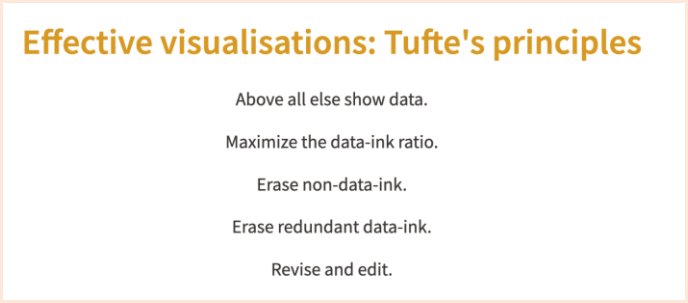
BIOSTATS 640 – Introduction to R
Fall 2023
https://people.umass.edu/biep640w/webpages/demonstrations.html



https://joeroe.io/r4r_visualisation/r4r_visualisation_slides.html#34

03
Introduction to Data Visualization
Using `ggplot2`
September 22, 2023

Right click to download excel dataset
`framingham_didactic.xlsx`

Welcome to Lesson 03!
Who doesn't like producing a pretty graph. There are lots of ways to do this in R. Using the package ggplot2 is one of the best. In this lesson, I will introduce you to how to make some basic graphs using the package **`{ggplot2}`.**

Dataset Used: **`framingham_didactic.xlsx`**
Packages Used: **`tidyverse, ggplot2, ggExtra`**

1. Highlights of Lesson 02
Numerical Summarization and One and Two Sample Inference

R needs to know where to read and write. Always set your working directory at the start of your R session	From the top toolbar drop down menus Session > Set Working Directory > Choose Directory From the console window setwd("FULLPATH") # set getwd() # check
Often you will use functions in packages that you must install and attach.	Step 1: Install (one time ever) File/Plots/Packages pane > Install Step 2: Attach (one time each session) library(packagename) # no quotes
How to import excel data into R Studio/Posit using menus	From the top toolbar drop down menu, import ".csv" File > Import Dataset > From Text (readr) From the top toolbar drop down menu, import ".xlsx" File > Import Dataset > From Excel From the console window read.csv("FILENAME.csv")
Factors. R cannot work with character/string data. If you want to work with categorical data, you must work with factors in R. By default, factor levels are stored alphabetically. TIP – set these yourself as shown at right.	From character → factor newvar <- factor(oldvar, levels=c("string1","string2"), labels=c("label1", "label2"), ordered=TRUE) # if ordinal From number → factor newvar <- factor(oldvar, levels=c(number1, number2), labels=c("label1", "label2"), ordered=TRUE) # if ordinal

Description and inference using pre-installed functions	`summary(dataframe)`
	`summary(dataframe$variable)`
	`myvars <- c("var1", "var2", "var3")`
	`summary(dataframe[myvars])`
	`table(discrete1,discrete2)`
	`t.test(outcome ~1,data=df,mu=nullmean) # one sample`
	`t.test(df$pre,df$post,paired=TRUE)  # paired wide`
	`t.test(outcome~group,data=df)  # two samples`
	`binom.test(x=#events,n=ntrials)  # one sample`
	`fisher.test(df$rowvar,df$colvar)  # two samples`
	`fisher.test(table)  # tabular data`
	
	`To get confidence interval,add $conf.int`
	`t.test(y~1,data=df,conf.level=.90)$conf.int`

Some packages for description and inference	{summarytools}, {stargazer}, {DescTools}

2. Introduction to the Framingham Heart Study Didactic Data

framingham_didactic.xlsx

Source:
The Framingham Didactic dataset was contributed by Dr. Amy Nowacki, Associate Professor, Cleveland Clinic. Please refer to this resource as: Amy S. Nowacki, "Framingham Didactic Dataset", *TSHS Resources Portal (2015)*. Available at https://www.causeweb.org/tshs/framingham-didactic/.

Description:

Cardiovascular disease (CVD) is the leading cause of death and serious illness in the United States. In 1948, the Framingham Heart Study - under the direction of the National Heart Institute (now known as the National Heart, Lung, and Blood Institute or NHLBI) was initiated.

The objective of the Framingham Heart Study was to identify the common factors or characteristics that contribute to CVD by following its development over a long period of time in a large group of participants who had not yet developed overt symptoms of CVD or suffered a heart attack or stroke.

In this illustration, we will explore the fitting of a multiple predictor model to a different transformation of systolic blood pressure. Y = -1/sqrt(sbp). The predictors of interest will be sex (sex), body mass index (bmi), serum cholesterol (scl), and age (age).

Data dictionary/Codebook

Position	Variable	Label	Type	Codings
1	id	Patient identifier		
2	sex	Sex at birth	numeric	1=male 2=female
3	sbp	Systolic Blood Pressure (mm Hg)	numeric	
4	dbp	Diastolic Blood Pressure (mm Hg)	numeric	
5	scl	Serum cholesterol (mg/100 ml)	numeric	
6	age	Age at baseline exam, years	numeric	
7	bmi	Body Mass index (kg/m^2)	numeric	
8	month	Month of year of baseline exam	numeric	
9	followup	Follow-up: days since baselinel	numeric	
10	chdfate	Event of CHD at follow up	numeric	1 = event had developed CHD 0 = otherwise

3. Introduction to ggplot2

The **grammar of a ggplot** consists of:

1st -- Some minimal components (required); plus

2nd – Additional specifications (as you like, but not required)

Grammar of a ggplot graph

Required (minimal) component layers:

data =	data to use (**Tip** – this must be a dataframe)
aes( )	define x-axis, y-axis, 3rd variable, as appropriate
geom_XXX( )	type of plot (e.g., dot, box, scatterplot, etc.)

Additional Specifications layers:

aesthetic	asethetics pertaining to position, size, color, shape, fill, etc.
scale	customize scale; e.g. – log scale, color scale, size, shape
stat =	show statistics (e.g., regression line, overlay normal)
facets	plot by group or create multi-panel graphs.

Build your ggplot plot **layer by layer, editing and correcting as you go along!**

How to Build Your Plot Layer by Layer:

Step 1: Attach packages. Either of the following works
library(ggplot2) or
library(tidyverse)

Step 2 *(optional, recommended):* Create each plot in an R Script or in its own R Markdown chunk

Step 3 *(optional, recommended):* Code your graph line by line, layering as you go.

```
First line:                          # Execute and correct as needed
 data = dataframename

Second line is added                 # Execute and correct as needed
 data = dataframename  +
 aes( )

Third line is added:                 # Execute and correct as needed
 data = dataframename  +
 aes( )  +
geom_xxx( )
```

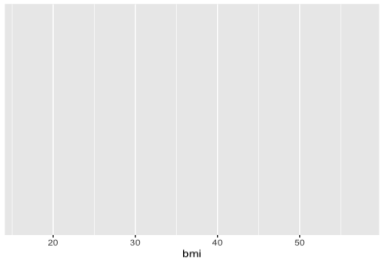
Tips

- The continuation + MUST BE at the end of the line (not at the start of the next line)
- As you add lines, execute all of the accumulating layers
- Check your work and correct errors, layer by layer

Illustration of Layer by Layer

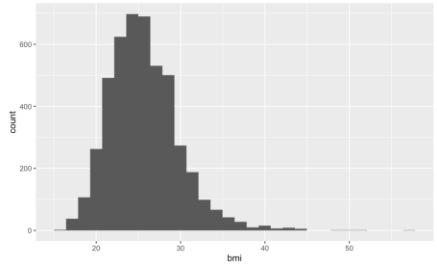
Note: In what follows the red color of the + at the end of each line is my coloring for emphasis

```
# Attach ggplot2 or tidyverse
library(ggplot2)

# Minimal Components: data= and aes( )
# Tell R which data to use.   Specify single variable for histogram
ggplot(data=framinghamdf) +
      aes(x=bmi)
```



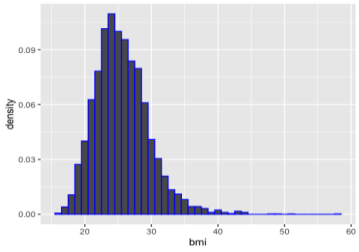
Yes, a blank plot to start!

```
# Next layer: + geom_XXX( )
# Tell R which kind of plot to produce
ggplot(data=framinghamdf) +
      aes(x=bmi) +
      geom_histogram( )
```



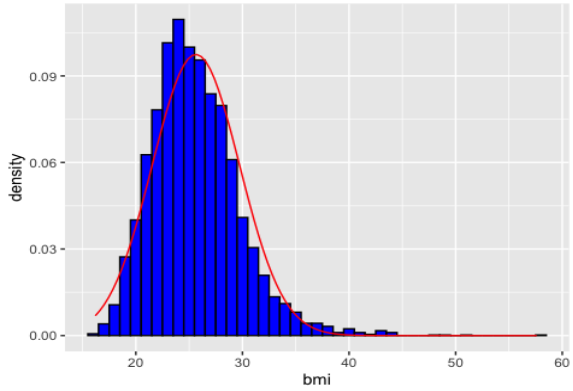
geom_histogram default plot

```
# Along the way: fine tune geom_histogram specifications
# binwidth, color, y-axis
ggplot(data=framinghamdf) +
      aes(x=bmi) +
      geom_histogram(binwidth=1,
                     colour="blue",
                     aes(y=..density..))
```



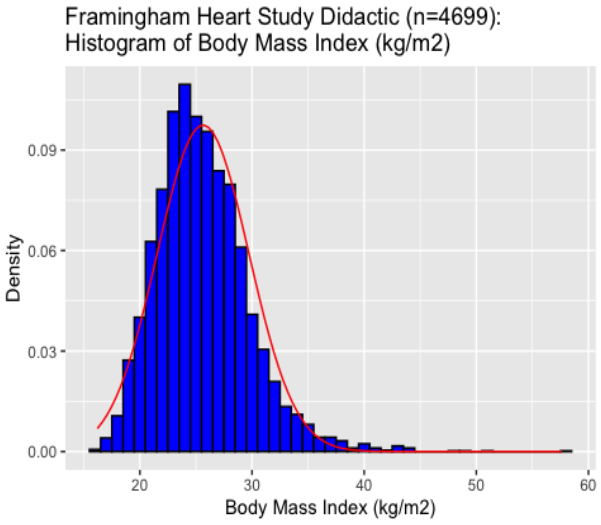
This looks a little better…

```
# Next layer: + stat_function( )
# Here we are telling R overlay a statistical calculation, in particular an overlay normal curve
# Tip:  Be sure to include the option na.rm=TRUE.  Reason:  Calculations will not
# happen if there are missing values

ggplot(data=framinghamdf) +
      aes(x=bmi) +
      geom_histogram(binwidth=1,
                     colour="blue",
                     aes(y=..density..))  +
      stat_function(fun=dnorm, color="red",
                    args=list(mean=mean(framinghamdf$bmi,na.rm=TRUE),
                    sd=sd(framinghamdf$bmi,na.rm=TRUE))
```



Pretty!

```
# Next layers: +  ADD TITLE, LABELS, AXIS LIMITS, etc
ggplot(data=framinghamdf) +
      aes(x=bmi) +
      geom_histogram(binwidth=1,
                     colour="blue",
                     aes(y=..density..))  +
      stat_function(fun=dnorm,
                    color="red",
                    args=list(mean=mean(framinghamdf$bmi,na.rm=TRUE),
                    sd=sd(framinghamdf$bmi,na.rm=TRUE)) +
       ggtitle("Framingham Heart Study Didactic (n=4699):  \nHistogram of Body Mass Index (kg/m2)") +
       xlab("Body Mass Index (kg/m2)") +
       ylab("Density")
```



Don't forget to save your graph!

How to Save Your Graph

STEP 1: Attach the packags {ggplot2}
library(ggplot2)

STEP 2: Edit your R Script or your R Markdown code so as to create your graph as an object
Create your graph as an object using whatever name you like. Don't forget. If you want to see your plot as it develops, layer by layer, you will have to print it. For example, if your graph object is named p, then to print it, simply type p

```
p <- ggplot(stuff) +
     next layer +
     next layer +
     etc
```

STEP 3: Use the command ggsave( ) to save your graph
ggsave(file="FILENAME.extension",(p, option, option). For example
ggsave(file="mygraph.tiff",p, width=7, height=5, units="in")

Your Turn!
Initialize Session

```
setwd("/cloud/project")
getwd()

## [1] "/cloud/project"

rm(list = ls())
```

Load framingham_didactic. Inspect

```
library(tidyverse)
library(readxl)
framingham <- read_excel("framingham_didactic.xlsx")
glimpse(framingham)

## Rows: 4,699
## Columns: 10
## $ id       <dbl> 2642, 4627, 2568, 4192, 3977, 659, 2290, 4267, 2035, 3587, 10…
## $ sex      <dbl> 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 2, 1, 2, 2, 2, 1, 1, 1, 2, 1…
## $ sbp      <dbl> 120, 130, 144, 92, 162, 212, 140, 174, 142, 115, 202, 130, 13…
## $ dbp      <dbl> 80, 78, 90, 66, 98, 118, 85, 102, 94, 70, 124, 94, 88, 72, 10…
## $ scl      <dbl> 267, 192, 207, 231, 271, 182, 276, 259, 242, 242, 260, 326, 1…
## $ age      <dbl> 55, 53, 61, 48, 39, 61, 44, 39, 47, 60, 58, 47, 43, 59, 56, 5…
## $ bmi      <dbl> 25.0, 28.4, 25.1, 26.2, 28.4, 33.3, 25.3, 27.9, 26.6, 30.8, 2…
## $ month    <dbl> 8, 12, 8, 11, 11, 2, 6, 11, 5, 10, 3, 10, 1, 9, 9, 9, 9, 8, 1…
## $ followup <dbl> 18, 35, 109, 147, 169, 199, 201, 209, 265, 278, 290, 300, 300…
## $ chdfate  <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1…
```

Be sure to attach the package ggplot2

```
library(ggplot2)
```

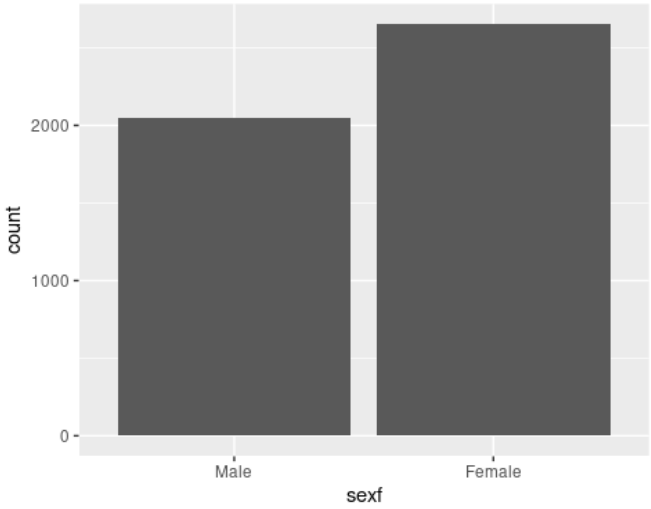
Create sexf, a factor version of the variable sex

```
framingham$sexf <- factor(framingham$sex,
                          levels=c(1,2),
                          labels=c("Male", "Female"))

table(framingham$sex,framingham$sexf)                    # show.

##
##     Male Female
##   1 2049      0
##   2    0   2650
```

4. Single Discrete Variable: Bar Chart

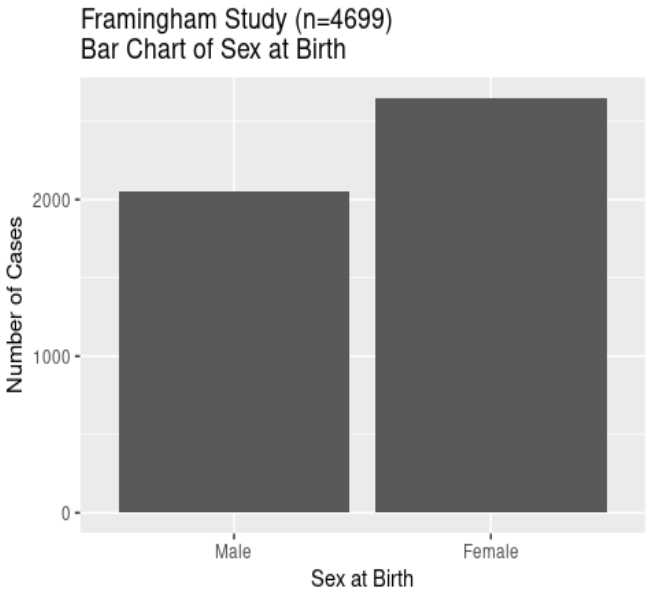
BAR Graph - default

```
ggplot(data=framingham) +                    # required component: data=
       aes(x=sexf) +                         # required component: aes( )
       geom_bar(na.rm=TRUE)                  # required component:  geom_SOMETHING
```



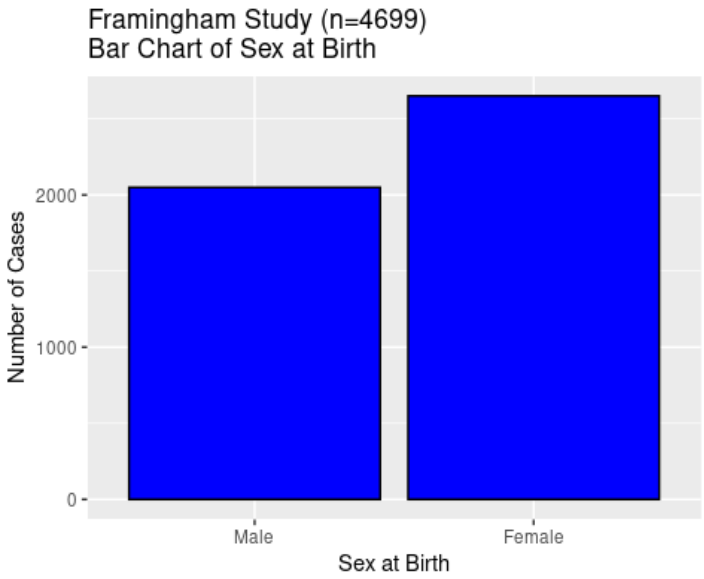
Bar Graph with aesthetics

```
ggplot(data=framingham) +                                                  # required component: data=
  aes(x=sexf) +                                                            # required component: aes( )
  geom_bar(na.rm=TRUE) +                                                   # required component:  geom_SOMETHING
  ggtitle("Framingham Study (n=4699)\nBar Chart of Sex at Birth") +         # \n starts a new line
  xlab("Sex at Birth") +
  ylab("Number of Cases")
```



Bar Graph with Aesthetics + COLOR

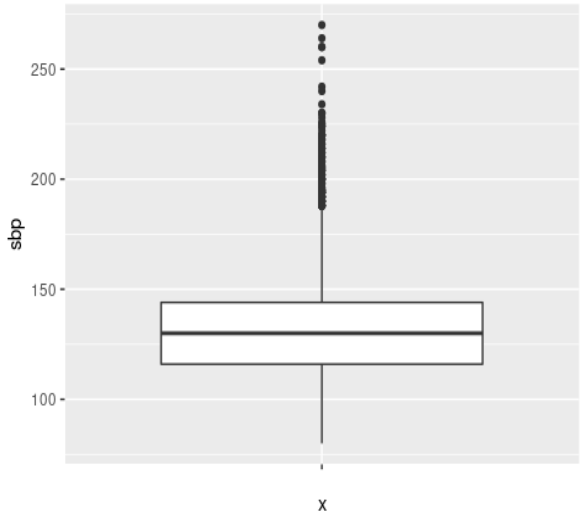
```
ggplot(data=framingham) +                                          # required component: data=
  aes(x=sexf) +                                                    # required component: aes( )
  geom_bar(na.rm=TRUE,
           color="black",                                          # aesthetics are added as options
           fill="blue") +                                          # required component:  geom_SOMETHING
  ggtitle("Framingham Study (n=4699)\nBar Chart of Sex at Birth") +
  xlab("Sex at Birth") +
  ylab("Number of Cases")
```



5. Single Continuous Variable: Box and Whisker Plot

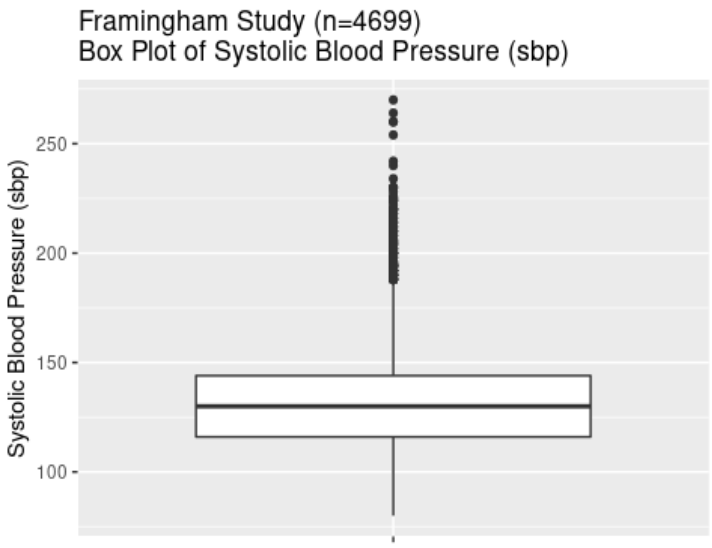
Box and Whisker PLot - default

```
ggplot(data=framingham) +                                    # required component: data=
    aes(x="", y=sbp) +                                       # required component: aes( )
    geom_boxplot(na.rm=TRUE)                                 # required component:  geom_SOMETHING
```

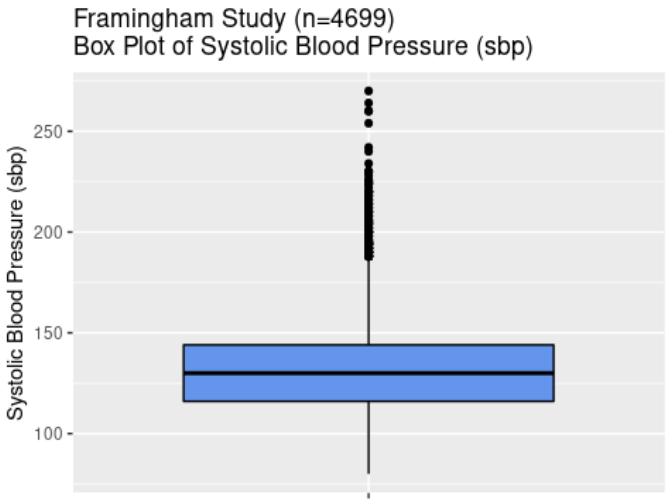


Box and Whisker Plot with Aesthetics

```
ggplot(data=framingham) +                                    # required component: data=
    aes(x="", y=sbp) +                                       # required component: aes( )
    geom_boxplot(na.rm=TRUE) +                               # required component:  geom_SOMETHING
    ggtitle("Framingham Study (n=4699)\nBox Plot of Systolic Blood Pressure (sbp)") +   # \n to start new line
    xlab("") +
    ylab("Systolic Blood Pressure (sbp)")
```




```
# BOX PLOT - Single continuous variable (with optional aesthetics) + color!
 ggplot(data=framingham) +                                                  # required component: data=
   aes(x="", y=sbp) +                                                       # required component: aes( )
   geom_boxplot(na.rm=TRUE,
                color="black",
                fill="cornflowerblue") +                                    # required component:  geom_SOMETHING
   ggtitle("Framingham Study (n=4699)\nBox Plot of Systolic Blood Pressure (sbp)") +
   xlab("") +
   ylab("Systolic Blood Pressure (sbp)")
```



6. XY Scatterplot

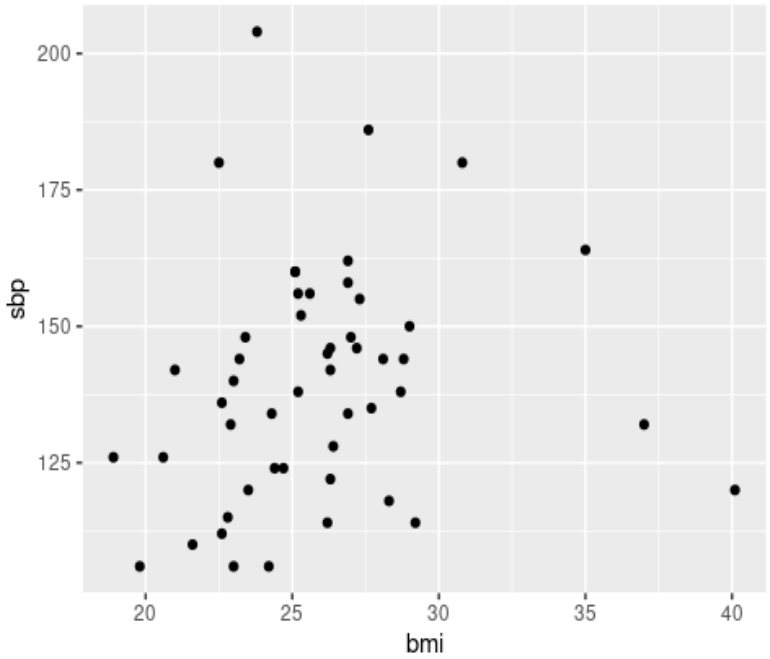
Preliminary (for illustration only): Use sample_n() in package {tidyverse} to obtain random sample

```
library(tidyverse)

temp <- framingham %>%
         sample_n(50)
 glimpse(temp)
```

```
## Rows: 50
## Columns: 11
## $ id       <dbl> 1337, 3926, 112, 4201, 1925, 1696, 4646, 412, 3346, 856, 2838…
## $ sex      <dbl> 1, 2, 1, 2, 1, 1, 2, 1, 2, 1, 2, 1, 2, 1, 1, 1, 2, 2, 2, 1, 2…
## $ sbp      <dbl> 134, 160, 138, 106, 144, 132, 155, 122, 120, 106, 134, 106, 1…
## $ dbp      <dbl> 92, 88, 85, 78, 96, 96, 100, 84, 75, 64, 82, 70, 80, 86, 98, …
## $ scl      <dbl> 305, 167, 271, 292, 209, 165, 200, 283, 344, 241, 275, 167, 2…
## $ age      <dbl> 56, 55, 43, 57, 45, 55, 44, 34, 54, 51, 53, 40, 55, 37, 43, 6…
## $ bmi      <dbl> 24.3, 25.1, 25.2, 23.0, 28.8, 37.0, 27.3, 26.3, 23.5, 24.2, 2…
## $ month    <dbl> 3, 11, 1, 11, 5, 4, 12, 1, 9, 2, 8, 8, 4, 11, 2, 3, 1, 3, 8, …
## $ followup <dbl> 5577, 10882, 7553, 5000, 10028, 5943, 11688, 11688, 9497, 504…
## $ chdfate  <dbl> 0, 1, 1, 0, 0, 1, 0, 0, 0, 1, 1, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0…
## $ sexf     <fct> Male, Female, Male, Female, Male, Male, Female, Male, Female,…
```

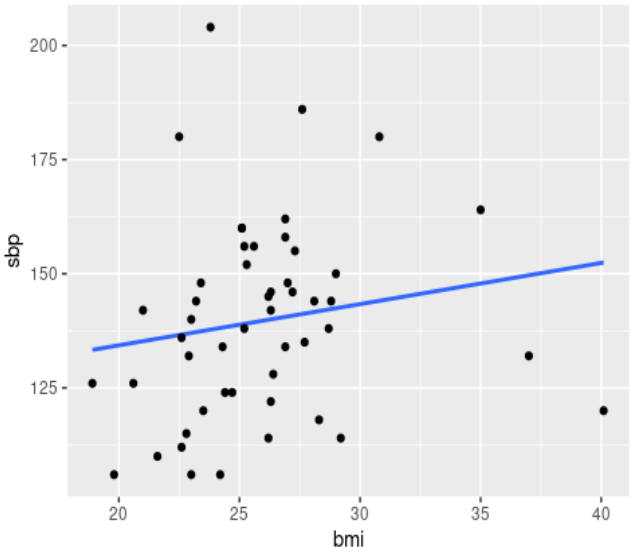
Scatterplot - default

```
ggplot(data=temp) +                                    # required component: data=
   aes(x=bmi, y=sbp) +                                 # required component: aes( )
   geom_point(na.rm=TRUE)                              # required component:  geom_SOMETHING
```



Scatterplot with overlay linear model straight line

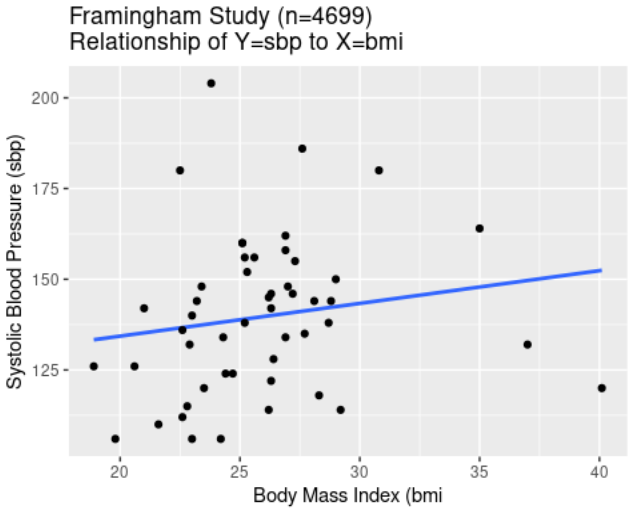
```
ggplot(data=temp) +                                    # required component: data=
  aes(x=bmi, y=sbp) +                                  # required component: aes( )
  geom_smooth(method=lm,se=FALSE) +                    # TIP - plot line first, then points on top
  geom_point(na.rm=TRUE)                               # required component:  geom_SOMETHING

## `geom_smooth()` using formula 'y ~ x'
```



Scatterplot with overlay straight line and aesthetics

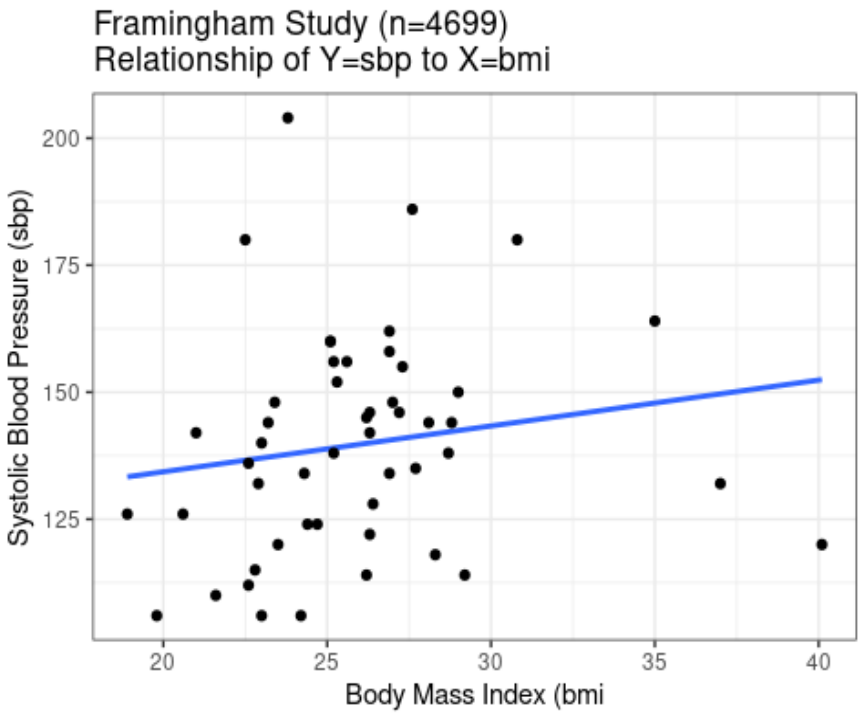
```
ggplot(data=temp) +                                    # required component: data=
  aes(x=bmi, y=sbp) +                                  # required component: aes( )
```

```
   geom_smooth(method=lm,se=FALSE) +                                    # TIP - plot line, then points on top
   geom_point(na.rm=TRUE) +                                             # required component:  geom_SOMETHING
   ggtitle("Framingham Study (n=4699)\nRelationship of Y=sbp to X=bmi") +
   xlab("Body Mass Index (bmi") +
   ylab("Systolic Blood Pressure (sbp)")

## `geom_smooth()` using formula 'y ~ x'
```



Add theme_bw() to obtain cleaner background

```
ggplot(data=temp) +                                                     # required component: data=
   aes(x=bmi, y=sbp) +                                                  # required component: aes( )
   geom_smooth(method=lm,se=FALSE) +                                    # TIP - plot line first, then points on top
   geom_point(na.rm=TRUE) +                                             # required component:  geom_SOMETHING
   ggtitle("Framingham Study (n=4699)\nRelationship of Y=sbp to X=bmi") +
   xlab("Body Mass Index (bmi") +
   ylab("Systolic Blood Pressure (sbp)") +
   theme_bw()

## `geom_smooth()` using formula 'y ~ x'
```



7. Some Good Resources

VIDEOS

__1. *(Source: Greg Martin, R Programming 101)*
ggplot2 for Plots and Graphs (video, 26:50)

__2. *(Source: Data Camp)*
Learn R: An Introduction to ggplot2 (video, 5:08)

CHEAT SHEET

__1. *(Source: https://www.maths.usyd.edu.au/u/UG/SM/STAT3022/r/current/Misc/data-visualization-2.1.pdf)*
Data Visualization with ggplot2 Cheat Sheet (pdf, 2 pp)

RESOURCE FOR LEARNING

__1. *(Source: Statistical Tools for High Throughput Data STHDA)*
ggplot2 Essentials (html)