The Basics of Plotting in R
R has a built-in Datasets Package:

- iris
- mtcars
- precip
- faithful
- state.x77
- USArrests
- presidents
- ToothGrowth
- USJudgeRatings

You can call built-in functions like `hist()` or `plot()` on a built-in data set to quickly produce a chart
Basic plotting in R

- `hist(nhtemp)`
- `plot(nhtemp)`
Basic plotting in R

attach(iris)
plot(Petal.Length ~ Petal.Width)
Basic plotting in R

```r
attach(iris)
plot(Petal.Length ~ Petal.Width, col = Species)
```
Basic plotting in R

```r
plot(Petal.Length ~ Petal.Width, col = Species, main = "Iris: Petal width vs. length")
```
Legends

legend("topleft", legend = unique(Species), fill = unique(Species))
Basic plotting in R

```r
attach(faithful)
duration = eruptions

plot(duration, waiting, xlab = "Eruption duration in minutes", ylab = "Time waited in minutes")

plot(duration, waiting, xlab = "Eruption duration in minutes", ylab = "Time waited in minutes", col = "seagreen")
```
Histograms

Histogram of waiting

hist(waiting)

Histogram of eruptions

hist(eruptions)
Histograms

```
hist(waiting, breaks = 5)
hist(waiting, breaks = 20)
```
Histograms

```r
hist(waiting,
    main = "Old Faithful",
    cex.main = 1.75,
    xlab = "Waiting Time in Minutes",
    ylab = "Frequency",
    cex.lab = 1.25)
```
Histograms

```
hist(waiting,
   main = "Old Faithful",
cex.main = 1.75,
xlab = "Waiting Time in Minutes",
ylab = "Frequency",
cex.lab = 1.25
col = "blue",
border = "orange")
```
Stem and leaf plot

> stem(waiting)

The decimal point is 1 digit(s) to the right of the |

```
4  | 3
4  | 5556666677788899999
5  | 0000011111222233333344444444
5  | 555556666778888999999999
6  | 00000022223334444
6  | 555667899
7  | 000011111233333334444
7  | 55555555666666666777777778888888888899999999999
8  | 00000000111111111222222222233333333333334444444444
8  | 555555666667788888899999
9  | 00000012334
9  | 6
```
> stem(eruptions)

The decimal point is 1 digit(s) to the left of the |

16 | 070355555588
18 | 00002223333355777777788888223357778888
20 | 00002223378800035778
22 | 002335578023578
24 | 00228
26 | 23
28 | 080
30 | 7
32 | 2337
34 | 250077
36 | 0000823577
38 | 233335582225577
40 | 000000335778888800223355557778
42 | 03335555778800233333555577778
44 | 0222335557780000000023333357778888
46 | 0000233357700000023578
48 | 00000022335800333
50 | 0370
Bar charts

> races_younger
[1] "Black" "Hispanic" "Other" "White"

> population_in Millions_younger
[1] 10.76 19.03 7.76 40.50

> barplot(population_in Millions_younger, names.arg = races_younger, main = "Younger than 18, 2014", ylab = "Population in Millions")
Bar charts

> races_all
[1] "Native" "Asian" "Black" "Hispanic" "Two" "White"

> population_in_millions_all
[1] 1.39 18.12 38.60 55.61 5.67 195.35

barplot(population_in_millions_all,
        names.arg = races_all,
        main = "All ages, 2014",
        ylab = "Population in Millions")
Bar charts

> races_all_other
[1] "Black" "Hispanic" "White" "Other"

> population_in_millions_all_other
[1] 38.60 55.61 195.35 25.19

barplot(population_in_millions_all_other,
        names.arg = races_all_other,
        main = "All ages, 2014",
        ylab = "Population in Millions")
Stacked and grouped bar charts
Pie charts

```r
pie_labels_younger <-
paste(races_younger,
population_in_millions_younger,
sep = "\n")

pie(population_in_millions_younger,
main = "Younger than 18\nPopulation in Millions",
labels = pie_labels_younger)
```
Pie charts

pie_labels_all_other <- paste(races_all_other, population_in_millions_all_other, sep = "\n")

pie(population_in_millions_all_other, main = "All Ages\nPopulation in Millions", labels = pie_labels_all_other)
Pie charts

Younger than 18 Population in Millions:
- Hispanic: 19.03
- Black: 10.76
- Other: 7.76
- White: 40.5

All Ages Population in Millions:
- Hispanic: 55.61
- Black: 38.6
- Other: 25.19
- White: 195.35
Dot plots

```r
states <- data.frame(state.x77)
sorted_states <- states[order(states$Income), ]
dotchart(sorted_states$Income, rownames(sorted_states), cex.lab = .25, main = "Income per capita")
```
Box plots

```r
boxplot(Petal.Length ~ Species,
       main = "Iris Petal Length by Species",
       xlab = "Species",
       ylab = "Petal Length")
```
Notched Box plots

attach(ToothGrowth)

boxplot(len ~ supp * dose,
       data = Toothgrowth, notch = TRUE,
       col = (c("gold", "darkgreen")),
       main = "Tooth Growth",
       xlab = "Supplement and Dose")

If the notches do not overlap, then the medians of the groups are different (because their confidence intervals do not overlap).
Simple Scatterplots

```r
plot(USJudgeRatings$RTEN ~ USJudgeRatings$FAMI,
xlab = "Familiarity with Law",
ylab = "Worthy of Retention",
main = "Law Familiarity vs. Worthy of Retention",
pch = "+")
```
Scatterplot Matrices

INTG Judicial integrity.
DMNR Demeanor.
DILG Diligence.

pairs(~USJudgeRatings$CONT +
    USJudgeRatings$INTG +
    USJudgeRatings$DMNR +
    USJudgeRatings$DILG,
    main = "US Judge Ratings")
features <- c("Contacts", "Integrity", "Demeanor", "Diligence")

pairs(~USJudgeRatings$CONT + USJudgeRatings$INTG + USJudgeRatings$DMNR + USJudgeRatings$DILG, labels = features, main = "US Judge Ratings")
library(scatterplot3d)

scatterplot3d(mtcars$wt, mtcars$disp, mtcars$mpg, main = "3D Scatterplot")
Graphical parameters

- **Text and symbol size** \((\text{cex: \text{axis, lab, main}})\)
- **Fonts** \((\text{font: \text{axis, lab, main}})\):
  - 1=plain, 2=bold, 3=italic, 4=bold italic, 5=symbol
- **Colors** \((\text{col})\): [colors](http://www.statmethods.net/advgraphs/parameters.html), and more [colors](http://www.statmethods.net/advgraphs/parameters.html)
Graphical parameters (cont’d)

Plotting symbols (pch)

Line type (lty)

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