4. Adding Features to Plots

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In this session

R has very flexible built-in graphing capabilities to add a wide-range of features to a plot.

- Plotting options
- Adding points, lines, and segments to existing plots
- Creating a legend for a plot

Scatterplot Options

The command `plot(x,y)` will create a scatterplot when x and y are numeric. The default setting will plot points but one can graph lines or both (or neither):

- `plot(x,y,type="p")` is the default option that plots points
- `plot(x,y,type="l")` connects points by lines but does not plot point symbols
- `plot(x,y,type="b")` plots point symbols connected by lines
- `plot(x,y,type="o")` plots point symbols connected by lines, points on top of lines
- `plot(x,y,type="h"` will plot histogram-like (a.k.a. high-density) vertical lines
- `plot(x,y,type="n")` plots axes only, no symbols

Examples: Plotting two variables

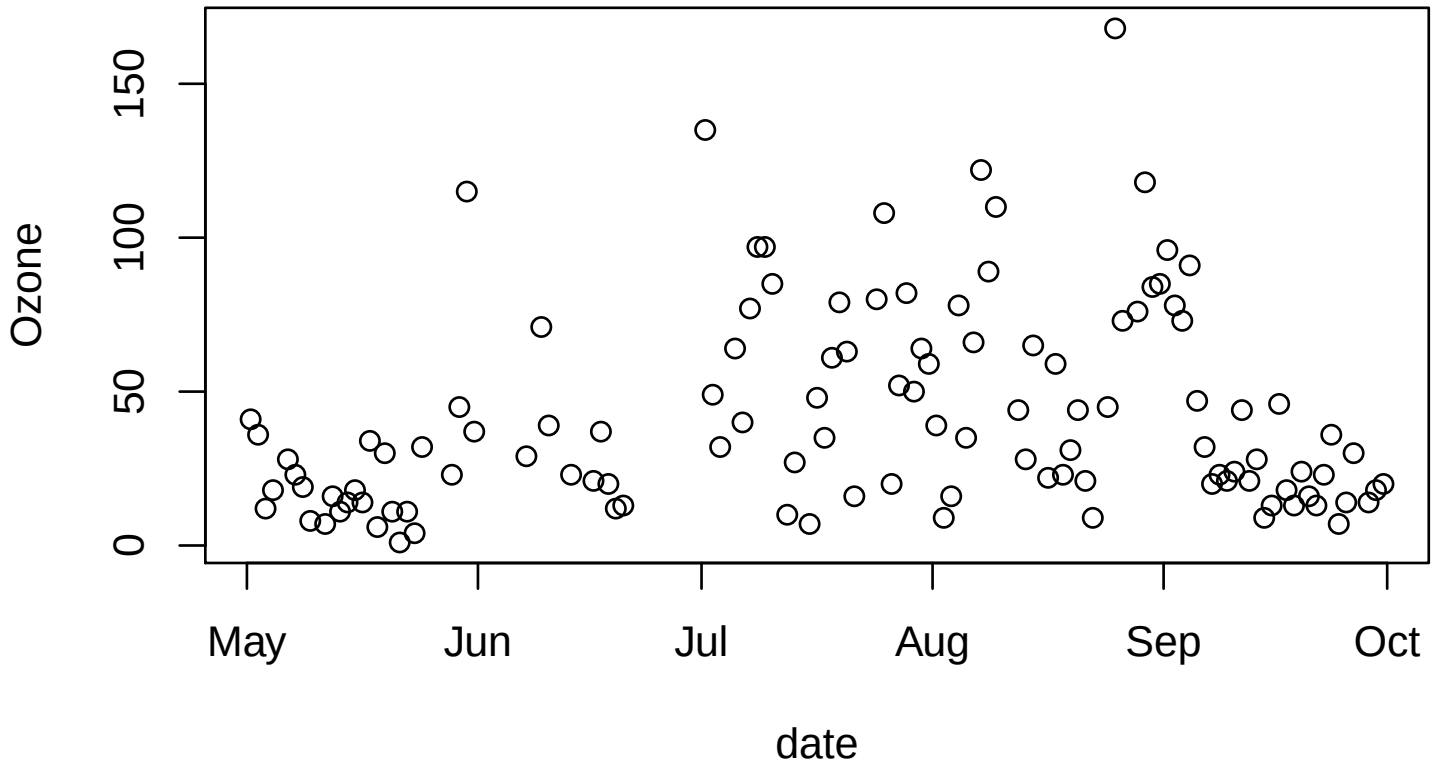
Let's consider the *airquality* dataset.

```
data(airquality)
names(airquality)
airquality$date<-with(airquality, ISOdate(1973,Month,Day))
```

(`ISOdate()` takes year/month/day information and returns an object containing the same information, but in a format R recognizes as numeric information.)

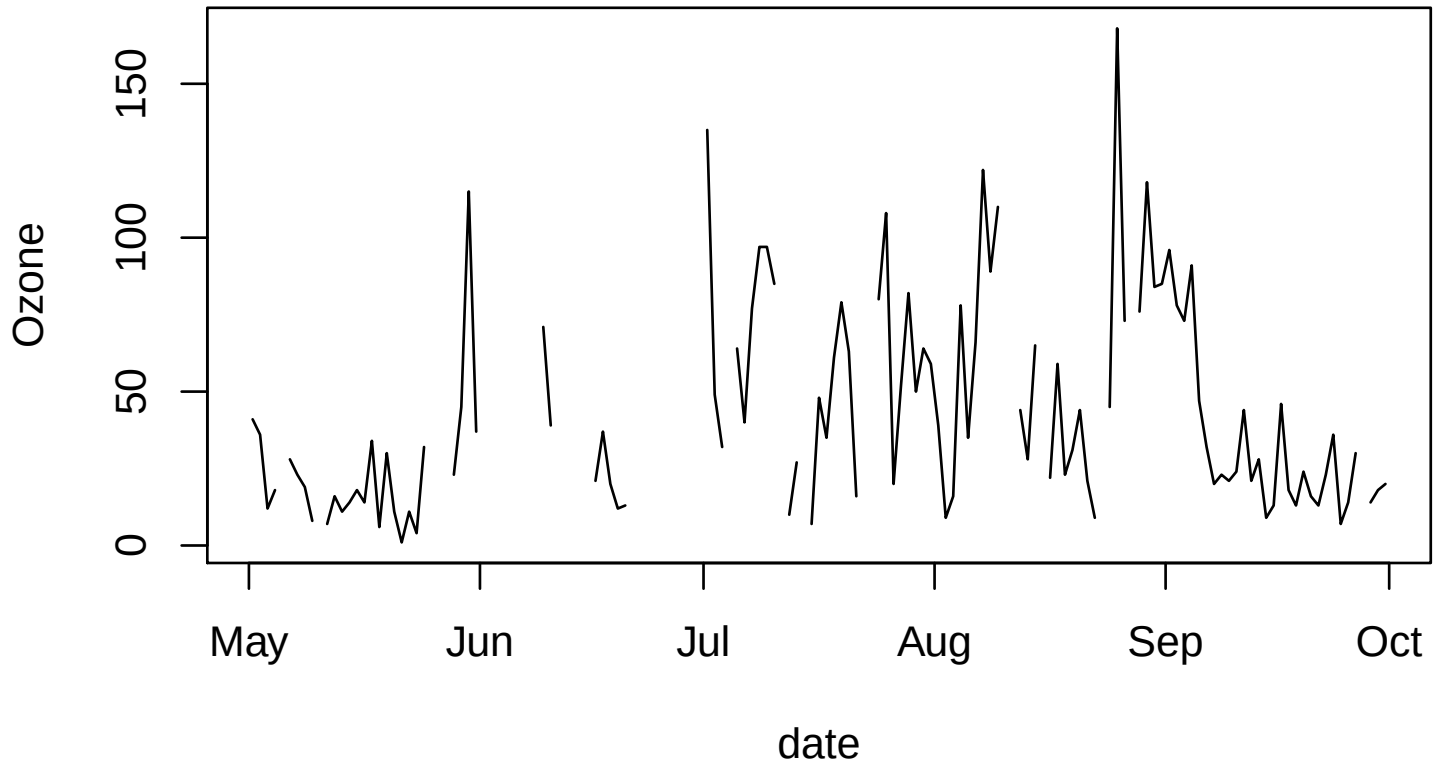
Examples: Plotting two variables

```
plot(Ozone~date, data=airquality)
```



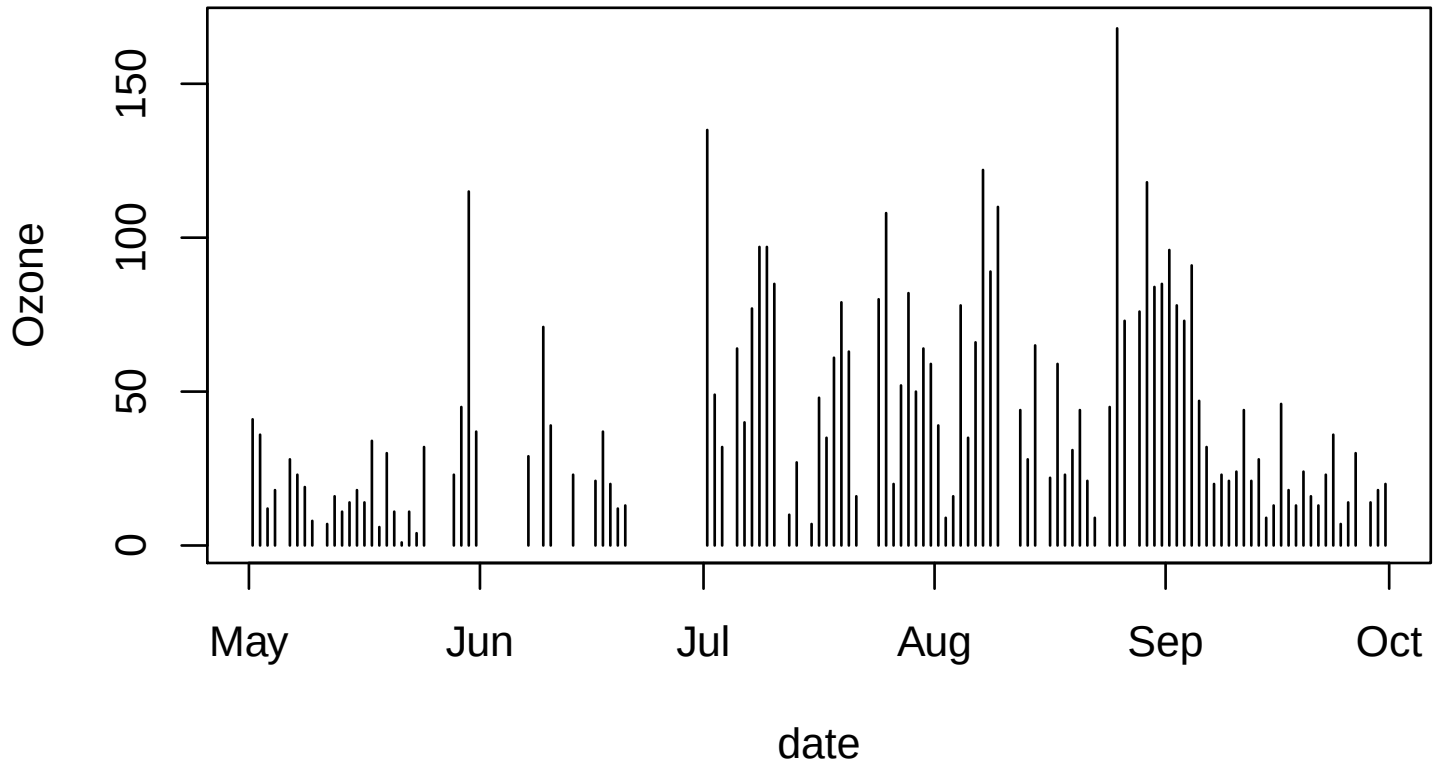
Examples: Plotting two variables

```
plot(Ozone~date, data=airquality,type="l")
```



Examples: Plotting two variables

```
plot(Ozone~date, data=airquality,type="h")
```



Adding points to a graph

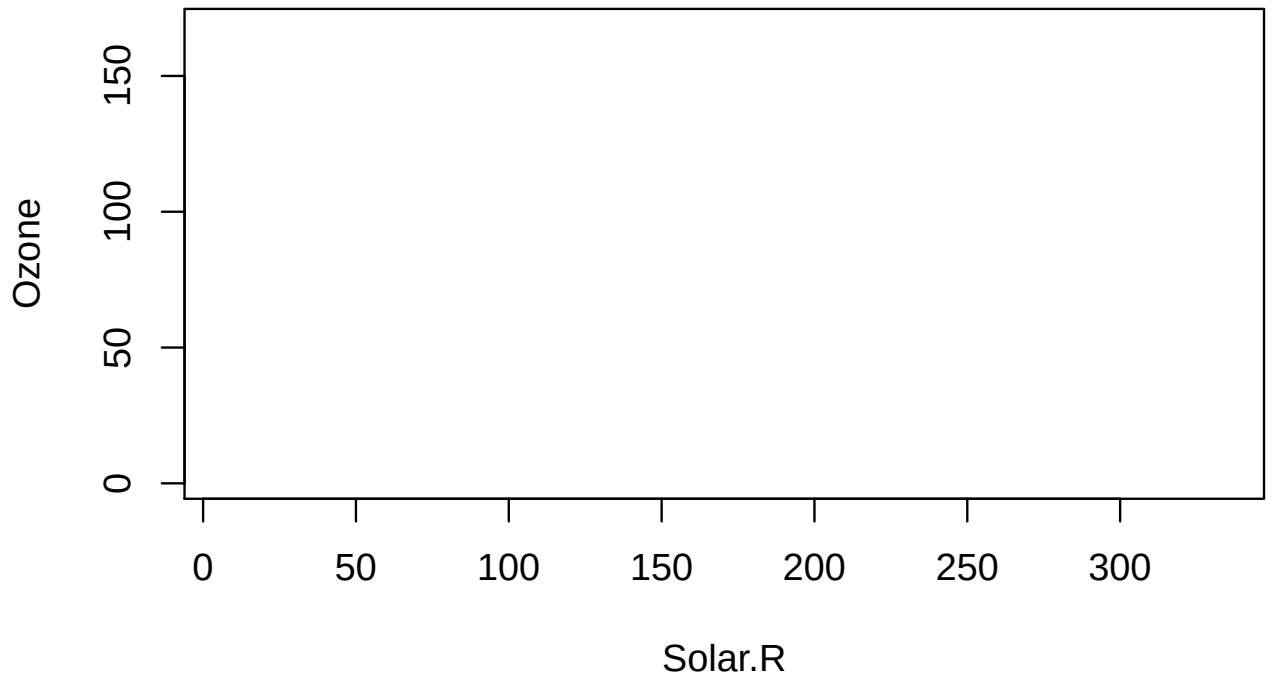
We can add points to an existing plot with the command `points(x,y)`

The `lines(x,y)` command can be used to add connected points by lines to an existing plot without symbols

Adding points to a graph

For example, create a graph that contains axes only.

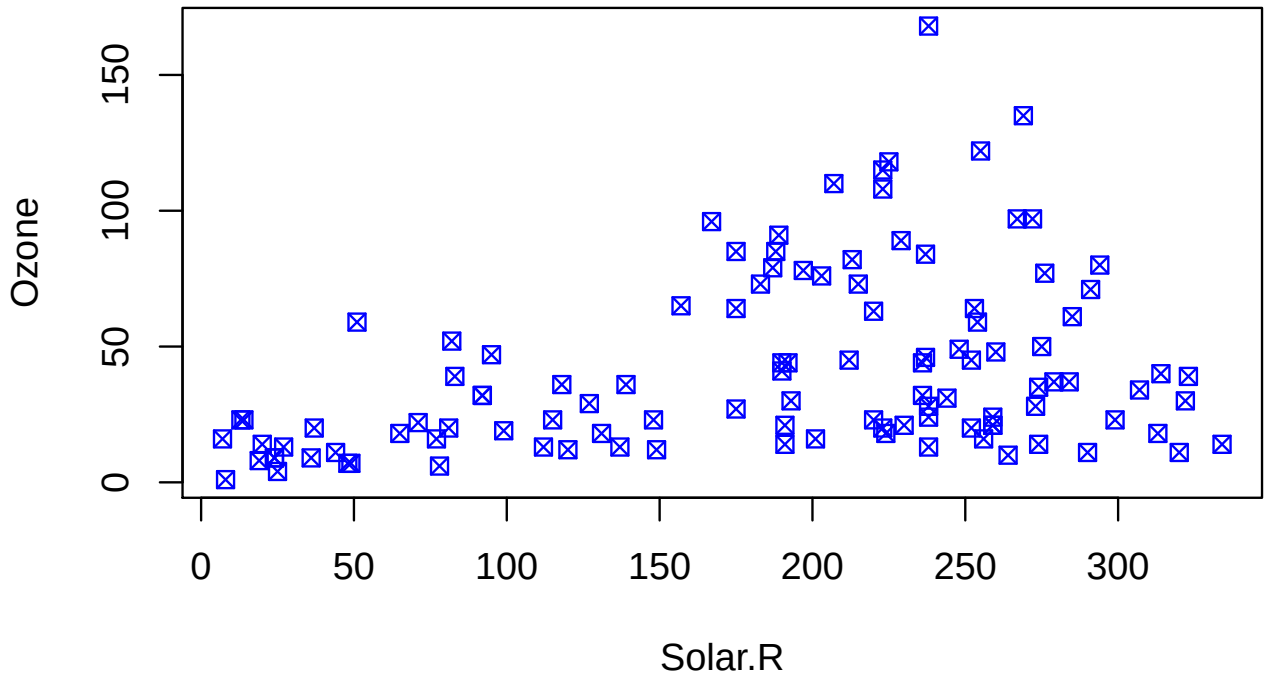
```
plot(Ozone~Solar.R, data=airquality,type="n")
```



Adding points to a graph

Now add the points to the graph:

```
points(airquality$Solar.R,airquality$Ozone,col="blue",pch=7)
```



Adding lines to plots

Horizontal, vertical, and sloped lines can be added to an existing plot with `abline()`:

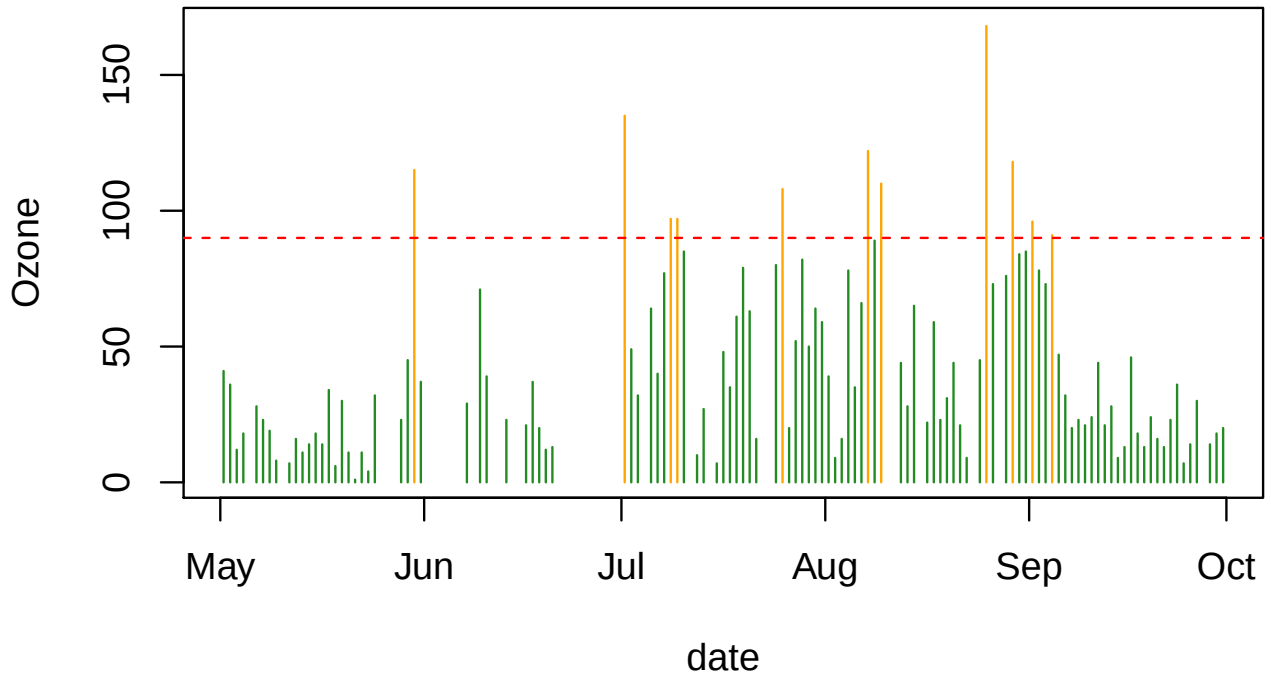
- `abline(h=ycoordinate)` adds a horizontal line at the specified y-coordinate
- `abline(v=xcoordinate)` adds a vertical line at the specified x-coordinate
- `abline(intercept,slope)` adds a line with the specified intercept and slope

As well as using `lines()`, line segments can also be added to an existing plot with `segments()`:

- `segments(x0,y0,x1,y1)` adds a line segment from (x0,y0) to (x1,y1)

Adding lines to plots

```
bad <- ifelse(airquality$Ozone>=90, "orange","forestgreen")
plot(Ozone~date,data=airquality,type="h",col=bad)
abline(h=90,lty=2,col="red")
```



Adding text to plots

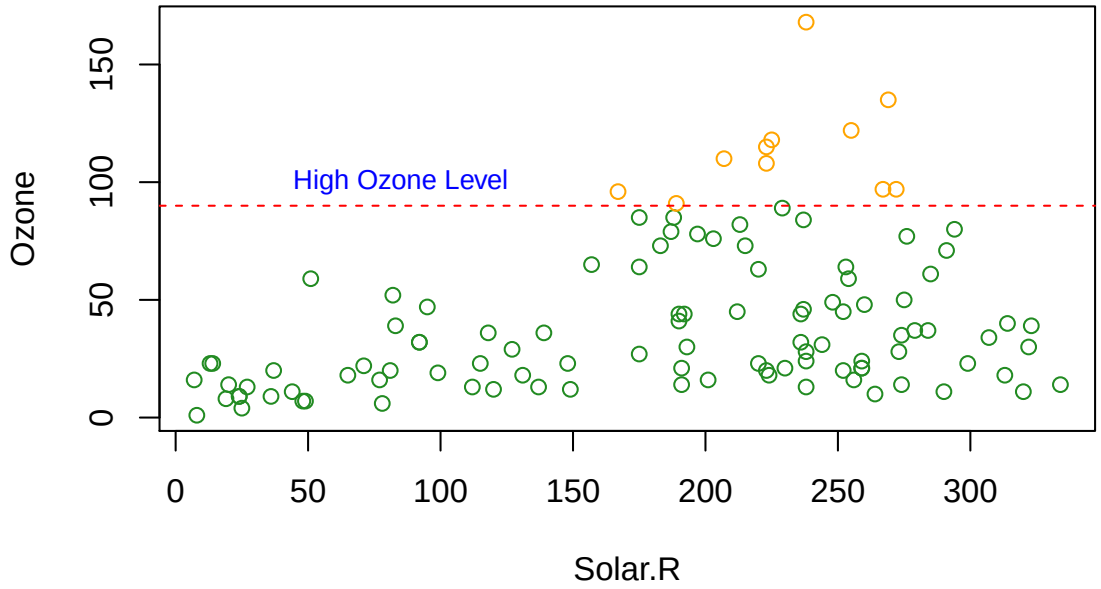
Text labels can be added to a plot with the `text()` command:

- `text(x,y,"Here is my text")` adds text centered at the specified (x,y) coordinates

Text colors and size can be specified with the options *col* and *cex*, respectively.

Adding text to plots

```
bad <- ifelse(airquality$Ozone>=90, "orange", "forestgreen")
plot(Ozone~Solar.R, data=airquality, col=bad)
abline(h=90, lty=2, col="red")
text(85,100,"High Ozone Level",cex=.8,col="blue")
```



Adding a legend to a plot

Including a legend is often essential for explaining symbols, colors, or line types used in a plot. The `legend()` command can be used to add a legend to an existing plot:

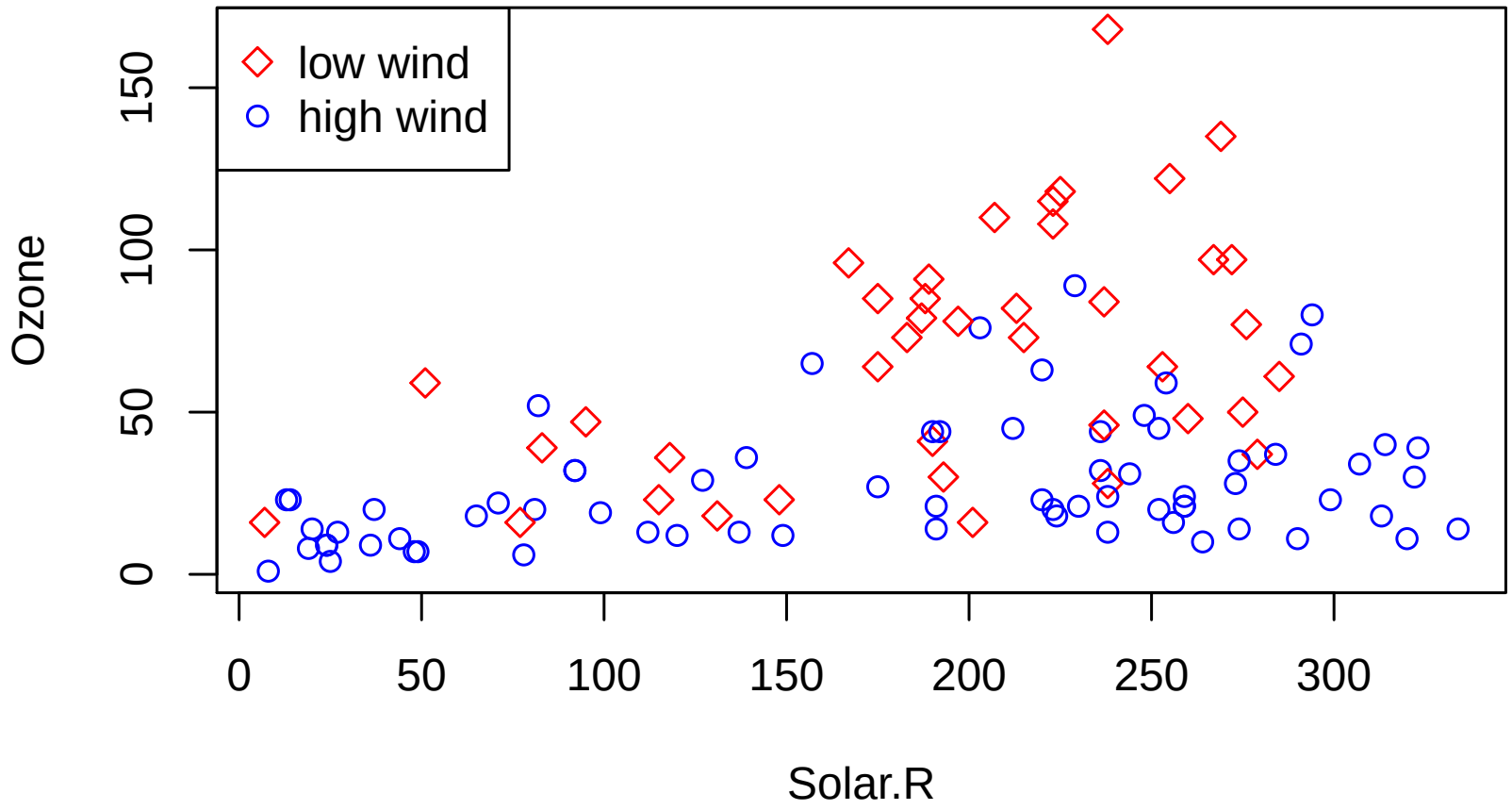
- The position of the legend can be specified by (x,y) coordinates or by using preset positions:
  - `legend(x,y,c("name1","name2"), pch=c(1,5))` adds a legend to the plot with its top-left corner at coordinate (x,y)
  - `legend("topright",c("name1","name2"),pch=c(1,5))` adds a legend in the top right corner of the plot. Can also use "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center".

Adding a legend to a plot

Options such as symbols (*pch*), colors (*col*), and line types (*lty*) can be specified in the legend command. See `?legend` for more details.

```
lowwinds <- ifelse(airquality$Wind<=8, "red", "blue")
symbols <- ifelse(airquality$Wind<=8, 5,1)
plot(Ozone~Solar.R,data=airquality,col=lowwinds,pch=symbols)
legend("topleft",c("low wind","high wind"),col=c("red","blue"),
                pch=c(5,1))
```

Adding a legend to a plot



Smoothing

A straight line may not adequately represent the relationship between two variables.

Smoothing is a way of illustrating the *local* relationship between two variables over parts of their ranges, which may differ from their *global* relationship.

Locally weighted scatterplot smoothing (LOWESS) can be performed in `R` with the `lowess()` function, which calculates a smooth curve that fits the relationship between y and x locally.

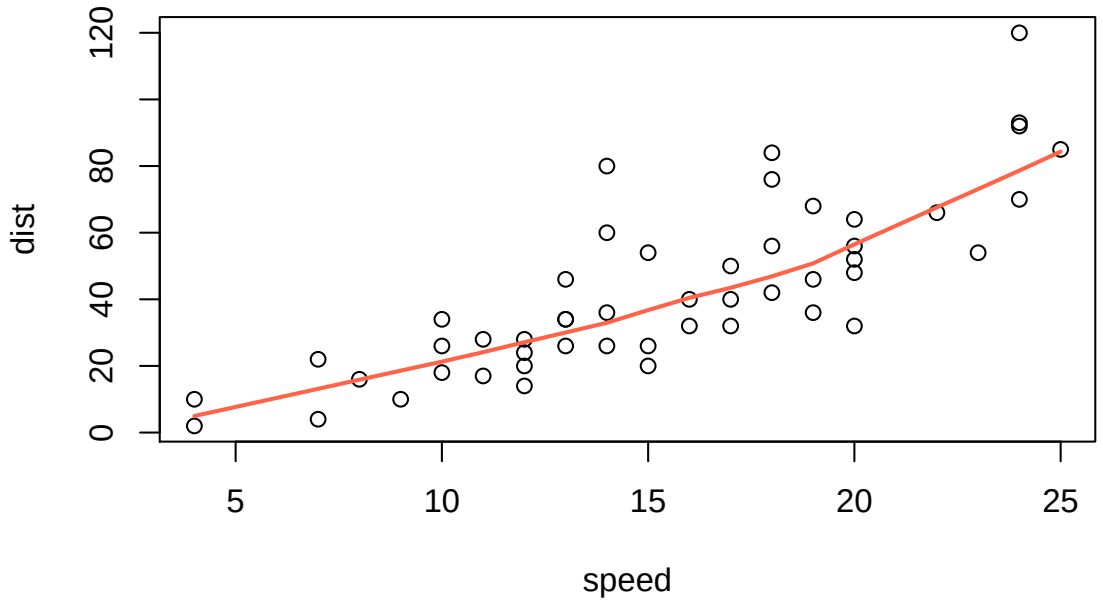
The `supsmu()` function can also be used for smoothing.

The output from both smoothing functions have attributes `$x` and `$y` that can be used with the generic plotting function `lines()`

Smoothing

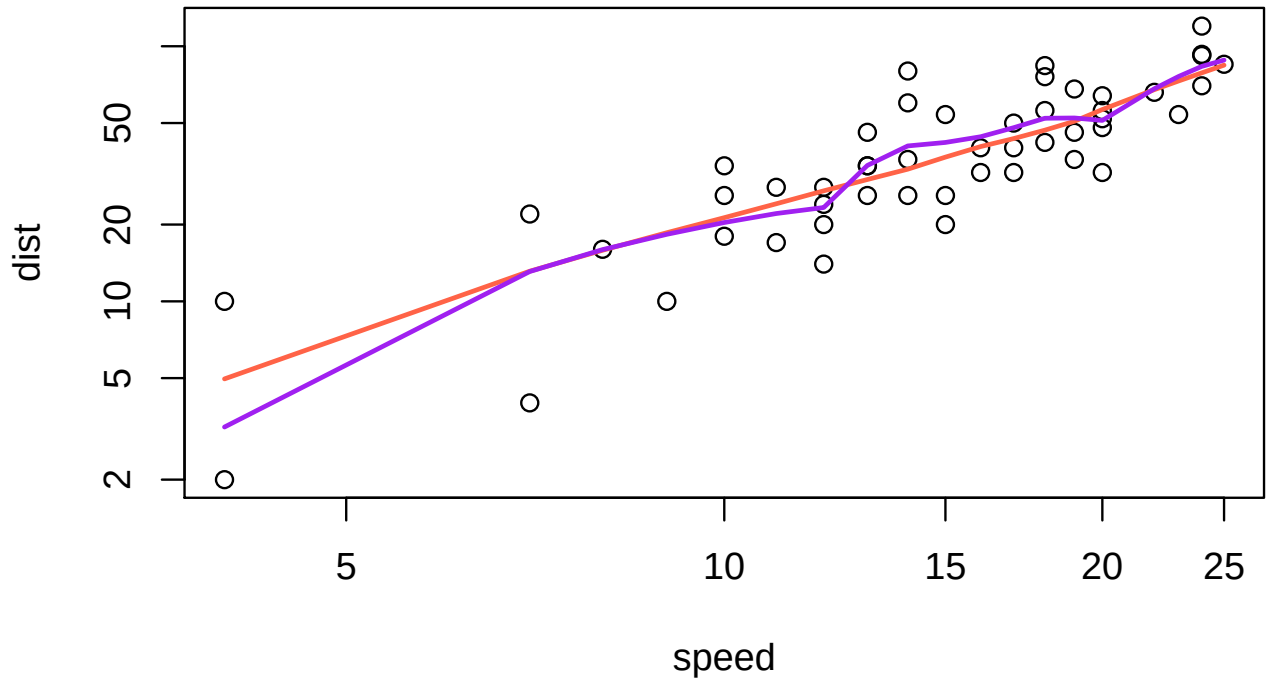
Consider the built-in dataset *cars*.

```
data(cars)
plot(dist~speed,data=cars)
with(cars, lines(lowess(speed, dist), col="tomato", lwd=2))
```



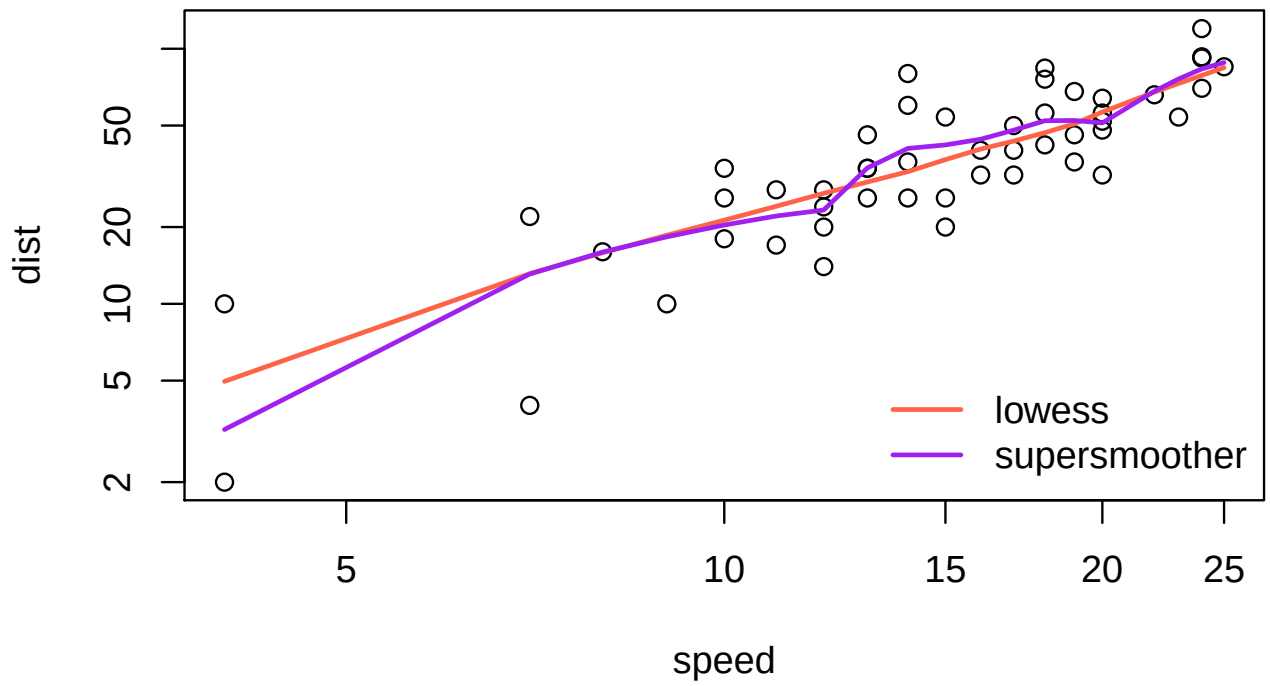
Smoothing

```
plot(dist~speed,data=cars, log="xy")
with(cars, lines(lowess(speed, dist), col="tomato", lwd=2))
with(cars, lines(supsmu(speed, dist), col="purple", lwd=2))
```



Smoothing

```
legend("bottomright", legend=c("lowess","supersmoother"),bty="n",
  lwd=2, col=c("tomato","purple"))
```



Multiple plots in a single figure

The `par()` and `layout()` functions can be used for drawing several plots in one figure.

`par()` with the option `mfrow=c(nrows,ncols)` creates a matrix of *nrows* $\times$ *ncols* plots that are filled in by row.

Using `par( mfcol=c(nrows,ncols) )` fills in the matrix by columns instead.

`layout(mat)` allows for a more customized panel with multiple plots, where *mat* is a matrix object that specifies the locations of the plots in the figure.

Multiple plots in a single figure

The `ToothGrowth` dataset, supplied with R, contains data from a study on the the effect of vitamin C on tooth growth in 10 guinea pigs.

- There are two treatments/supplement types: orange juice and ascorbic acid
- There are three vitamin C dose levels for each of the two treatments: 0.5, 1, and 2mg
- The response is length of odontoblast;

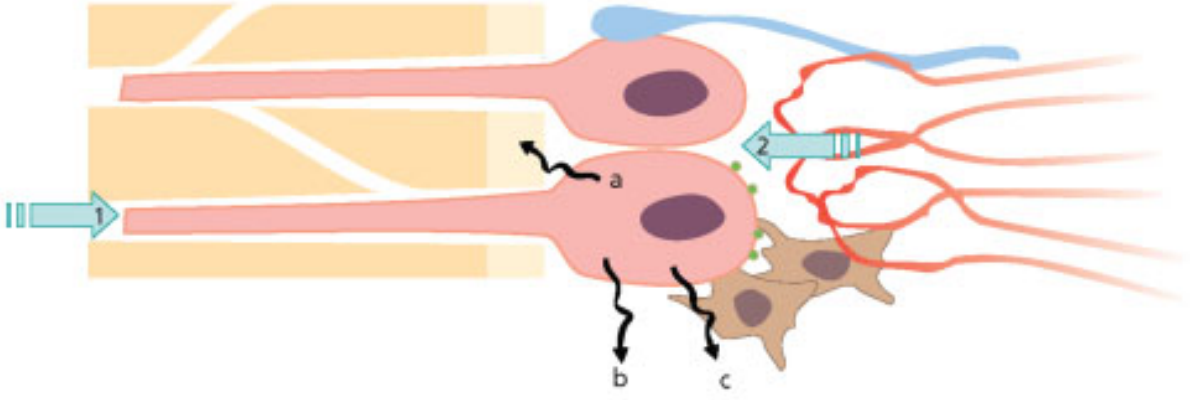


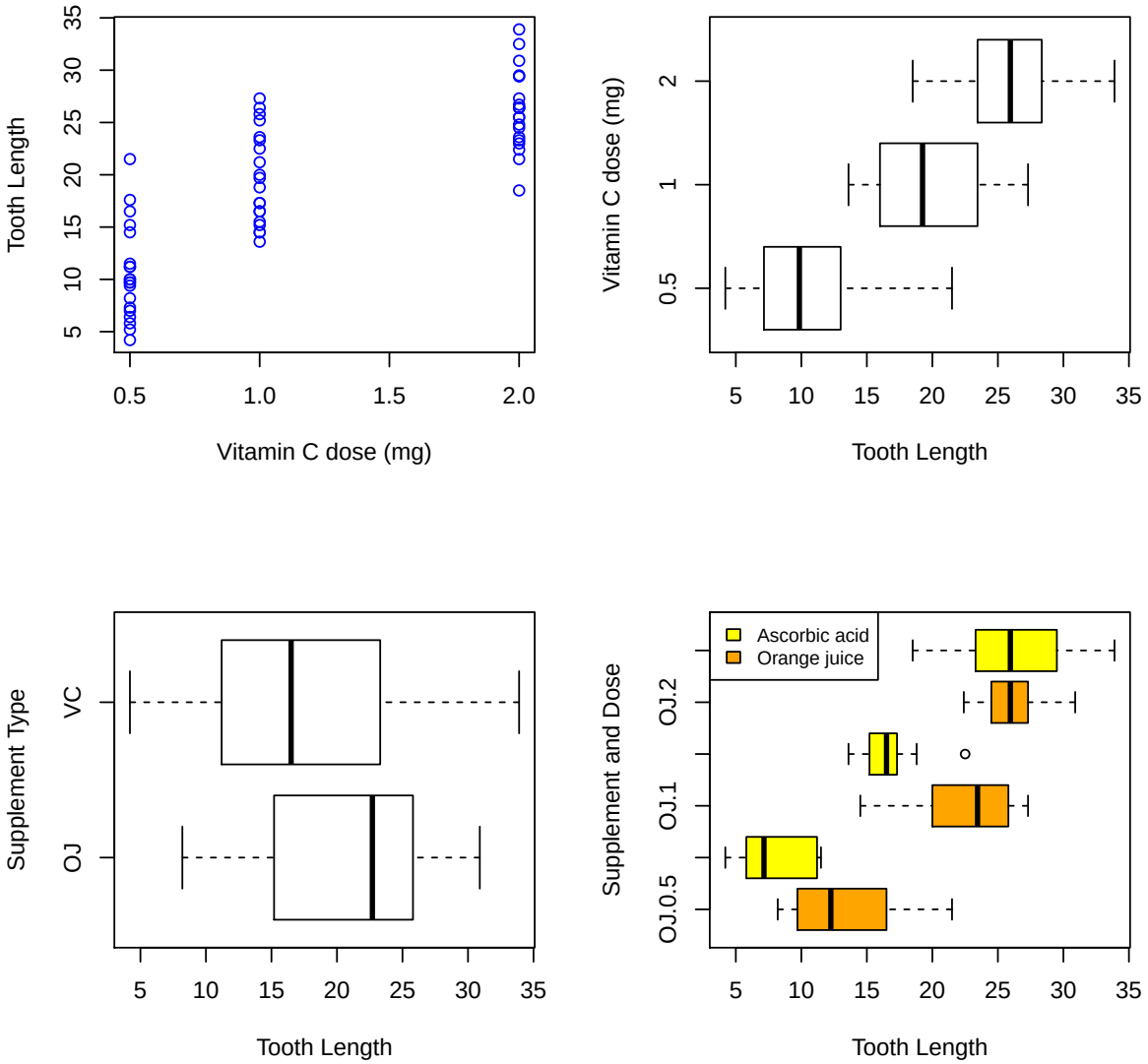
Fig. 2.5 The odontoblast has many functions which change during tooth development, maturation and injury of teeth. (a) *Sensor*: 1. affected from outside by antigens, mechanical forces, thermal gradients; 2. bombarded from inside by circulating hormones, paracrine and autocrine substances. (b) *Secretory cell*: a. for dentin lay down, b. for maintenance, c. for immune defense. (c) *Pain mediator*: acting as a transducer between external stimuli and pulpal sensory nerves.

Multiple plots in a single figure

Commands for plotting multiple figures with the ToothGrowth dataset, using `par()`;

```
data(ToothGrowth) # load data into current R session
par(mfrow=c(2,2)) # Set up a 2x2 layout

#1st Plot - scatterplot of length vs dose;
plot(len~dose, data=ToothGrowth, xlab="Vitamin C dose (mg)",
     ylab="Tooth Length", col="blue" ,cex.main=.8)

#2nd plot - boxplot of length vs dose;
boxplot(len~dose, data=ToothGrowth, horizontal=TRUE,
        ylab="Vitamin C dose (mg)", xlab="Tooth Length", cex.main=.8)

#3rd plot - boxplot of length vs type of supplement;
boxplot(len~supp, data=ToothGrowth, horizontal=TRUE,
        ylab="Supplement Type", xlab="Tooth Length", cex.main=.8)

#4th plot - length vs *interaction* (i.e. all combinations) of supp and dose;
boxplot(len~supp*dose,data=ToothGrowth,horizontal=TRUE,col=c("orange","yellow"),
         ylab="Supplement and Dose", xlab="Tooth Length")

#... and give this one a legend
legend("topleft", c("Ascorbic acid", "Orange juice"), fill=c("yellow","orange"))
```

Multiple plots in a single figure



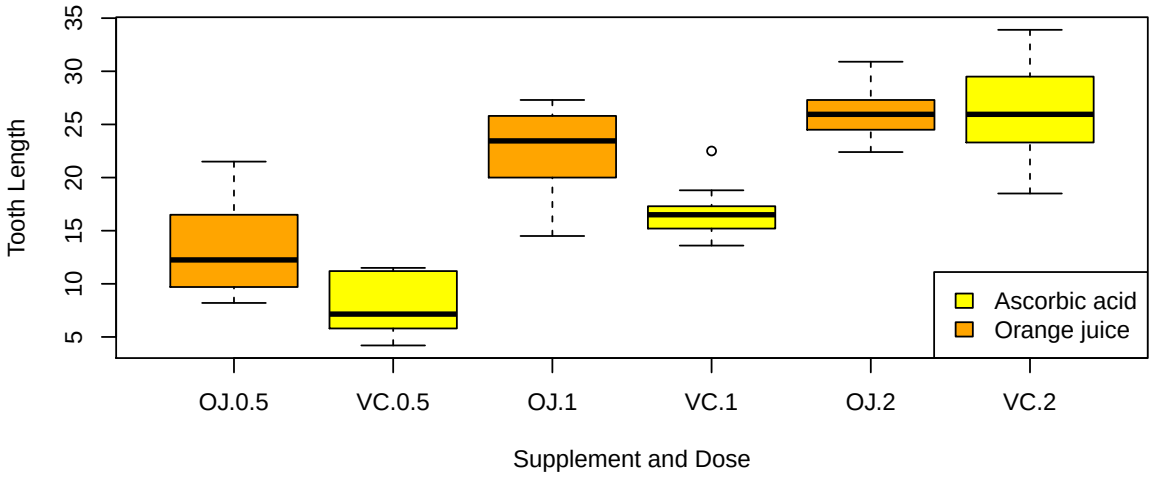
Multiple plots in a single figure

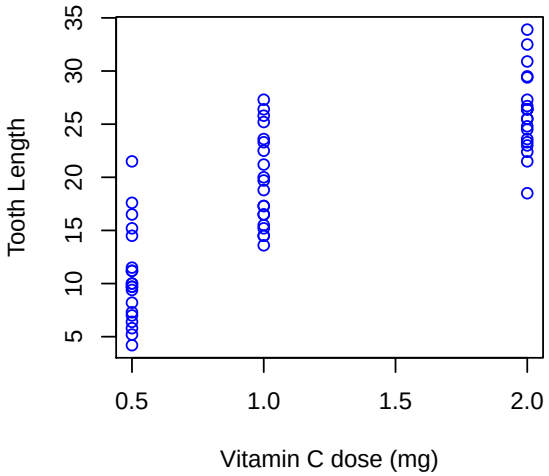
Commands for a more customized multiple-plot figure using `layout()`

```
#set up a 2x2 layout, but merge first 2 cells, i.e. the top row
layout(matrix(c(1,1,2,3), 2, 2, byrow = TRUE))

#1st plot - the interactions again, with a legend added
boxplot(len~supp*dose, data=ToothGrowth, col=c("orange","yellow"),
        xlab="Supplement and Dose",ylab="Tooth Length")

legend("bottomright",c("Ascorbic acid", "Orange juice"),
       fill = c("yellow", "orange"))

#2nd plot (in bottom left position) - scatterplot length vs dose
plot(len~dose, data=ToothGrowth, xlab="Vitamin C dose (mg)",
     ylab="Tooth Length", col="blue", cex.main=.8)

#3rd plot (in bottom right position) - histogram of tooth length
hist(ToothGrowth$len, xlab="Tooth Length", main="", cex.main=.8)
```

(This is far too much effort for a quick look at your data – but useful for making slides, or final copies of your paper)

Multiple plots in a single figure





Summary

- R has a variety of plotting options
- `points()` adds points to an existing plot and `lines()` adds connected points by lines to an existing plot without symbols
- `abline()` draws a single straight line on a plot
- `lowess()` and `supsmu()` are scatterplot smoothers
- `legend()` adds a legend to a plot
- `par()` and `layout()` can be used for multi-panel plotting