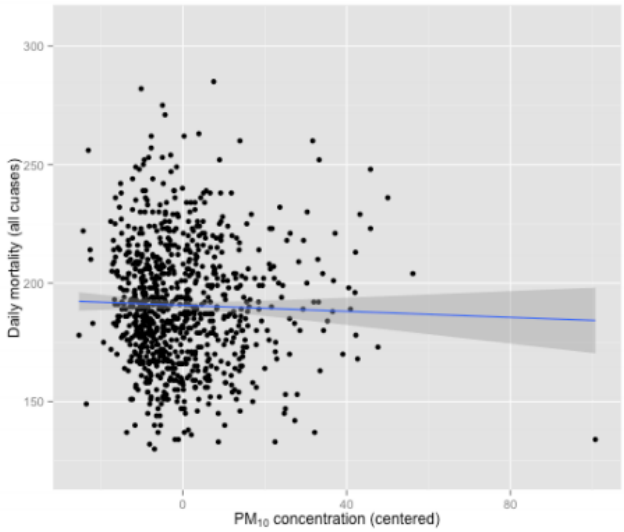
Exploratory Data Analysis Course Notes

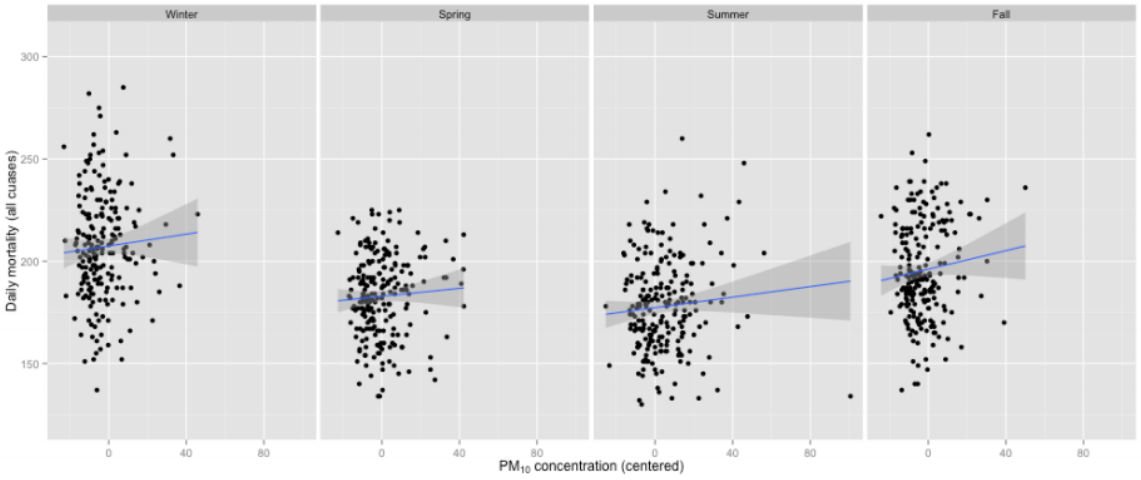
Contents

Principle of Analytic Graphics

- **Principle 1: Show Comparisons**
  - always comparative (compared to what)
  - randomized trial - compare control group to test group
  - evidence for a hypothesis is always relative to another competing hypothesis
- **Principle 2: Show causality/mechanism/explanation/systematic structure**
  - form hypothesis to evidence showing a relationship (causal framework, why something happened)
- **Principle 3: Show multivariate data**
  - more than 2 variables because the real world is multivariate
  - show as much data on a plot as you can
  - ***example***



- slightly negative relationship between pollution and mortality
  - when split up by season, the relationships are all positive → season = confounding variable



- **Principle 4: Integration of evidence**
  - use as many modes of evidence/displaying evidence as possible (modes of data presentation)
  - integrate words/numbers/images/diagrams (information rich)
  - analysis should drive the tool
- **Principle 5: Describe/document evidence with appropriate labels/scales/sources**
  - add credibility to that data graphic
- **Principle 6: Content is the most important**
  - analytical presentations ultimately stand/fall depending on quality/relevance/integrity of content

Exploratory Graphs (examples)

- **Purpose**: understand data properties, find pattern in data, suggest modeling strategies, debug
- **Characteristics**: made quickly, large number produced, gain personal understanding, appearances and presentation are aren't as important

One Dimension Summary of Data

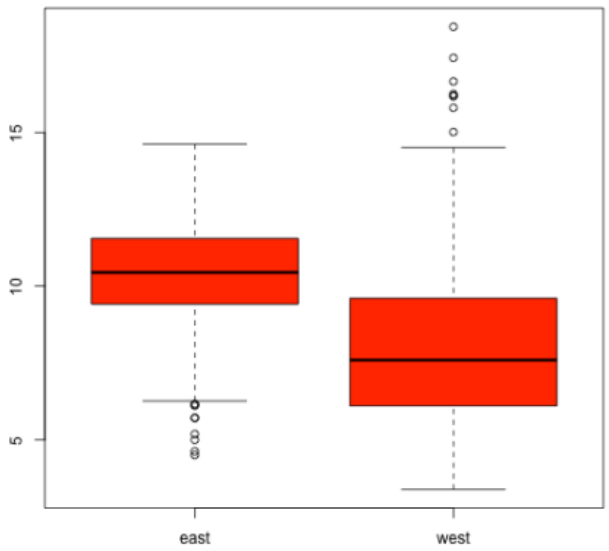
- `summary(data)` = returns min, 1st quartile, median, mean, 3rd quartile, max
- `boxplot(data, col = "blue")` = produces a box with middles 50% highlighted in the specified color
  - `whiskers` = $\pm 1.58 IQR/\sqrt{n}$

    - IQR = interquartile range, Q_3 - Q_1
  - `box` = 25%, median, 75%

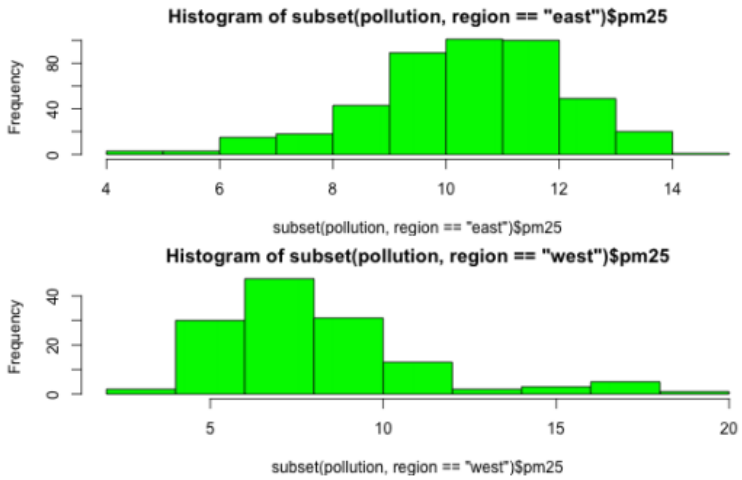
- `histograms(data, col = "green")` = produces a histogram with specified breaks and color
  - `breaks = 100` = the higher the number is the smaller/narrower the histogram columns are
- `rug(data)` = density plot, add a strip under the histogram indicating location of each data point
- `barplot(data, col = wheat)` = produces a bar graph, usually for categorical data
- **Overlaying Features**
- `abline(h/v = 12)` = overlays horizontal/vertical line at specified location
  - `col = "red"` = specifies color
  - `lwd = 4` = line width
  - `lty = 2` = line type

Two Dimensional Summaries

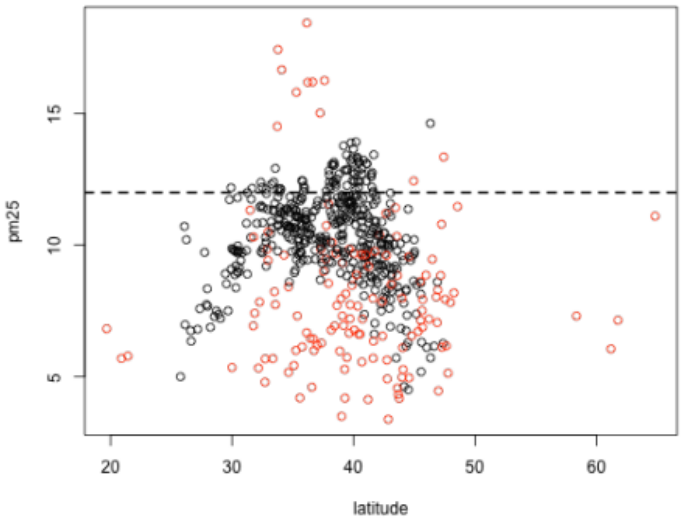
- multiple/overlay 1D plots (using lattice/ggplot2)
- **box plots**: `boxplot(pm25 ~ region, data = pollution, col = "red")`



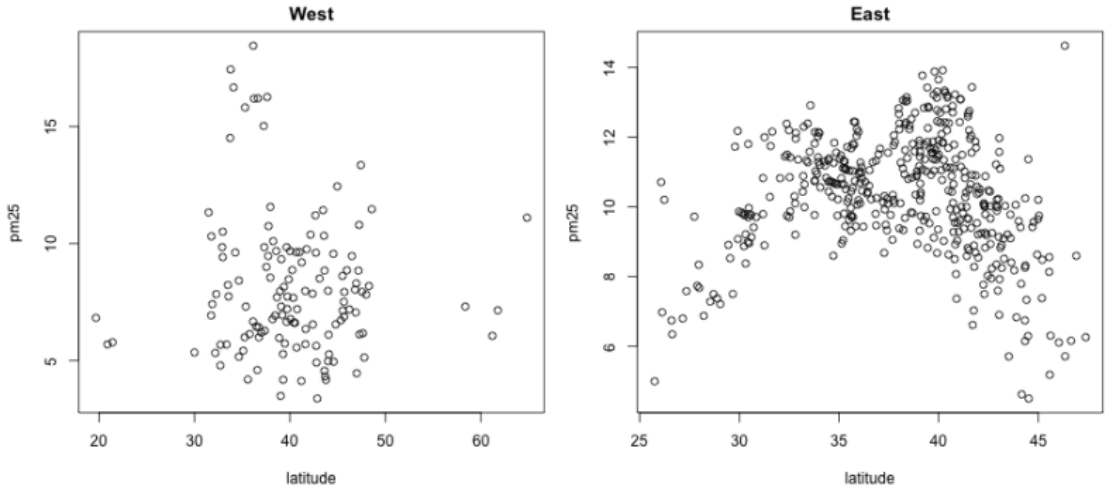
- **histogram**:
  - `par(mfrow = c(2, 1), mar = c(4, 4, 2, 1))` = set margin
  - `hist(subset(pollution, region == "east")$pm25, col = "green")` = first histogram
  - `hist(subset(pollution, region == "west")$pm25, col = "green")` = second histogram



- **scatterplot**
  - `with(pollution, plot(latitude, pm25, col = region))`
  - `abline(h = 12, lwd = 2, lty = 2)` = plots horizontal dotted line
  - `plot(jitter(child, 4)~parent, galton)` = spreads out data points at the same position to simulate measurement error/make high frequency more visibble



- **multiple scatter plots**
  - `par(mfrow = c(1, 2), mar = c(5, 4, 2, 1))` = sets margins
  - `with(subset(pollution, region == "west"), plot(latitude, pm25, main = "West"))` = left scatterplot
  - `with(subset(pollution, region == "east"), plot(latitude, pm25, main = "East"))` = right scatterplot



Process of Making a Plot/Considerations

- where will plot be made? screen or file?
- how will plot be used? viewing on screen/web browser/print/presentation?
- large amount of data vs few points?
- need to be able to dynamically resize?
- **plotting system**: base, lattice, ggplot2?

Base Plotting

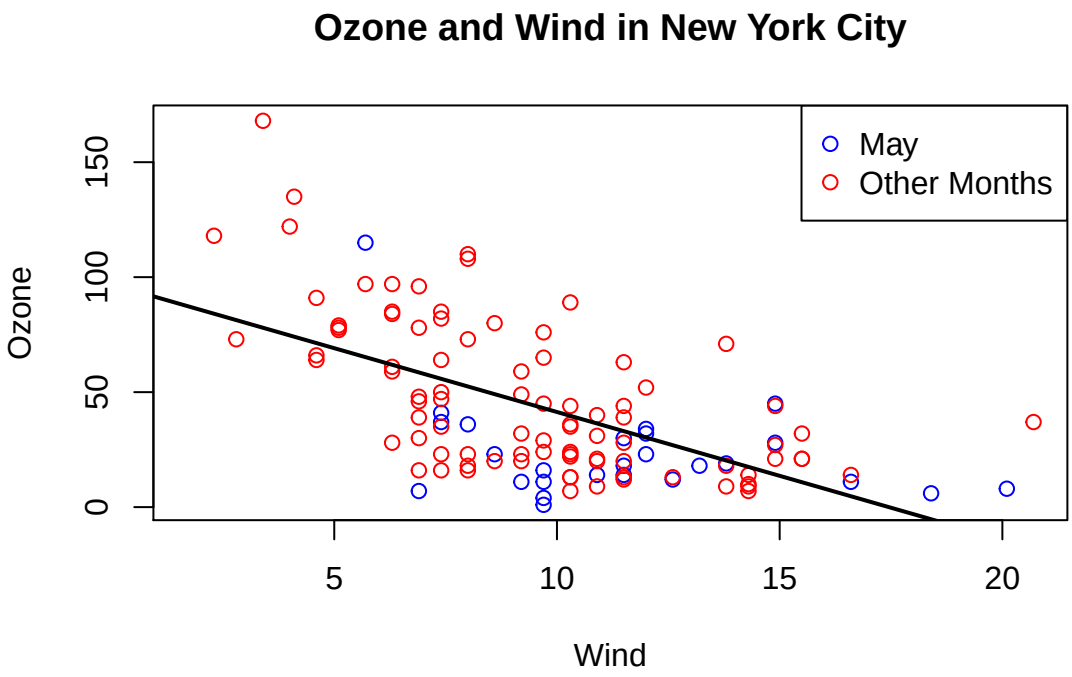
- blank canvas, "artist's palette", start with plot function
- annotations - text, lines, points, axis
- convenient, but cannot go back when started (need to plan ahead)
- everything need to be manually set carefully to be able to achieve the desired effect (margins)
- core plotting/graphics engine in R encapsulated in the following
  - ***graphics***: plotting functions for vase graphing system (plot, hist, boxplot, text)
  - ***grDevices***: contains all the code implementing the various graphics devices (x11, PDF, PostScript, PNG, etc)
- ***Two phase***: initialize, annotate
- calling `plot(x, y)` or `hist(x)` will launch a graphics device and draw a plot on device
  - if no argument specified, default called
  - parameters documented in "`?par`"
  - ***Note****: it is some times necessary to convert column/variable to factor to make plotting easier*
    - `airquality <- transform(airquality, Month = factor(month))`

Base Graphics Functions and Parameters

- **arguments**
  - `pch`: plotting symbol (default = open circle)
  - `lty`: line type (default is solid)
    - 0=blank, 1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash
  - `lwd`: line width (integer)
  - `col`: plotting color (number string or hexcode, colors() returns vector of colors)
  - `xlab`, `ylab`: x-y label character strings
  - `cex`: numerical value giving the amount by which plotting text/symbols should be magnified relative to the default
    - `cex = 0.15 * variable`: plot size as an additional variable
- `par()` function = specifies global graphics parameters, affects all plots in an R session (can be overridden)
  - `las`: orientation of axis labels
  - `bg`: background color
  - `mar`: margin size (order = bottom left top right)
  - `oma`: outer margin size (default = 0 for all sides)
  - `mfrow`: number of plots per row, column (plots are filled row-wise)
  - `mfcol`: number of plots per row, column (plots are filled column-wise)
  - can verify all above parameters by calling `par("parameter")`
- **plotting functions**
  - `lines`: adds liens to a plot, given a vector of x values and corresponding vector of y values
  - `points`: adds a point to the plot
  - `text`: add text labels to a plot using specified x,y coordinates
  - `title`: add annotations to x,y axis labels, title, subtitles, outer margin
  - `mtext`: add arbitrary text to margins (inner or outer) of plot
  - `axis`: specify axis ticks

Base Plot Example

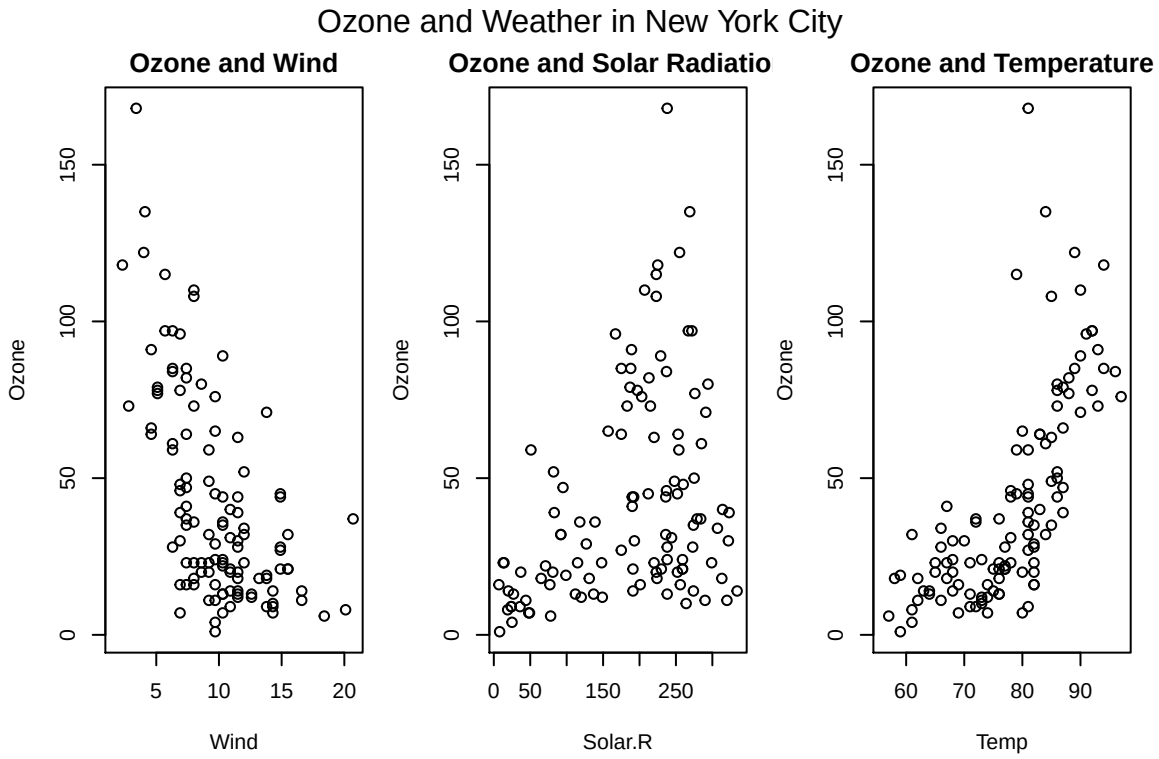
```
library(datasets)
# type ="n" sets up the plot and does not fill it with data
with(airquality, plot(Wind, Ozone, main = "Ozone and Wind in New York City", type = "n"))
# subsets of data are plotted here using different colors
with(subset(airquality, Month == 5), points(Wind, Ozone, col = "blue"))
with(subset(airquality, Month != 5), points(Wind, Ozone, col = "red"))
legend("topright", pch = 1, col = c("blue", "red"), legend = c("May", "Other Months"))
model <- lm(Ozone ~ Wind, airquality)
# regression line is produced here
abline(model, lwd = 2)
```



Multiple Plot Example

- ***Note**: typing `example(points)` in R will launch a demo of base plotting system and may provide some helpful tips on graphing*

```
# this expression sets up a plot with 1 row 3 columns, sets the margin and outer margins
par(mfrow = c(1, 3), mar = c(4, 4, 2, 1), oma = c(0, 0, 2, 0))
with(airquality, {
    # here three plots are filled in with their respective titles
    plot(Wind, Ozone, main = "Ozone and Wind")
    plot(Solar.R, Ozone, main = "Ozone and Solar Radiation")
    plot(Temp, Ozone, main = "Ozone and Temperature")
    # this adds a line of text in the outer margin*
    mtext("Ozone and Weather in New York City", outer = TRUE)}
)
```



Graphics Device

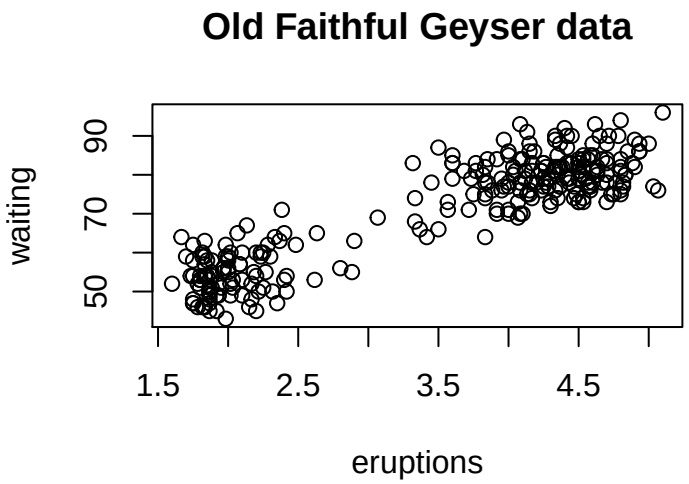
- A graphics device is something where you can make a plot appear
  - **window on screen** (screen device) = quick visualizations and exploratory analysis
  - **pdf** (file device) = plots that may be printed out or incorporated in to document
  - **PNG/JPEG** (file device) = plots that may be printed out or incorporated in to document
  - **scalable vector graphics** (SVG)
- When a plot is created in R, it has to be sent to a graphics device
- **Most common is screen device**
  - `quartz()` on Mac, `windows()` on Windows, `x11()` on Unix/Linux
  - `?Devices` = lists devices found
- **Plot creation**
  - screen device
    - call plot/xplot/qplot → plot appears on screen device → annotate as necessary → use
  - file devices
    - explicitly call graphics device → plotting function to make plot (write to file) → annotate as necessary → explicitly close graphics device with `dev.off()`
- **Graphics File Devices**
  - ***Vector Formats*** (good for line drawings/plots w/ solid colors, a modest number of points)
    - `pdf`: useful for line type graphics, resizes well, usually portable, not efficient if too many points
    - `svg`: XML based scalable vector graphics, support animation and interactivity, web based
    - `win.metafile`: Windows metafile format

    - `postscript`: older format, resizes well, usually portable, can create encapsulated postscript file, Windows often don't have postscript viewer (postscript = predecessor of PDF)
  - ***Bitmap Formats*** (good for plots w/ large number of points, natural scenes/webbased plots)
    - `png`: Portable Network Graphics, good for line drawings/image with solid colors, uses lossless compression, most web browsers read this natively, good for plotting a lot of data points, does not resize well
    - `JPEG`: good for photographs/natural scenes/gradient colors, size efficient, uses lossy compression, good for plotting many points, does not resize well, can be read by almost any computer/browser, not great for line drawings (aliasing on edges)
    - `tiff`: common bitmap format supports lossless compression
    - `bmp`: native Windows bitmapped format

- **Multiple Open Graphics Devices**
  - possible to open multiple graphics devices (screen, file, or both)
  - plotting occurs only one device at a time
  - `dev.cur()` = returns the currently active device
  - every open graphics device is assigned an integer >= 2
  - `dev.set(<integer>)` = change the active graphics device `<integer>` = number associated with the graphics device you want to switch to

- **Copying plots**
  - `dev.copy()` = copy a plot from one device to another
  - `dev.copy2pdf()` = specifically for copying to PDF files
  - ***Note****: copying a plot is not an exact operation, so the result may not be identical to the original*
  - ***example***

```
## Create plot on screen device
with(faithful, plot(eruptions, waiting))
## Add a main title
title(main = "Old Faithful Geyser data")
```




```
## Copy my plot to a PNG file
dev.copy(png, file = "geyserplot.png")
## Don't forget to close the PNG device!
dev.off()
```

`lattice` Plotting System

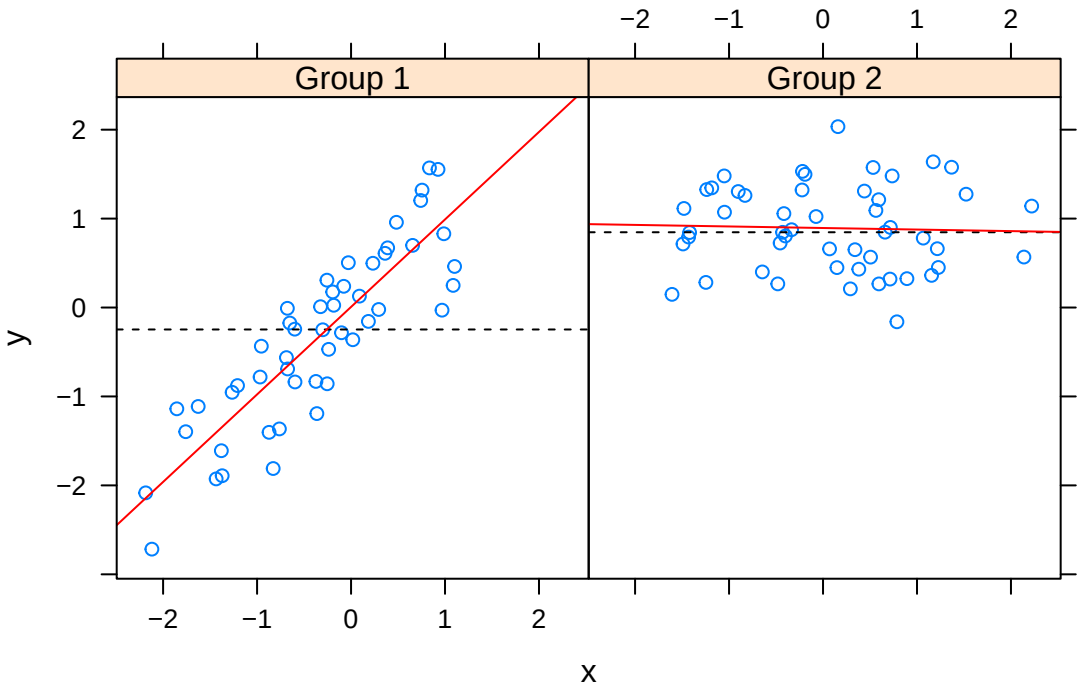
- `library(lattice)` = load lattice system
- implemented using the `lattice` and `grid` packages
  - `lattice` package = contains code for producing ***Trellis*** graphics (independent from base graphics system)
  - `grid` package = implements the graphing system; lattice build on top of grid
- all plotting and annotation is done with ***single function call***
  - margins/spacing/labels set automatically for entire plot, good for putting multiple on the screen
  - good for conditioning plots → examining same plots over different conditions how y changes vs x across different levels of z
  - `panel` functions can be specified/customized to modify the subplots
- lattice graphics functions return an object of class "trellis", where as base graphics functions plot data directly to graphics device
  - print methods for lattice functions actually plots the data on graphics device
  - trellis objects are auto-printed
  - `trellis.par.set()` → can be used to set global graphic parameters for all trellis objects
- hard to annotate, awkward to specify entire plot in one function call
- cannot add to plot once created, panel/subscript functions hard to prepare

`lattice` Functions and Parameters

- **Funtions**
  - `xyplot()` = main function for creating scatterplots
  - `bwplot()` = box and whiskers plots (box plots)
  - `histogram()` = histograms
  - `stripplot()` = box plot with actual points
  - `dotplot()` = plot dots on "violin strings"
  - `splom()` = scatterplot matrix (like pairs() in base plotting system)
  - `levelplot()`/`contourplot()` = plotting image data
- **Arguments** for `xyplot(y ~ x | f * g, data, layout, panel)`
  - default blue open circles for data points
  - formula notation is used here (`~`) = left hand side is the y-axis variable, and the right hand side is the x-axis variable
  - `f`/`g` = conditioning/categorical variables (optional)
    - basically creates multi-panelled plots (for different factor levels)
    - `*` indicates interaction between two variables
    - intuitively, the xyplot displays a graph between x and y for every level of `f` and `g`
  - `data` = the data frame/list from which the variables should be looked up
    - if nothing is passed, the parent frame is used (searching for variables in the workspace)
    - if no other arguments are passed, defaults will be used
  - `layout` = specifies how the different plots will appear
    - `layout = c(5, 1)` = produces 5 subplots in a horizontal fashion
    - padding/spacing/margin automatically set
  - [optional] `panel` function can be added to control what is plotted inside each panel of the plot
    - `panel` functions receive x/y coordinates of the data points in their panel (along with any additional arguments)
    - `?panel.xyplot` = brings up documentation for the panel functions
    - ***Note****: no base plot functions can be used for lattice plots*

`lattice` Example

```
library(lattice)
set.seed(10)
x <- rnorm(100)
f <- rep(0:1, each = 50)
y <- x + f - f * x+ rnorm(100, sd = 0.5)
f <- factor(f, labels = c("Group 1", "Group 2"))
## Plot with 2 panels with custom panel function
xyplot(y ~ x | f, panel = function(x, y, ...) {
    # call the default panel function for xyplot
    panel.xyplot(x, y, ...)
    # adds a horizontal line at the median
    panel.abline(h = median(y), lty = 2)
    # overlays a simple linear regression line
    panel.lmline(x, y, col = 2)
})
```



`ggplot2` Plotting System

- `library(ggplot2)` = loads ggplot2 package
- implementation of Grammar of Graphics by Leland Wilkinson, written by Hadley Wickham (created RStudio)

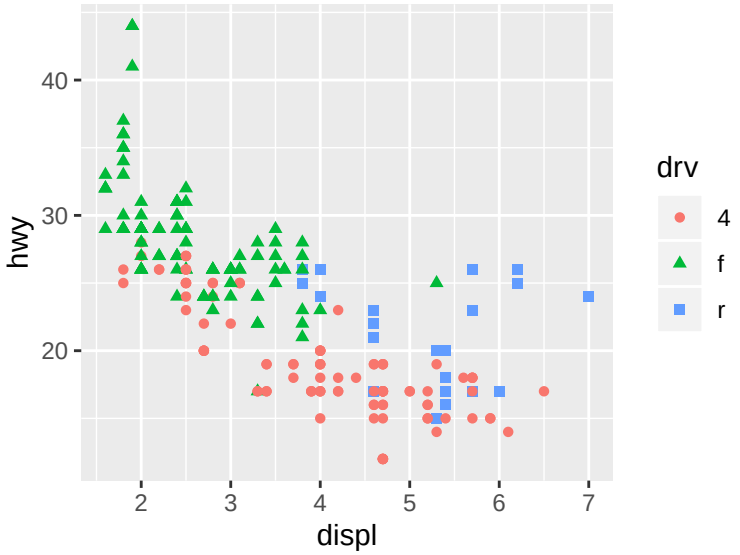
  "In brief, the grammar tells us that a statistical graphic is a mapping from data to aesthetic attributes (color, shape, size) of geometric objects (points, lines, bars). The plot may also contain statistical transformations of the data and is drawn on a specific coordinate system"

- grammar graphics plot, splits the different between base and lattice systems
- automatically sets spacings/text/tiles but also allows annotations to be added
- default makes a lot of choices, but still customizable

`ggplot2` Functions and Parameters

- **basic components** of a `ggplot2` graphic
  - **data frame** = source of data
  - **aesthetic mappings** = how data are mappped to color/size (x vs y)
  - **geoms** = geometric objects like points/lines/shapes to put on page
  - **facets** = conditional plots using factor variables/multiple panels
  - **stats** = statistical transformations like binning/quantiles/smoothing
  - **scales** = scale aesthetic map uses (i.e. male = red, female = blue)
  - **coordinate system** = system in which data are plotted
- `qplot(x, y, data , color, geom)` = quick plot, analogous to base system's `plot()` function
  - **default style**: gray background, white gridlines, x and y labels automatic, and solid black circles for data points
  - data always comes from data frame (in unspecified, function will look for data in workspace)
  - plots are made up of aesthetics (size, shape, color) and geoms (points, lines)
  - ***Note**: capable of producing quick graphics, but difficult to customize in detail*
- **factor variables**: important for graphing subsets of data = they should be labelled with specific information, and not just 1, 2, 3
  - `color = factor1` = use the factor variable to display subsets of data in different colors on the same plot (legend automatically generated)
  - `shape = factor2` = use the factor variable to display subsets of data in different shapes on the same plot (legend automatically generated)
  - ***example***

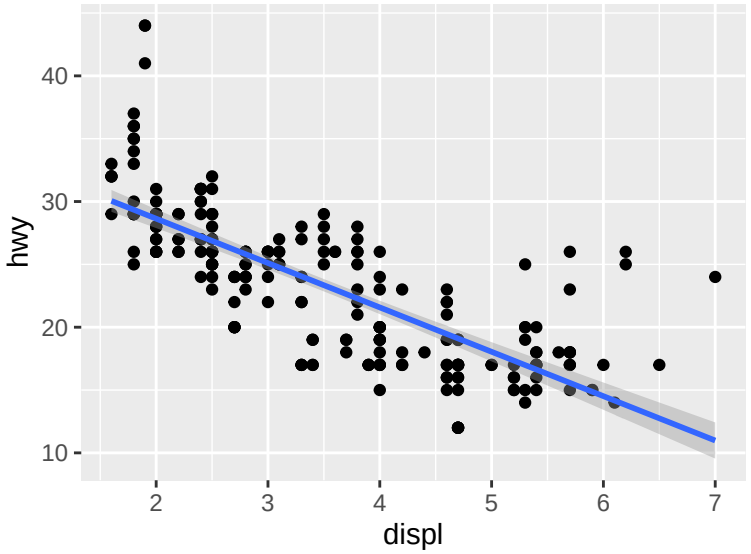
```
library(ggplot2)
qplot(displ, hwy, data = mpg, color = drv, shape = drv)
```



- **adding statistics**: `geom = c("points", "smooth")` = add a smoother/"low S"
  - "points" plots the data themselves, "smooth" plots a smooth mean line in blue with an area of 95% confidence interval shaded in dark gray
  - `method = "lm"` = additional argument method can be specified to create different lines/confidence intervals
    - `lm` = linear regression
  - ***example***

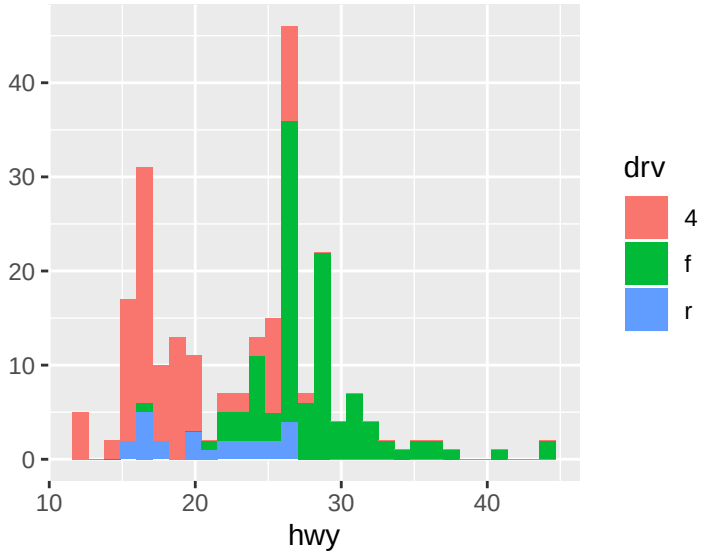
```
qplot(displ, hwy, data = mpg, geom = c("point", "smooth"), method="lm")
```

```
## Warning: Ignoring unknown parameters: method
```



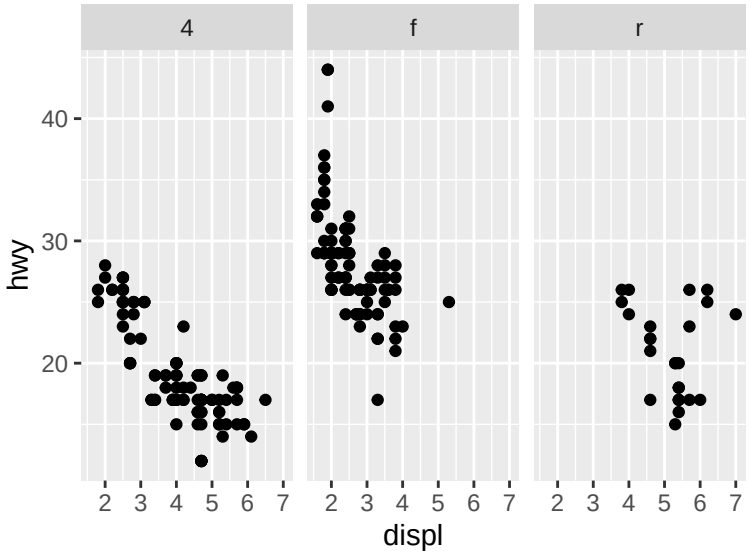
- **histograms**: if only one value is specified, a histogram is produced
  - `fill = factor1` = can be used to fill the histogram with different colors for the subsets (legend automatically generated)
  - ***example***

```
qplot(hwy, data = mpg, fill = drv)
```

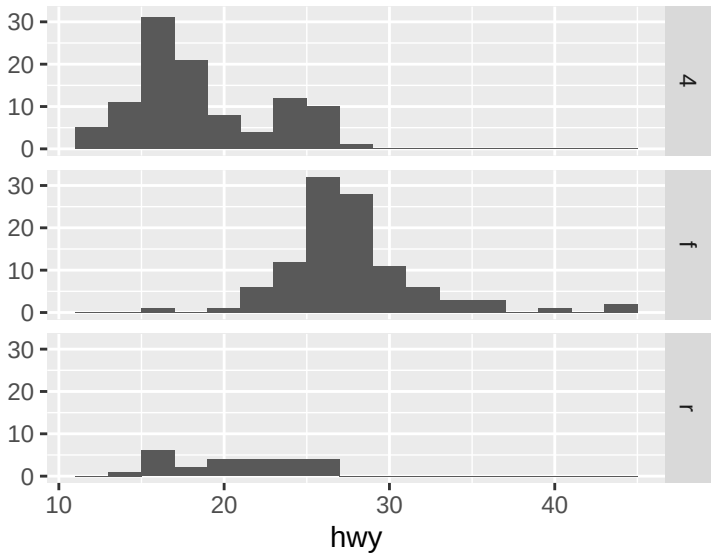


- **facets**: similar to panels in lattice, split data according to factor variables
  - `facets = rows ~ columns` = produce different subplots by factor variables specified (rows/columns)
  - `"."` indicates there are no addition row or column
  - `facets = . ~ columns` = creates 1 by col subplots
  - `facets = row ~ .` = creates row row by 1 subplots
  - labels get generated automatically based on factor variable values
  - ***example***

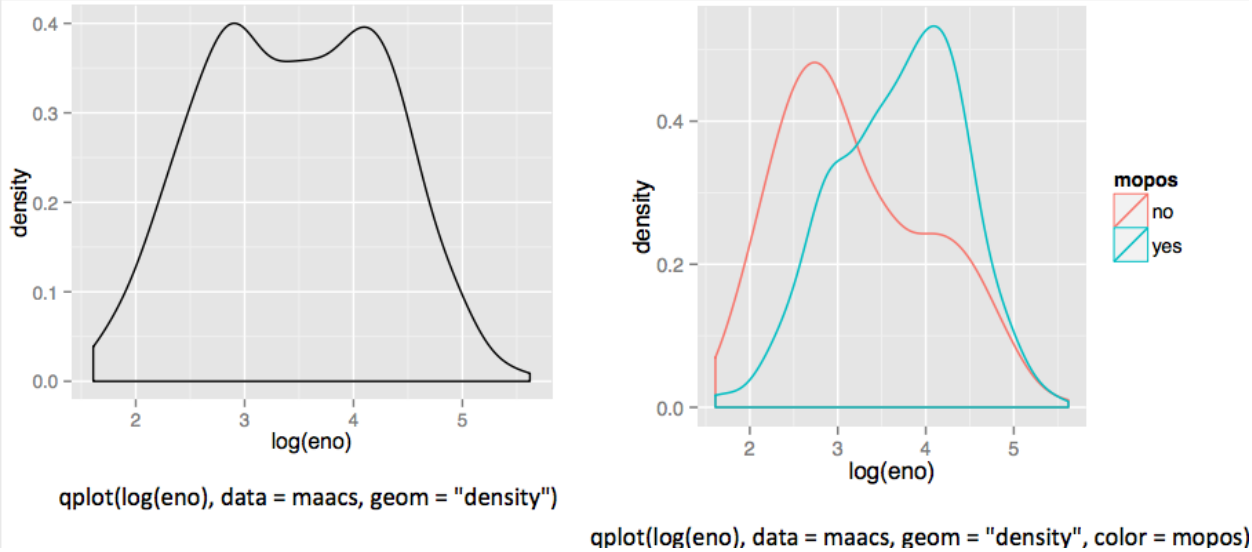
```
qplot(displ, hwy, data = mpg, facets = . ~ drv)
```




```
qplot(hwy, data = mpg, facets = drv ~ ., binwidth = 2)
```



- **density smooth**: smooths the histograms into a line tracing its shape
  - `geom = "density"` = replaces the default scatterplot with density smooth curve
  - ***example***



- `ggplot()`
  - built up in layers/modularly (similar to base plotting system)
    - data → overlay summary → metadata/annotation
  - `g <- ggplot(data, aes(var1, var2))`
    - initiates call to `ggplot` and specifies the data frame that will be used
    - `aes(var1, var2)` = specifies aesthetic mapping, or var1 = x variable, and var2 = y variable
    - `summary(g)` = displays summary of ggplot object

    * `print(g)` = returns error ("no layer on plot") which means the plot does know how to draw the data yet
- `g + geom_point()` = takes information from g object and produces scatter plot
- `+ geom_smooth()` = adds low S mean curve with confidence interval
    * `method = "lm"` = changes the smooth curve to be linear regression
    * `size = 4`, `linetype = 3` = can be specified to change the size/style of the line
    * `se = FALSE` = turns off confidence interval
- `+ facet_grid(row ~ col)` = splits data into subplots by factor variables (see facets from `qplot()`)
    * conditioning on continous variables is possible through cutting/making a new categorical variable
    * `cutPts <- quantiles(df$cVar, seq(0, 1, length=4), na.rm = TRUE)` = creates quantiles where the continuous variable will be cut
        · `seq(0, 1, length=4)` = creates 4 quantile points
        · `na.rm = TRUE` = removes all NA values
    * `df$newFactor <- cut(df$cVar, cutPts)` = creates new categorical/factor variable by using the cutpoints
        · creates n-1 ranges from n points = in this case 3
- ***annotations***:
    * `xlab()`, `ylab()`, `labs()`, `ggtitle()` = for labels and titles
        · `labs(x = expression("log " * PM[2.5]), y = "Nocturnal")` = specifies x and y labels
        · `expression()` = used to produce mathematical expressions
    * `geom` functions = many options to modify
    * `theme()` = for global changes in presentation
        · ***example***: `theme(legend.position = "none")`
    * two standard themes defined: `theme_gray()` and `theme_bw()`
    * `base_family = "Times"` = changes font to Times
- ***aesthetics***
    * `+ geom_point(color, size, alpha)` = specifies how the points are supposed to be plotted on the graph (style)
        · ***Note****: this translates to geom_line()/other forms of plots*
        · `color = "steelblue"` = specifies color of the data points
        · `aes(color = var1)` = wrapping color argument this way allows a factor variable to be assigned to the data points, thus subsetting it with different colors based on factor variable values
        · `size = 4` = specifies size of the data points
        · `alpha = 0.5` = specifies transparency of the data points
    * ***example***

- ***axis limits***
    * `+ ylim(-3, 3)` = limits the range of y variable to a specific range
        · ***Note****: ggplot will exclude (not plot) points that fall outside of this range (outliers), potentially leaving gaps in plot*
    * `+ coord_cartesian(ylim(-3, 3))` = this will limit the visible range but plot all points of the data

`ggplot2` Comprehensive Example

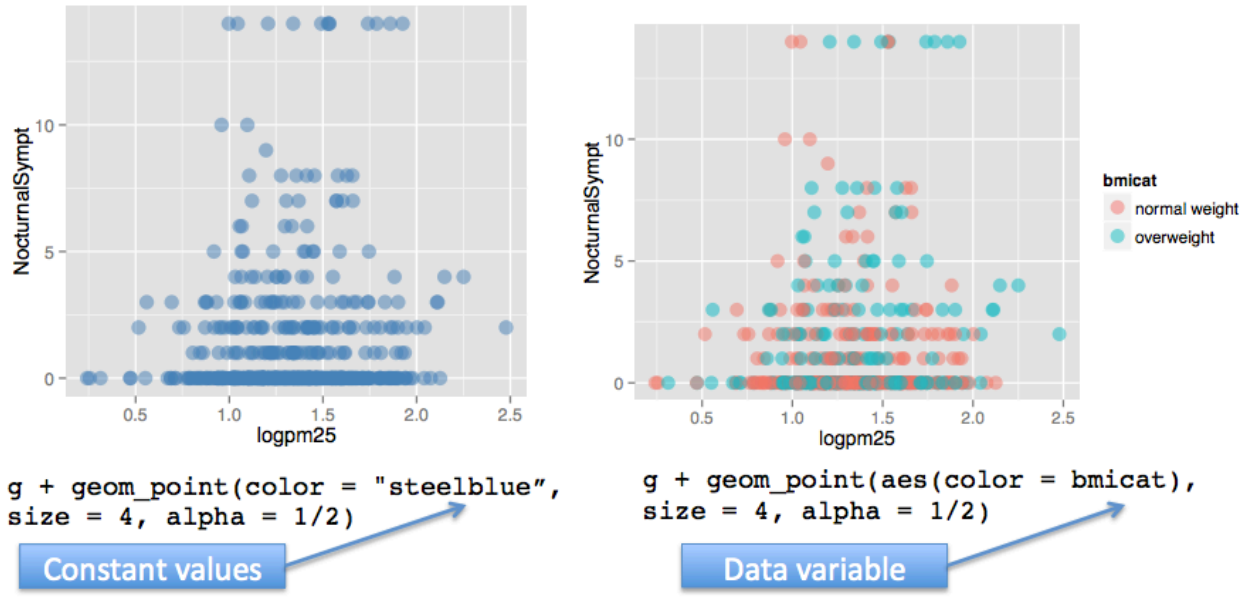


Figure 1: Alpha Level

```
# initiates ggplot
g <- ggplot(maacs, aes(logpm25, NocturnalSympt))
g + geom_point(alpha = 1/3)                              # adds points
  + facet_wrap(bmicat ~ no2dec, nrow = 2, ncol = 4)      # make panels
  + geom_smooth(method="lm", se=FALSE, col="steelblue") # adds smoother
  + theme_bw(base_family = "Avenir", base_size = 10)     # change theme
  + labs(x = expression("log " * PM[2.5]))               # add labels
  + labs(y = "Nocturnal Symptoms")
  + labs(title = "MAACS Cohort")
```

Color Packages in R Plots

- proper use of color can help convey the message by improving clarity/contrast of data presented
- default color schemes for most plots in R are fairly terrible, so some external packages are helpful

`grDevices` Package

- `colors()` function = lists names of colors available in any plotting function
- **`colorRamp` function**
  - takes any set of colors and return a function that takes values between 0 and 1, indicating the extremes of the color palette (e.g. see the `gray` function)
  - `pal <- colorRamp(c("red", "blue"))` = defines a `colorRamp` function
  - `pal(0)` returns a 1 x 3 matrix containing values for RED, GREEN, and BLUE values that range from 0 to 255
  - `pal(seq(0, 1, len = 10))` returns a 10 x 3 matrix of 10 colors that range from RED to BLUE (two ends of spectrum defined in the object)
  - ***example***

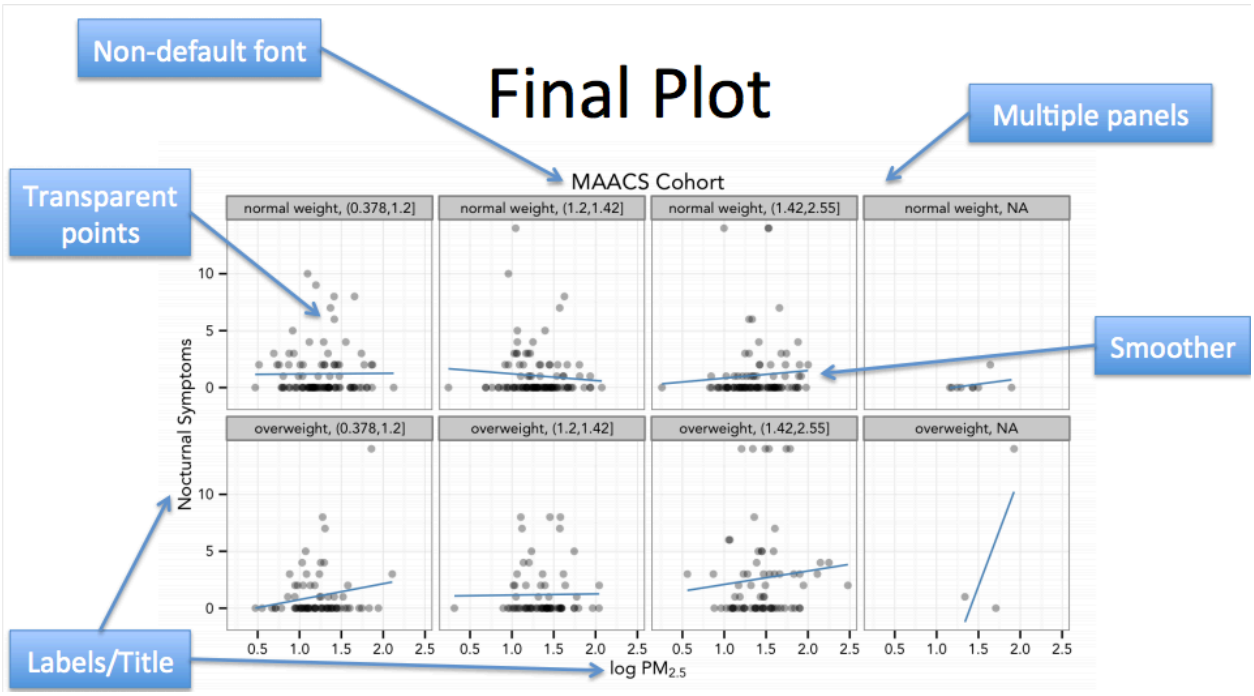


Figure 2: Final Plot

```
# define colorRamp function
pal <- colorRamp(c("red", "blue"))
# create a color
pal(0.67)
```

```
##       [,1] [,2]   [,3]
## [1,] 84.15    0 170.85
```

- **`colorRampPalette` function**
  - takes any set of colors and return a function that takes integer arguments and returns a vector of colors interpolating the palette (like `heat.colors` or `topo.colors`)
  - `pal <- colorRampPalette(c("red", "yellow"))` defines a `colorRampPalette` function
  - `pal(10)` returns 10 interpolated colors in hexadecimal format that range between the defined ends of spectrum
  - ***example***

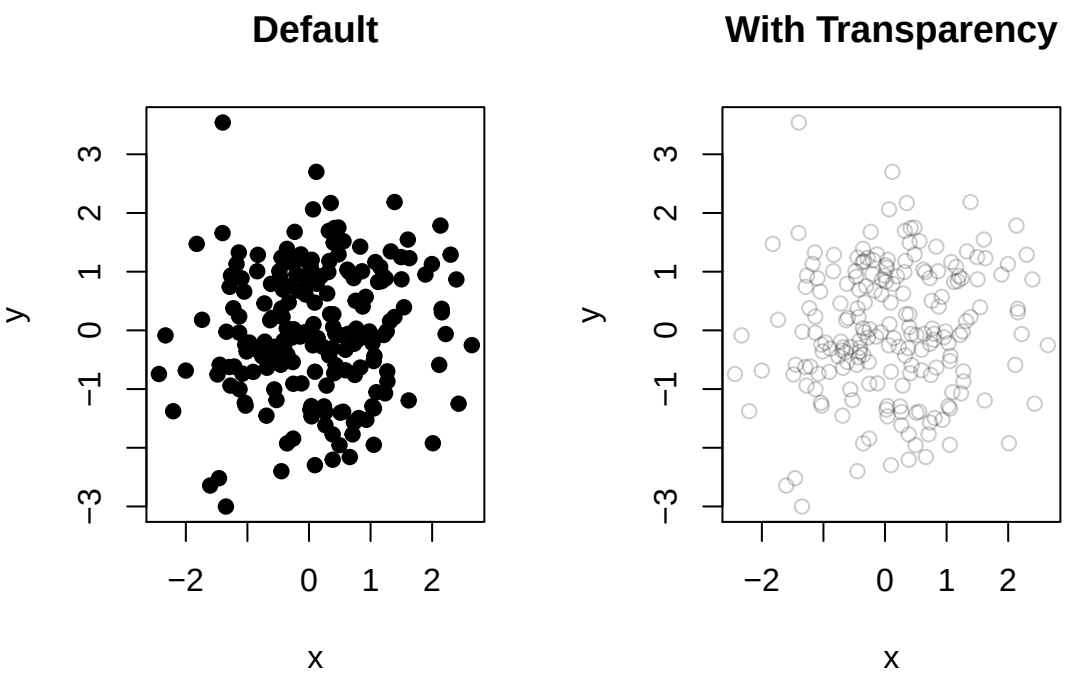
```
# define colorRampPalette function
pal <- colorRampPalette(c("red", "yellow"))
# create 10 colors
pal(10)
```

```
##  [1] "#FF0000" "#FF1C00" "#FF3800" "#FF5500" "#FF7100" "#FF8D00" "#FFAA00"
##  [8] "#FFC600" "#FFE200" "#FFFF00"
```

- **`rgb` function**
  - `red`, `green`, and `blue` arguments = values between 0 and 1

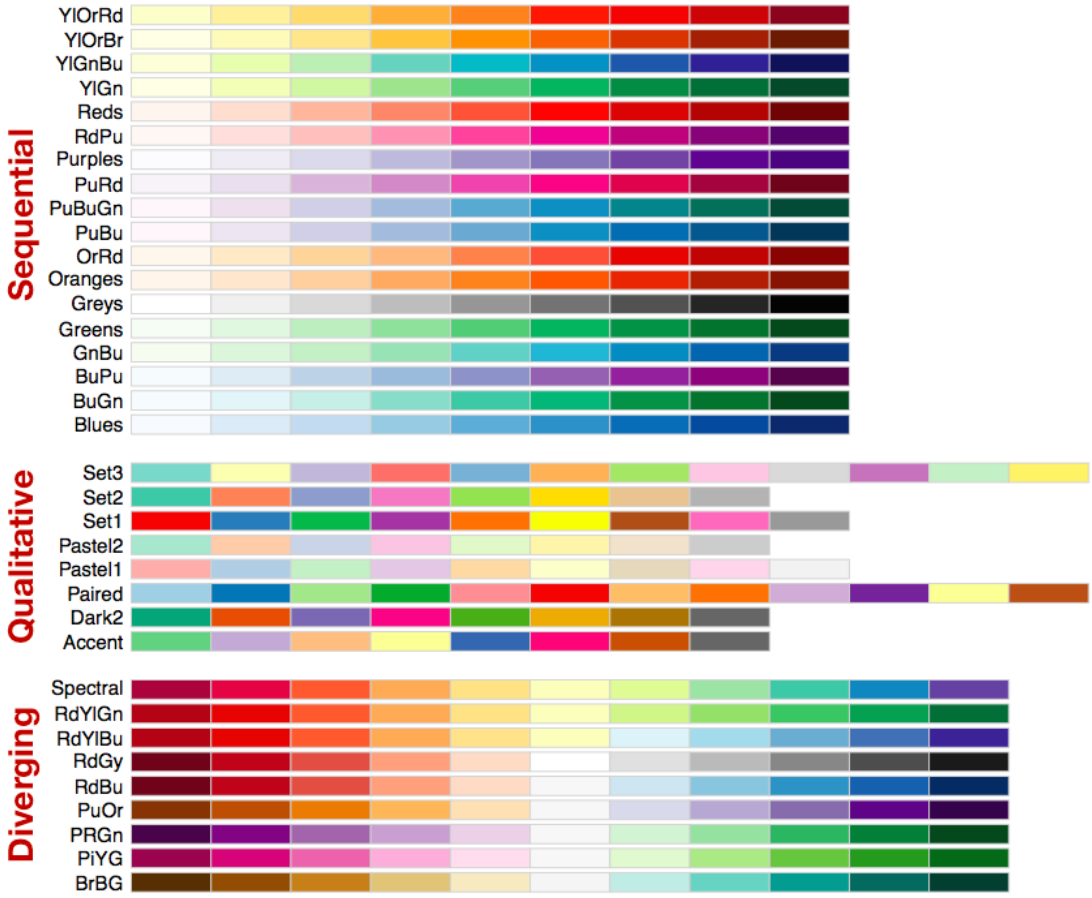
  - `alpha = 0.5` = transparency control, values between 0 and 1
  - returns hexadecimal string for color that can be used in `plot/image` commands
  - `colorspace` package `cna` be used for different control over colors
  - ***example***

```
x <- rnorm(200); y <- rnorm(200)
par(mfrow=c(1,2))
# normal scatter plot
plot(x, y, pch = 19, main = "Default")
# using transparency shows data much better
plot(x, y, col = rgb(0, 0, 0, 0.2), main = "With Transparency")
```



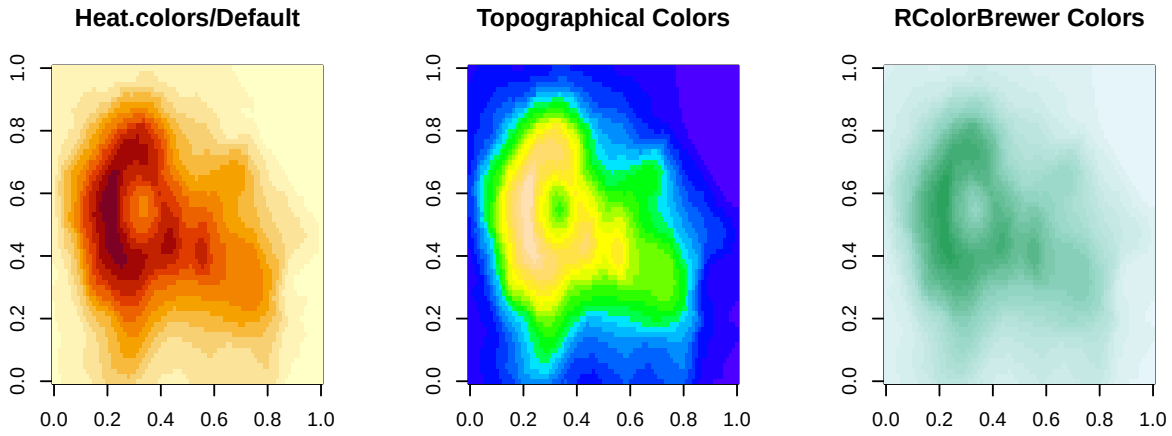
`RColorBrewer` Package

- can be found on CRAN that has predefined color palettes
  - `library(RColorBrewer)`
- **types of palettes**
  - *Sequential* = numerical/continuous data that is ordered from low to high
  - *Diverging* = data that deviate from a value, increasing in two directions (i.e. standard deviations from the mean)
  - *Qualitative* = categorical data/factor variables
- palette information from the `RColorBrewer` package can be used by `colorRamp` and `colorRampPalette` functions
- **available colors palettes**



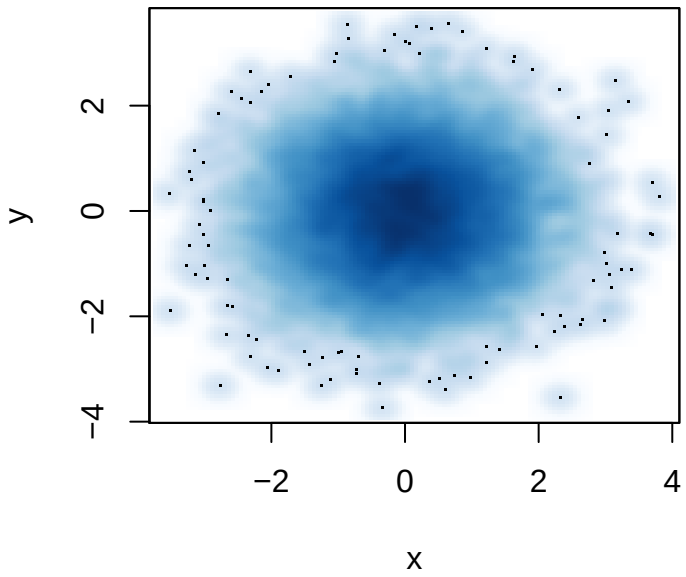
- **`brewer.pal(n, "BuGn")` function**
  - `n` = number of colors to generated
  - `"BuGn"` = name of palette
    - `?brewer.pal` list all available palettes to use
  - returns list of `n` hexadecimal colors
- ***example***

```
library(RColorBrewer)
# generate 3 colors using brewer.pal function
cols <- brewer.pal(3, "BuGn")
pal <- colorRampPalette(cols)
par(mfrow=c(1,3))
# heat.colors/default
image(volcano, main = "Heat.colors/Default")
# topographical colors
image(volcano, col = topo.colors(20), main = "Topographical Colors")
# RColorBrewer colors
image(volcano, col = pal(20), main = "RColorBrewer Colors")
```



- **`smoothScatter` function**
  - used to plot large quantities of data points
  - creates 2D histogram of points and plots the histogram
  - default color scheme = "Blues" palette from `RColorBrewer` package
  - ***example***

```
x <- rnorm(10000); y <- rnorm(10000)
smoothScatter(x, y)
```



Case Study: Human Activity Tracking with Smart Phones

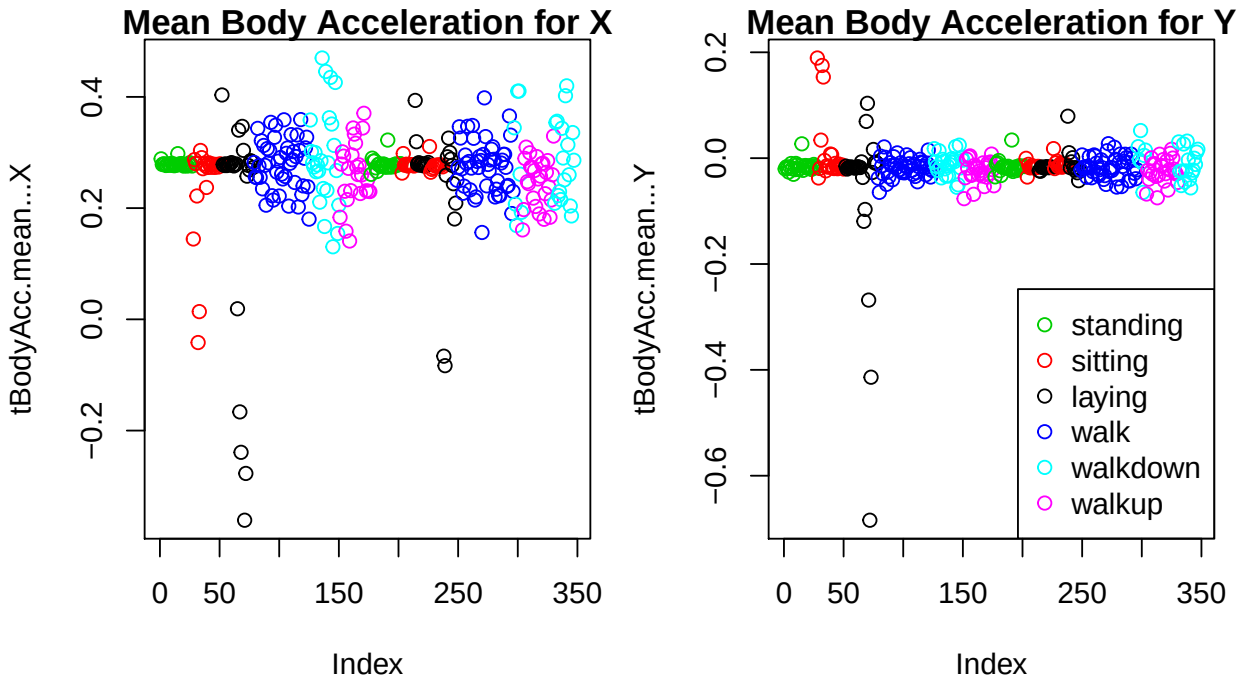
Loading Training Set of Samsung S2 Data from UCI Repository

```
# load data frame provided
load("samsungData.rda")
# table of 6 types of activities
table(samsungData$activity)
```

```
##
##   laying  sitting standing     walk walkdown   walkup
##     1407     1286     1374     1226      986     1073
```

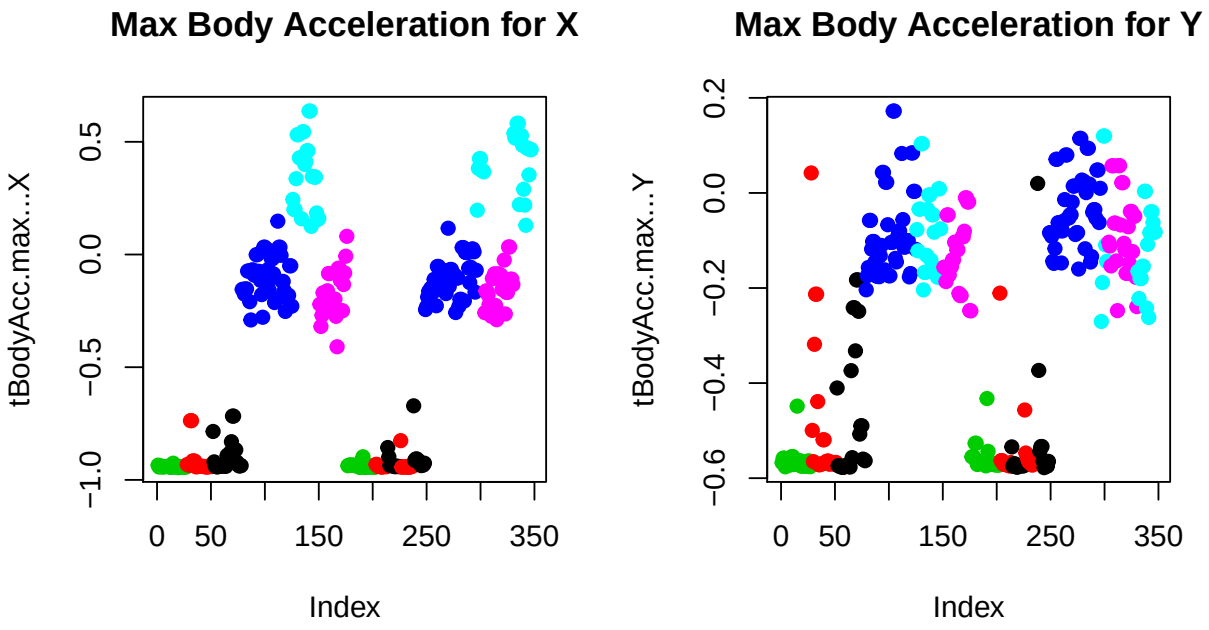
Plotting Average Acceleration for First Subject

```
# set up 1 x 2 panel plot
par(mfrow=c(1, 2), mar = c(5, 4, 1, 1))
# converts activity to a factor variable
samsungData <- transform(samsungData, activity = factor(activity))
# find only the subject 1 data
sub1 <- subset(samsungData, subject == 1)
# plot mean body acceleration in X direction
plot(sub1[, 1], col = sub1$activity, ylab = names(sub1)[1],
    main = "Mean Body Acceleration for X")
# plot mean body acceleration in Y direction
plot(sub1[, 2], col = sub1$activity, ylab = names(sub1)[2],
    main = "Mean Body Acceleration for Y")
# add legend
legend("bottomright",legend=unique(sub1$activity),col=unique(sub1$activity), pch = 1)
```



Plotting Max Acceleration for the First Subject

```
# create 1 x 2 panel
par(mfrow=c(1,2))
# plot max accelecrations in x and y direction
plot(sub1[,10],pch=19,col=sub1$activity,ylab=names(sub1)[10],
    main = "Max Body Acceleration for X")
plot(sub1[,11],pch=19,col = sub1$activity,ylab=names(sub1)[11],
    main = "Max Body Acceleration for Y")
```



Case Study: Fine Particle Pollution in the U.S. from 1999 to 2012

Read Raw Data from 1999 and 2012

```
# read in raw data from 1999
pm0 <- read.table("pm25_data/RD_501_88101_1999-0.txt", comment.char = "#", header = FALSE, sep = "|", na
# read in headers/column lables
cnames <- readLines("pm25_data/RD_501_88101_1999-0.txt", 1)
# convert string into vector
cnames <- strsplit(substring(cnames, 3), "|", fixed = TRUE)
# make vector the column names
names(pm0) <- make.names(cnames[[1]])
# we are interested in the pm2.5 readings in the "Sample.Value" column
x0 <- pm0$Sample.Value
# read in the data from 2012
pm1 <- read.table("pm25_data/RD_501_88101_2012-0.txt", comment.char = "#", header = FALSE, sep = "|",
    na.strings = "", nrow = 1304290)
# make vector the column names
```

```
names(pm1) <- make.names(cnames[[1]])
# take the 2012 data for pm2.5 readings
x1 <- pm1$Sample.Value
```

Summaries for Both Periods

```
# generate 6 number summaries
summary(x1)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##  -10.00    4.00    7.63    9.14   12.00  908.97   73133
```

```
summary(x0)
```

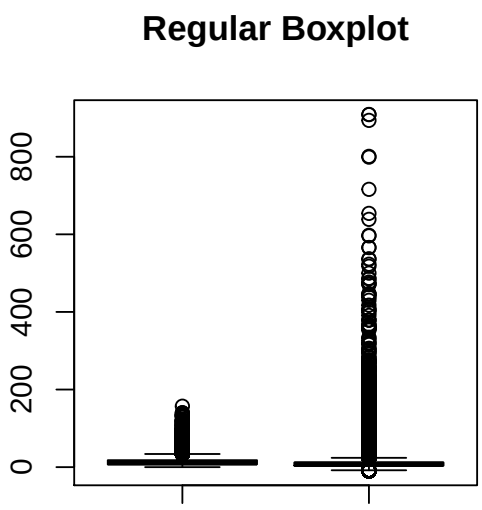
```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    0.00    7.20   11.50   13.74   17.90  157.10   13217
```

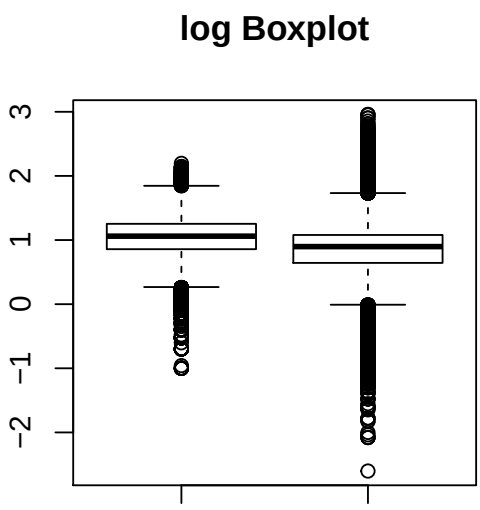
```
# calculate % of missing values, Are missing values important here?
data.frame(NA.1990 = mean(is.na(x0)), NA.2012 = mean(is.na(x1)))
```

```
##     NA.1990    NA.2012
## 1 0.1125608 0.05607125
```

Make a boxplot of both 1999 and 2012

```
par(mfrow = c(1,2))
# regular boxplot, data too right skewed
boxplot(x0, x1, main = "Regular Boxplot")
# log boxplot, significant difference in means, but more spread
boxplot(log10(x0), log10(x1), main = "log Boxplot")
```





Check for Negative Values in 'x1'

```
# summary again
summary(x1)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##  -10.00    4.00    7.63    9.14   12.00  908.97   73133
```

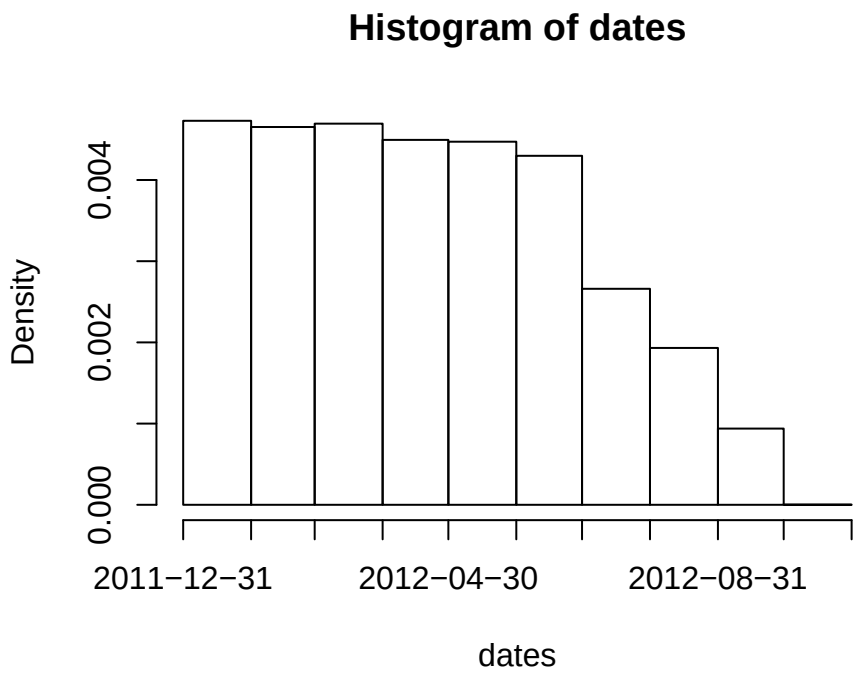
```
# create logical vector for
negative <- x1 < 0
# count number of negatives
sum(negative, na.rm = T)
```

```
## [1] 26474
```

```
# calculate percentage of negatives
mean(negative, na.rm = T)
```

```
## [1] 0.0215034
```

```
# capture the date data
dates <- pm1$Date
dates <- as.Date(as.character(dates), "%Y%m%d")
# plot the histogram
hist(dates, "month")  ## Check what's going on in months 1--6
```



Check Same New York Monitors at 1999 and 2012

```
# find unique monitors in New York in 1999
site0 <- unique(subset(pm0, State.Code == 36, c(County.Code, Site.ID)))
# find unique monitors in New York in 2012
site1 <- unique(subset(pm1, State.Code == 36, c(County.Code, Site.ID)))
# combine country codes and siteIDs of the monitors
site0 <- paste(site0[,1], site0[,2], sep = ".")
site1 <- paste(site1[,1], site1[,2], sep = ".")
# find common monitors in both
both <- intersect(site0, site1)
# print common monitors in 1999 and 2012
print(both)
```

```
##  [1] "1.5"     "1.12"    "5.80"    "13.11"   "29.5"    "31.3"    "63.2008"
##  [8] "67.1015" "85.55"   "101.3"
```

Find how many observations available at each monitor

```
# add columns for combined county/site for the original data
pm0$county.site <- with(pm0, paste(County.Code, Site.ID, sep = "."))
pm1$county.site <- with(pm1, paste(County.Code, Site.ID, sep = "."))
# find subsets where state = NY and county/site = what we found previously
cnt0 <- subset(pm0, State.Code == 36 & county.site %in% both)
cnt1 <- subset(pm1, State.Code == 36 & county.site %in% both)
# split data by the county/size values and count oberservations
sapply(split(cnt0, cnt0$county.site), nrow)
```

```
##    1.12     1.5   101.3   13.11    29.5    31.3    5.80 63.2008 67.1015   85.55
##      61     122     152      61      61     183      61     122     122       7
```

```
sapply(split(cnt1, cnt1$county.site), nrow)
```

```
##    1.12     1.5   101.3   13.11    29.5    31.3    5.80 63.2008 67.1015   85.55
##      31      64      31      31      33      15      31      30      31      31
```

Choose Monitor where County = 63 and Side ID = 2008

```
# filter data by state/county/siteID
pm1sub <- subset(pm1, State.Code == 36 & County.Code == 63 & Site.ID == 2008)
pm0sub <- subset(pm0, State.Code == 36 & County.Code == 63 & Site.ID == 2008)
# there are 30 observations from 2012, and 122 from 1999
dim(pm1sub)
```

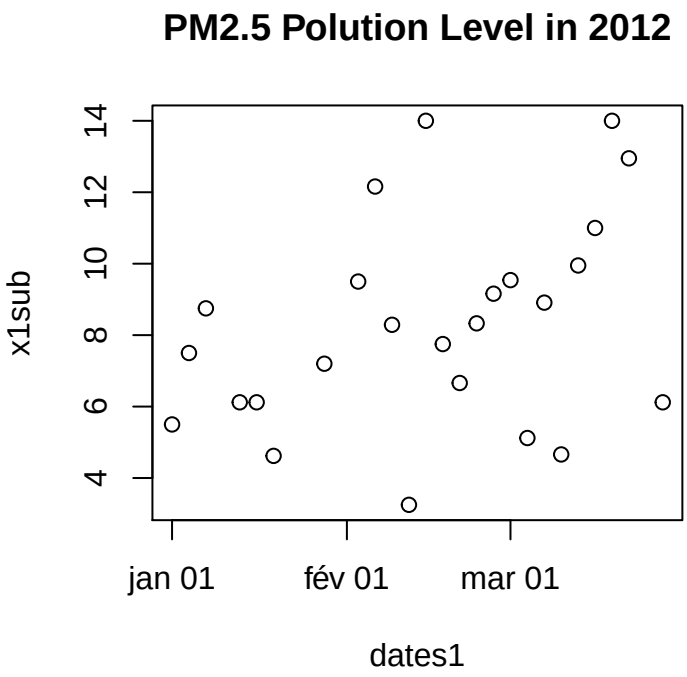
```
## [1] 30 29
```

```
dim(pm0sub)
```

```
## [1] 122  29
```

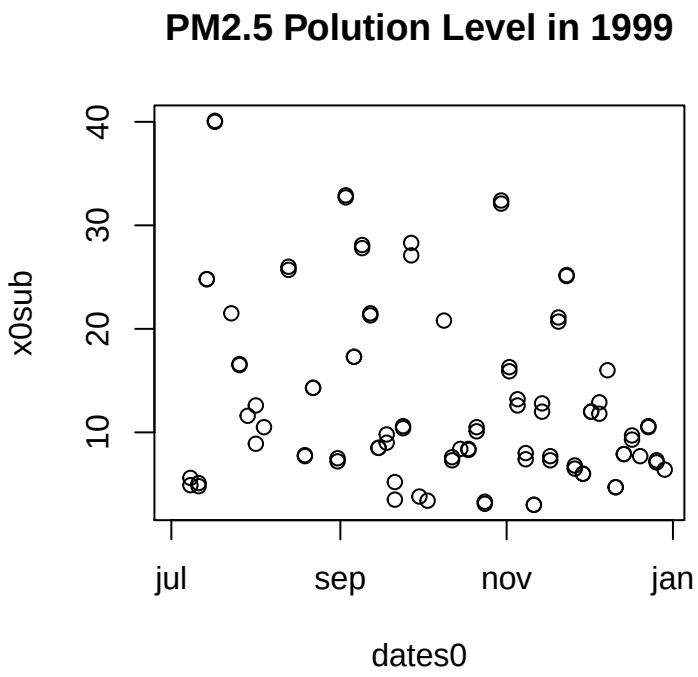
Plot Data for 2012

```
# capture the dates of the subset of data
dates1 <- pm1sub$Date
# capture measurements for the subset of data
x1sub <- pm1sub$Sample.Value
# convert dates to appropriate format
dates1 <- as.Date(as.character(dates1), "%Y%m%d")
# plot pm2.5 value vs time
plot(dates1, x1sub, main = "PM2.5 Polution Level in 2012")
```



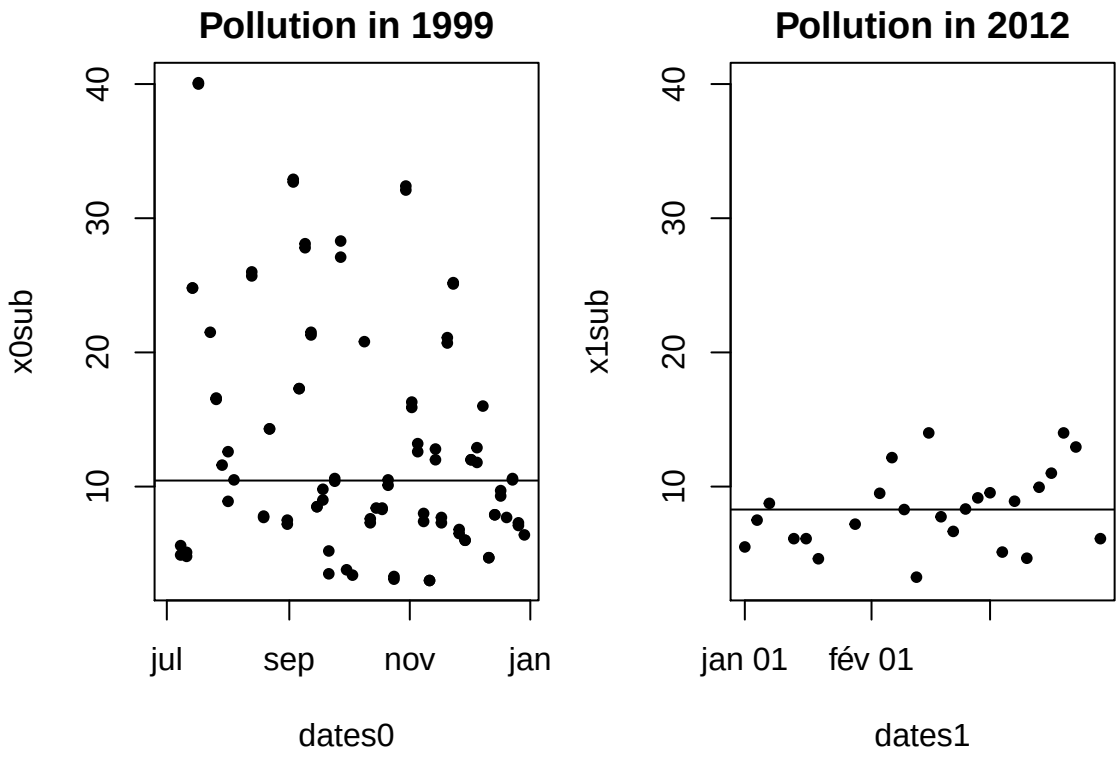
Plot data for 1999

```
# capture the dates of the subset of data
dates0 <- pm0sub$Date
# convert dates to appropriate format
dates0 <- as.Date(as.character(dates0), "%Y%m%d")
# capture measurements for the subset of data
x0sub <- pm0sub$Sample.Value
# plot pm2.5 value vs time
plot(dates0, x0sub, main = "PM2.5 Polution Level in 1999")
```



Panel Plot for Both Years

```
# find max range for data
rng <- range(x0sub, x1sub, na.rm = T)
# create 1 x 2 panel plot
par(mfrow = c(1, 2), mar = c(4, 4, 2, 1))
# plot time series plot for 1999
plot(dates0, x0sub, pch = 20, ylim = rng, main="Pollution in 1999")
# plot the median
abline(h = median(x0sub, na.rm = T))
# plot time series plot for 2012
plot(dates1, x1sub, pch = 20, ylim = rng, main="Pollution in 2012")
# plot the median
abline(h = median(x1sub, na.rm = T))
```



Find State-wide Means and Trend

```
# divide data by state and find tne mean of pollution level for 1999
mn0 <- with(pm0, tapply(Sample.Value, State.Code, mean, na.rm = T))
# divide data by state and find tne mean of pollution level for 1999
mn1 <- with(pm1, tapply(Sample.Value, State.Code, mean, na.rm = T))
# convert to data frames while preserving state names
d0 <- data.frame(state = names(mn0), mean = mn0)
d1 <- data.frame(state = names(mn1), mean = mn1)
# merge the 1999 and 2012 means by state
mrg <- merge(d0, d1, by = "state")
# dimension of combined data frame
dim(mrg)
```

```
## [1] 52  3
```

```
# first few lines of data
head(mrg)
```

```
##   state    mean.x    mean.y
## 1     1 19.956391 10.126190
## 2    10 14.492895 11.236059
## 3    11 15.786507 11.991697
## 4    12 11.137139  8.239690
## 5    13 19.943240 11.321364
## 6    15  4.861821  8.749336
```

```r
# plot the pollution levels data points for 1999
with(mrg, plot(rep(1, 52), mrg[, 2], xlim = c(.8, 2.2), ylim = c(3, 20),
    main = "PM2.5 Pollution Level by State for 1999 & 2012",
    xlab = "", ylab = "State-wide Mean PM"))
# plot the pollution levels data points for 2012
with(mrg, points(rep(2, 52), mrg[, 3]))
# connected the dots
segments(rep(1, 52), mrg[, 2], rep(2, 52), mrg[, 3])
# add 1999 and 2012 labels
axis(1, c(1, 2), c("1999", "2012"))
```