Module 10

Data Visualization

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Basic Plots

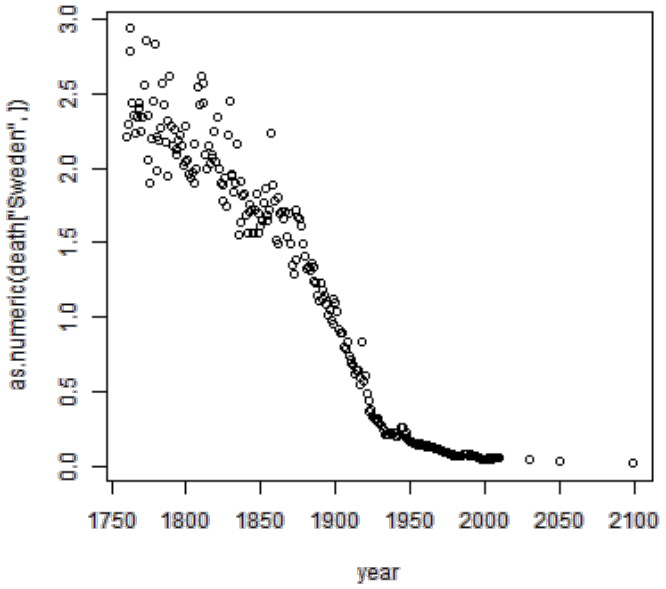
We covered some basic plots on Wednesday, but we are going to expand the ability to customize these basic graphics first.

But first...

Some cool graphics made in R by us.

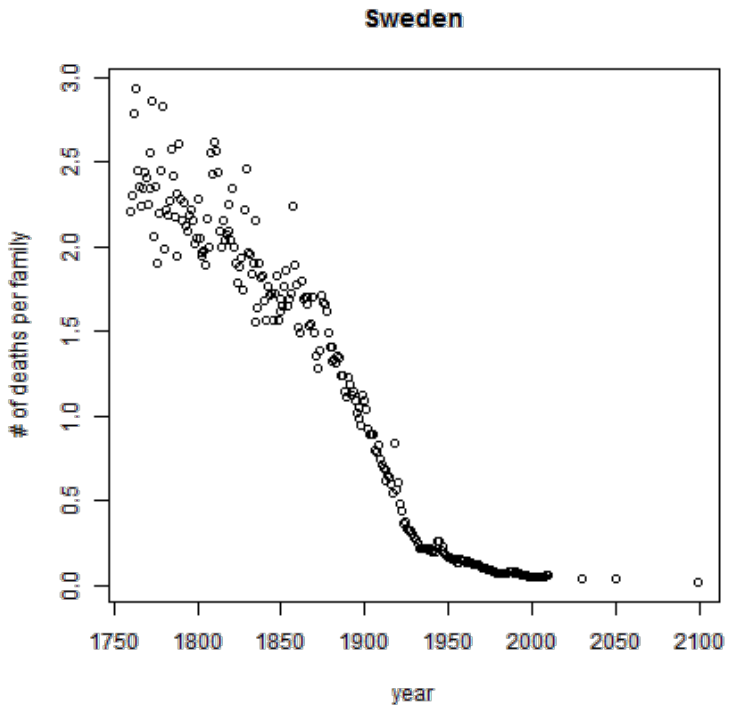
Basic Plots

```
> death = read.csv("http://biostat.jhsph.edu/~ajaffe/files/indicatordeadkids35.csv",
+     as.is = T, header = TRUE, row.names = 1)
> year = as.integer(gsub("X", "", names(death)))
> plot(as.numeric(death["Sweden", ]) ~ year)
```



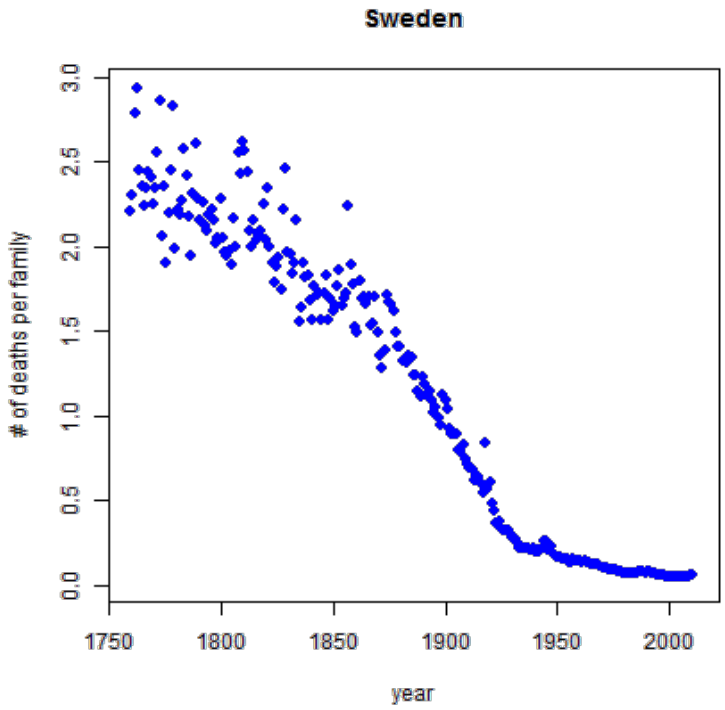
Basic Plots

```
> plot(as.numeric(death["Sweden", ]) ~ year, ylab = "# of deaths per family",
+     main = "Sweden")
```



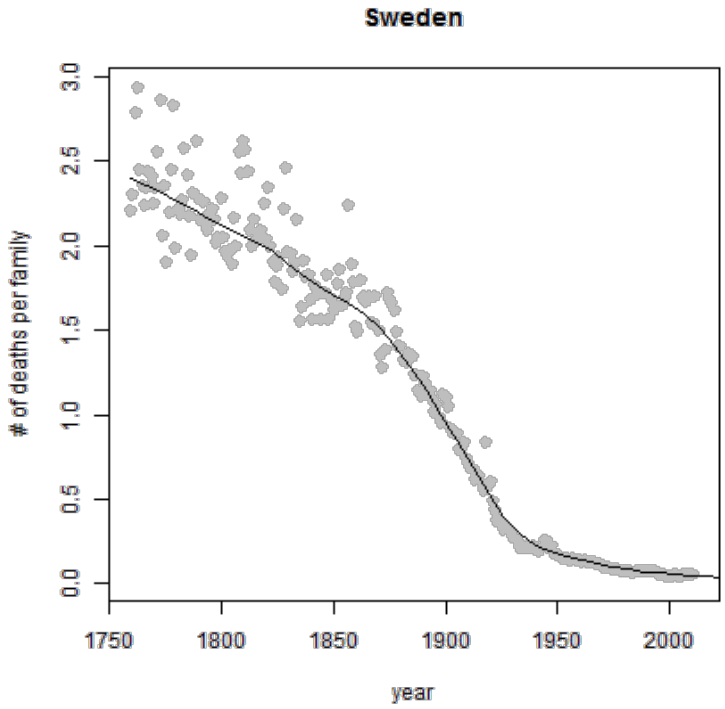
Basic Plots

```
> plot(as.numeric(death["Sweden", ]) ~ year, ylab = "# of deaths per family",
+     main = "Sweden", xlim = c(1760, 2012), pch = 19, cex = 1.2, col = "blue")
```



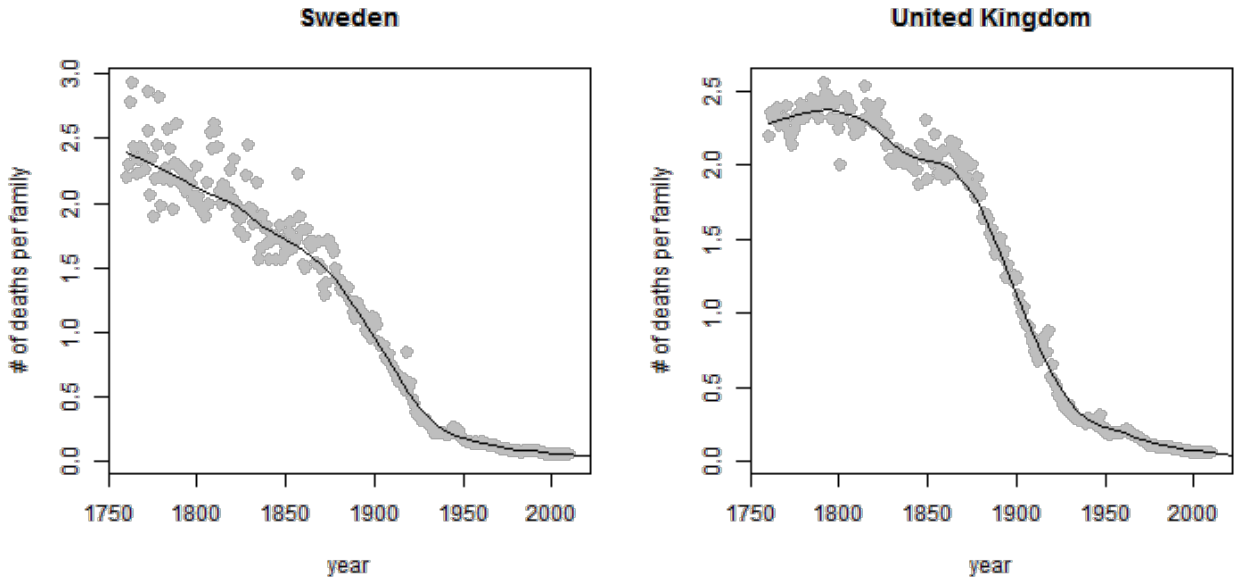
Basic Plots

```
> scatter.smooth(as.numeric(death["Sweden", ]) ~ year, span = 0.2, ylab = "# of deaths per family",
+     main = "Sweden", lwd = 3, xlim = c(1760, 2012), pch = 19, cex = 0.9, col = "grey")
```



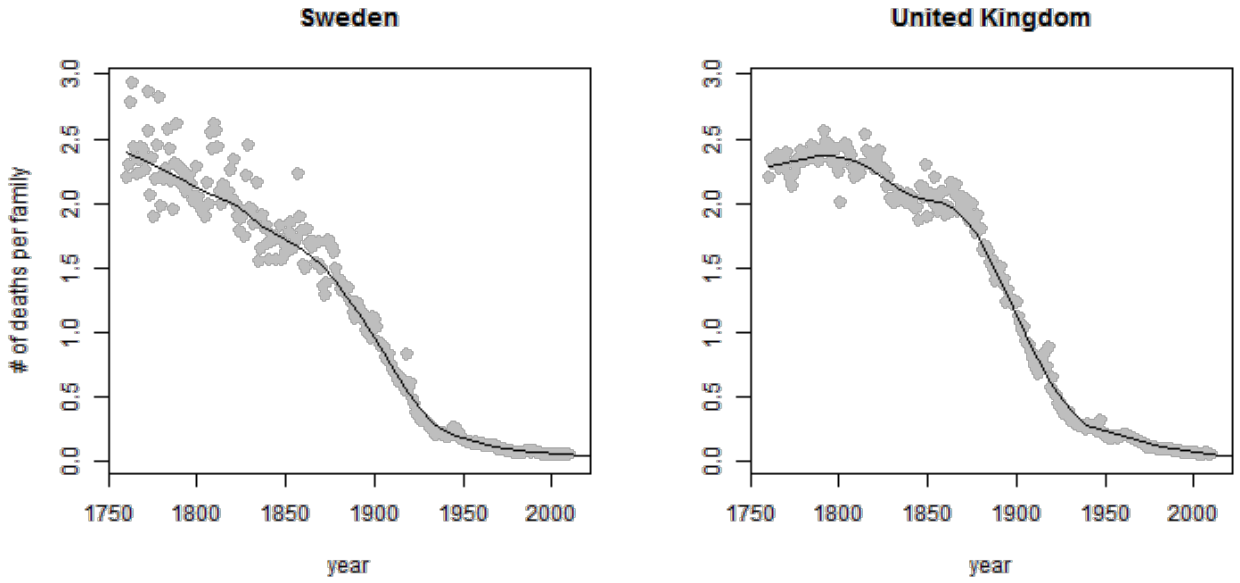
Basic Plots

```
> par(mfrow = c(1, 2))
> scatter.smooth(as.numeric(death["Sweden", ]) ~ year, span = 0.2, ylab = "# of deaths per family",
+     main = "Sweden", lwd = 3, xlim = c(1760, 2012), pch = 19, cex = 0.9, col = "grey")
> scatter.smooth(as.numeric(death["United Kingdom", ]) ~ year, span = 0.2, ylab = "# of deaths per famil
+     main = "United Kingdom", lwd = 3, xlim = c(1760, 2012), pch = 19, cex = 0.9,
+     col = "grey")
```



Basic Plots

```
> par(mfrow = c(1, 2))
> yl = range(death[c("Sweden", "United Kingdom"), ])
> scatter.smooth(as.numeric(death["Sweden", ]) ~ year, span = 0.2, ylim = yl,
+     ylab = "# of deaths per family", main = "Sweden", lwd = 3, xlim = c(1760,
+         2012), pch = 19, cex = 0.9, col = "grey")
> scatter.smooth(as.numeric(death["United Kingdom", ]) ~ year, span = 0.2, ylab = "",
+     main = "United Kingdom", lwd = 3, ylim = yl, xlim = c(1760, 2012), pch = 19,
+     cex = 0.9, col = "grey")
```



Graphical parameters

par() can be used to set or query graphical parameters. Parameters can be set by specifying them as arguments to par in tag = value form, or by passing them as a list of tagged values.

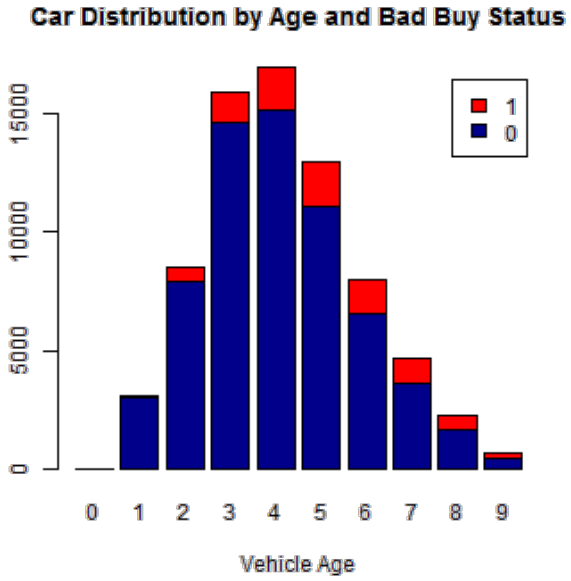
Note that some parameters are passed from plot(,...) calls whereas others need to be explicitly set using par() - like above with par(mfrow = c(nrow,ncol))

Note that some parameters are both very flexible but also very finicky, especially margins.

Bar Plots

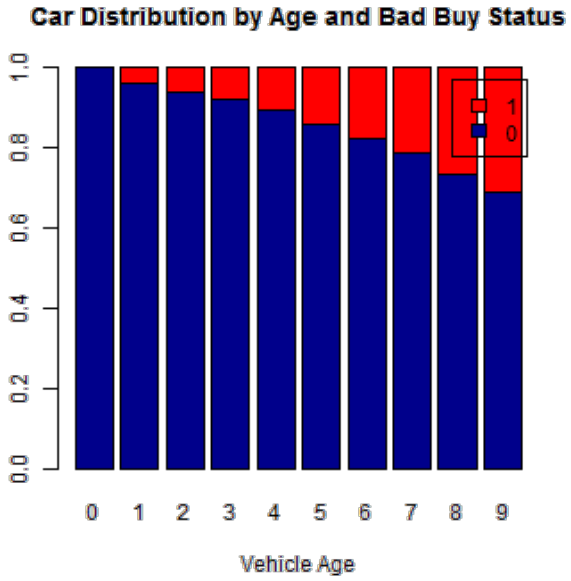
- Stacked Bar Charts are sometimes wanted to show how

```
> ## Stacked Bar Charts
> cars = read.csv("http://biostat.jhsph.edu/~ajaffe/files/kaggleCarAuction.csv",
+     as.is = T)
> counts <- table(cars$IsBadBuy, cars$VehicleAge)
> barplot(counts, main = "Car Distribution by Age and Bad Buy Status", xlab = "Vehicle Age",
+     col = c("darkblue", "red"), legend = rownames(counts))
```



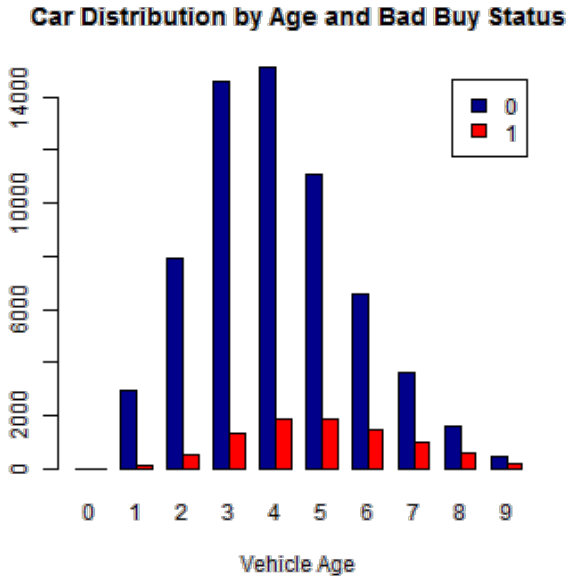
Bar Plots

```
> ## Use percentages (column percentages)
> barplot(prop.table(counts, 2), main = "Car Distribution by Age and Bad Buy Status",
+     xlab = "Vehicle Age", col = c("darkblue", "red"), legend = rownames(counts))
```



Bar Plots

```
> # Stacked Bar Plot with Colors and Legend
> barplot(counts, main = "Car Distribution by Age and Bad Buy Status", xlab = "Vehicle Age",
+     col = c("darkblue", "red"), legend = rownames(counts), beside = TRUE)
```



Graphics parameters

Set within most plots in the base 'graphics' package:

- pch = point shape, http://voteview.com/symbols_pch.htm
- cex = size/scale
- xlab, ylab = labels for x and y axes
- main = plot title
- lwd = line density
- col = color
- cex.axis, cex.lab, cex.main = scaling/sizing for axes marks, axes labels, and title

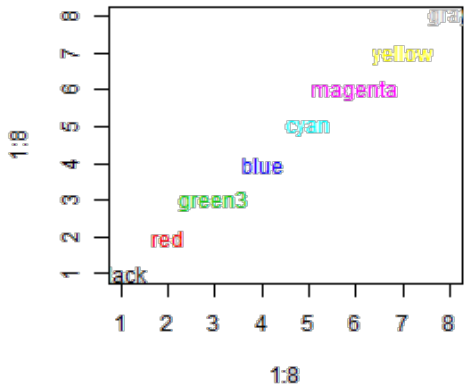
Colors

R relies on color 'palettes'.

```
> palette()
```

```
[1] "black"   "red"     "green3"  "blue"    "cyan"    "magenta" "yellow"
[8] "gray"
```

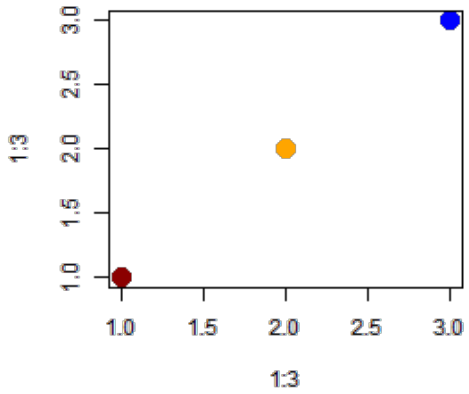
```
> plot(1:8, 1:8, type = "n")
> text(1:8, 1:8, lab = palette(), col = 1:8)
```



Colors

The default color palette is pretty bad, so you can try to make your own.

```
> palette(c("darkred", "orange", "blue"))
> plot(1:3, 1:3, col = 1:3, pch = 19, cex = 2)
```



Colors

It's actually pretty hard to make a good color palette. Luckily, smart and artistic people have spent a lot more time thinking about this. The result is the 'RColorBrewer' package

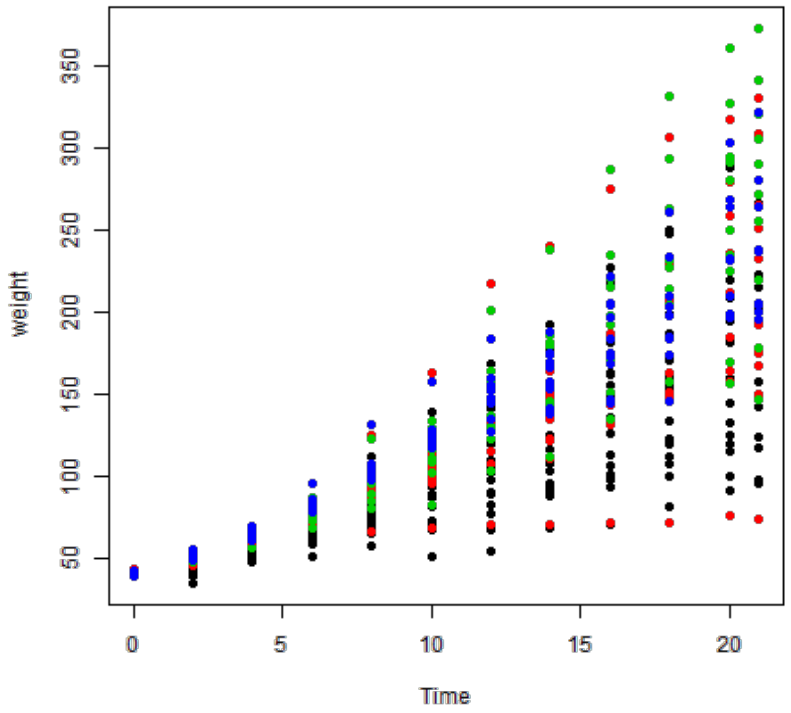
RColorBrewer::display.brewer.all() will show you all of the palettes available. You can even print it out and keep it next to your monitor for reference.

The help file for brewer.pal() gives you an idea how to use the package.

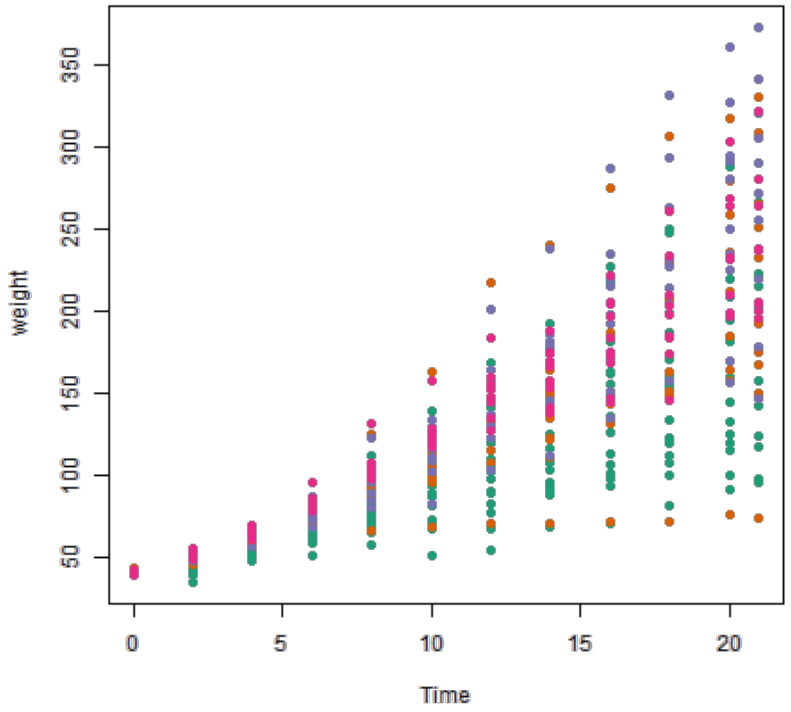
You can also get a "sneak peek" of these palettes at: www.colorbrewer2.com . You would provide the number of levels or classes of your data, and then the type of data: sequential, diverging, or qualitative. The names of the RColorBrewer palettes are the string after 'pick a color scheme:'

Colors

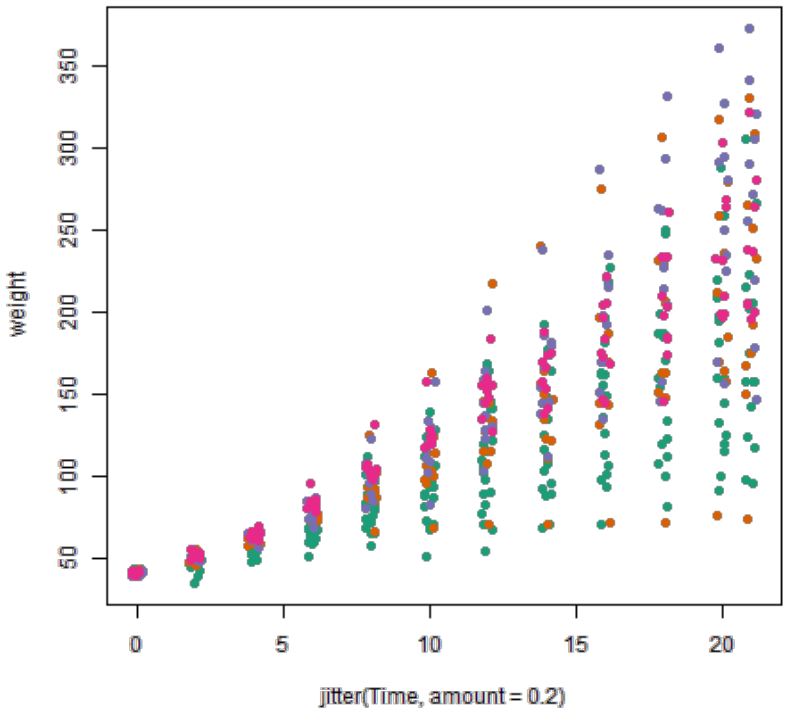
```
> palette("default")
> with(ChickWeight, plot(weight ~ Time, pch = 19, col = Diet))
```



```
> library(RColorBrewer)
> palette(brewer.pal(5, "Dark2"))
> with(ChickWeight, plot(weight ~ Time, pch = 19, col = Diet))
```



```
> library(RColorBrewer)
> palette(brewer.pal(5, "Dark2"))
> with(ChickWeight, plot(weight ~ jitter(Time, amount = 0.2), pch = 19, col = Diet),
+     xlab = "Time")
```



Adding legends

The legend() command adds a legend to your plot. There are tons of arguments to pass it.

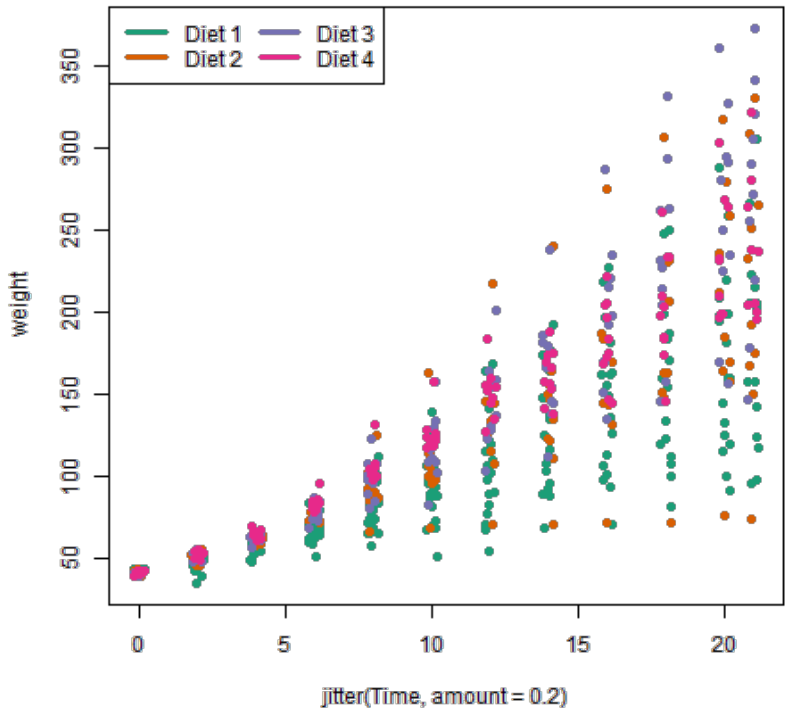
x, y=NULL: this just means you can give (x,y) coordinates, or more commonly just give x, as a character string: "top","bottom","topleft","bottomleft","topright","bottomright".

legend: unique character vector, the levels of a factor

pch, lwd: if you want points in the legend, give a pch value. if you want lines, give a lwd value.

col: give the color for each legend level

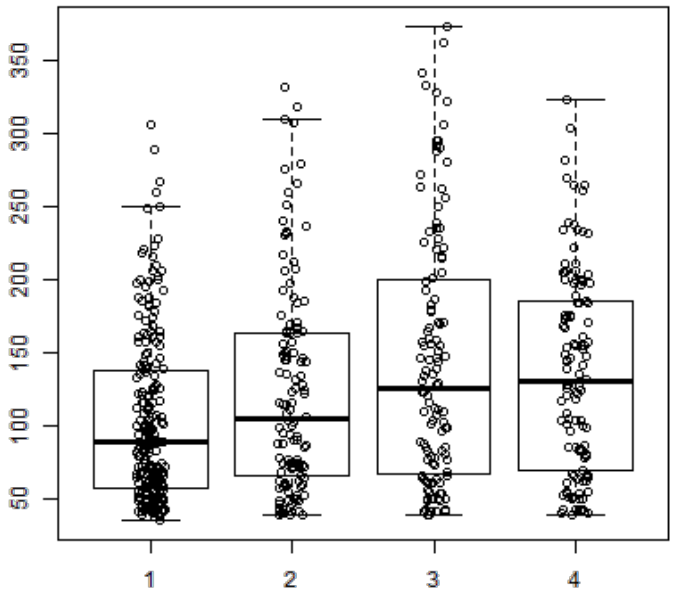
```
> palette(brewer.pal(5, "Dark2"))
> with(ChickWeight, plot(weight ~ jitter(Time, amount = 0.2), pch = 19, col = Diet),
+     xlab = "Time")
> legend("topleft", paste("Diet", levels(ChickWeight$Diet)), col = 1:length(levels(ChickWeight$Diet)),
+     lwd = 3, ncol = 2)
```



Boxplots, revisited

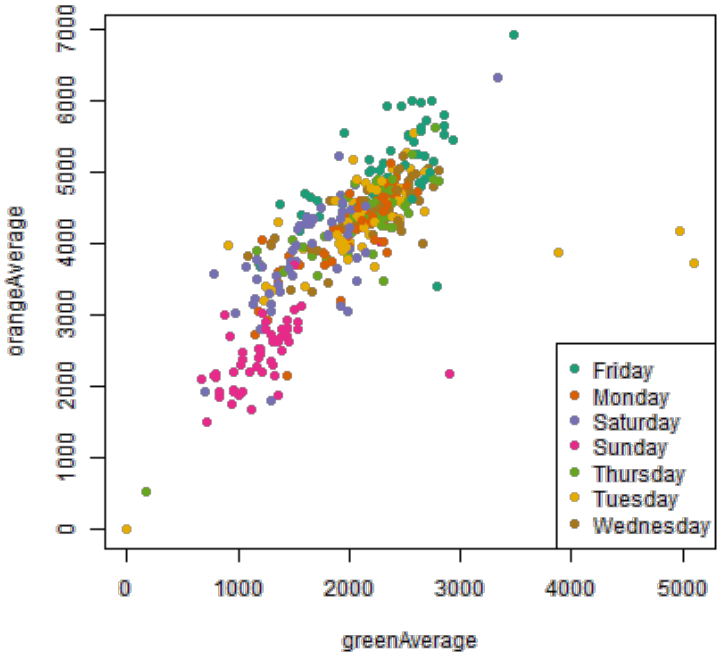
These are one of my favorite plots. They are way more informative than the barchart + antenna...

```
> with(ChickWeight, boxplot(weight ~ Diet, outline = FALSE))
> points(ChickWeight$weight ~ jitter(as.numeric(ChickWeight$Diet), 0.5))
```



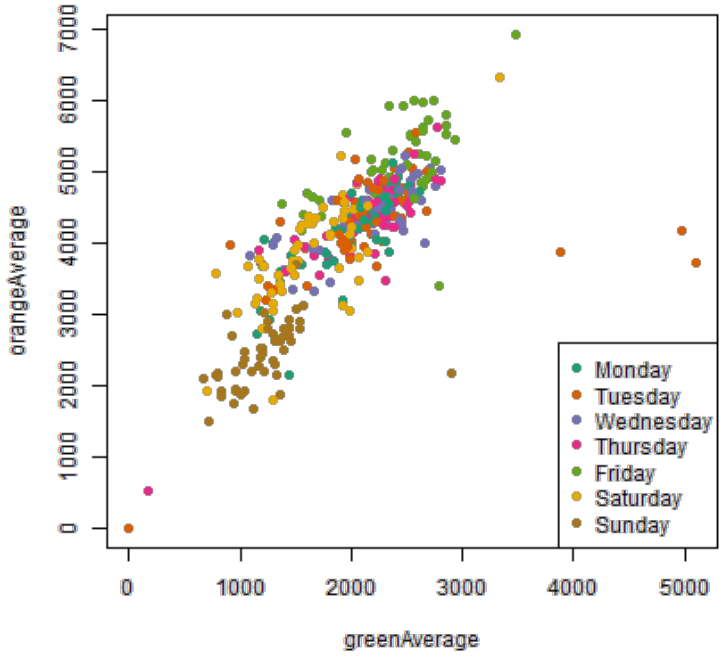
Coloring by variable

```
> load("data/charmcirc.rda")
> palette(brewer.pal(7, "Dark2"))
> dd = factor(dat$day)
> with(dat, plot(orangeAverage ~ greenAverage, pch = 19, col = as.numeric(dd)))
> legend("bottomright", levels(dd), col = 1:length(dd), pch = 19)
```



Coloring by variable

```
> dd = factor(dat$day, levels = c("Monday", "Tuesday", "Wednesday", "Thursday",
+     "Friday", "Saturday", "Sunday"))
> with(dat, plot(orangeAverage ~ greenAverage, pch = 19, col = as.numeric(dd)))
> legend("bottomright", levels(dd), col = 1:length(dd), pch = 19)
```



Devices

By default, R displays plots in a separate panel. From there, you can export the plot to a variety of image file types, or copy it to the clipboard.

However, sometimes its very nice to save many plots made at one time to one pdf file, say, for flipping through. Or being more precise with the plot size in the saved file.

R has 5 additional graphics devices: bmp(), jpeg(), png(), tiff(), and pdf()

The syntax is very similar for all of them:

```
pdf("filename.pdf", width=8, height=8) # inches
plot() # plot 1
plot() # plot 2
# etc
dev.off()
```

Basically, you are creating a pdf file, and telling R to write any subsequent plots to that file. Once you are done, you turn the device off. Note that failing to turn the device off will create a pdf file that is corrupt, that you cannot open.

More powerful graphics

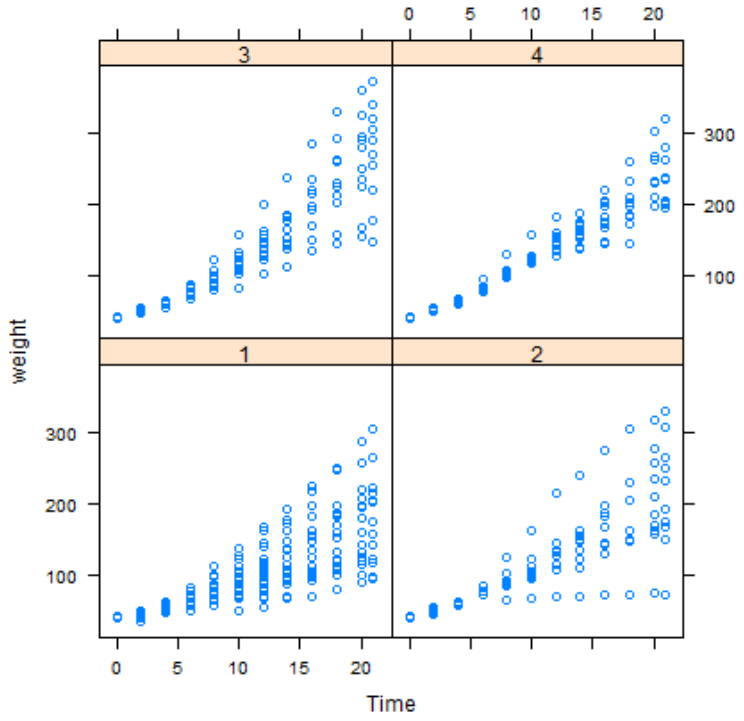
There are two very common packages for making very nice looking graphics.

lattice: http://lmdvr.r-forge.r-project.org/figures/figures.html

ggplot2: http://docs.ggplot2.org/current/index.html

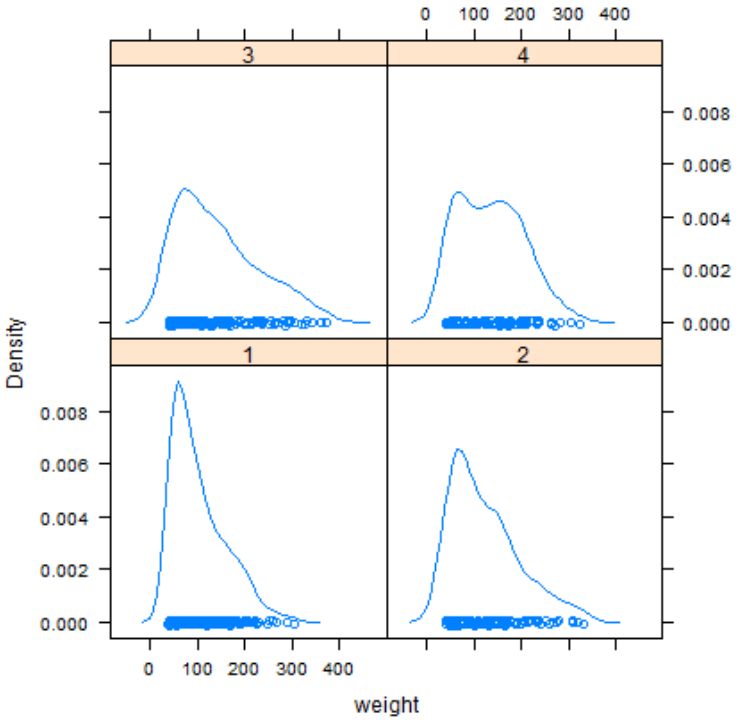
Lattice

```
> library(lattice)
> xyplot(weight ~ Time | Diet, data = ChickWeight)
```



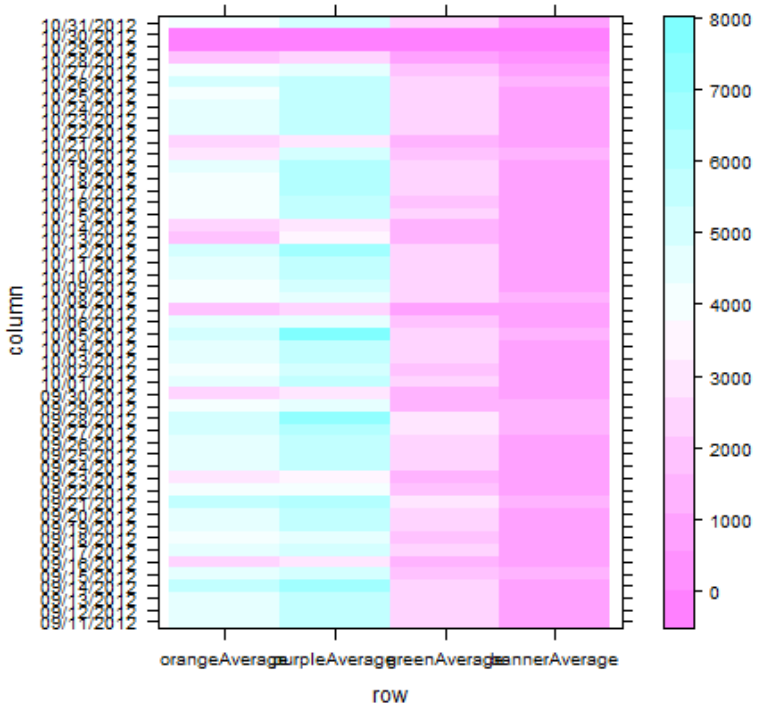
Lattice

```
> densityplot(~weight | Diet, data = ChickWeight)
```



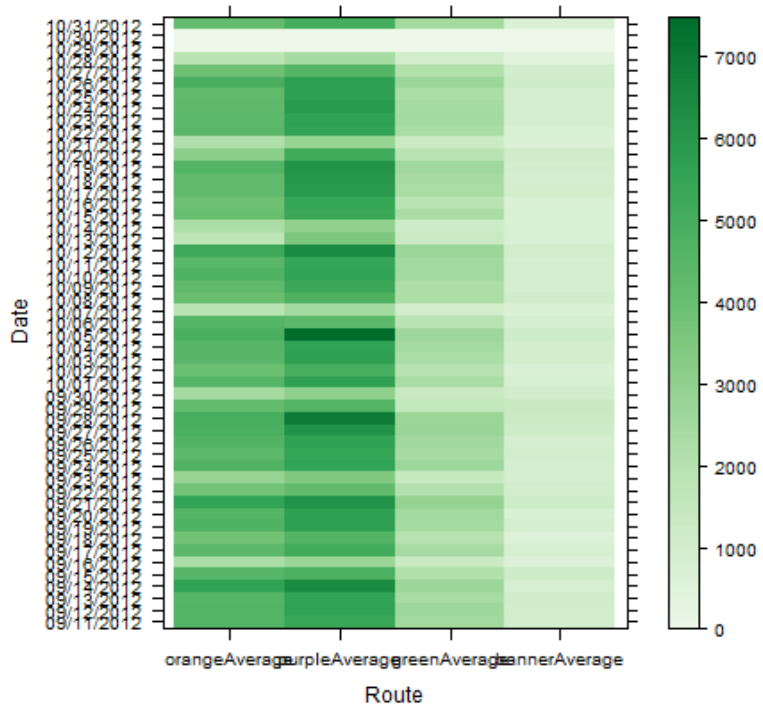
Lattice

```
> rownames(dat2) = dat2$date
> mat = as.matrix(dat2[975:nrow(dat2), 3:6])
> levelplot(t(mat), aspect = "fill")
```



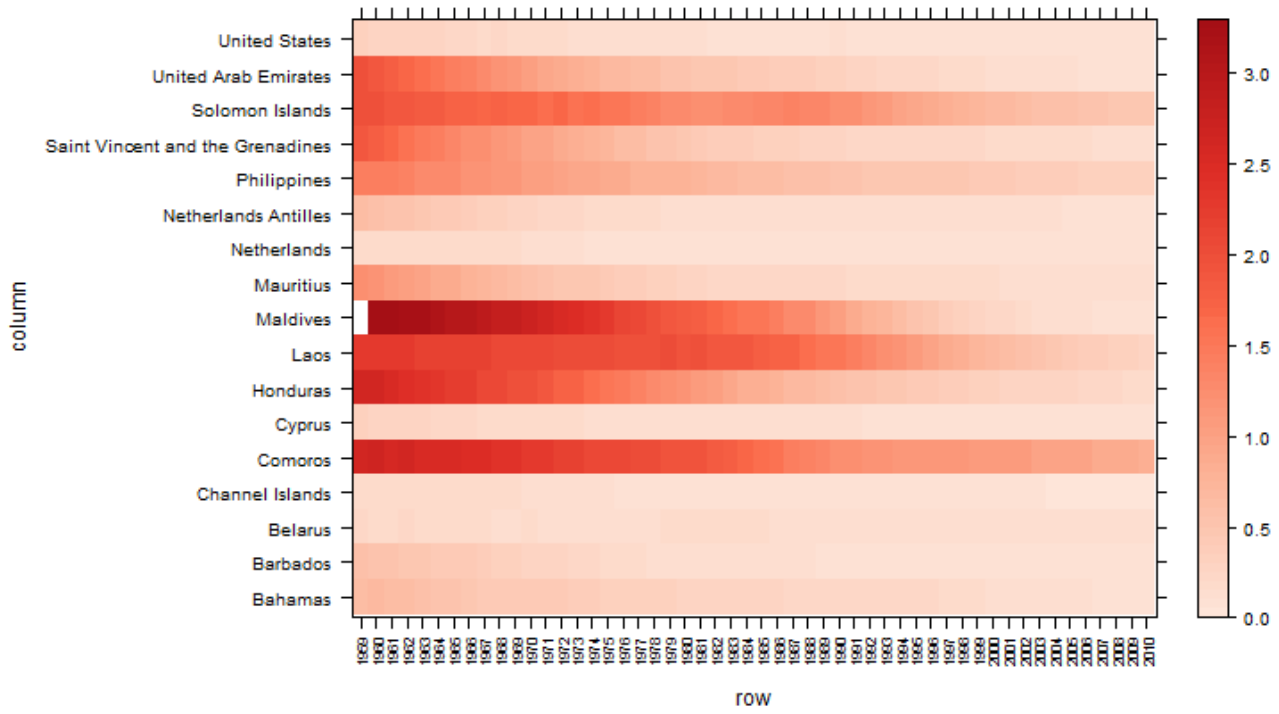
Lattice

```
> theSeq = seq(0, max(mat), by = 50)
> my.col <- colorRampPalette(brewer.pal(5, "Greens"))(length(theSeq))
> levelplot(t(mat), aspect = "fill", at = theSeq, col.regions = my.col, xlab = "Route",
+     ylab = "Date")
```



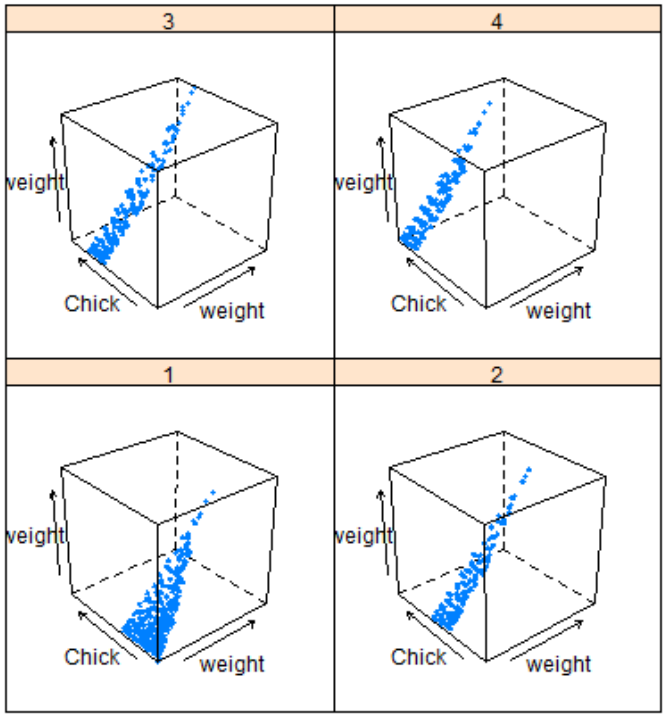
Lattice

```
> tmp = death[grep("s$", rownames(death)), 200:251]
> yr = gsub("X", "", names(tmp))
> theSeq = seq(0, max(tmp, na.rm = TRUE), by = 0.05)
> my.col <- colorRampPalette(brewer.pal(5, "Reds"))(length(theSeq))
> levelplot(t(tmp), aspect = "fill", at = theSeq, col.regions = my.col, scales = list(x = list(label = y
+     rot = 90, cex = 0.7)))
```



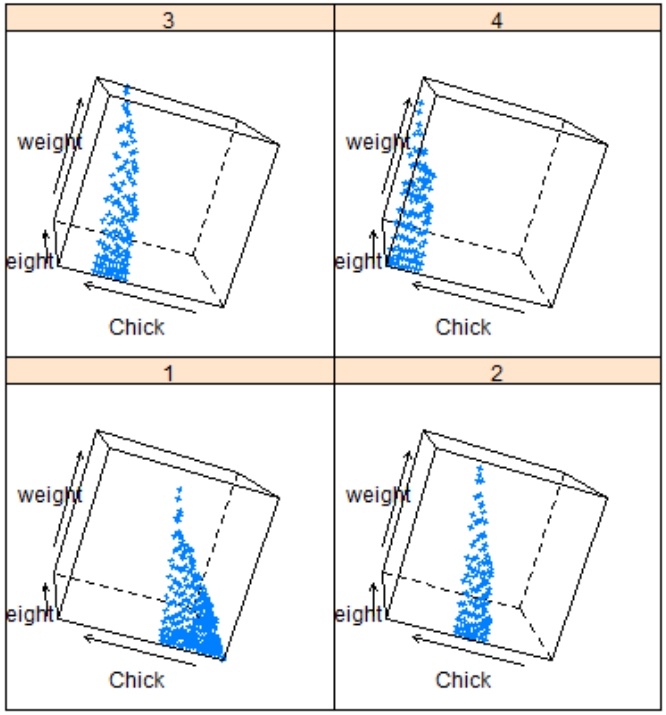
Lattice

```
> cloud(weight ~ weight * Chick | Diet, data = ChickWeight)
```



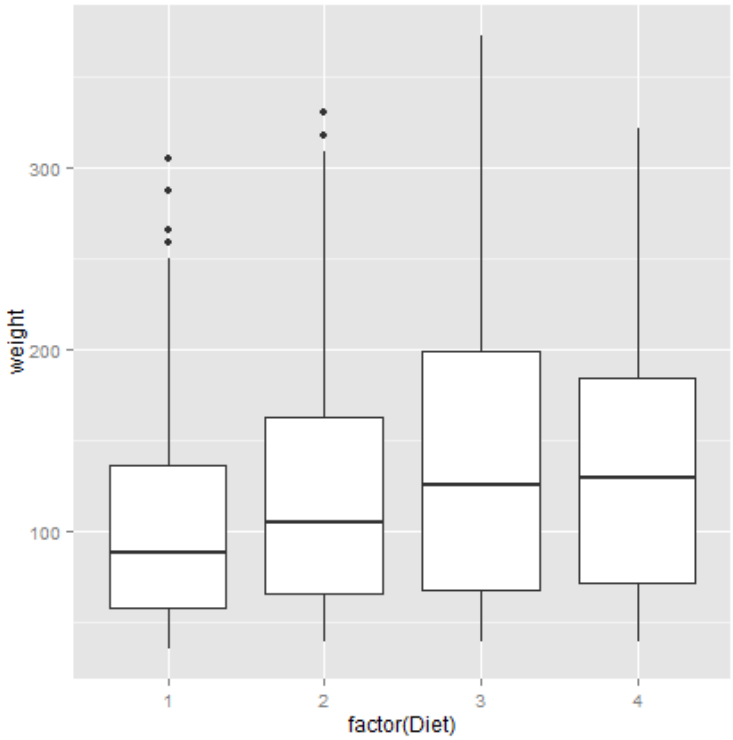
Lattice

```
> cloud(weight ~ weight * Chick | Diet, data = ChickWeight, screen = list(z = 40,
+     x = -70, y = 60))
```



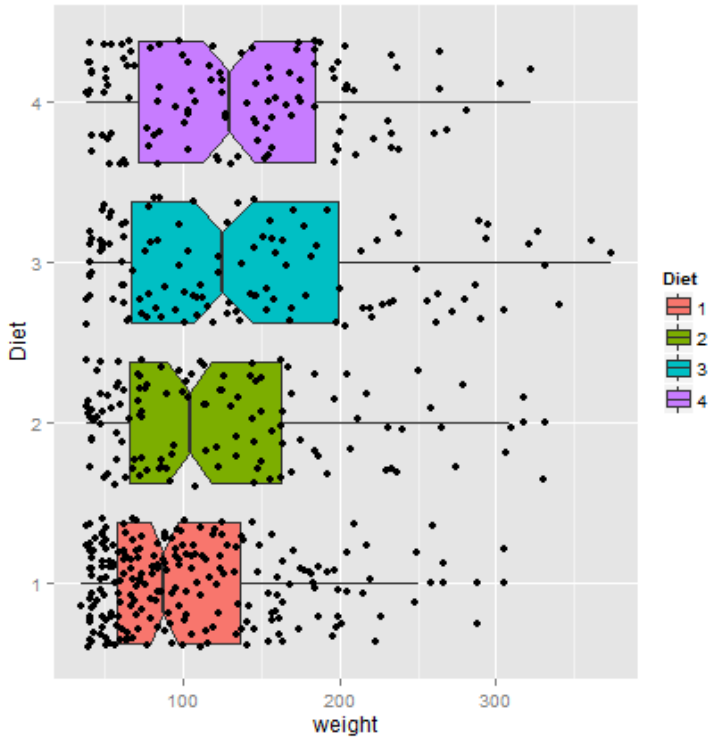
ggplot2

```
> library(ggplot2)
> qplot(factor(Diet), weight, data = ChickWeight, geom = "boxplot")
```



ggplot2

```
> p = ggplot(ChickWeight, aes(Diet, weight))
> p + geom_boxplot(notch = TRUE, aes(fill = Diet)) + geom_jitter() + coord_flip()
```



ggplot2

Useful links:

- http://docs.ggplot2.org/0.9.3/index.html
- http://www.cookbook-r.com/Graphs/