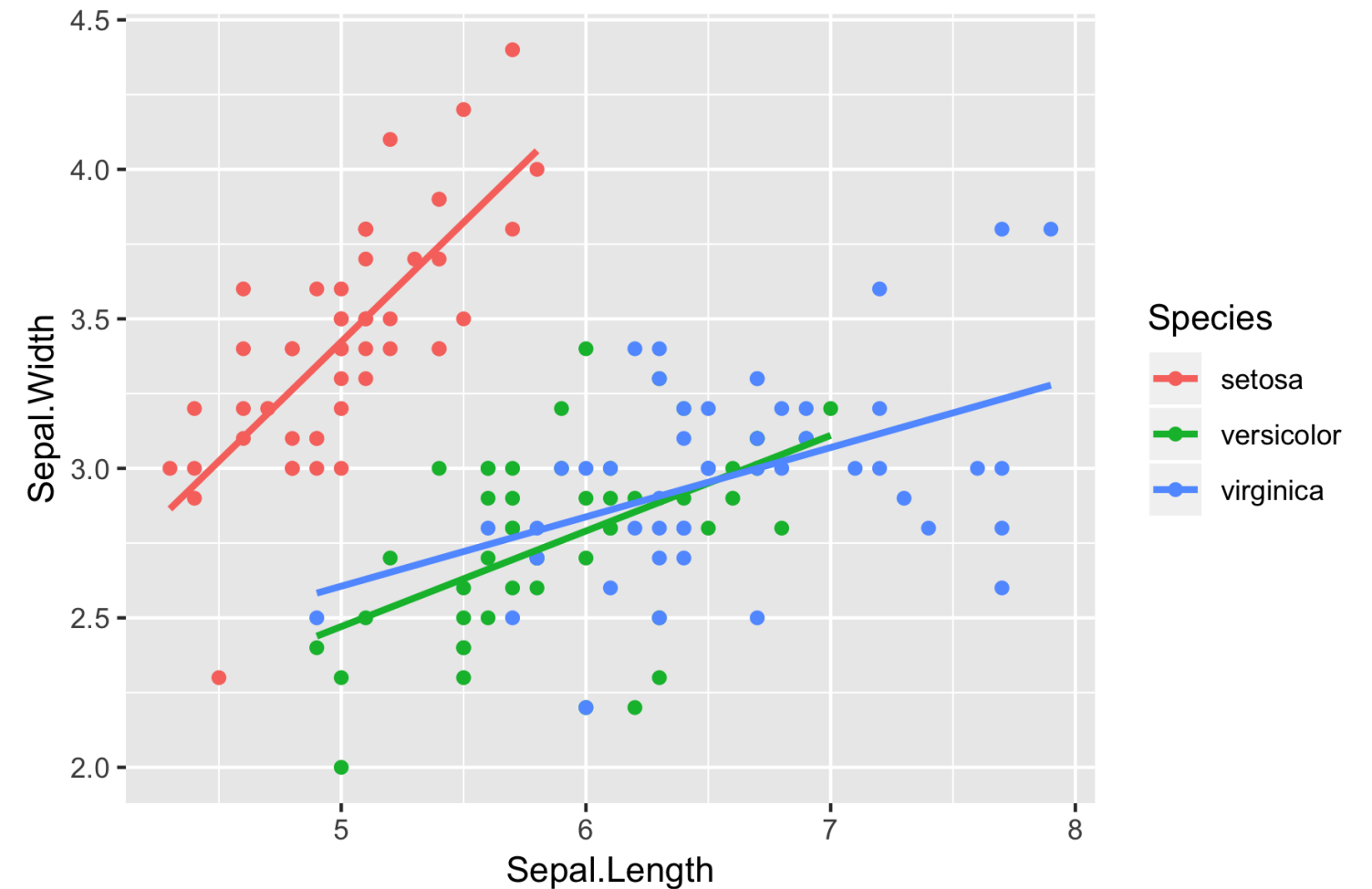
```
ggplot(iris, aes(x = Sepal.Length,  
                 y = Sepal.Width,  
                 color = Species)) +  
  geom_point() +  
  geom_smooth(se = FALSE, span = 0.4)
```

geom_smooth() using method = 'loess' and
formula 'y ~ x'



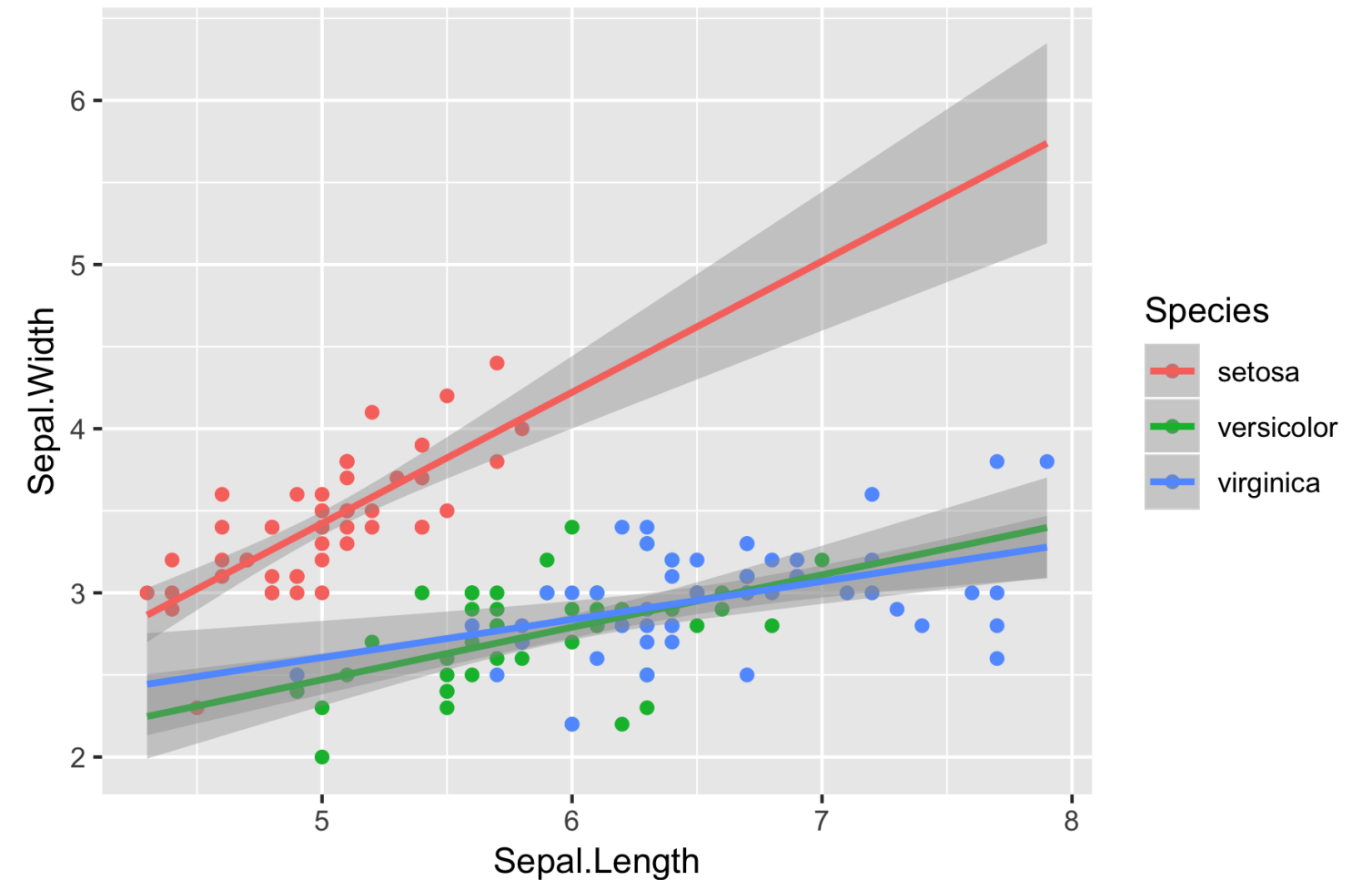
geom_smooth(method = "lm")

```
ggplot(iris, aes(x = Sepal.Length,  
                 y = Sepal.Width,  
                 color = Species)) +  
  geom_point() +  
  geom_smooth(method = "lm", se = FALSE)
```



geom_smooth(fullrange = TRUE)

```
ggplot(iris, aes(x = Sepal.Length,  
                 y = Sepal.Width,  
                 color = Species)) +  
  geom_point() +  
  geom_smooth(method = "lm",  
             fullrange = TRUE)
```



The geom_/stat_ connection

| stat_ | geom_ |
|---------------|------------------------------------|
| stat_bin() | geom_histogram() , geom_freqpoly() |
| stat_count() | geom_bar() |
| stat_smooth() | geom_smooth() |

Other stat_ functions

| stat_ | geom_ |
|-----------------------------|-----------------------------|
| <code>stat_boxplot()</code> | <code>geom_boxplot()</code> |

Other stat_ functions

| stat_ | geom_ |
|-----------------------------|-----------------------------|
| <code>stat_boxplot()</code> | <code>geom_boxplot()</code> |
| <code>stat_bindot()</code> | <code>geom_dotplot()</code> |
| <code>stat_bin2d()</code> | <code>geom_bin2d()</code> |
| <code>stat_binhex()</code> | <code>geom_hex()</code> |

Other stat_ functions

| stat_ | geom_ |
|------------------------------|------------------------------|
| <code>stat_boxplot()</code> | <code>geom_boxplot()</code> |
| <code>stat_bindot()</code> | <code>geom_dotplot()</code> |
| <code>stat_bin2d()</code> | <code>geom_bin2d()</code> |
| <code>stat_binhex()</code> | <code>geom_hex()</code> |
| <code>stat_contour()</code> | <code>geom_contour()</code> |
| <code>stat_quantile()</code> | <code>geom_quantile()</code> |
| <code>stat_sum()</code> | <code>geom_count()</code> |

Let's practice!

INTERMEDIATE DATA VISUALIZATION WITH GGPLOT2

Stats: sum and quantile

INTERMEDIATE DATA VISUALIZATION WITH GGPLOT2



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Recall from course 1

| | Cause of Over-plotting | Solutions |
|----|---------------------------------|--|
| 1. | Large datasets | Alpha-blending, hollow circles, point size |
| 2. | Aligned values on a single axis | As above, plus change position |
| 3. | Low-precision data | Position: jitter |
| 4. | Integer data | Position: jitter |

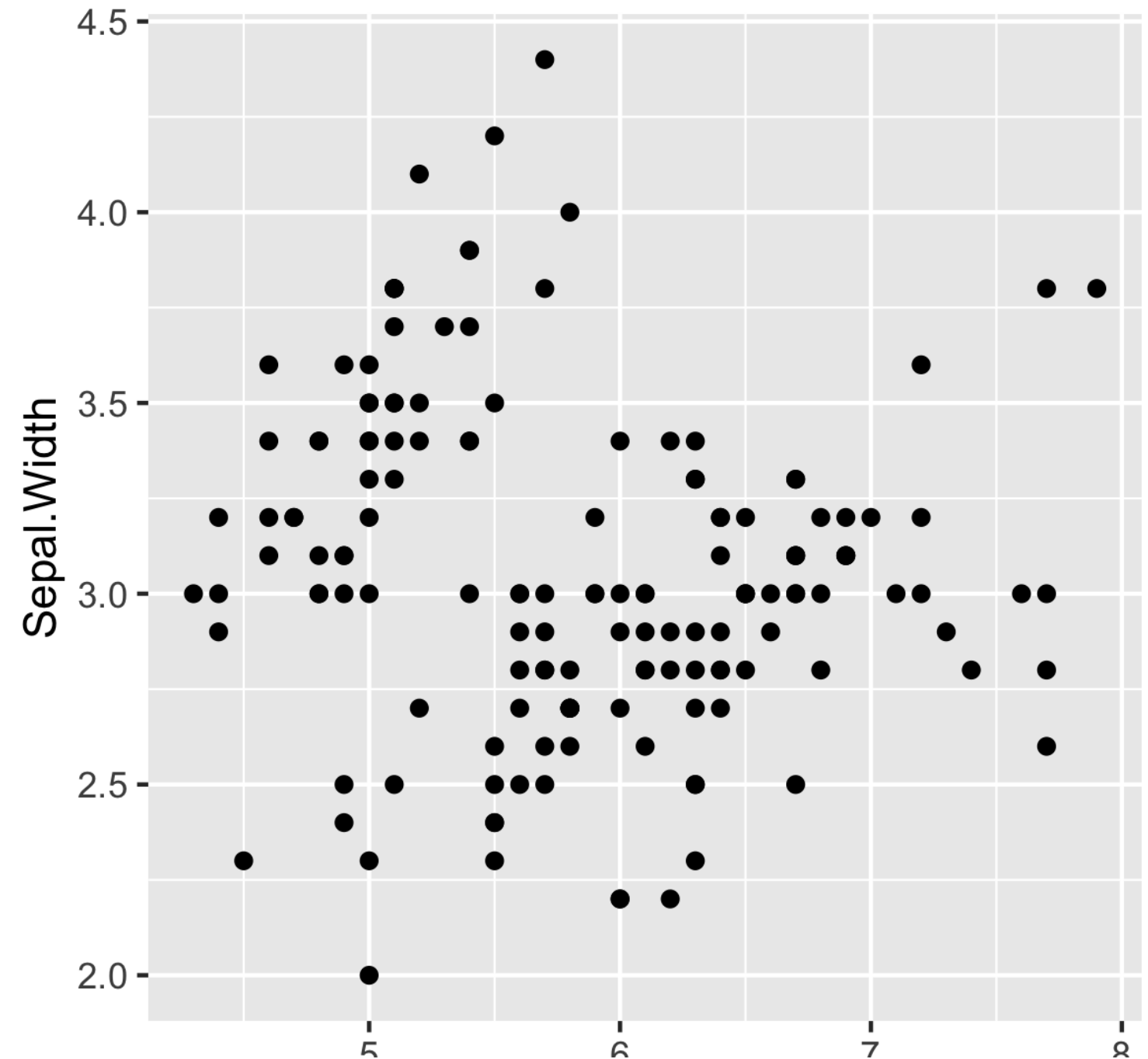
Plot counts to overcome over-plotting

| | Cause of Over-plotting | Solutions | Here... |
|----|---------------------------------|--|---------------------------|
| 1. | Large datasets | Alpha-blending, hollow circles, point size | |
| 2. | Aligned values on a single axis | As above, plus change position | |
| 3. | Low-precision data | Position: jitter | <code>geom_count()</code> |
| 4. | Integer data | Position: jitter | <code>geom_count()</code> |

Low precision (& integer) data

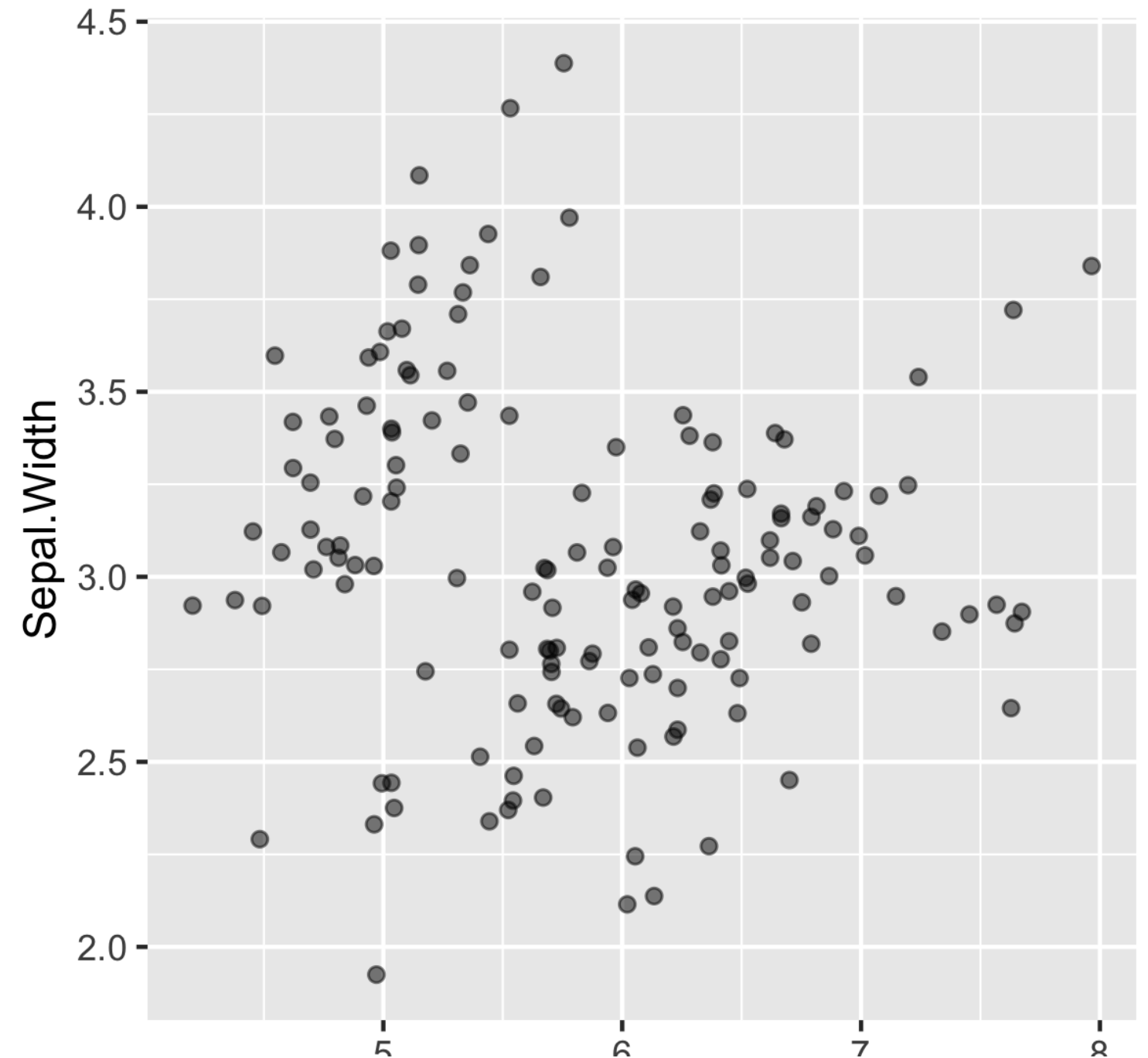
```
p <- ggplot(iris, aes(Sepal.Length,  
                      Sepal.Width))
```

```
p + geom_point()
```



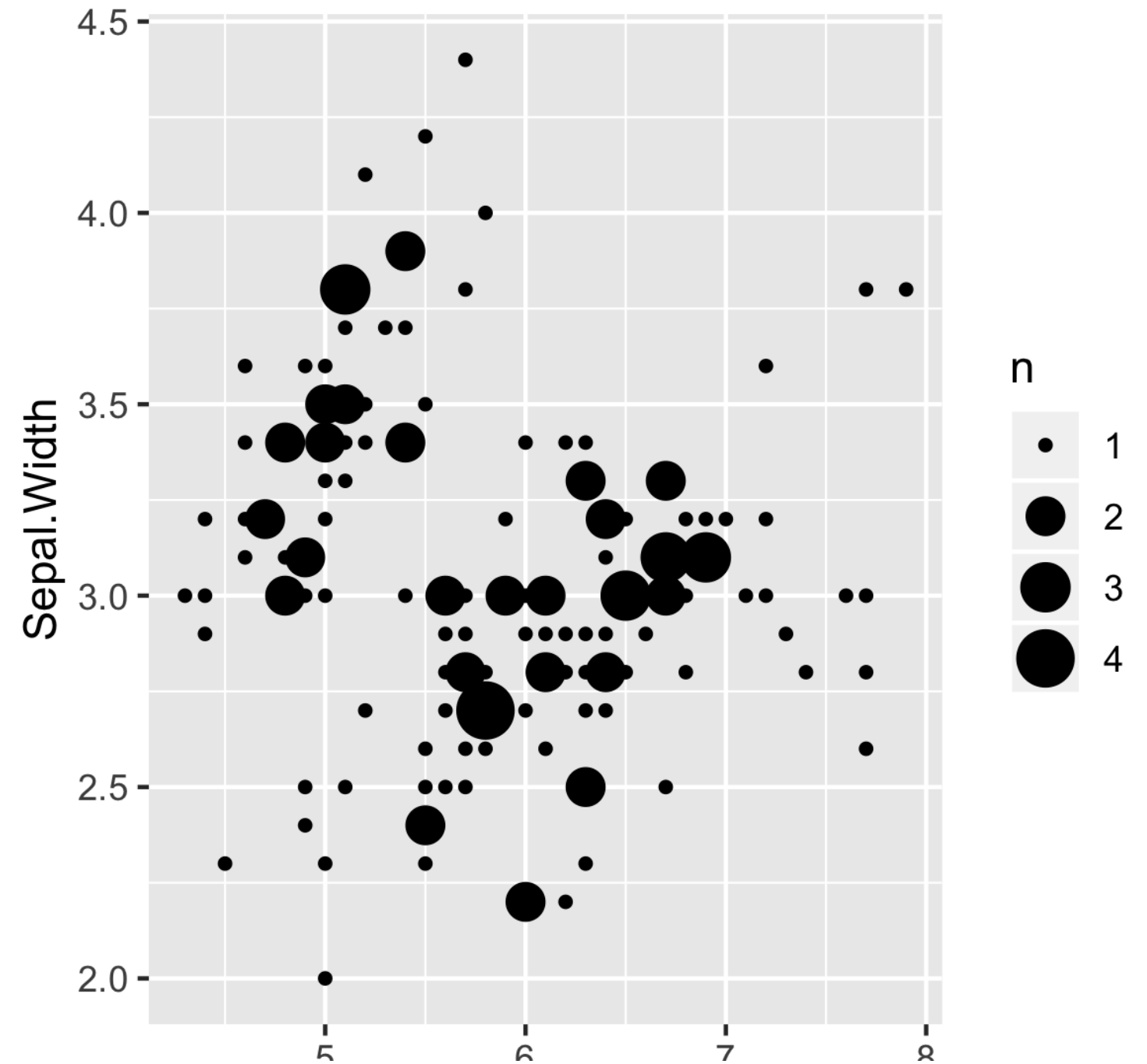
Jittering may give a wrong impressions

```
p + geom_jitter(alpha = 0.5,  
                width = 0.1,  
                height = 0.1)
```



geom_count()

```
p +  
  geom_count()
```

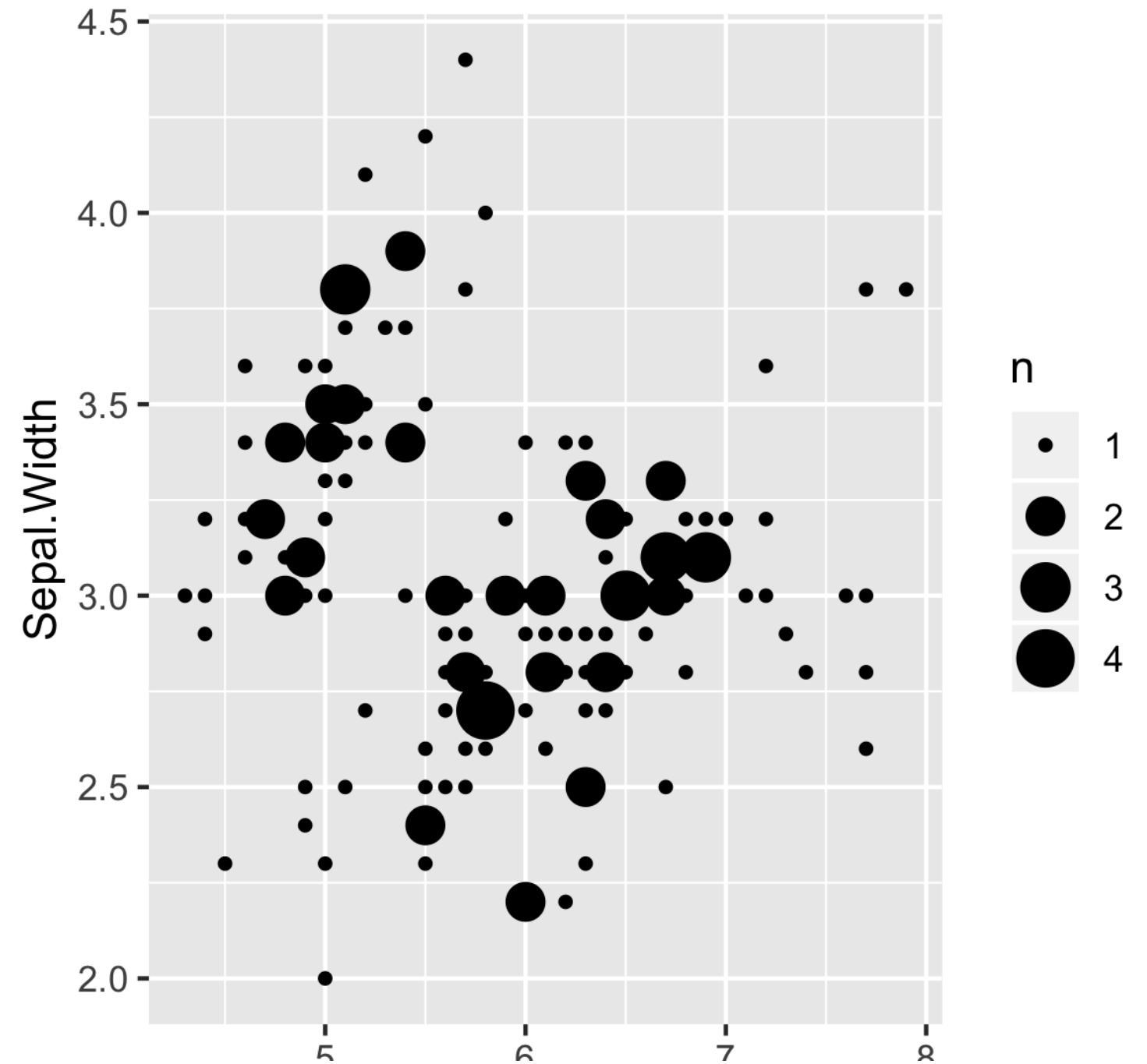


The geom/stat connection

| geom_ | stat_ |
|---------------------------|-------------------------|
| <code>geom_count()</code> | <code>stat_sum()</code> |

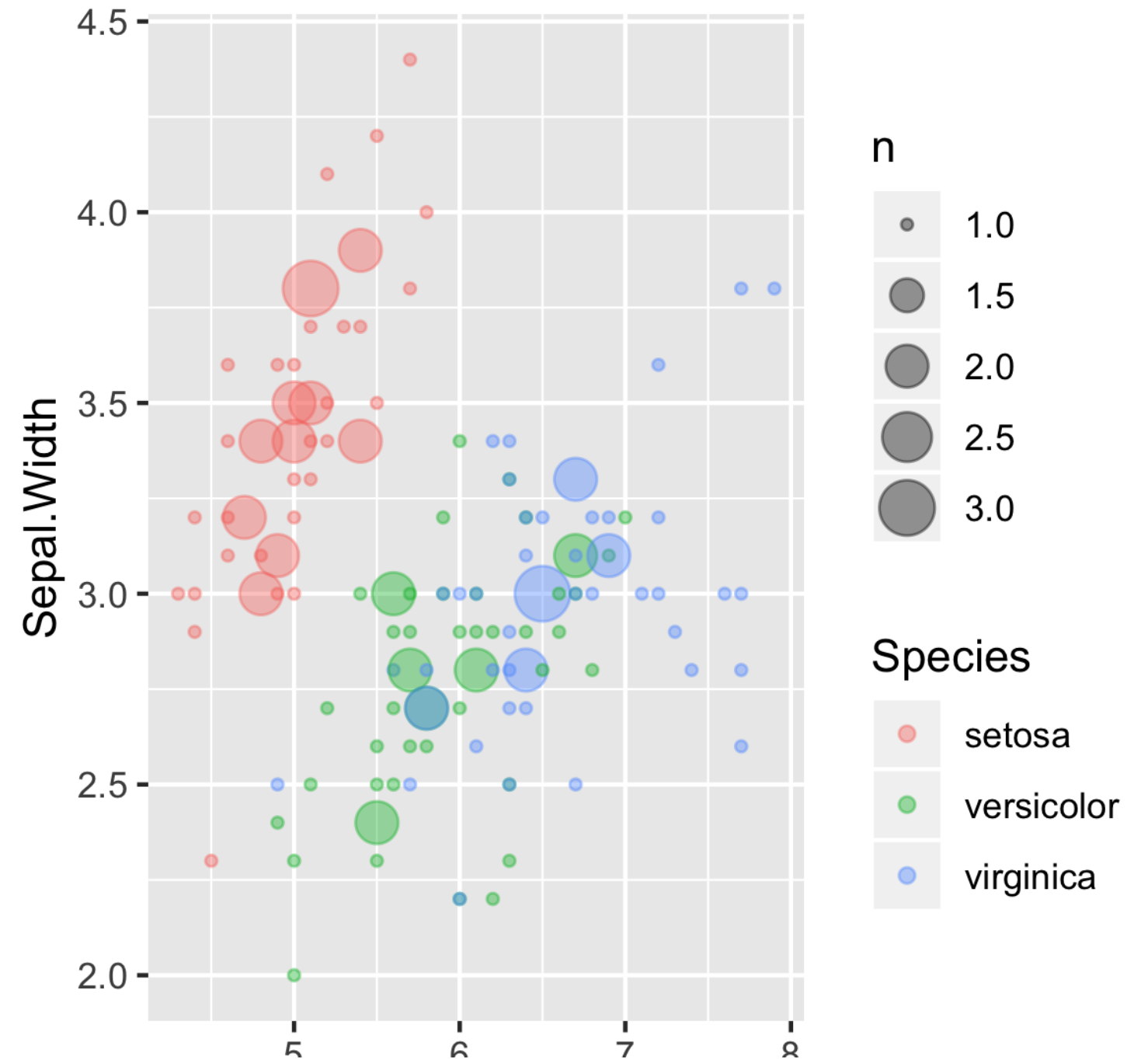
stat_sum()

```
p +  
  stat_sum()
```



Over-plotting can still be a problem!

```
ggplot(iris, aes(Sepal.Length,  
                Sepal.Width,  
                color = Species)) +  
  geom_count(alpha = 0.4)
```



geom_quantile()

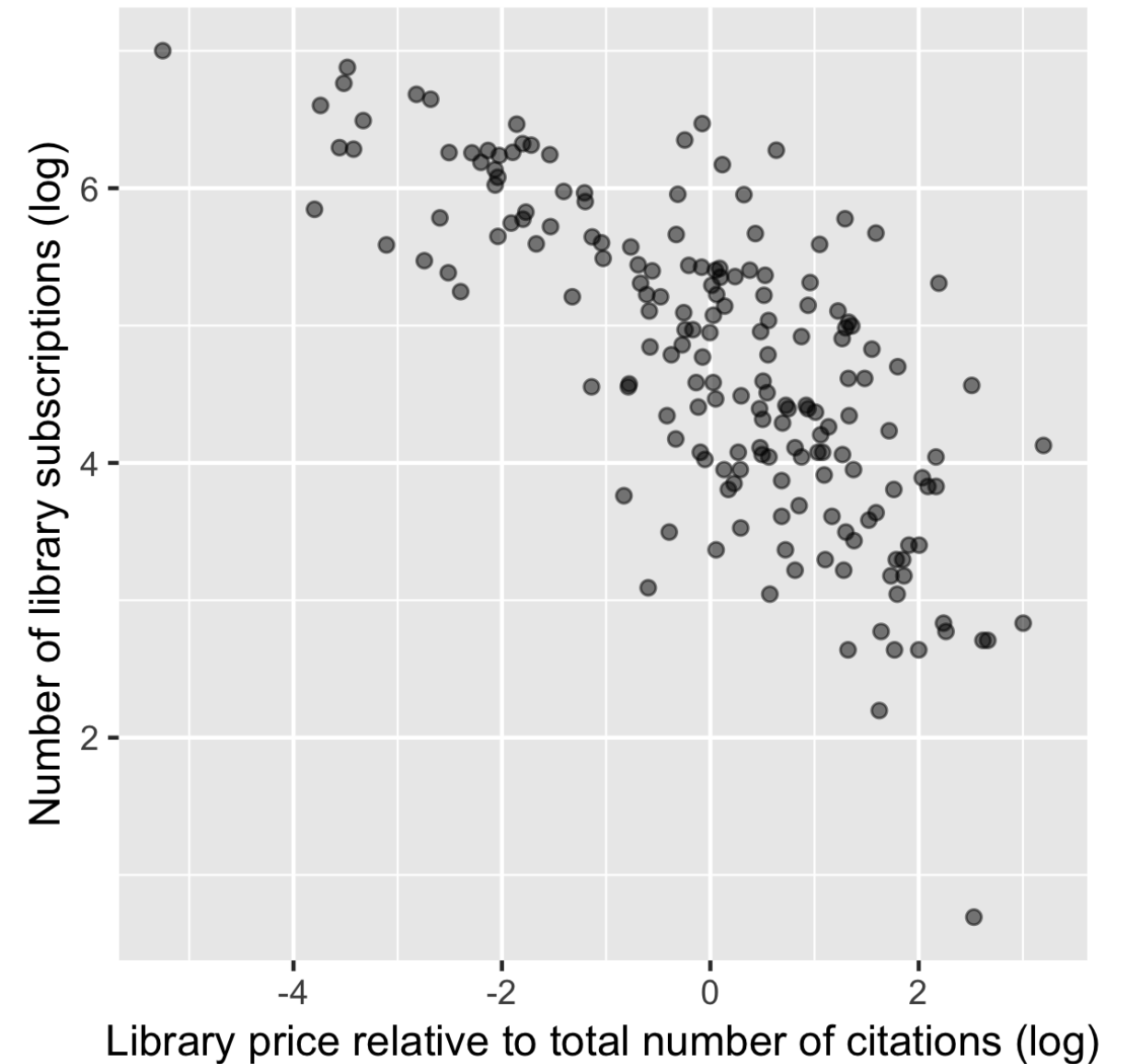
```
ggplot(iris, aes(Sepal.Length,  
                 Sepal.Width,  
                 color = Species)) +  
  geom_count(alpha = 0.4)
```

Dealing with heteroscedasticity

```
library(AER)
data(Journals)

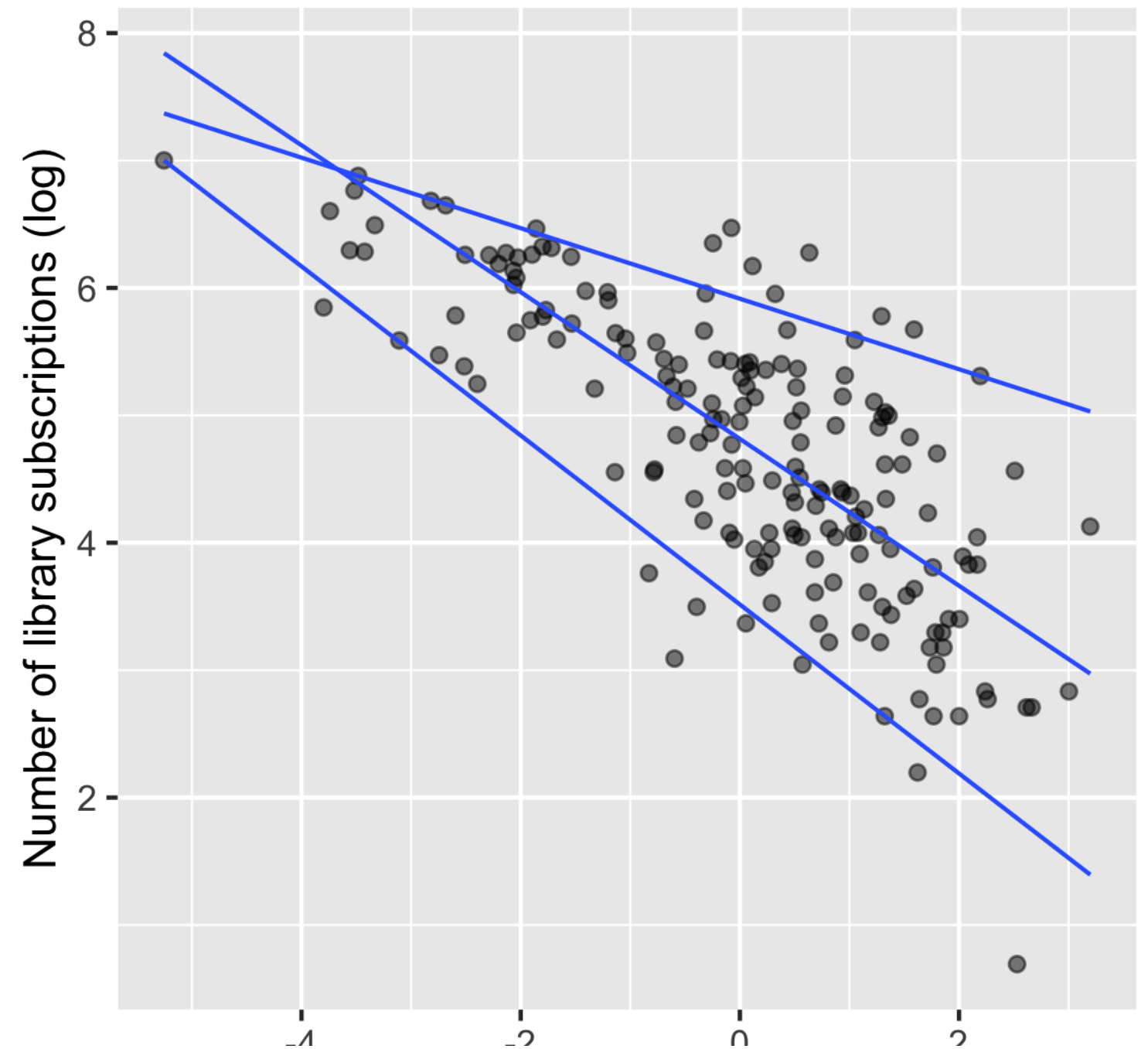
p <- ggplot(Journals,
            aes(log(price/citations),
                log(subs)))) +
  geom_point(alpha = 0.5) +
  labs(...)
```

p



Using geom_quantiles

```
p +  
  geom_quantile(quantiles =  
    c(0.05, 0.50, 0.95))
```



The geom/stat connection

| geom_ | stat_ |
|------------------------------|------------------------------|
| <code>geom_count()</code> | <code>stat_sum()</code> |
| <code>geom_quantile()</code> | <code>stat_quantile()</code> |

Ready for exercises!

INTERMEDIATE DATA VISUALIZATION WITH GGPLOT2

Stats outside geoms

INTERMEDIATE DATA VISUALIZATION WITH GGPLOT2

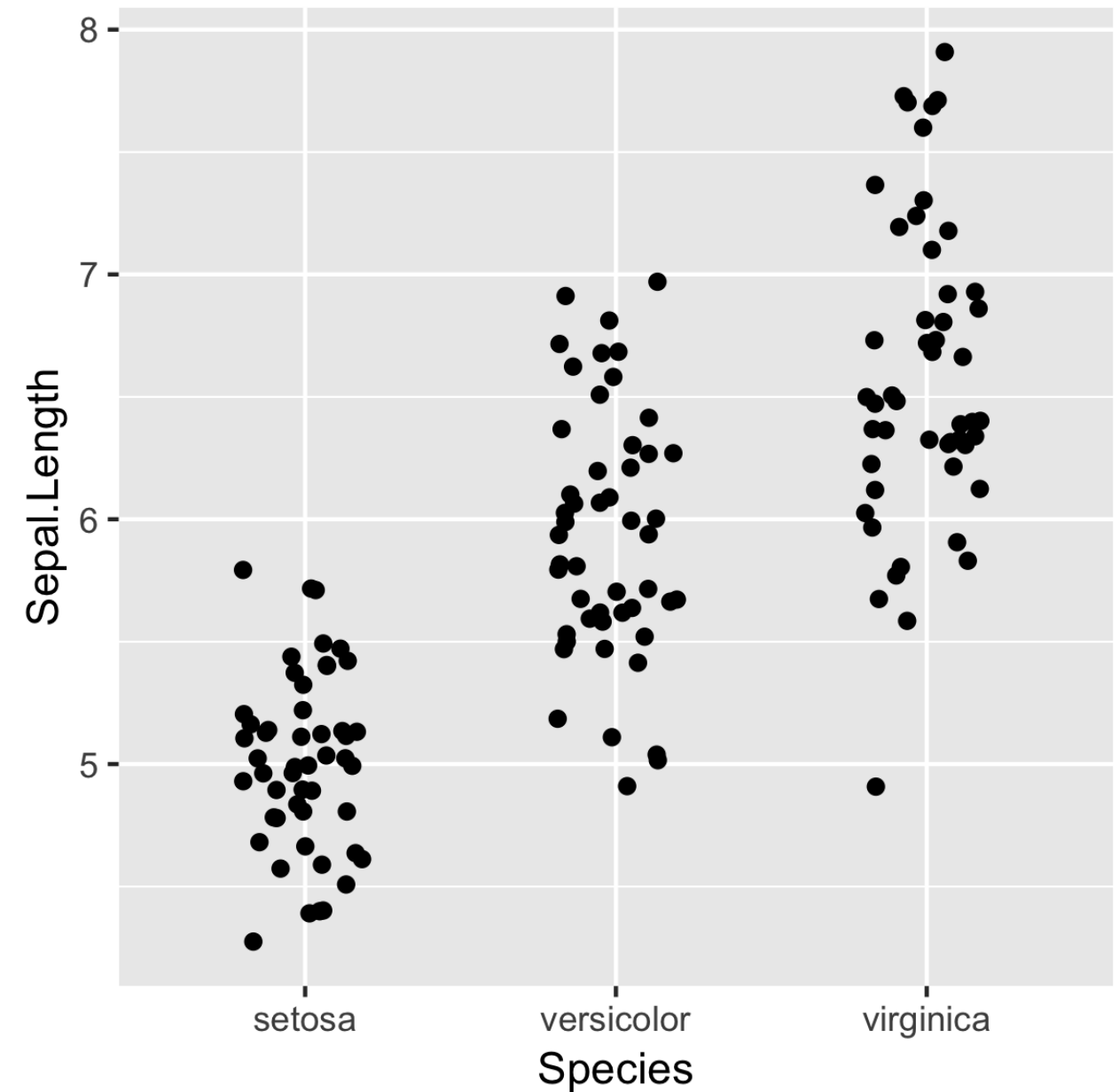


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Basic plot

```
ggplot(iris, aes(x = Species,  
                 y = Sepal.Length)) +  
  geom_jitter(width = 0.2)
```



Calculating statistics

```
set.seed(123)  
xx <- rnorm(100)  
mean(xx)
```

```
[1] 0.09040591
```

```
mean(xx) + (sd(xx) * c(-1, 1))
```

```
[1] -0.822410  1.003222
```

Calculating statistics

```
set.seed(123)
xx <- rnorm(100)

# Hmisc
library(Hmisc)
smean.sdl(xx, mult = 1)
```

| | Mean | Lower | Upper |
|--|------------|-------------|------------|
| | 0.09040591 | -0.82240997 | 1.00322179 |

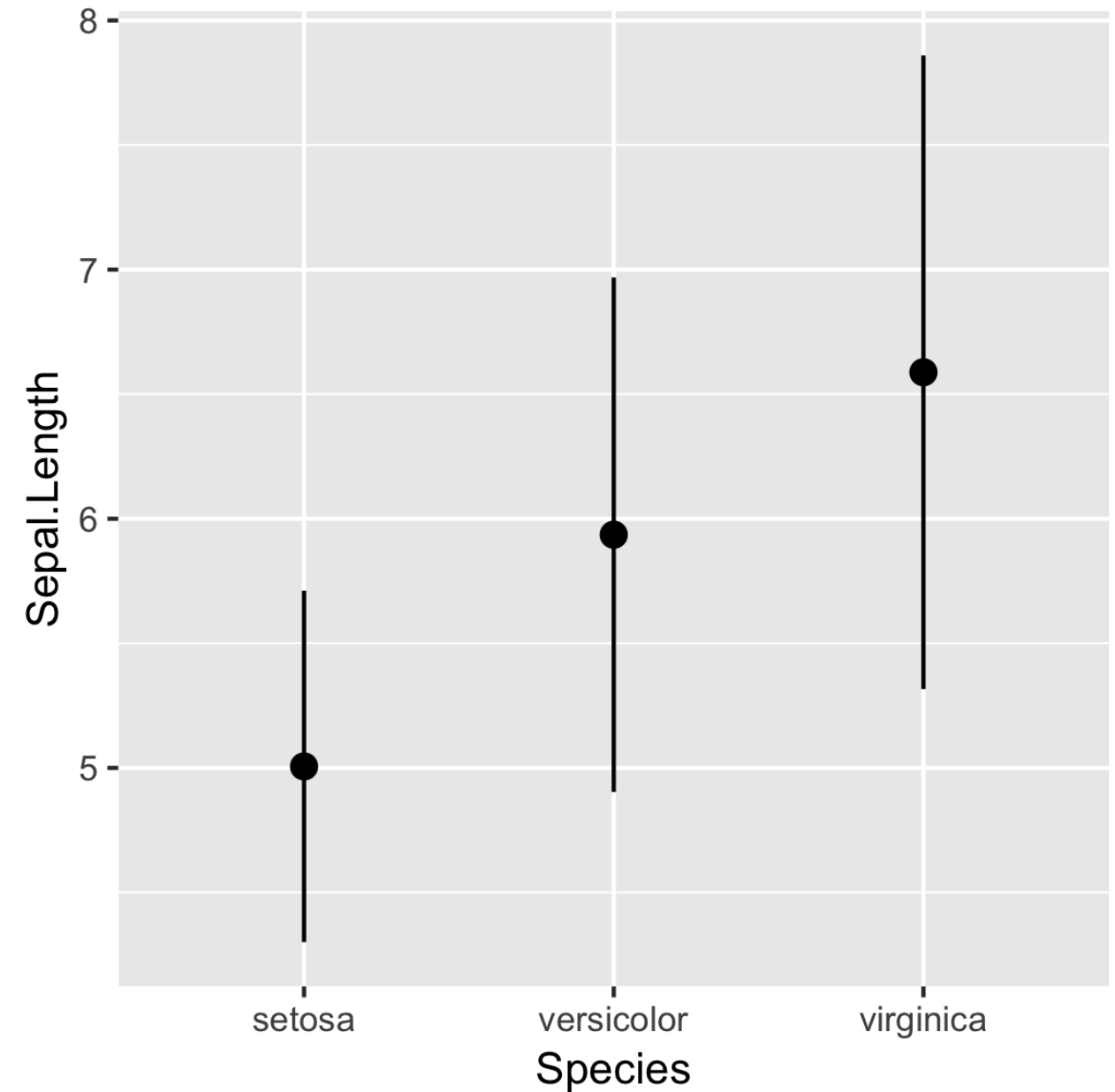
```
# ggplot2
mean_sdl(xx, mult = 1)
```

| | y | ymin | ymax |
|---|------------|----------|----------|
| 1 | 0.09040591 | -0.82241 | 1.003222 |

stat_summary()

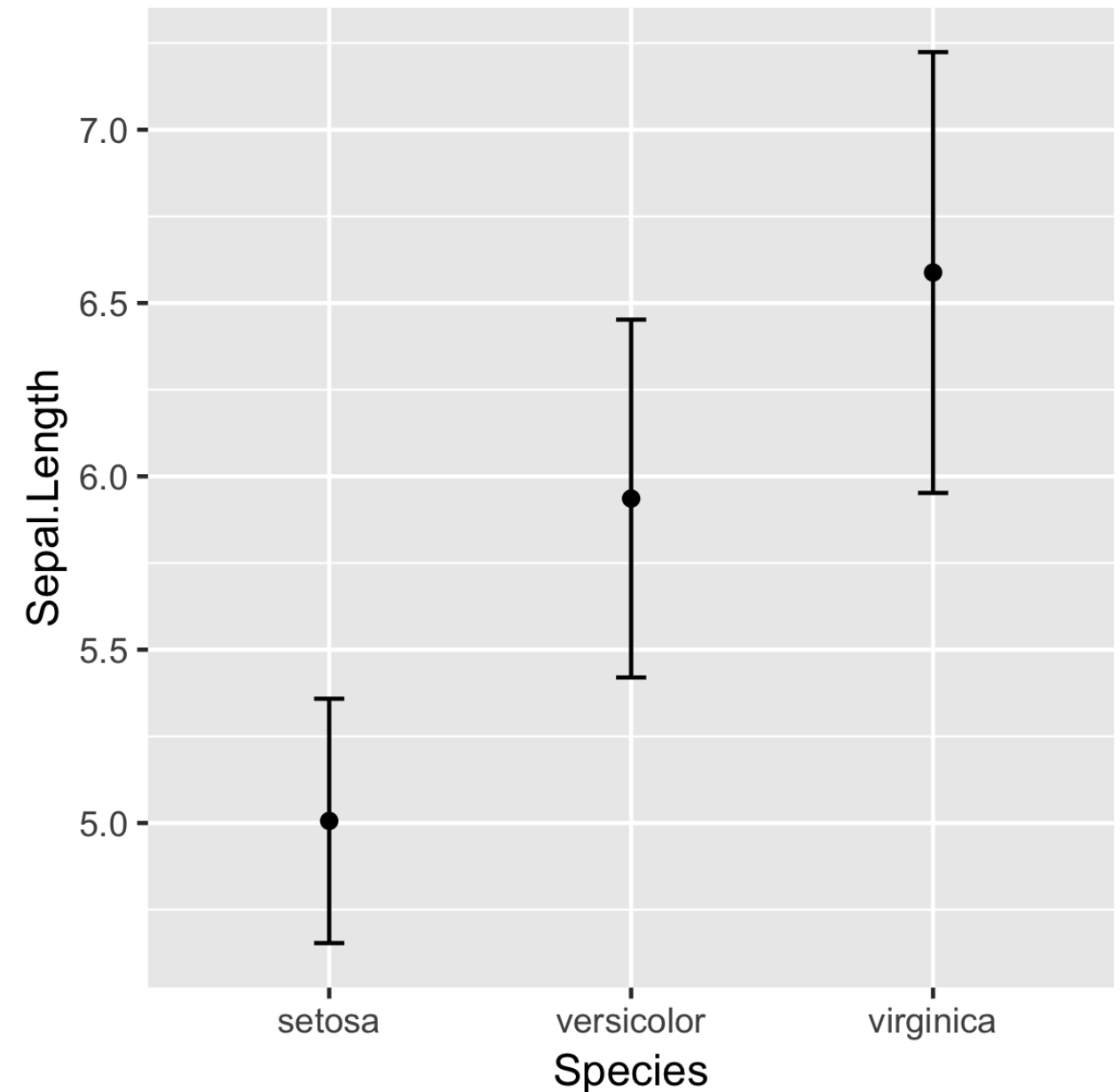
```
ggplot(iris, aes(x = Species,  
                 y = Sepal.Length)) +  
  stat_summary(fun.data = mean_sdl,  
              fun.args = list(mult = 1))
```

- Uses `geom_pointrange()` by default

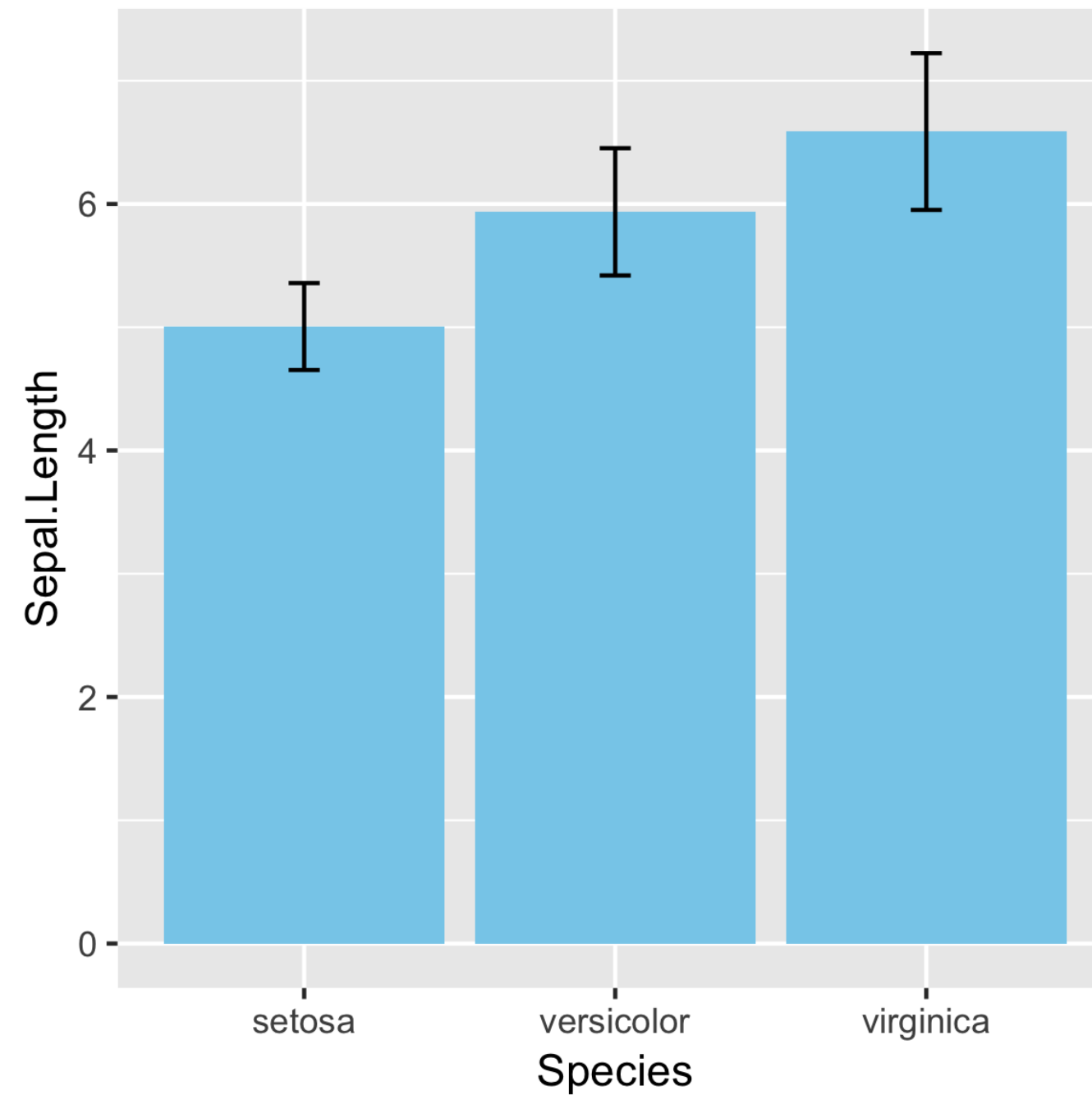


stat_summary()

```
ggplot(iris, aes(x = Species,  
                 y = Sepal.Length)) +  
  stat_summary(fun = mean,  
              geom = "point") +  
  stat_summary(fun.data = mean_sdl,  
              fun.args = list(mult = 1),  
              geom = "errorbar",  
              width = 0.1)
```



Not recommended!



95% confidence interval

```
ERR <- qt(0.975, length(xx) - 1) * (sd(xx) / sqrt(length(xx)))  
mean(xx)
```

```
0.09040591
```

```
mean(xx) + (ERR * c(-1, 1)) # 95% CI
```

```
-0.09071657  0.27152838
```

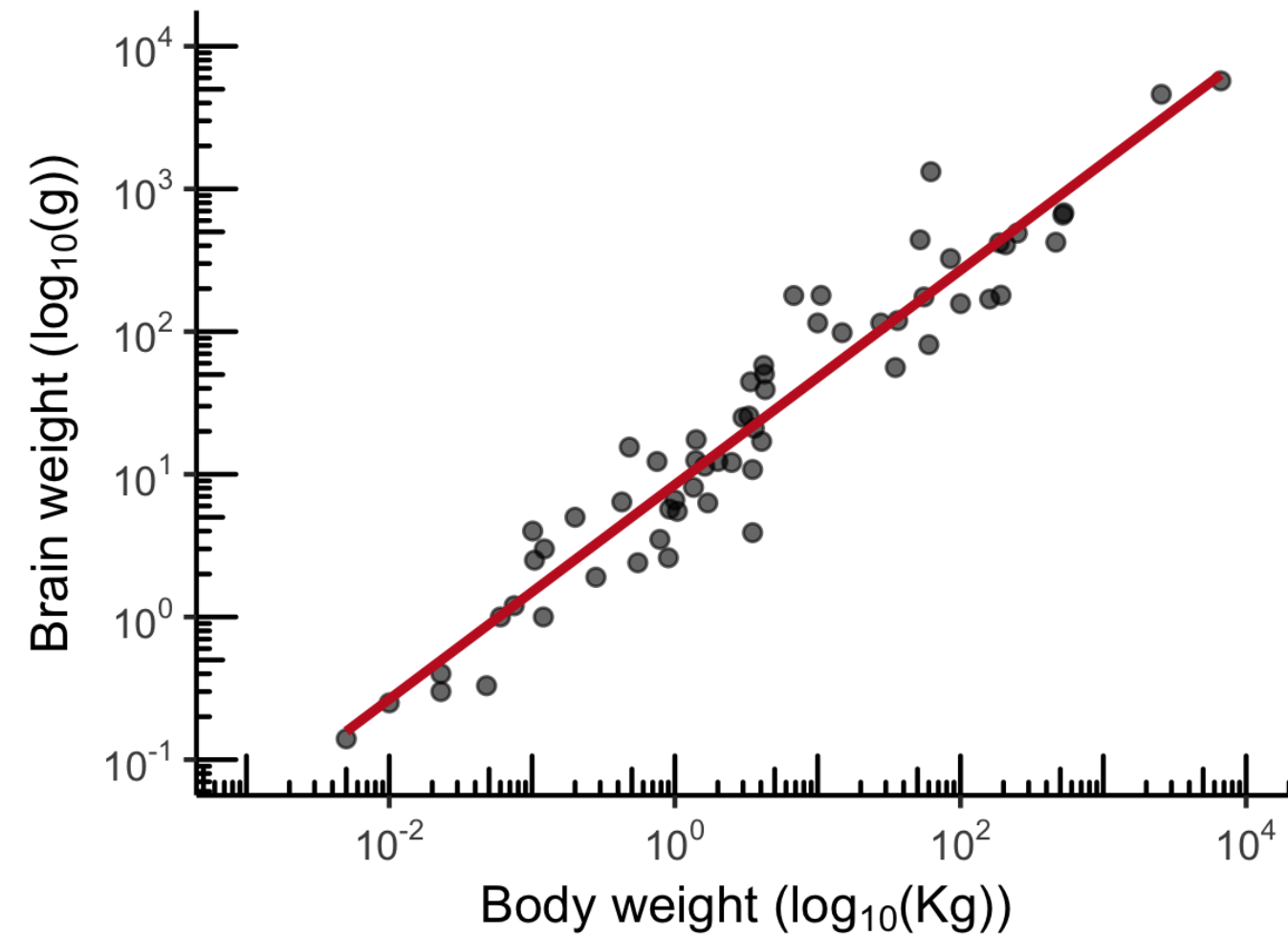
```
mean_cl_normal(xx)
```

```
      y      ymin      ymax  
0.09040591 -0.09071657 0.2715284
```

Other stat_ functions

| stat_ | Description |
|------------------------------|--|
| <code>stat_summary()</code> | summarize y values at distinct x values. |
| <code>stat_function()</code> | compute y values from a function of x values. |
| <code>stat_qq()</code> | perform calculations for a quantile-quantile plot. |

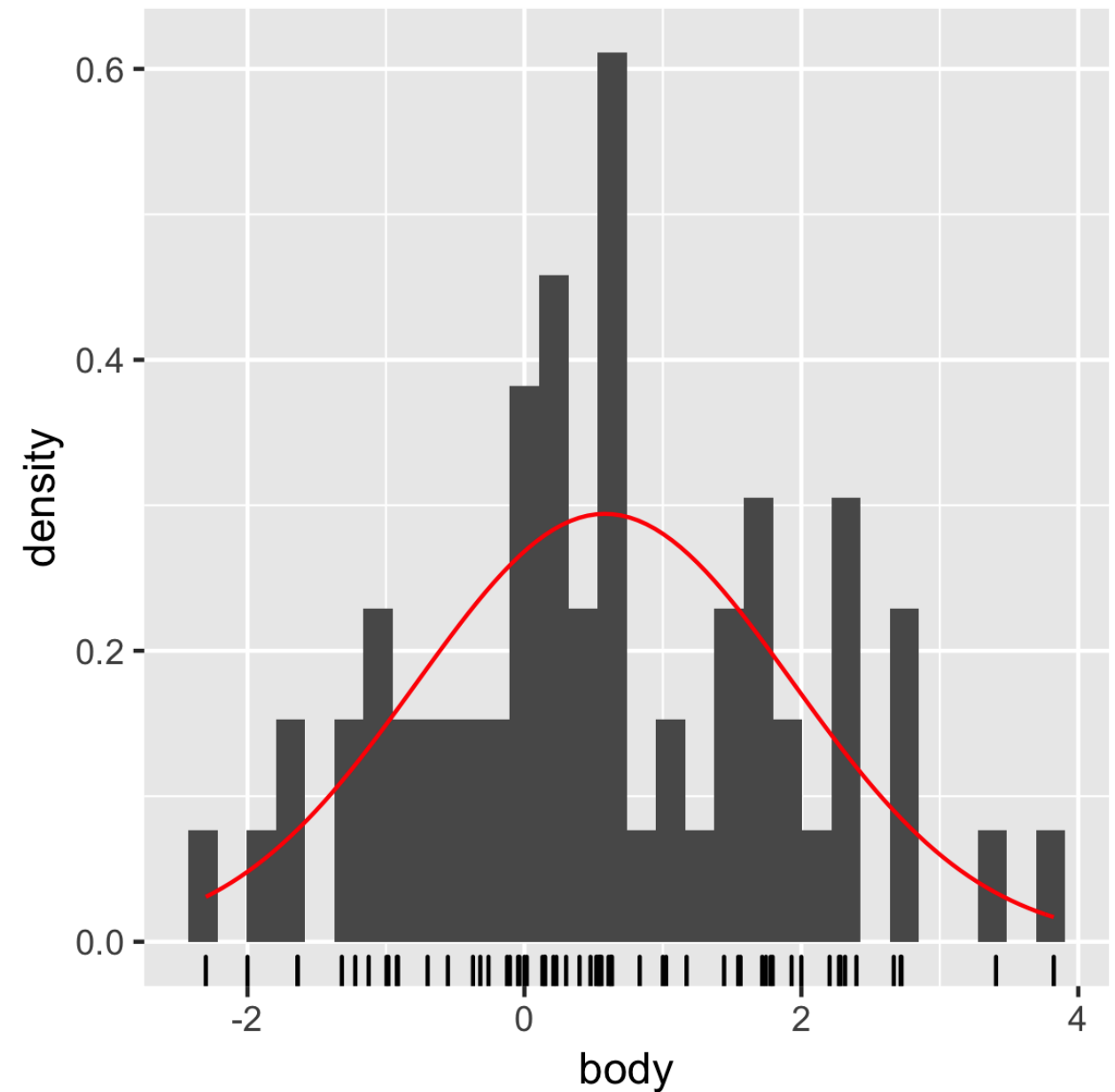
MASS::mammals



Normal distribution

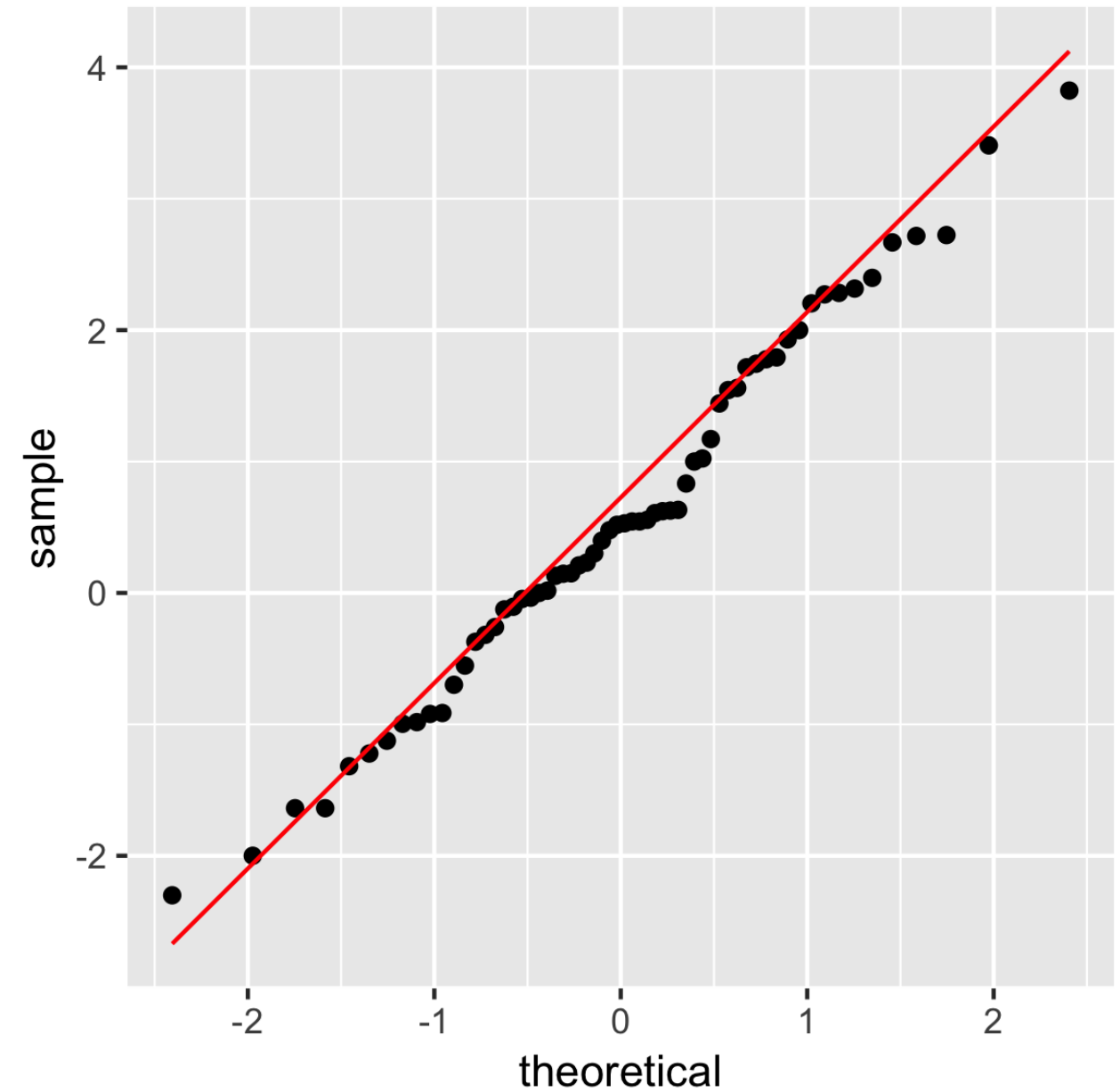
```
mam.new <- data.frame(body = log10(mammals$body))

ggplot(mam.new, aes(x = body)) +
  geom_histogram(aes( y = ..density..)) +
  geom_rug() +
  stat_function(fun = dnorm, color = "red",
               args = list(mean = mean(mam.new$body),
                             sd = sd(mam.new$body)))
```



QQ plot

```
ggplot(mam.new, aes(sample = body)) +  
  stat_qq() +  
  geom_qq_line(col = "red")
```



Your turn!

INTERMEDIATE DATA VISUALIZATION WITH GGLOT2