In-class worksheet 3

Jan 29, 2019

1. Plotting the iris data set

We will work with the `iris` data set available in R. This data set gives the measurements in centimeters of the variables sepal length and width and petal length and width, respectively, for 50 flowers from each of 3 species of iris. The species are *Iris setosa*, *versicolor*, and *virginica:*

```
head(iris)
```

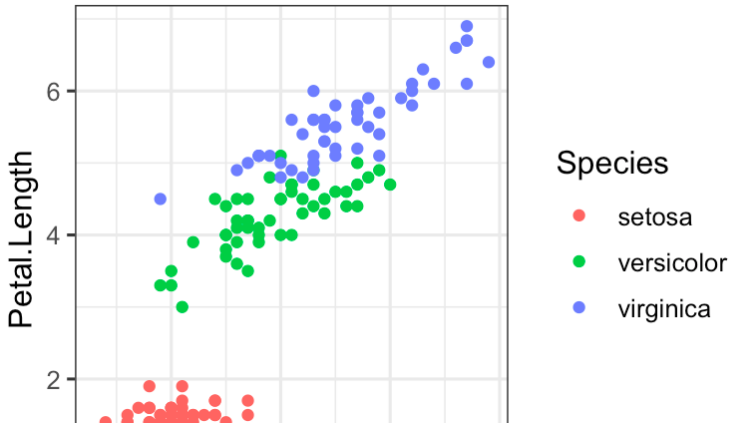
```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

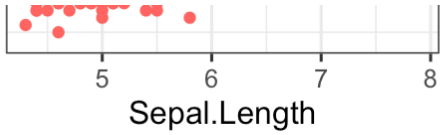
In this worksheet, we will work with the library ggplot2, so we need to load it. We also set a theme that doesn't use a gray background grid:

```
library(ggplot2) # load ggplot2 library
theme_set(theme_bw(base_size=12)) # set the default plot theme for the ggplot2 library
```

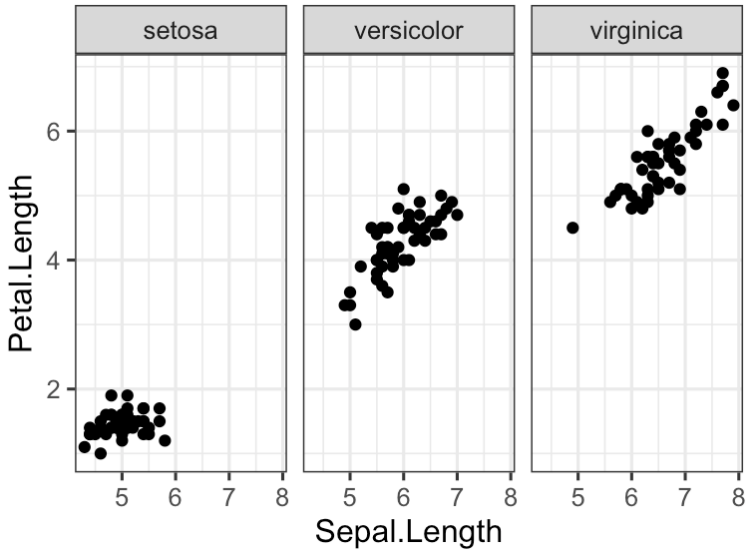
Using ggplot, make a scatter plot of petal length vs. sepal length for the three species. Then do the same plot but facet by species instead of coloring.

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



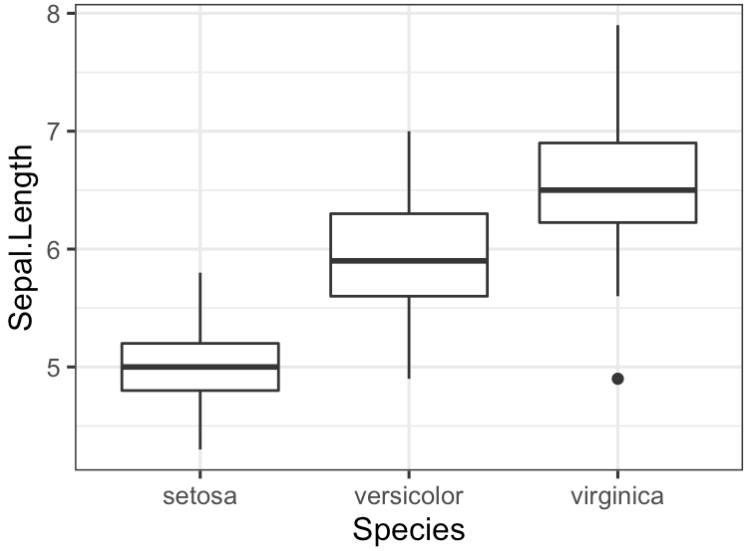



```
ggplot(iris, aes(x=Sepal.Length, y=Petal.Length)) + geom_point() + facet_wrap(~
Species)
```



Now make side-by-side boxplots of sepal lengths for the three species of iris. The geom you need to use is `geom_boxplot()`. See if you can guess the correct aesthetic mapping.

```
ggplot(iris, aes(y=Sepal.Length, x=Species)) + geom_boxplot()
```



2. Plotting tree-growth data

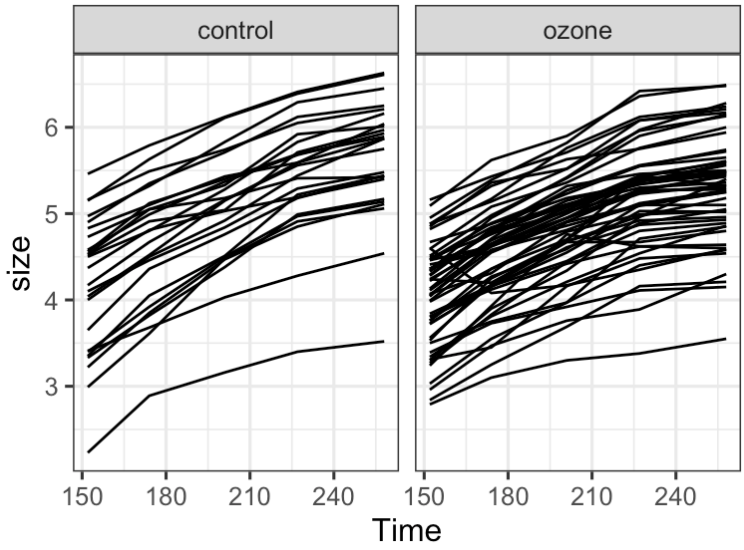
The data set `sitka` contains repeated measurements of tree size for 79 Sitka spruce trees, which were grown either in ozone-enriched chambers or under control conditions. It contains four columns: `size` measures the size of the tree (height times diameter squared, on a log scale). `Time` measures the time, in days since Jan. 1, 1988. `tree` indicates the tree we are working with, consecutively numbered from 1 to 79. `treat` indcates the treatment trees were subjected to, either `ozone` for an ozone-enriched chamber or `control`.

```
# download the sitka data set:
sitka <- read.csv("http://wilkelab.org/classes/SDS348/data_sets/sitka.csv")
head(sitka)
```

```
##   size Time tree treat
## 1 4.51  152    1 ozone
## 2 4.98  174    1 ozone
## 3 5.41  201    1 ozone
## 4 5.90  227    1 ozone
## 5 6.15  258    1 ozone
## 6 4.24  152    2 ozone
```

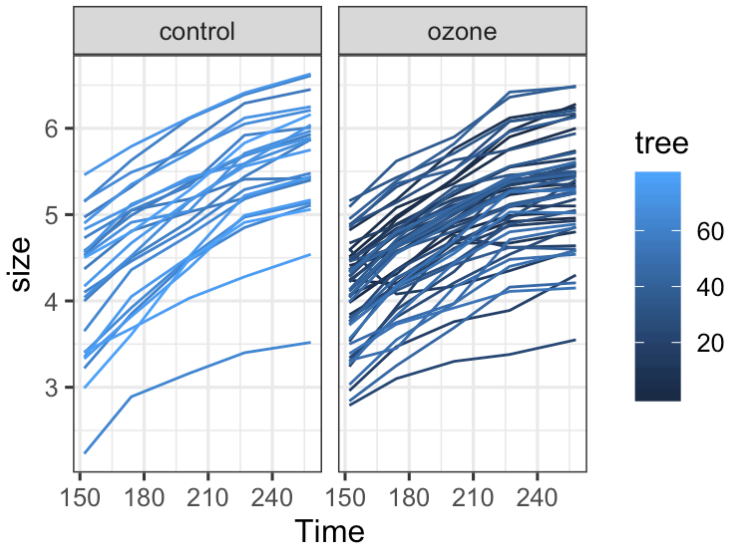
Make line plots of tree size vs. time, for each tree, faceted by treatment. First, use the same color for all lines. Hint: you will need to use the `group` aesthetic to tell ggplot that you want to have a separate line for each tree.

```
ggplot(sitka, aes(x=Time, y=size, group=tree)) + geom_line() + facet_wrap(~trea
t)
```



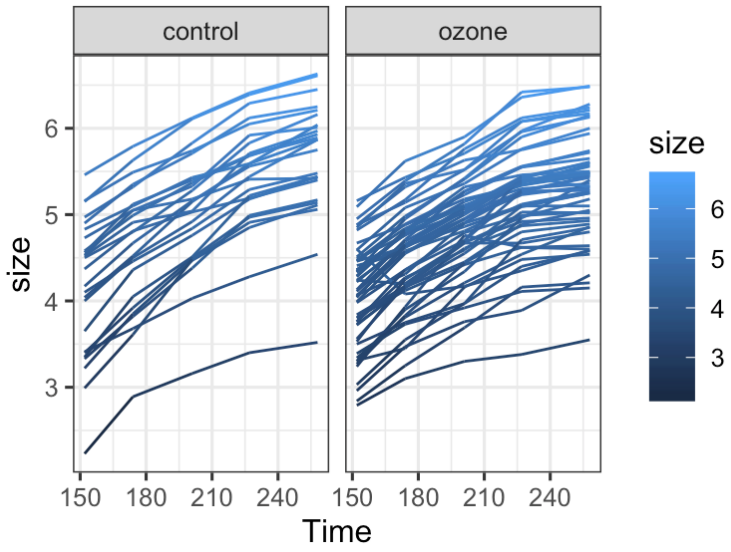
Now, make a variant of this plot where each tree has a separate color.

```
ggplot(sitka, aes(x=Time, y=size, color=tree, group=tree)) + geom_line() + face
t_wrap(~treat)
```



Finally, color each tree by its by size.

```
ggplot(sitka, aes(x=Time, y=size, color=size, group=tree)) + geom_line() + face
t_wrap(~treat)
```



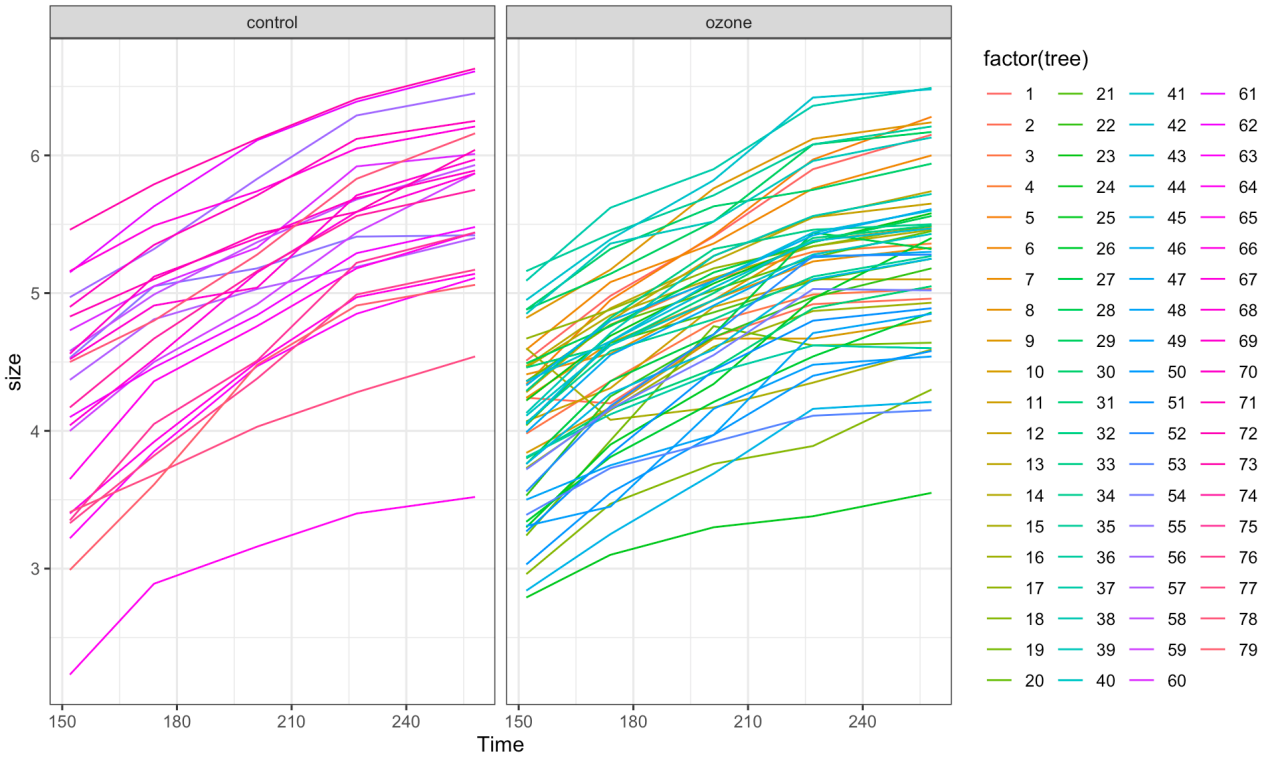
In this last example, the lines actually change color from left to right. It would be nicer to have a single, uniform color for each tree, and, e.g., color by maximum size. To do this efficiently we need the dplyr package, which we will discuss soon.

3. If this was easy

In the sitka tree example, when you colored each tree by a different color, do you understand why ggplot used a continuous color scale? And how would you make it use a discrete color scale with a different color for each tree?

Since the trees are consecutively numbered, R treats these values as a numerical variable and uses a continuous color scale for plotting. To make it use a discrete scale, we need to convert the `tree` *variable into a factor.*

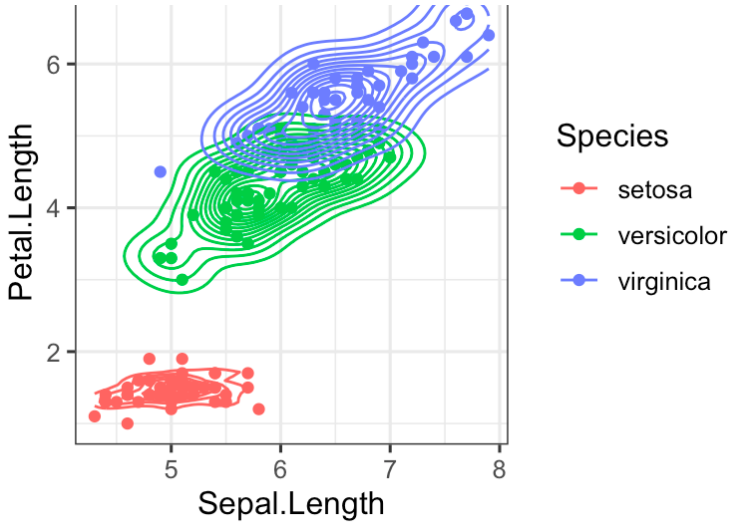
```
ggplot(sitka, aes(x=Time, y=size, color=factor(tree), group=tree)) + geom_line(
) + facet_wrap(~treat)
```



(Note that I have told R Markdown to make a larger figure, by starting the code block with `{r fig.height=6, fig.width=10}` *instead of* `{r}`*, because the default figure size is too small to show the resulting legend.)*

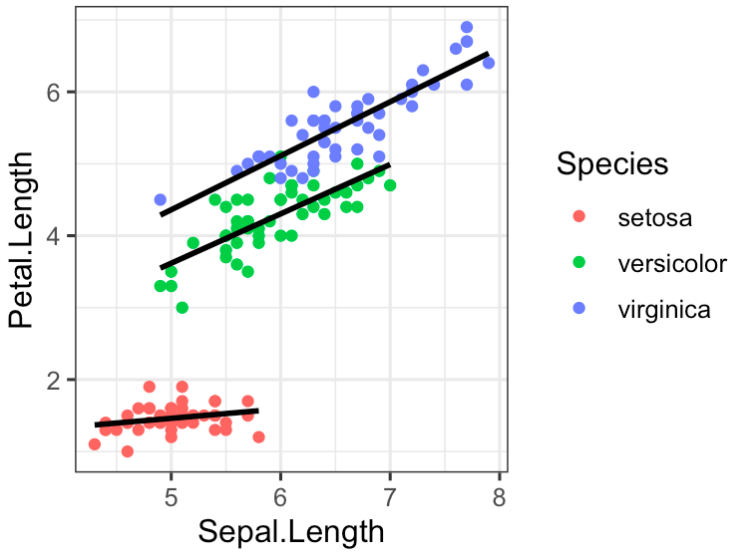
For the `iris` data set, make a plot of the 2d distribution of petal length vs. sepal length, by making an x-y plot that shows the individual data points as well as contour lines indicating the density of points in a given spatial region.

```
ggplot(iris, aes(x=Sepal.Length, y=Petal.Length, color=Species)) + geom_point()
+ geom_density2d()
```



If this was still easy, now instead of contour lines add a fitted straight black line (not a curve, and no confidence band!) to each group of points.

```
ggplot(iris, aes(x=Sepal.Length, y=Petal.Length, color=Species)) + geom_point()
+ geom_smooth(aes(group=Species), method=lm, color='black', se=F)
```



In this last example, because we are manually overriding the color of the lines, we need to set the group aesthetic to tell ggplot2 to draw a separate line for each species.