# Functions & Data Visualization

## Fundamental Techniques in Data Science

Utrecht University

Kyle M. Lang

Department of Methodology & Statistics
Utrecht University

# Outline

Functions

Data Visualization

- Base R Graphics
- GGPlot
- Saving Graphics

# FUNCTIONS

# R Functions

Functions are the foundation of R programming.

- Other than data objects, almost everything else that you interact with when using R is a function.
- Any R command written as a word followed by parentheses, `()`, is a function.
  - `mean()`
  - `library()`
  - `mutate()`
- Infix operators are aliased functions.
  - `<-`
  - `+`, `-`, `*`
  - `>`, `<`, `==`

# User-Defined Functions

We can define our own functions using the `function()` function.

```
square <- function(x) {
    out <- x^2
    out
}
```

After defining a function, we call it in the usual way.

```
square(5)
```

```
[1] 25
```

One-line functions don't need braces.

```
square <- function(x) x^2
square(5)
```

```
[1] 25
```

# User-Defined Functions

Function arguments are not strictly typed.

```
square(1:5)

[1]  1  4  9 16 25

square(pi)

[1] 9.869604

square(TRUE)

[1] 1
```

But there are limits.

```
square("bob") # But one can only try so hard

Error in x^2:  non-numeric argument to binary operator
```

# User-Defined Functions

Functions can take multiple arguments.

```
mod <- function(x, y) x %% y
mod(10, 3)

[1] 1
```

Sometimes it's useful to specify a list of arguments.

```
getLsBeta <- function(datList) {
    X <- datList$X
    y <- datList$y

    solve(crossprod(X)) %*% t(X) %*% y
}
```

# User-Defined Functions

```
X        <- matrix(runif(500), ncol = 5)
datList <- list(y = X %*% rep(0.5, 5), X = X)

getLsBeta(datList = datList)

     [,1]
[1,]  0.5
[2,]  0.5
[3,]  0.5
[4,]  0.5
[5,]  0.5
```

# User-Defined Functions

Functions are first-class objects in R.

- We can treat functions like any other R object.

R views an unevaluated function as an object with type ”closure”.

```
class(getLsBeta)

[1] "function"

typeof(getLsBeta)

[1] "closure"
```

An evaluated functions is equivalent to the objects it returns.

```
class(getLsBeta(datList))

[1] "matrix" "array"

typeof(getLsBeta(datList))

[1] "double"
```

# User-Defined Functions

We can use functions as arguments to other operations and functions.

```
fun1 <- function(x, y) x + y

## What will this command return?
fun1(1, fun1(1, 1))

[1] 3
```

Why would we care?

```
s2 <- var(runif(100))
x  <- rnorm(100, 0, sqrt(s2))
```

# User-Defined Functions

```
X[1:8, ]
```

```
           [,1]       [,2]       [,3]      [,4]       [,5]
[1,] 0.52431382 0.67136447 0.28228726 0.7148383 0.54204681
[2,] 0.01926742 0.11693762 0.09148502 0.6929171 0.88371944
[3,] 0.05100735 0.18432074 0.43547799 0.6097462 0.09026598
[4,] 0.60566972 0.12944127 0.21000143 0.2441917 0.68141473
[5,] 0.48737303 0.94030405 0.23988619 0.4915910 0.36353771
[6,] 0.19941958 0.96670678 0.11455820 0.1243947 0.24253273
[7,] 0.95507804 0.38705829 0.49733535 0.2968470 0.81001800
[8,] 0.11093197 0.07731757 0.84923006 0.8653987 0.61914193
```

```
c(1, 3, 6:9, 12)
```

```
[1]  1  3  6  7  8  9 12
```

# Data Visualization

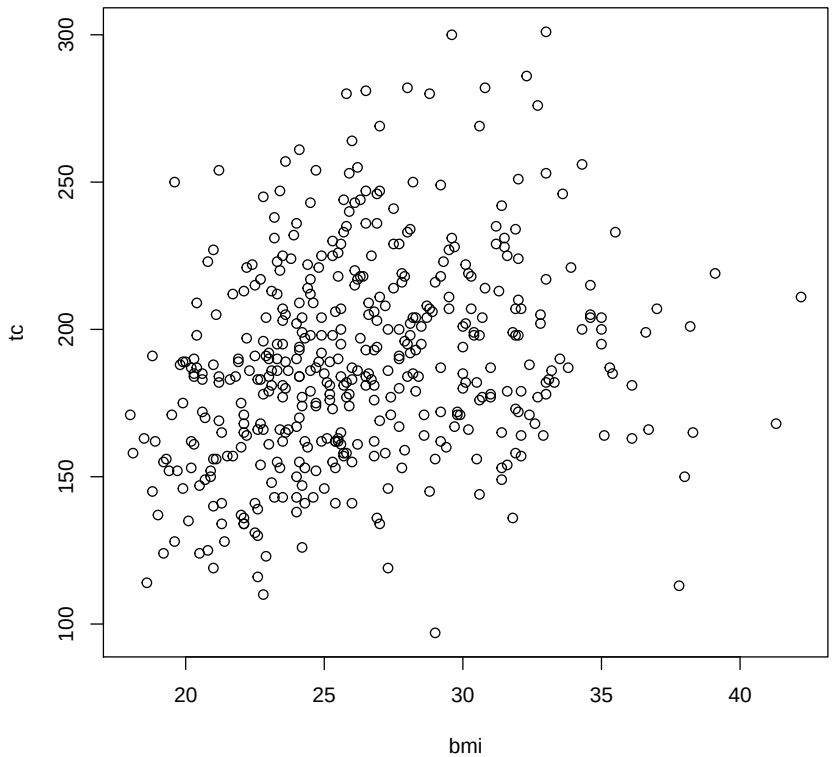
# Setup

```
dataDir  <- "../../../data/"

## Load some data:
diabetes <- readRDS(paste0(dataDir, "diabetes.rds"))
titanic  <- readRDS(paste0(dataDir, "titanic.rds"))
bfi      <- readRDS(paste0(dataDir, "bfi.rds"))

## Convert survival indicator to a numeric dummy code:
titanic <- titanic %>% mutate(survived = as.numeric(survived) - 1)
```

# Base R Graphics: Scatterplots

We can create a basic scatterplot using the `plot()` function.

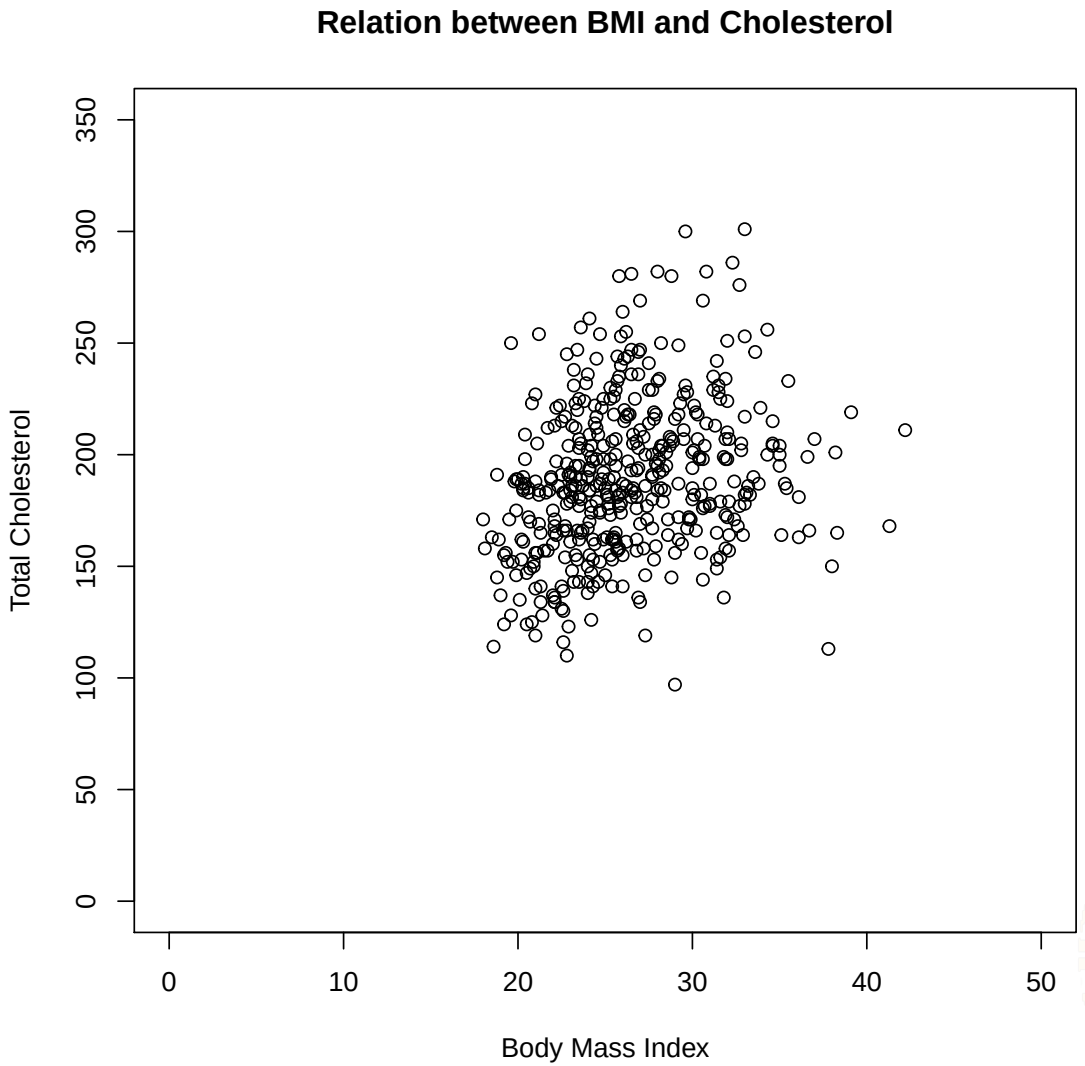
```
diabetes %$% plot(y = tc, x = bmi)
```



# Base R Graphics: Scatterplots

```
diabetes %$% plot(y = tc,
                  x = bmi,
                  ylab = "Total Cholesterol",
                  xlab = "Body Mass Index",
                  main = "Relation between BMI and Cholesterol",
                  ylim = c(0, 350),
                  xlim = c(0, 50)
                  )
```

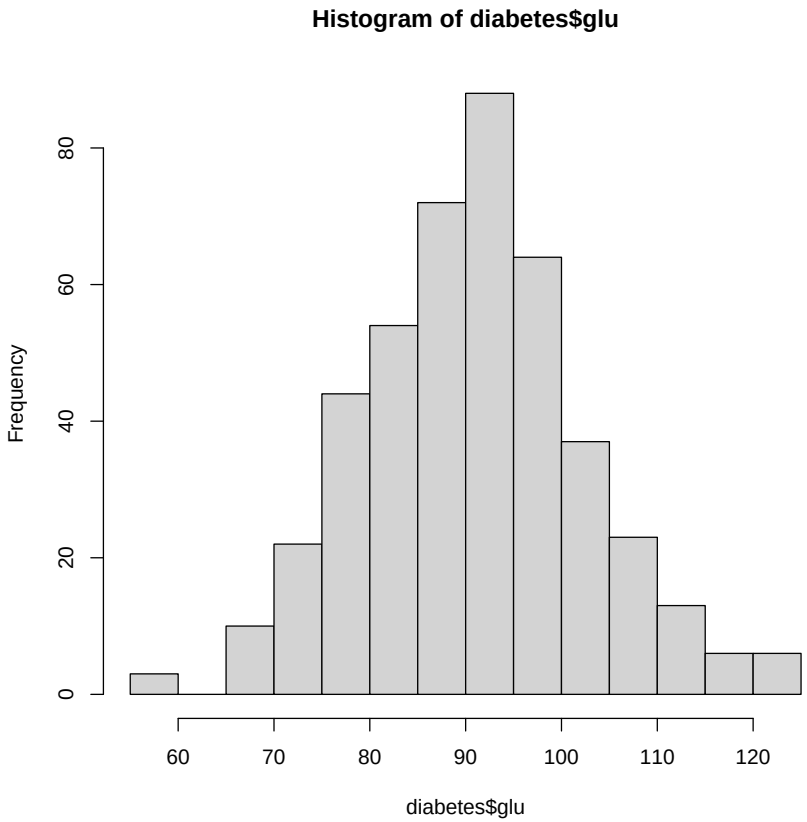
# Base R Graphics: Scatterplots



# Base R Graphics: Histograms

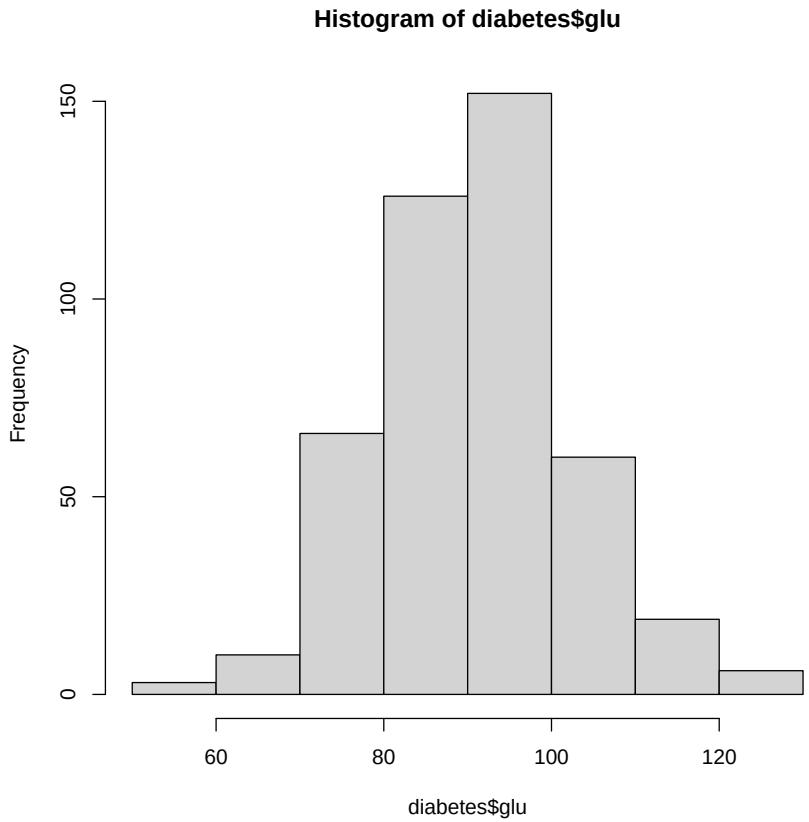
We can create a simple histogram with the `hist()` function.

```
hist(diabetes$glu)
```



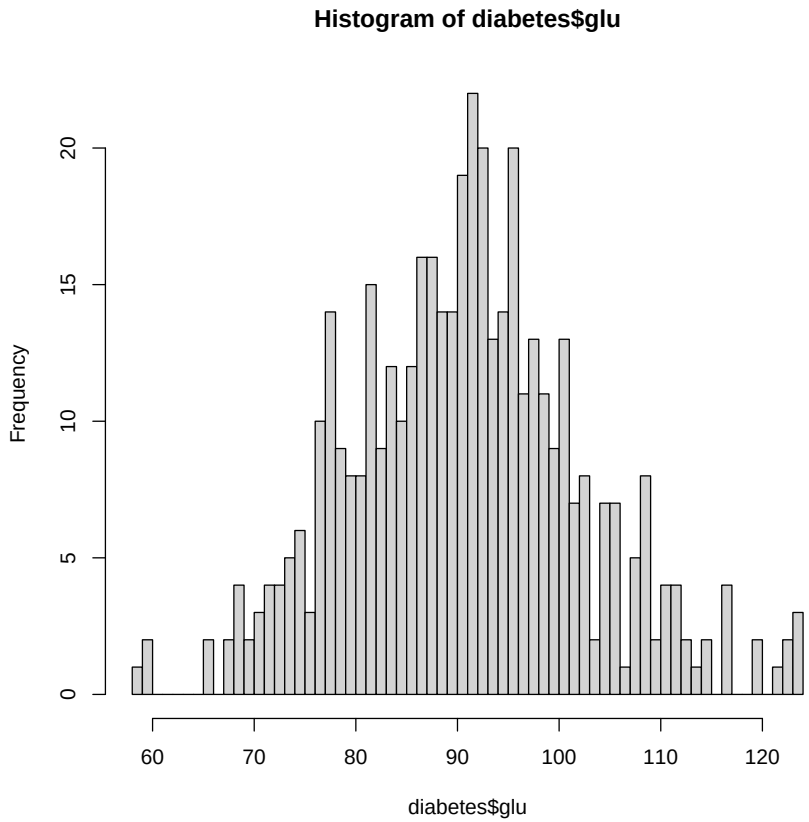
# Base R Graphics: Histograms

```
hist(diabetes$glu, breaks = 5)
```



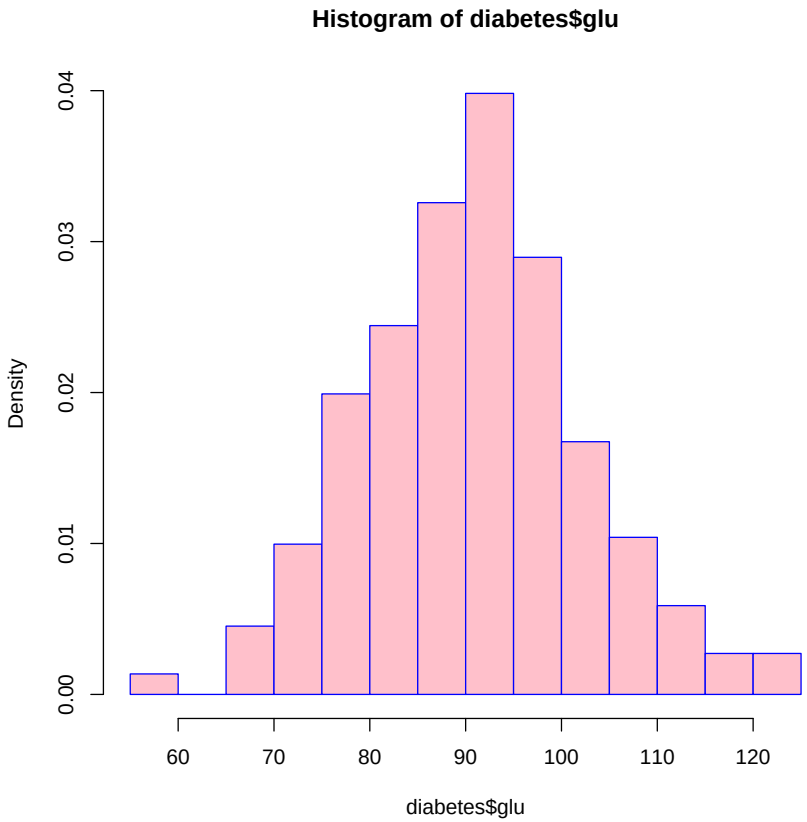
# Base R Graphics: Histograms

```
hist(diabetes$glu, breaks = 50)
```



# Base R Graphics: Histograms

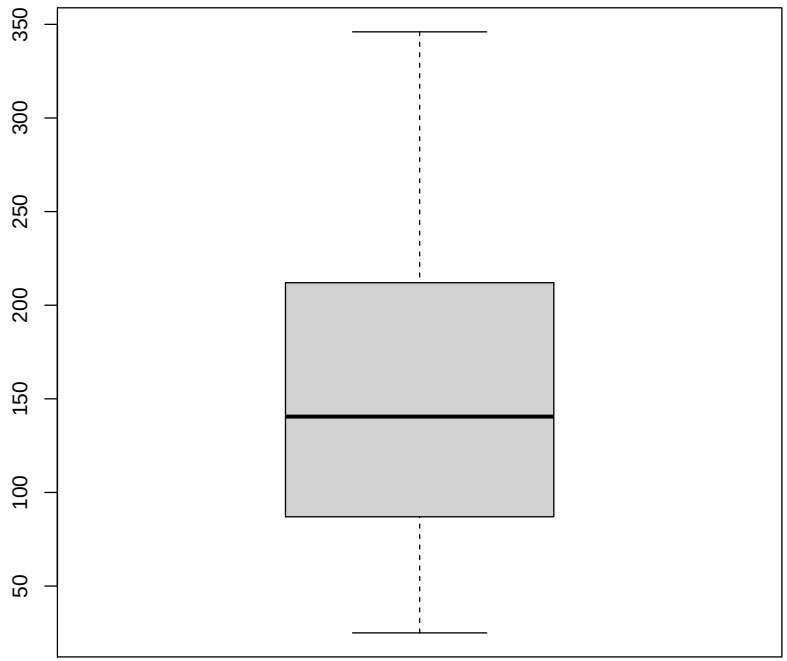
```
hist(diabetes$glu, col = "pink", border = "blue", probability = TRUE)
```



# Base R Graphics: Boxplots

We can create simple boxplots via the `boxplot()` function.

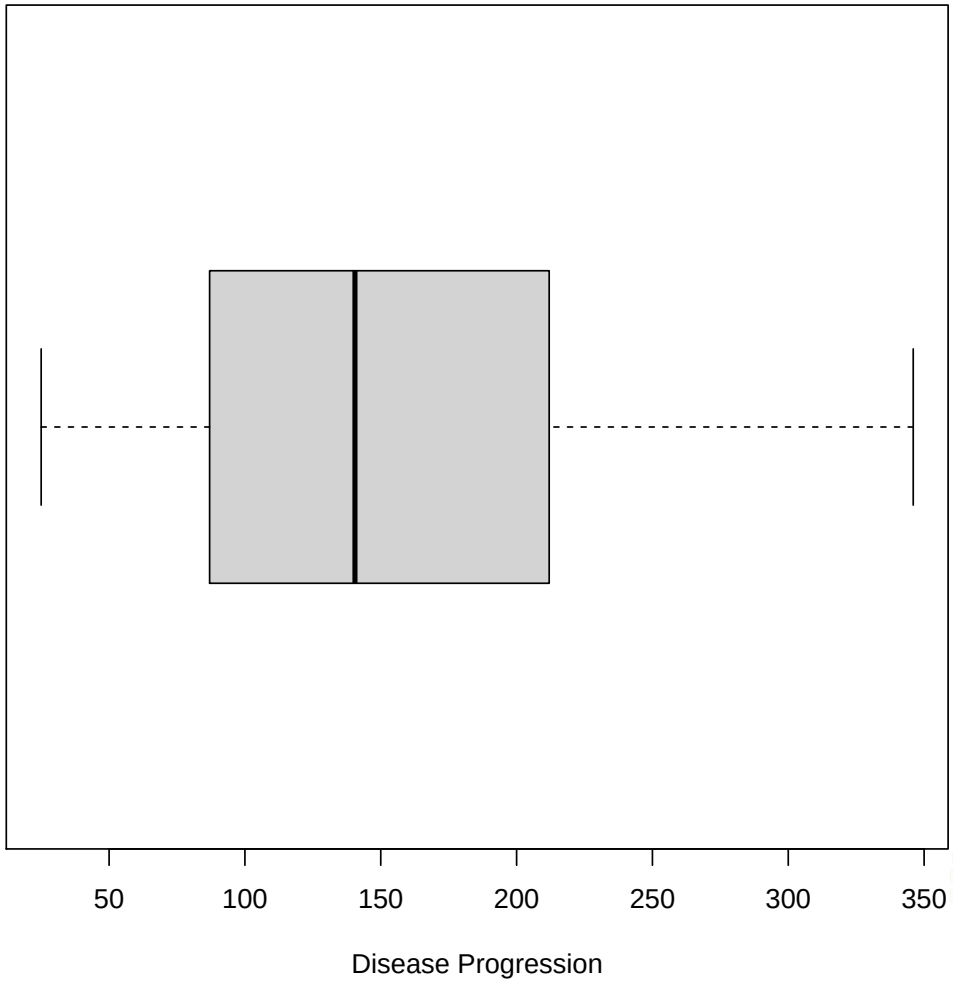
```
boxplot(diabetes$progress)
```



# Base R Graphics: Boxplots

```
boxplot(diabetes$progress,
        horizontal = TRUE,
        range = 3,
        xlab = "Disease Progression")
```

# Base R Graphics: Boxplots

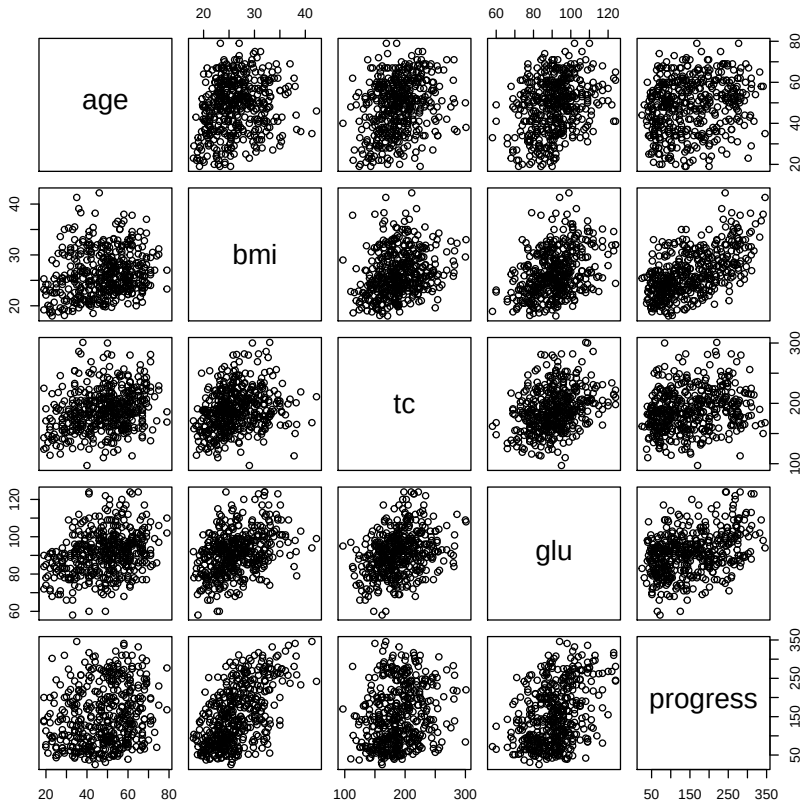



```
boxplot(prog
```

# Base R Graphics: Fancy Things

Plotting an entire data frame produces a scatterplot matrix.

```
diabetes %>% select(age, bmi, tc, glu, progress) %>% plot()
```

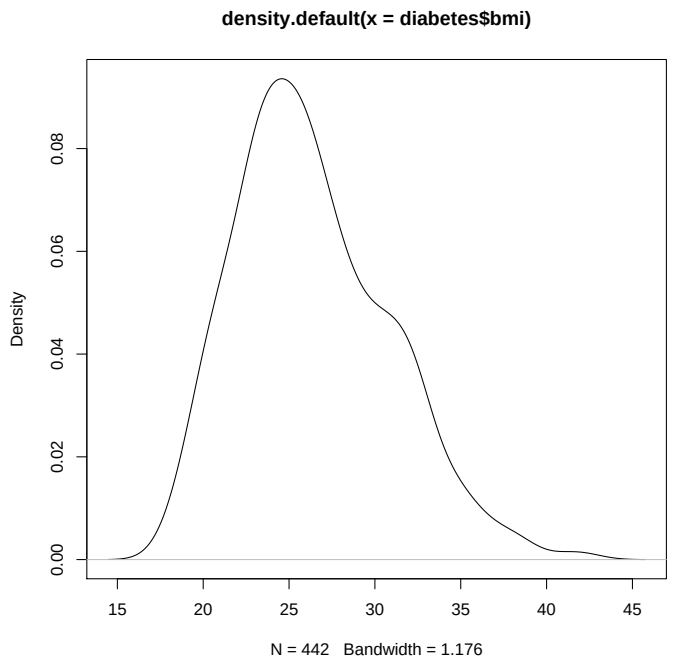


# Base R Graphics: Fancy Things

The `density()` function estimates the density of a variable.

- If we plot a density object, we get a kernel density plot.

```
density(diabetes$bmi) %>% plot()
```

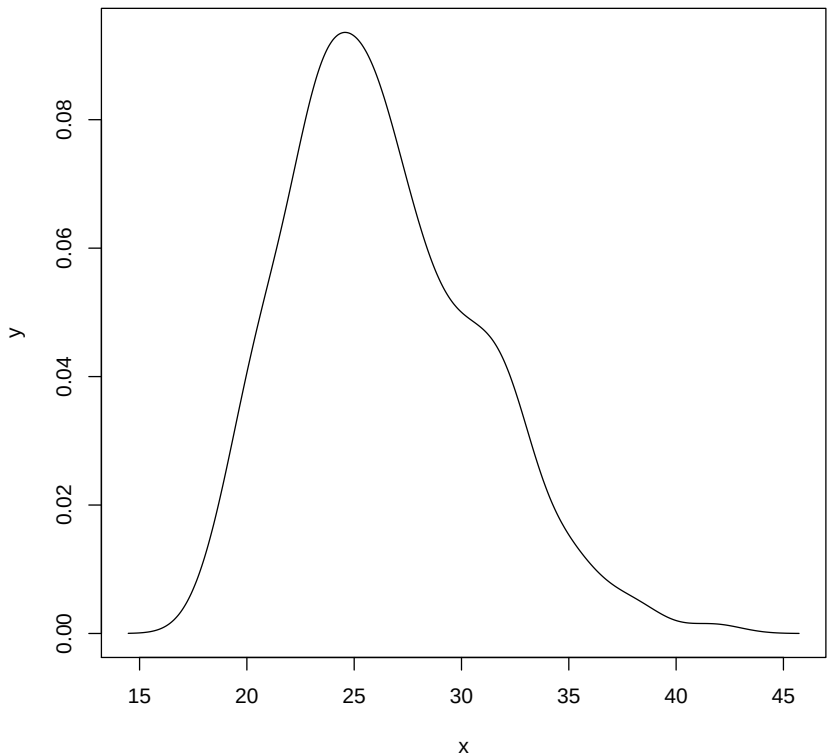


# Base R Graphics: Fancy Things

```
d <- density(diabetes$bmi)
ls(d)

[1] "bw"         "call"       "data.name" "has.na"
[5] "n"          "x"          "y"
```

# Base R Graphics: Fancy Things

```
d %$% plot(y = y, x = x, type = "l")
```

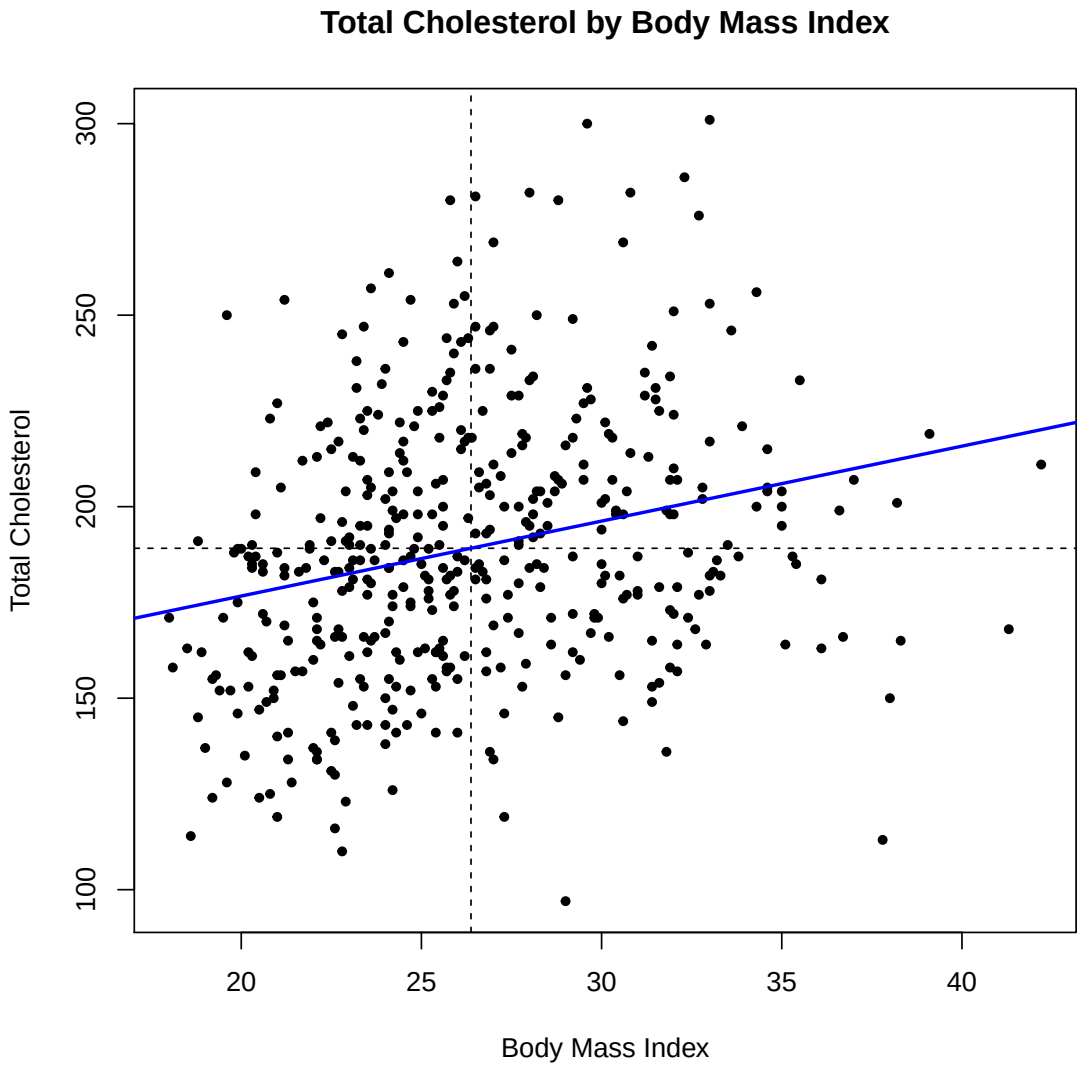


# Base R Graphics: Workflow

Base R graphics work by building up figures in layers.

```
## Start with a simple scatterplot:
diabetes %$% plot(y = tc, x = bmi, pch = 20, xlab = "", ylab = "")

## Use the abline() function to add lines representing the means of x and y:
abline(h = mean(diabetes$tc), v = mean(diabetes$bmi), lty = 2)

## Add the best fit line from a linear regression of 'tc' onto 'bmi':
diabetes %$%
    lm(tc ~ bmi) %>%
    coef() %>%
    abline(coef = ., col = "blue", lwd = 2)

## Add titles:
title(main = "Total Cholesterol by Body Mass Index",
      ylab = "Total Cholesterol",
      xlab = "Body Mass Index")
```

# Base R Graphics: Workflow

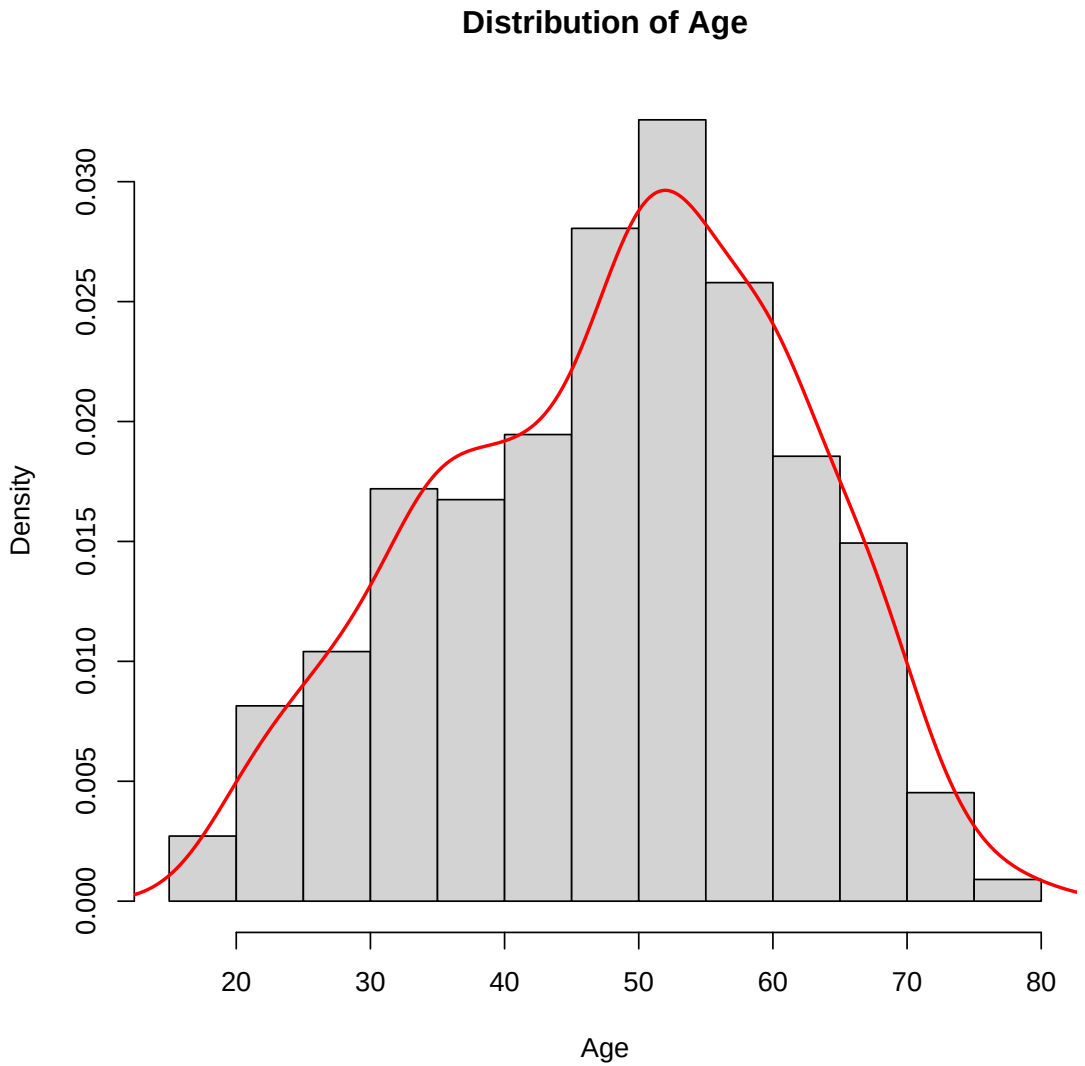


# Base R Graphics: Workflow

Add a kernel density plot on top of a histogram.

```
diabetes %$%
    hist(age,
         probability = TRUE,
         xlab = "Age",
         main = "Distribution of Age")

diabetes %$%
    density(age) %>%
    lines(col = "red", lwd = 2)
```

# Base R Graphics: Workflow



# GGPlot

Base R graphics are fine for quick-and-dirty visualizations (e.g., EDA, checking assumptions), but for publication quality graphics, you should probably use GGPlot.

- GGPlot uses the ”grammar of graphics” and ”tidy data” to build up a figure from modular components.

# GGPlot: Basic Setup

We start by calling the `ggplot()` function.

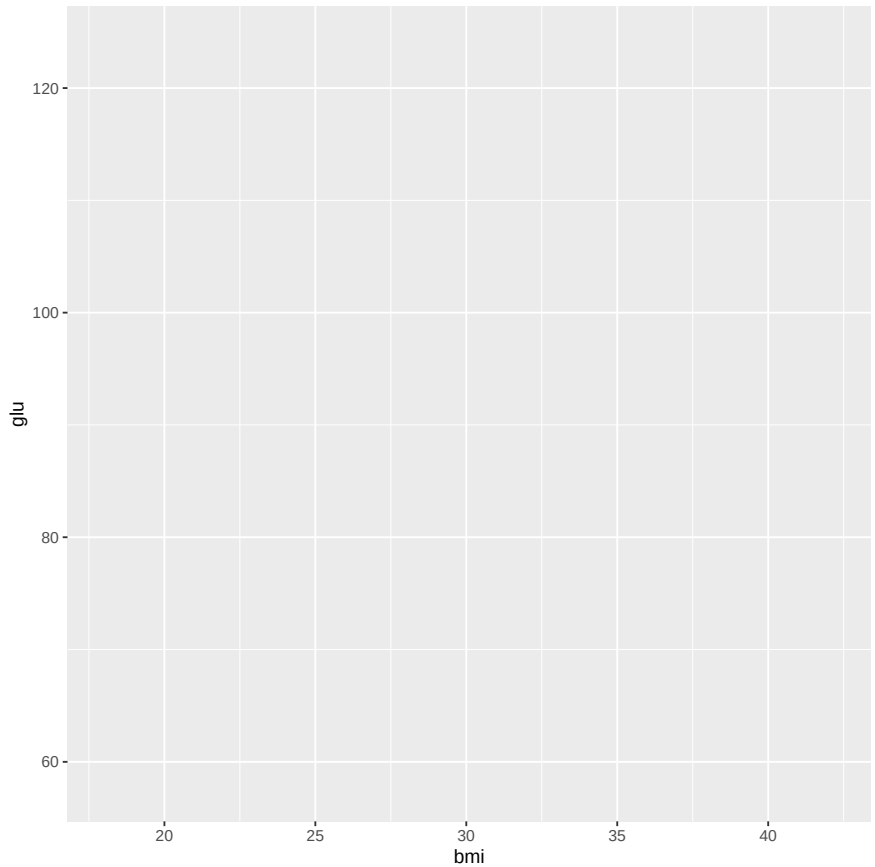
- We must define a data source.
- We must also give some aesthetic via the `aes()` function.

```
library(ggplot2)
p1 <- ggplot(data = diabetes, mapping = aes(x = bmi, y = glu))
```

# GGPlot: Basic Setup

At this point, our plot is pretty boring.

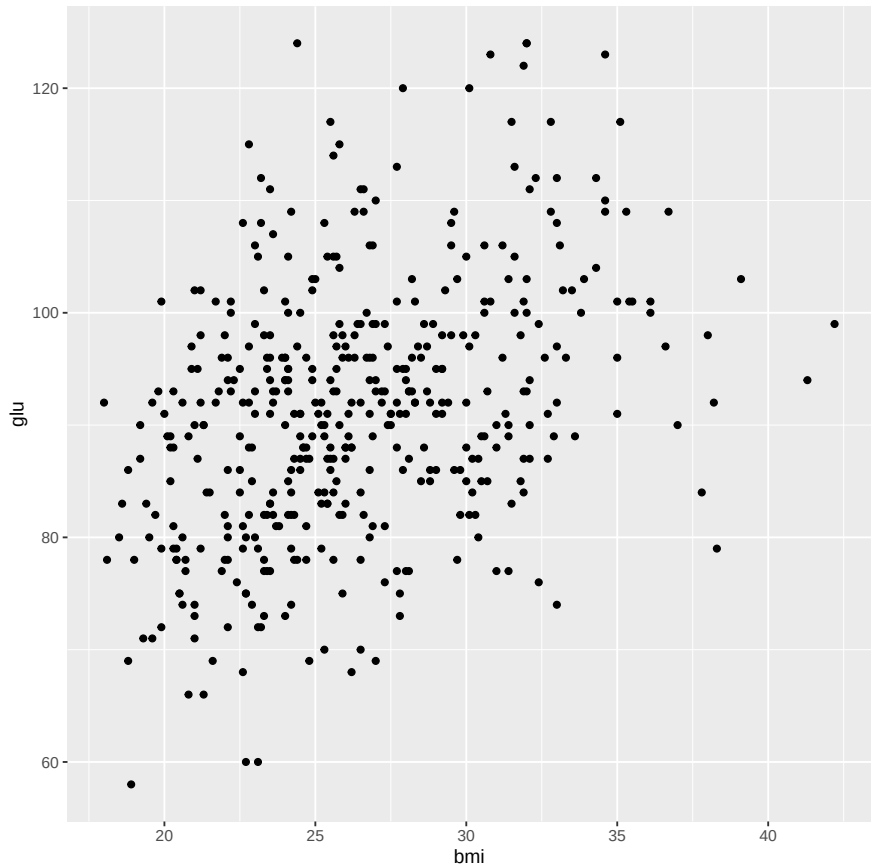
```
p1
```



# GGPlot: Geometries

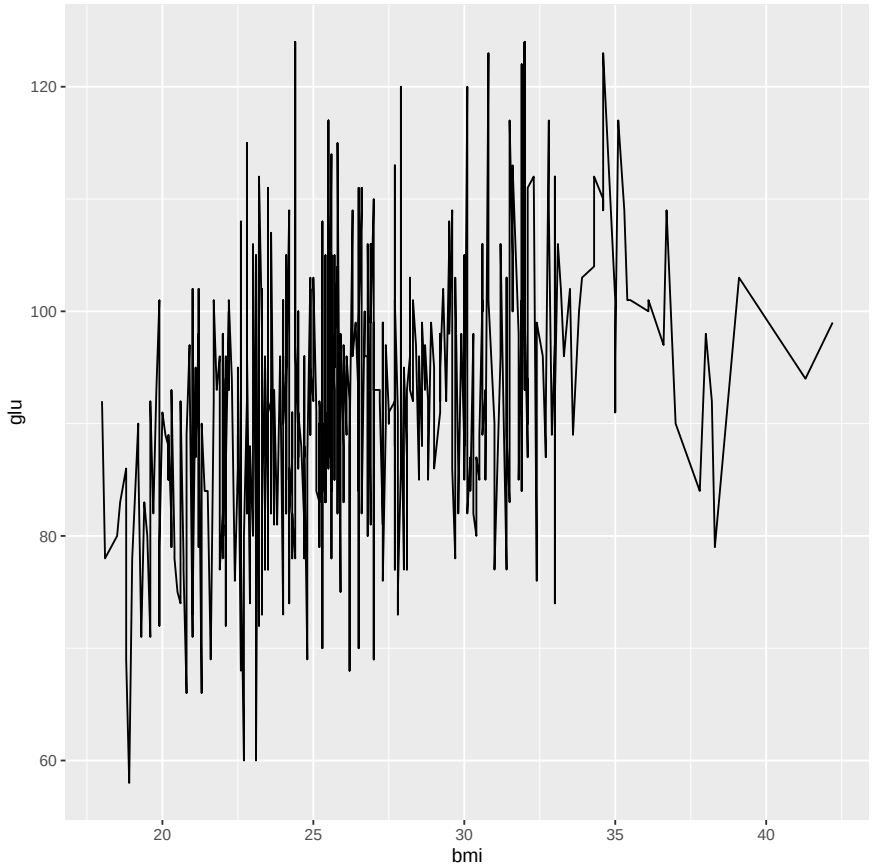
We need to define some geometry via a `geom_XXX()` function.

```
p1 + geom_point()
```



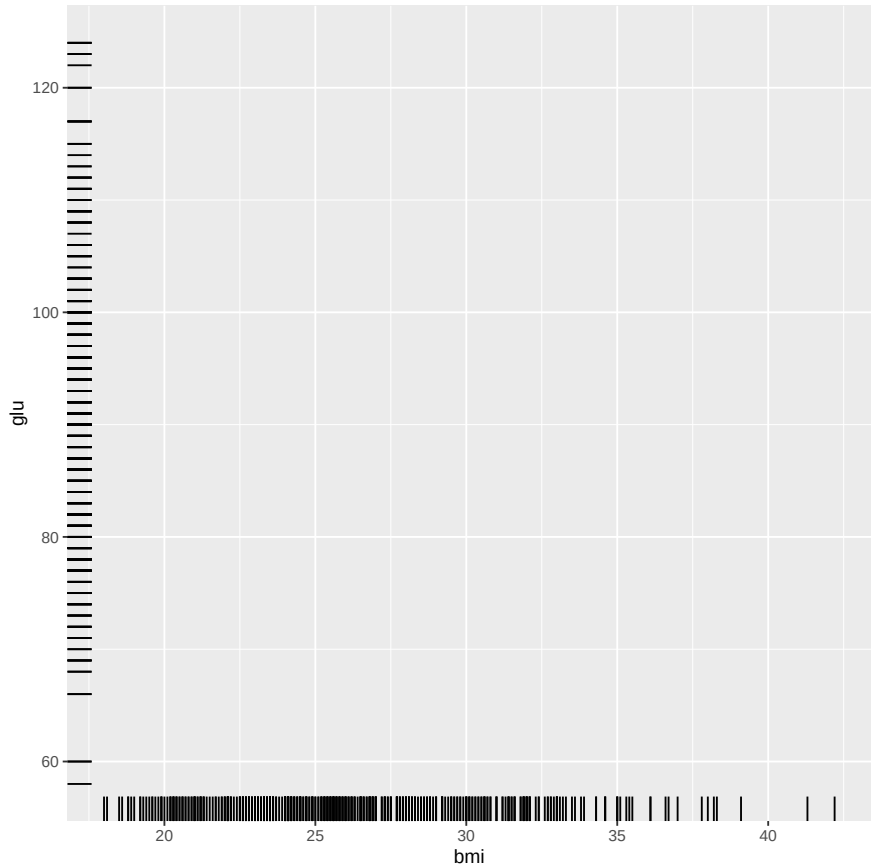
# GGPlot: Geometries

```
p1 + geom_line()
```



# GGPlot: Geometries

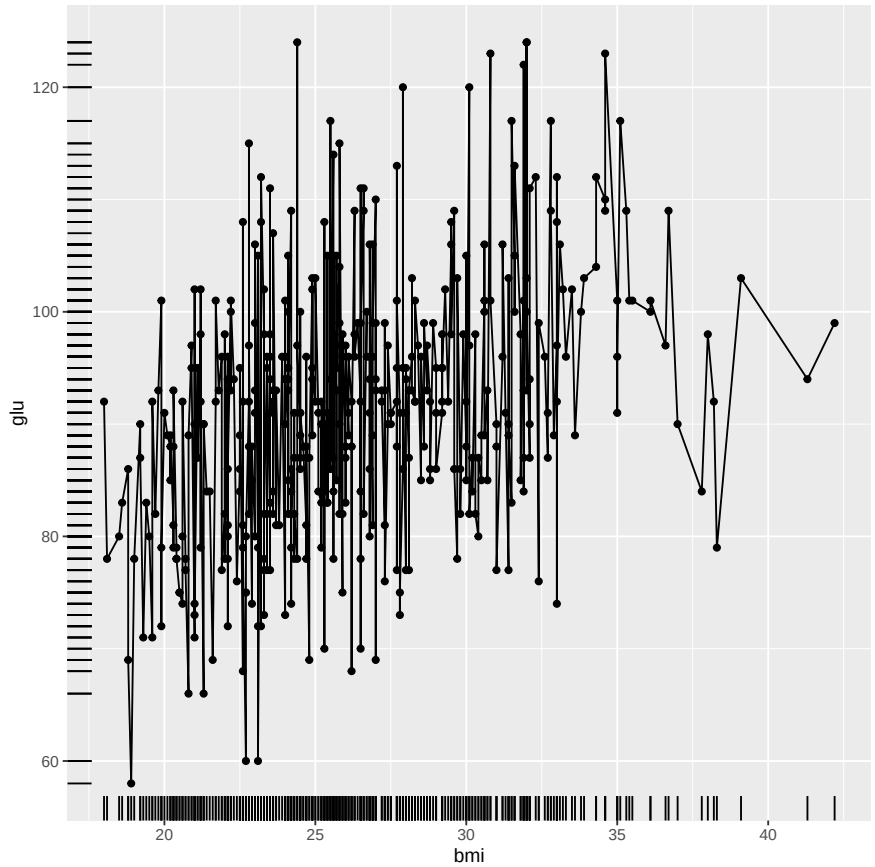
```
p1 + geom_rug()
```



# GGPlot: Geometries

We can also combine different geometries into a single figure

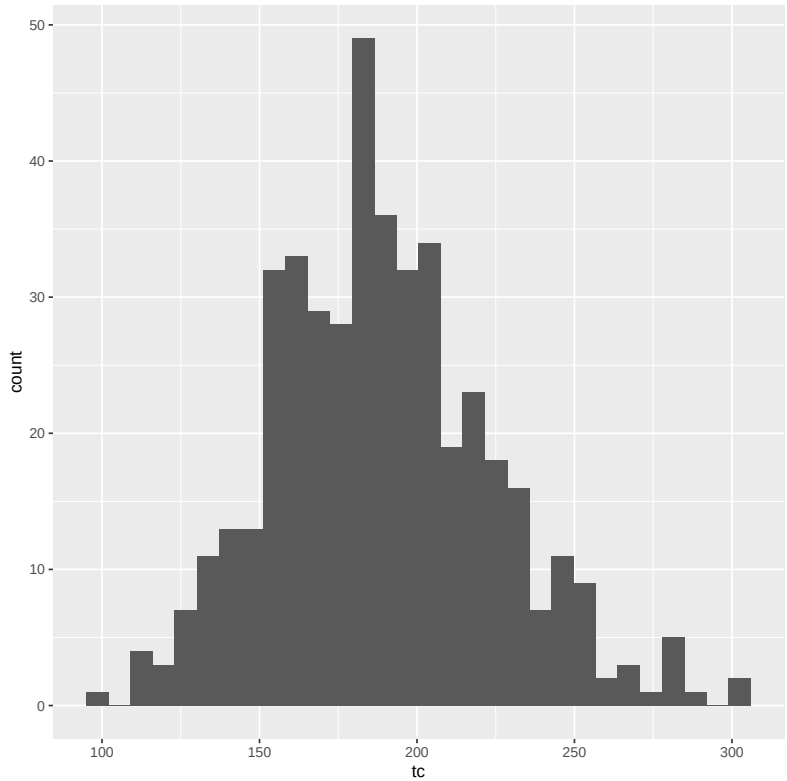
```
p1 + geom_point() + geom_line() + geom_rug()
```



# GGPlot: Geometries

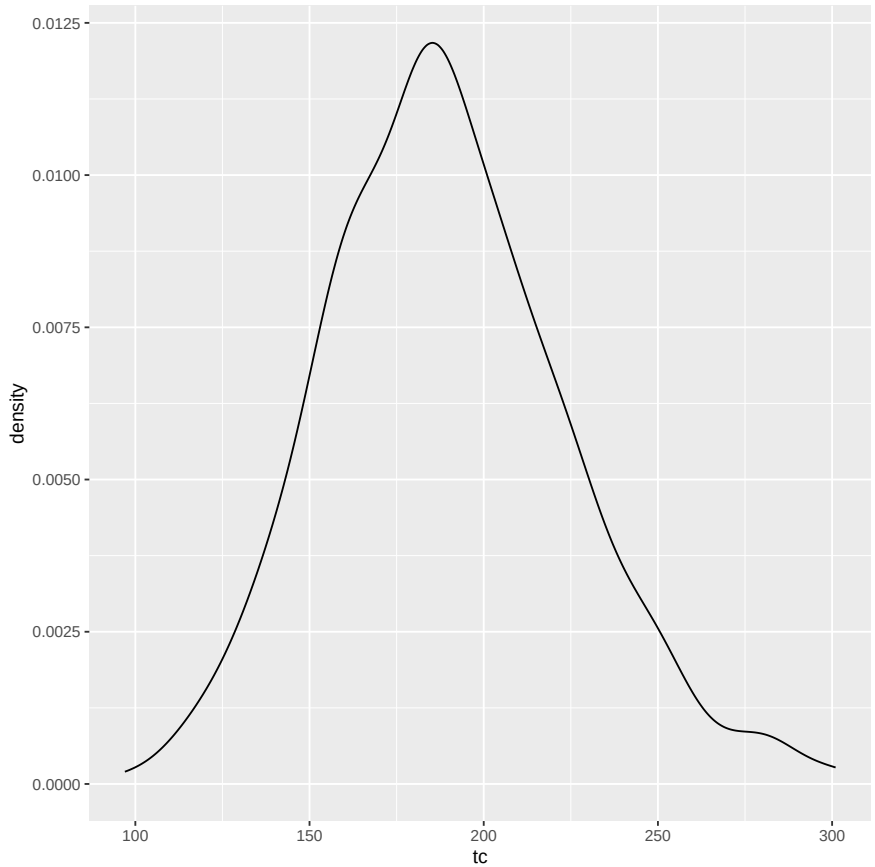
We can use different flavors of geometry for different types of data.

```
p2 <- ggplot(diabetes, aes(tc))
p2 + geom_histogram()
```



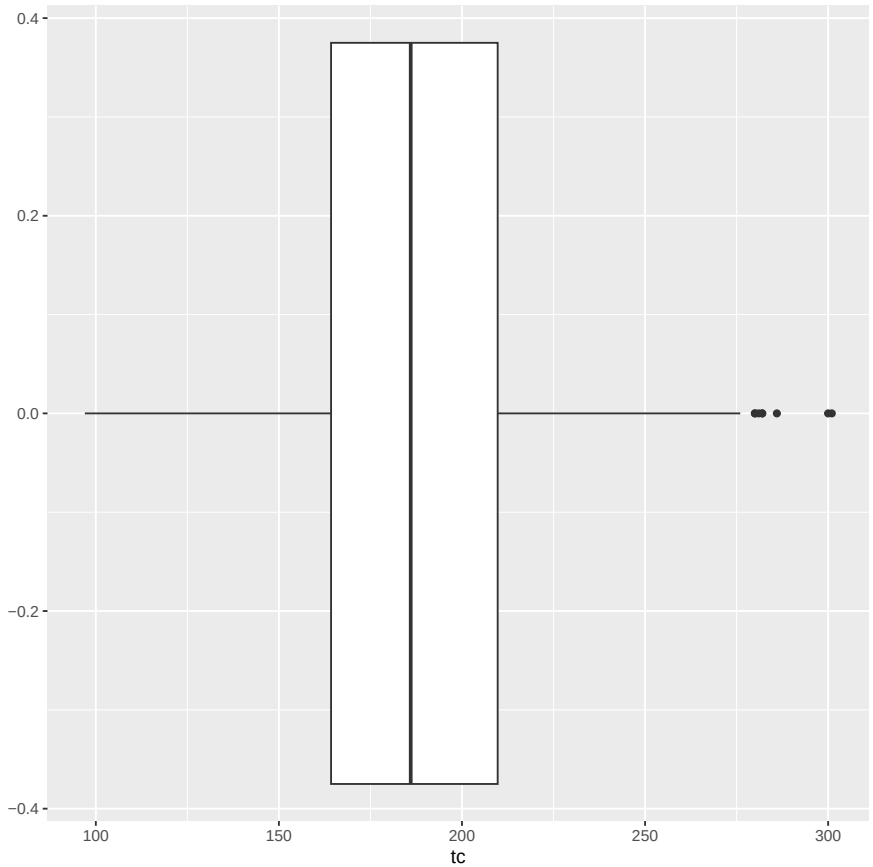
# GGPlot: Geometries

```
p2 + geom_density()
```



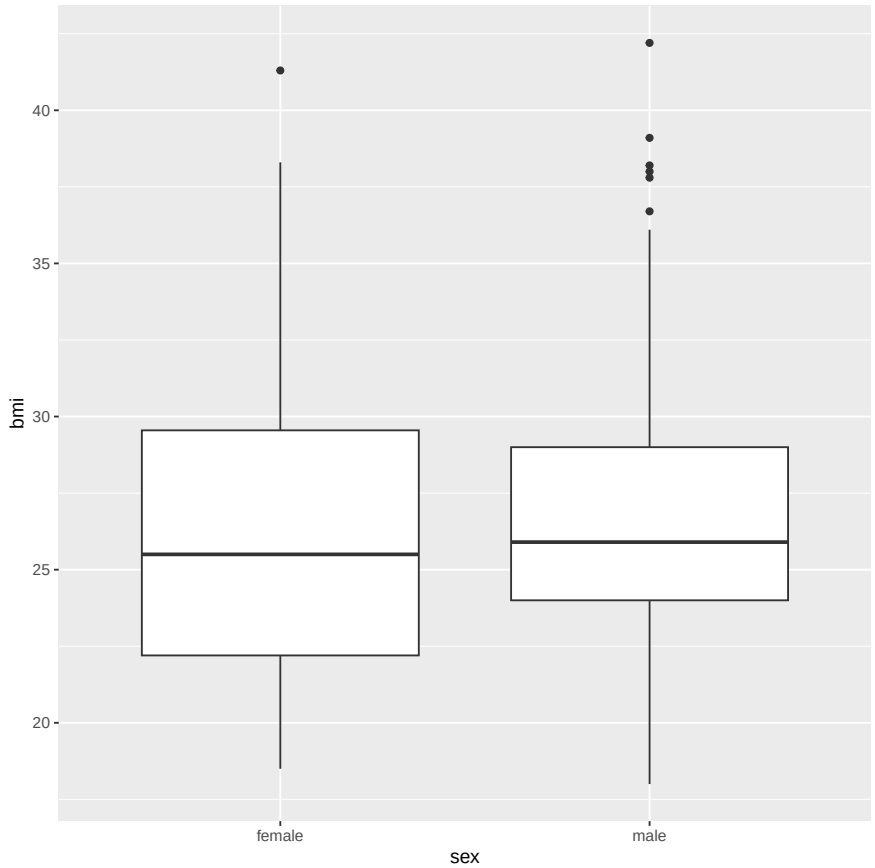
# GGPlot: Geometries

```
p2 + geom_boxplot()
```



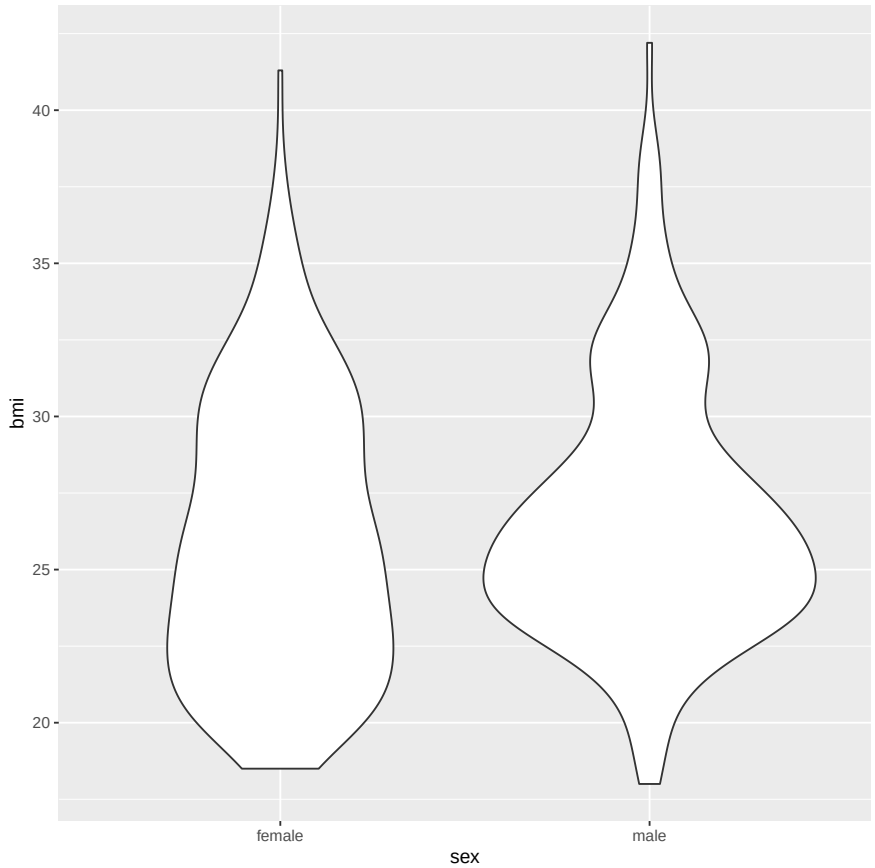
# GGPlot: Geometries

```
p3 <- ggplot(diabetes, aes(sex, bmi))
p3 + geom_boxplot()
```



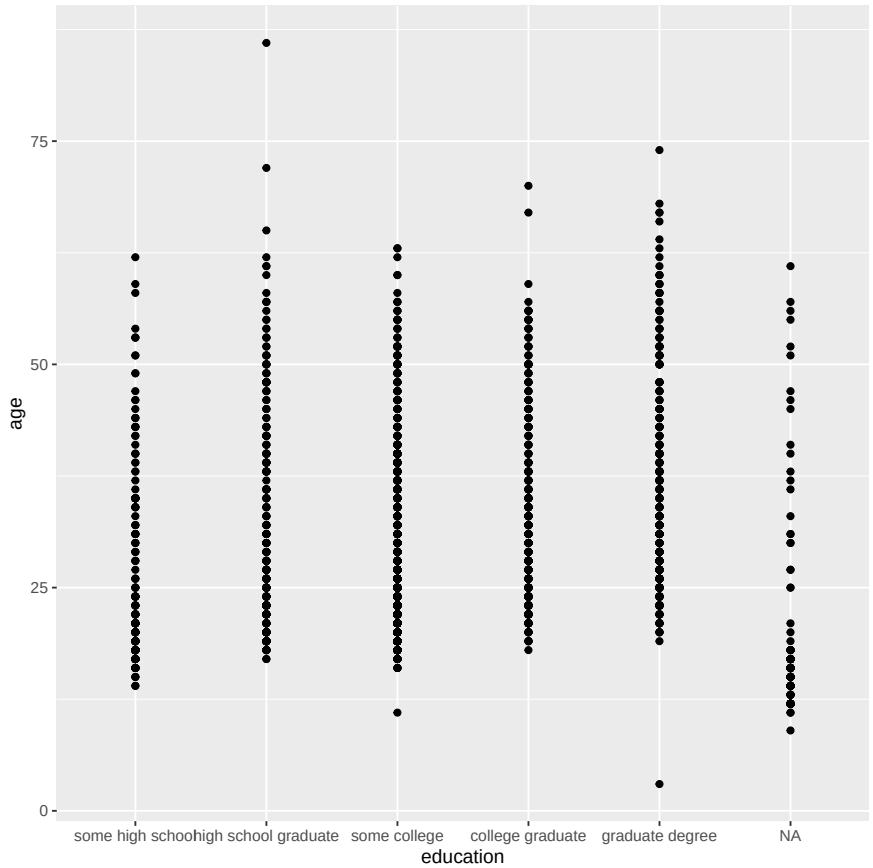
# GGPlot: Geometries

```
p3 + geom_violin()
```



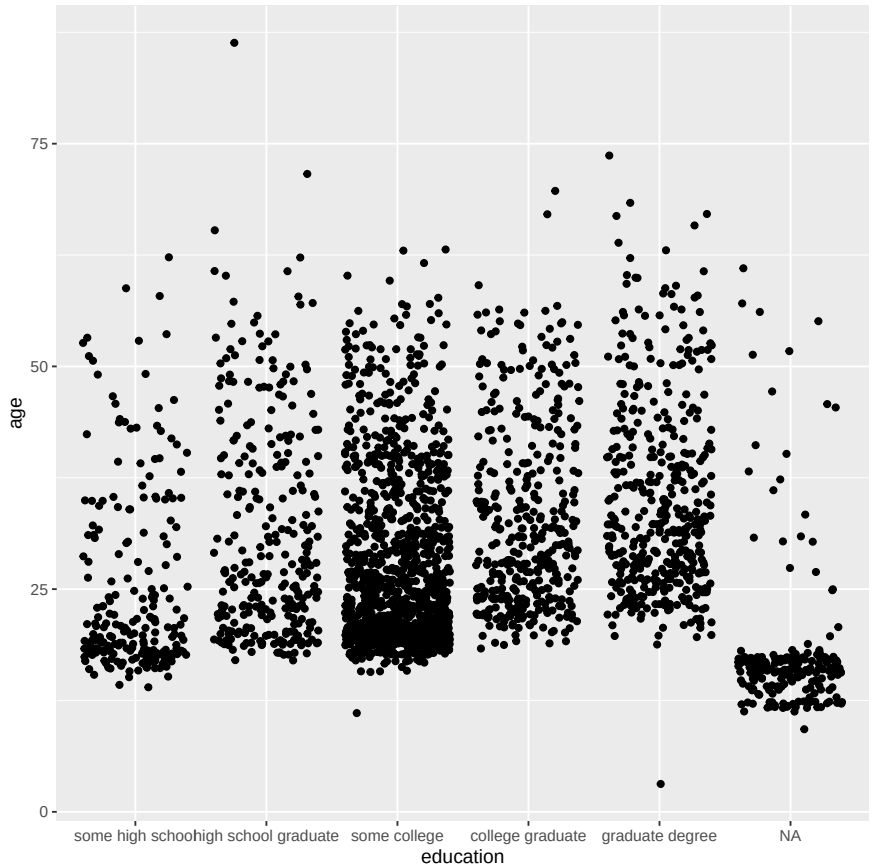
# GGPlot: Geometries

```
p4 <- ggplot(bfi, aes(education, age))
p4 + geom_point()
```



# GGPlot: Geometries

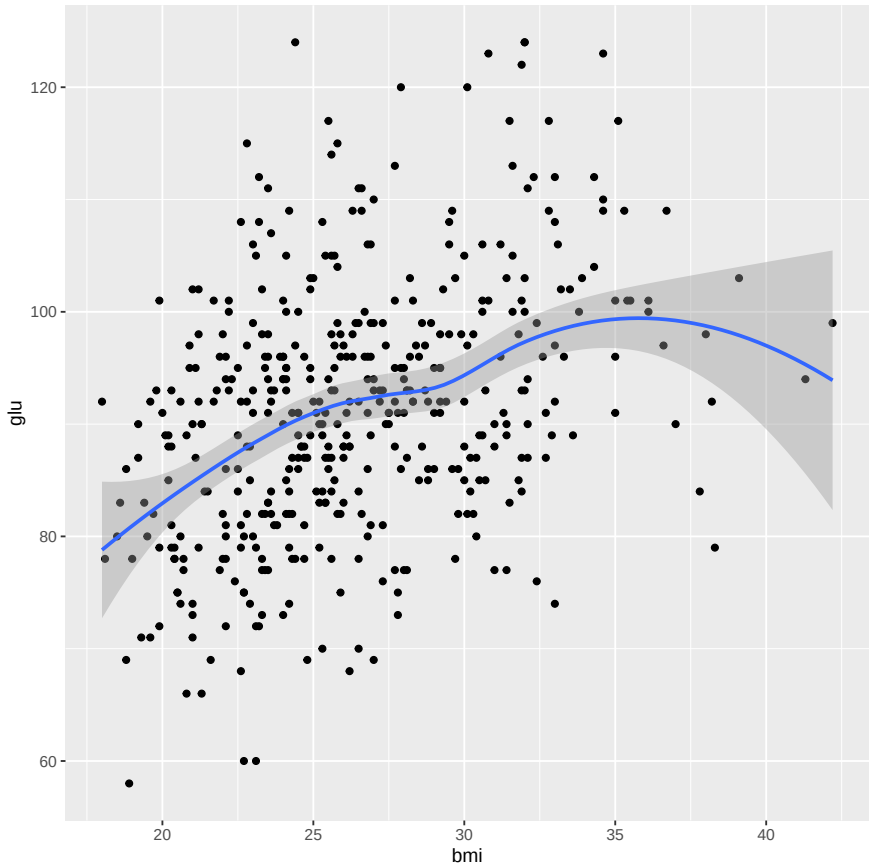
```
p4 + geom_jitter()
```



# GGPlot: Statistics

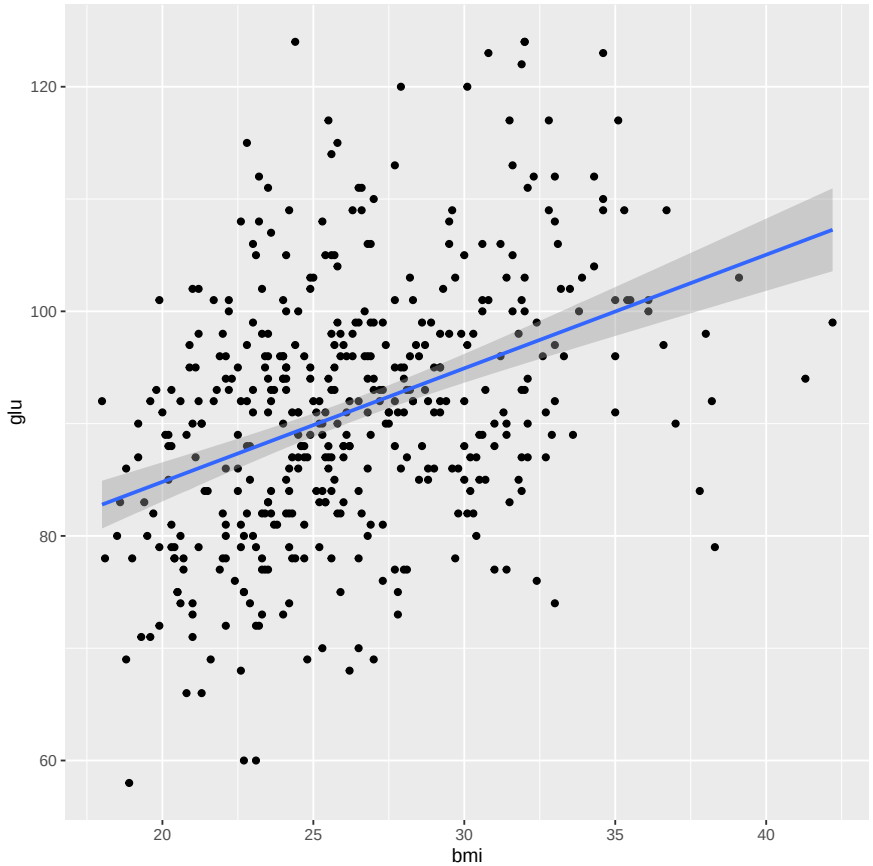
We can also add statistical summaries of the data.

```
p1 + geom_point() + geom_smooth()
```



# GGPlot: Statistics

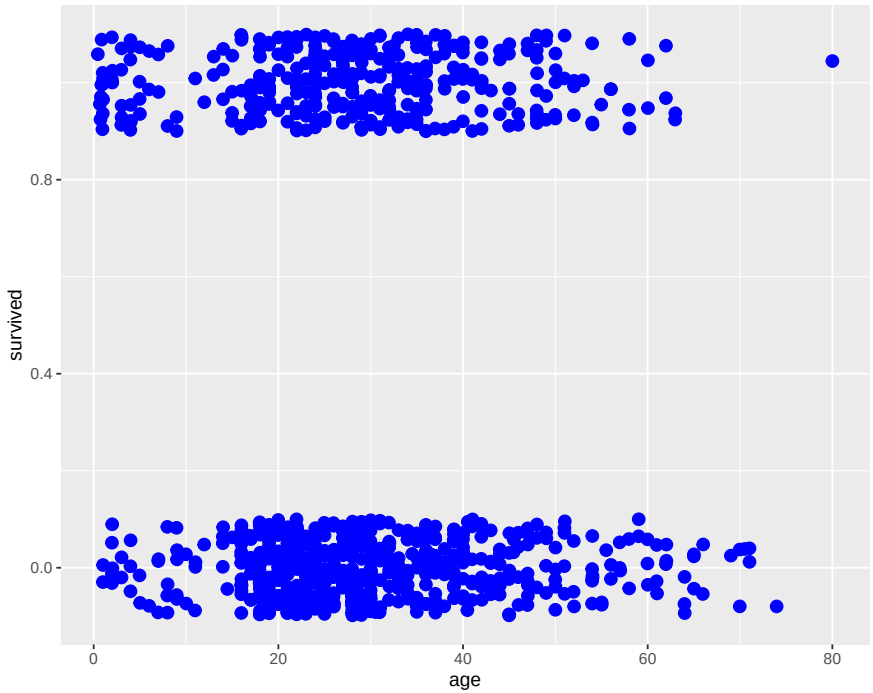
```
p1 + geom_point() + geom_smooth(method = "lm")
```



# GGPlot: Styling

Changing style options outside of the `aes()` function applies the styling to the entire plot.

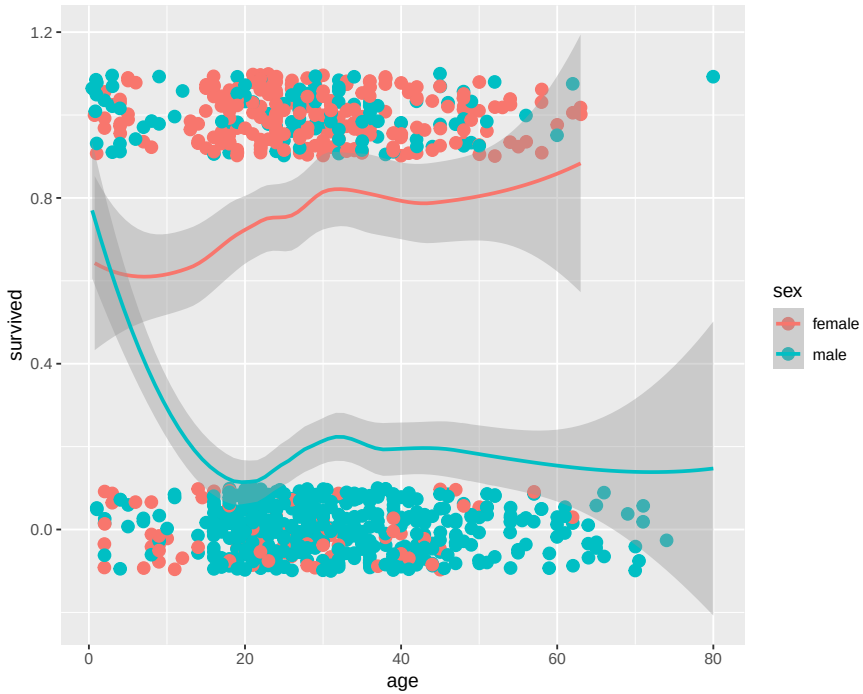
```
p5 <- ggplot(titanic, aes(age, survived))
p5 + geom_jitter(color = "blue", size = 3, height = 0.1)
```



# GGPlot: Styling

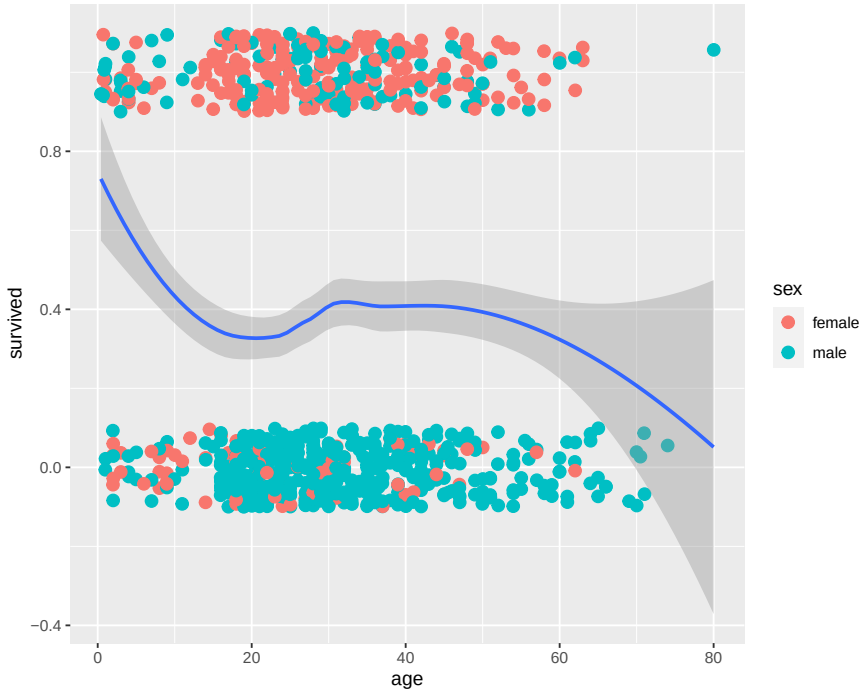
We can also apply styles as a function of variables by defining the style within the `aes()` function.

```
p6.1 <- ggplot(titanic, aes(age, survived, color = sex))
p6.1 + geom_jitter(size = 3, height = 0.1) + geom_smooth()
```



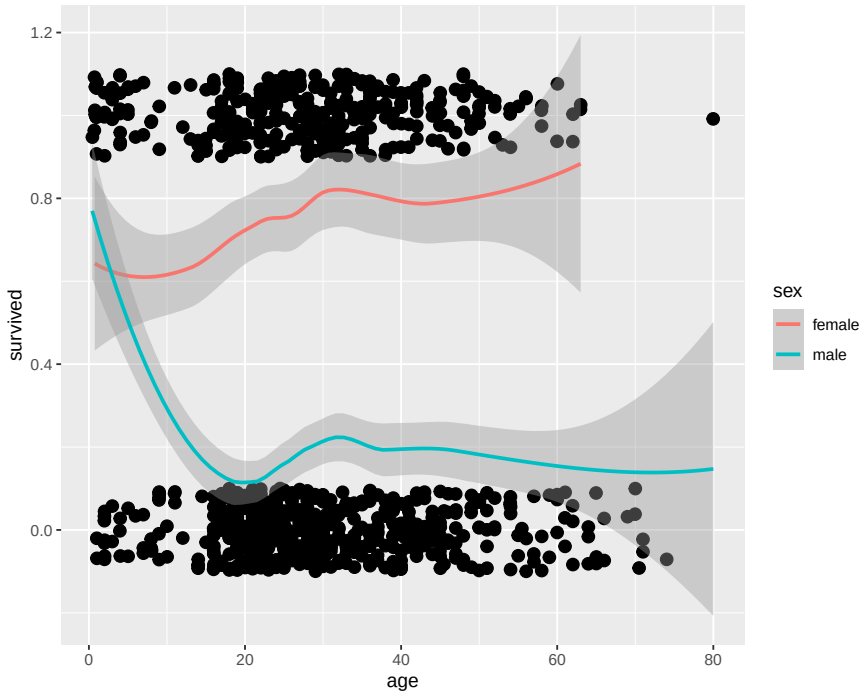
# GGPlot: Styling

```
p6.2 <- ggplot(titanic, aes(age, survived))
p6.2 + geom_jitter(aes(color = sex), size = 3, height = 0.1) +
    geom_smooth()
```



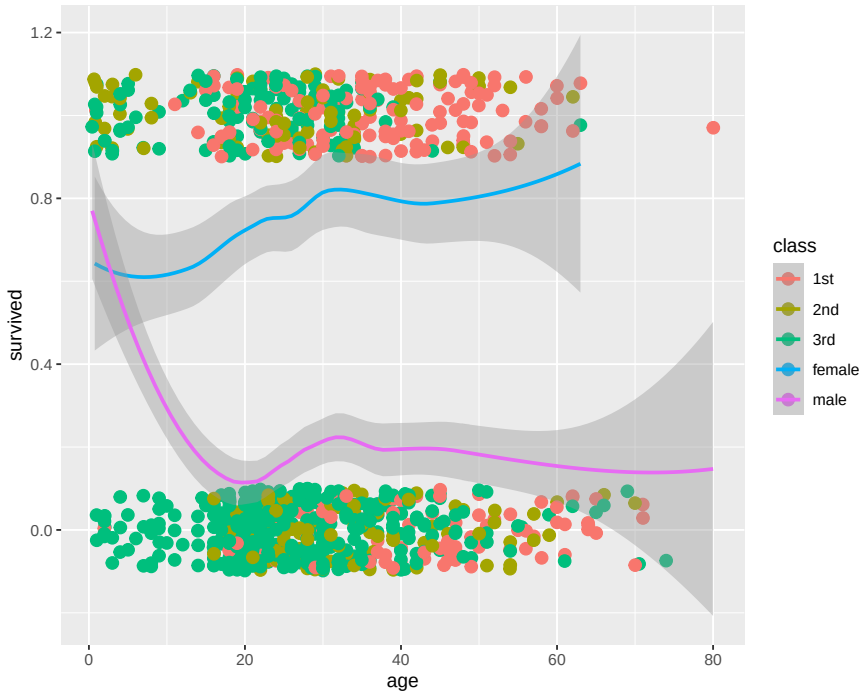
# GGPlot: Styling

```
p6.2 + geom_jitter(size = 3, height = 0.1) +
    geom_smooth(aes(color = sex))
```



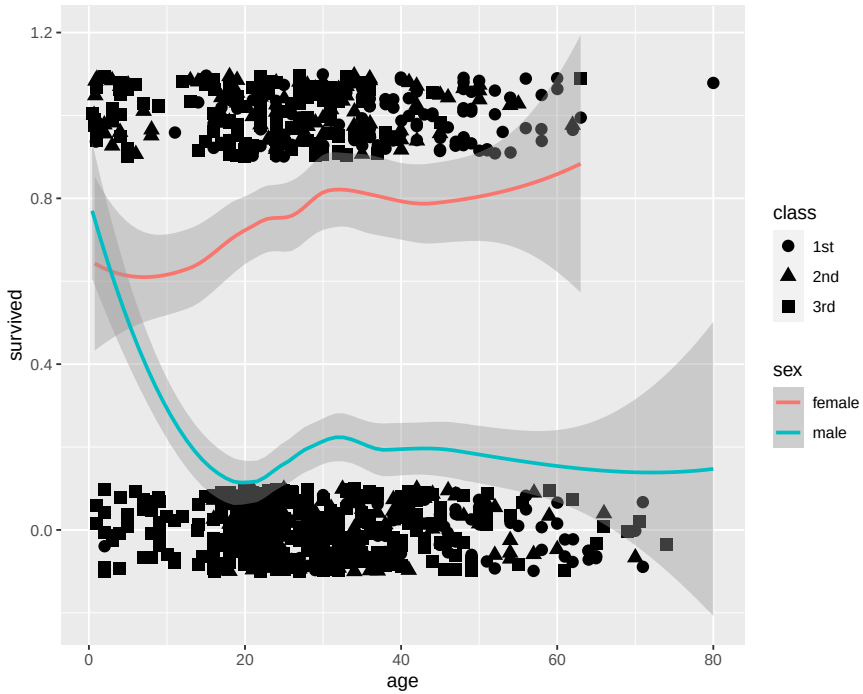
# GGPlot: Styling

```
p6.2 + geom_jitter(aes(color = class), size = 3, height = 0.1) +
    geom_smooth(aes(color = sex))
```



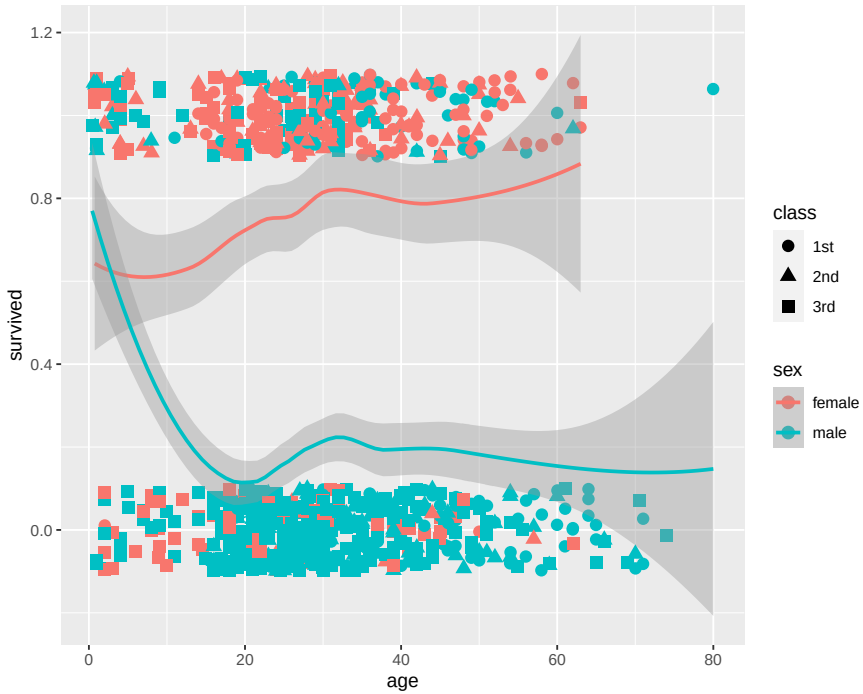
# GGPlot: Styling

```
p6.2 + geom_jitter(aes(shape = class), size = 3, height = 0.1) +
  geom_smooth(aes(color = sex))
```



# GGPlot: Styling

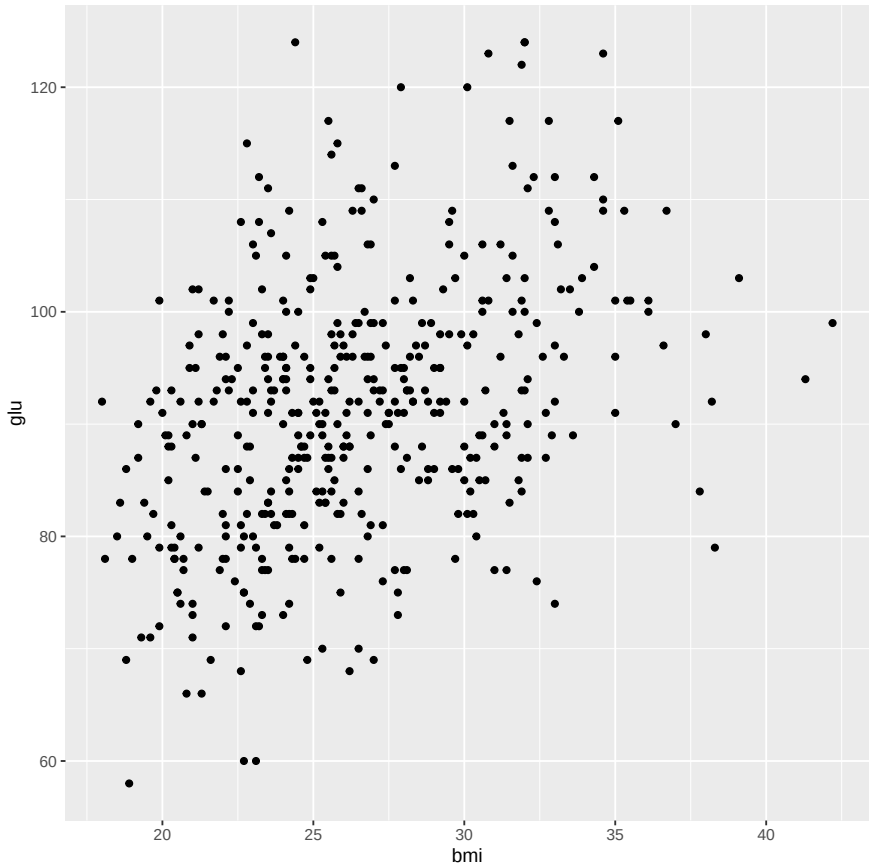
```
p6.1 + geom_jitter(aes(shape = class), size = 3, height = 0.1) +
  geom_smooth()
```



# GGPlot: Themes

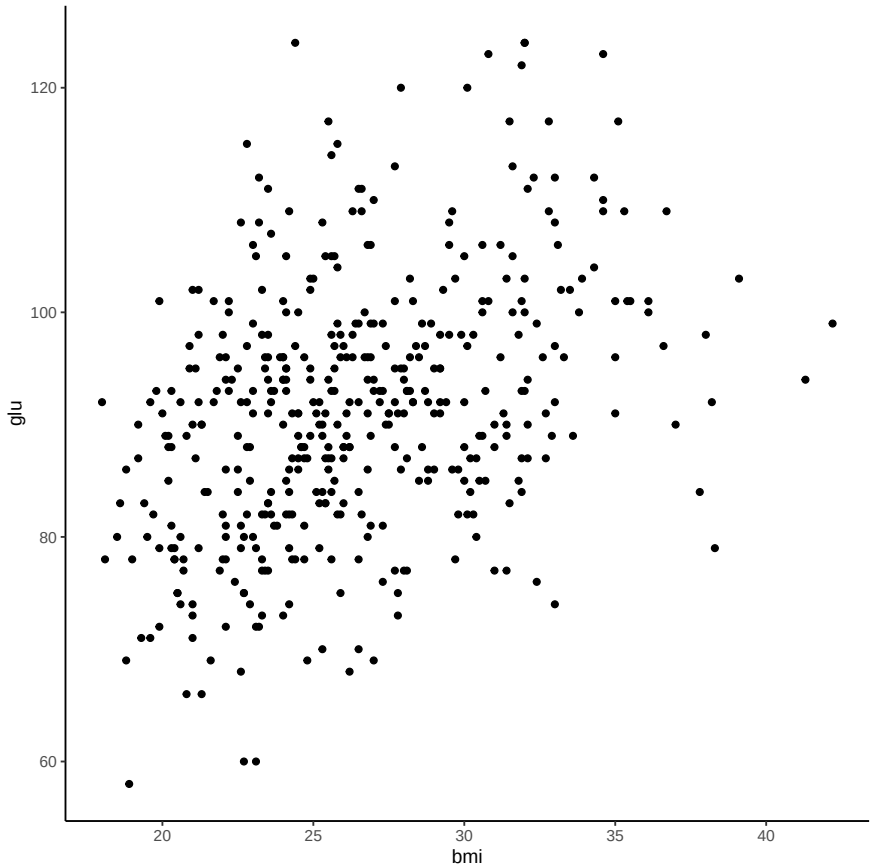
We can apply canned themes to adjust a plot's overall appearance.

```
(p1.1 <- p1 + geom_point())
```



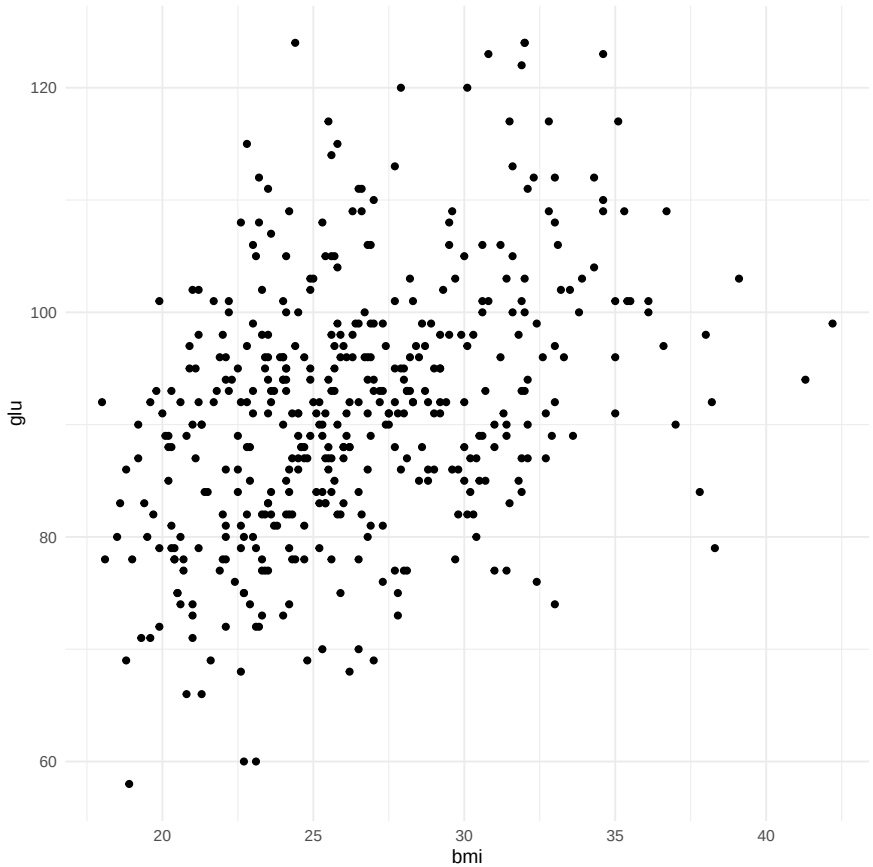
# GGPlot: Themes

```
p1.1 + theme_classic()
```



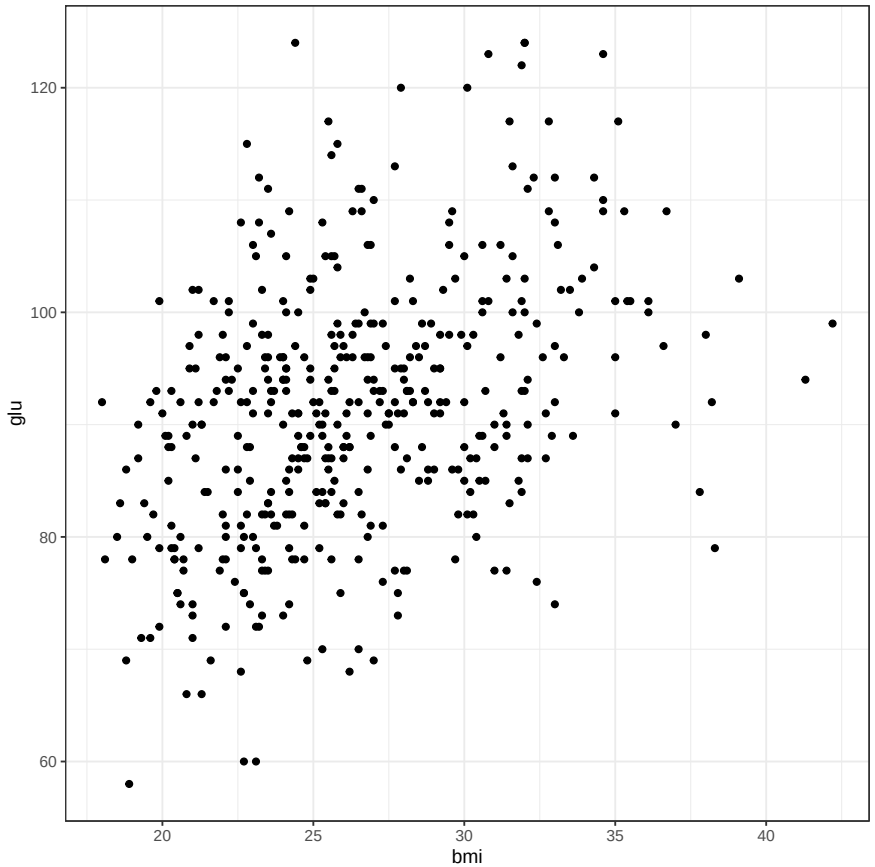
# GGPlot: Themes

```
p1.1 + theme_minimal()
```



# GGPlot: Themes

```
p1.1 + theme_bw()
```

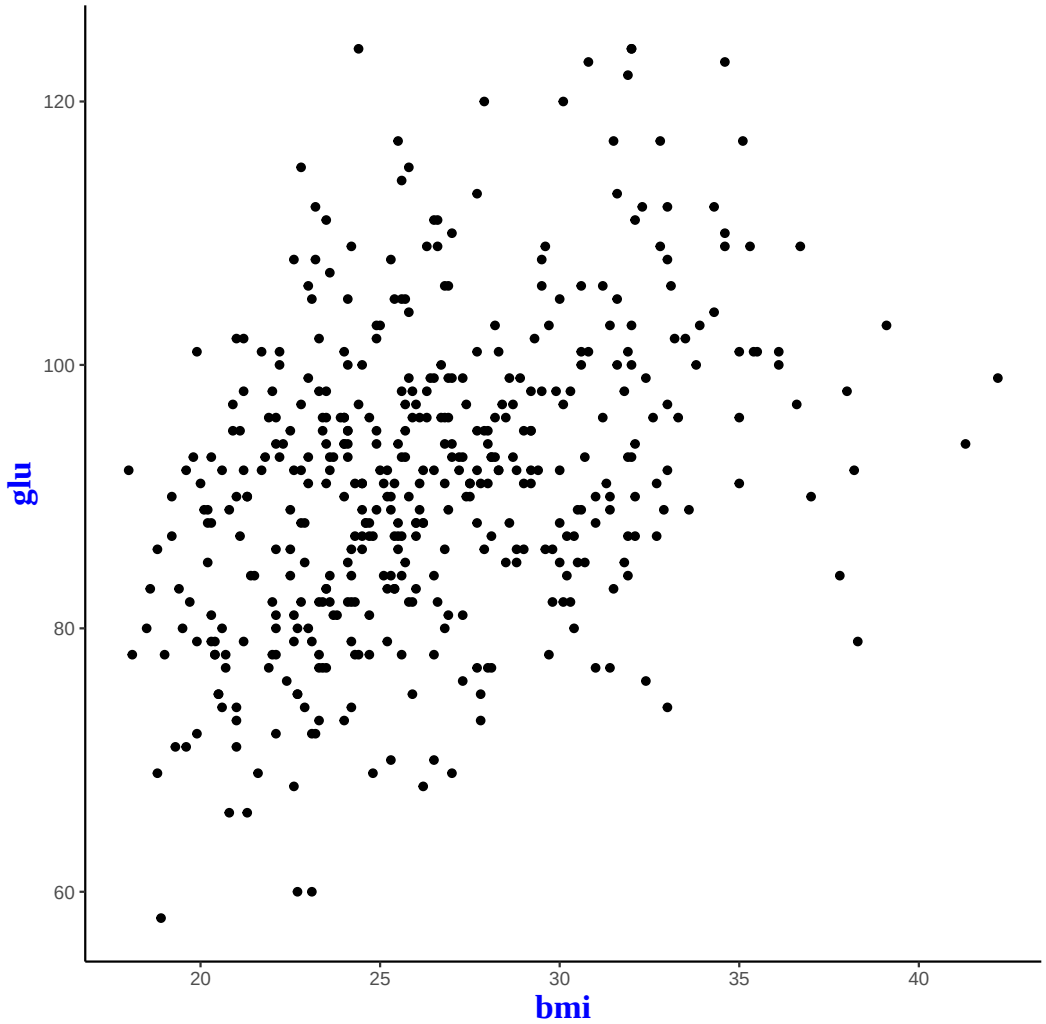


# GGPlot: Themes

We can also modify individual theme elements.

```
p1.1 + theme_classic() +
    theme(axis.title = element_text(size = 16,
                                    family = "serif",
                                    face = "bold",
                                    color = "blue"),
          aspect.ratio = 1)
```

# GGPlot: Themes

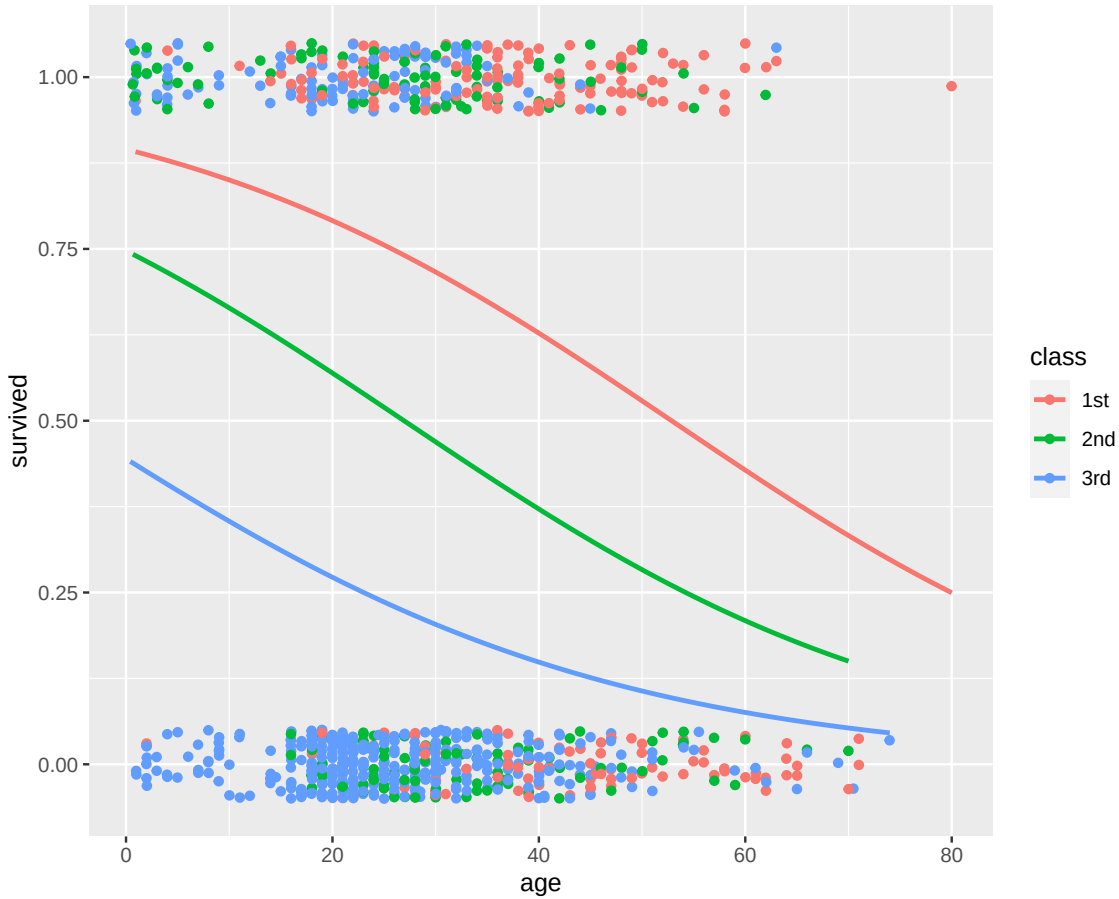


# GGPlot: Facets

Faceting allow us to make arrays of conditional plots.

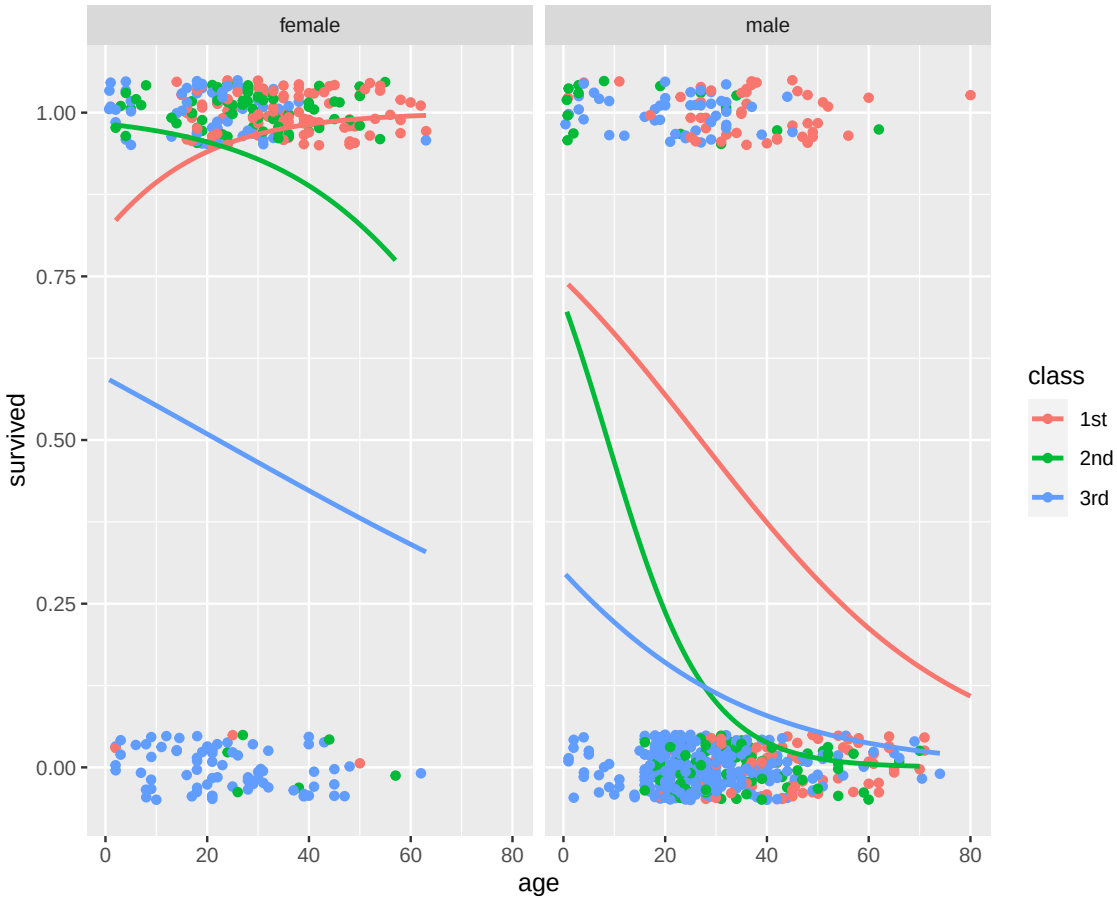
```
(p7 <- ggplot(titanic, aes(age, survived, color = class)) +
     geom_jitter(height = 0.05) +
     geom_smooth(method = "glm",
                 method.args = list(family = "binomial"),
                 se = FALSE)
)
```

# GGPlot: Facets



# GGPlot: Facets

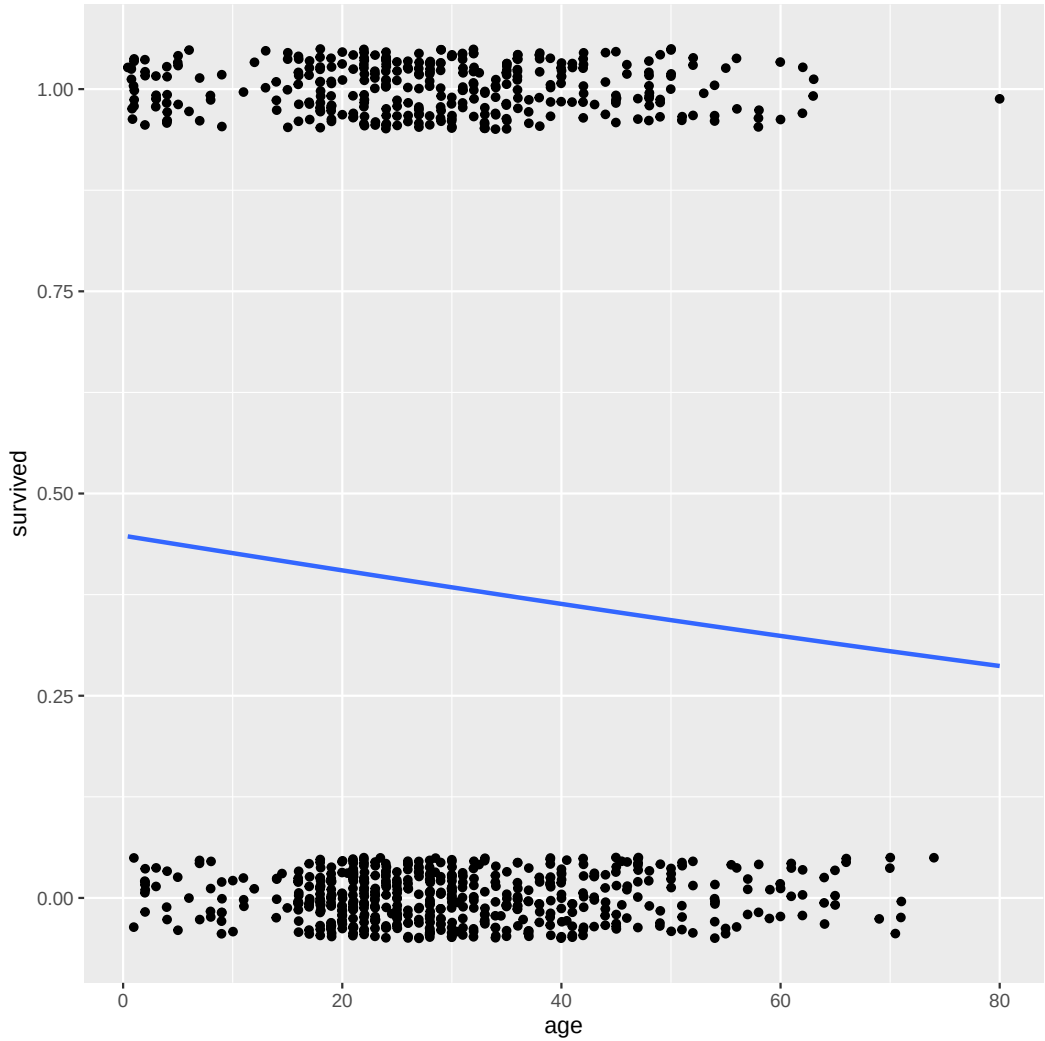
```
p7 + facet_wrap(vars(sex))
```



# GGPlot: Facets

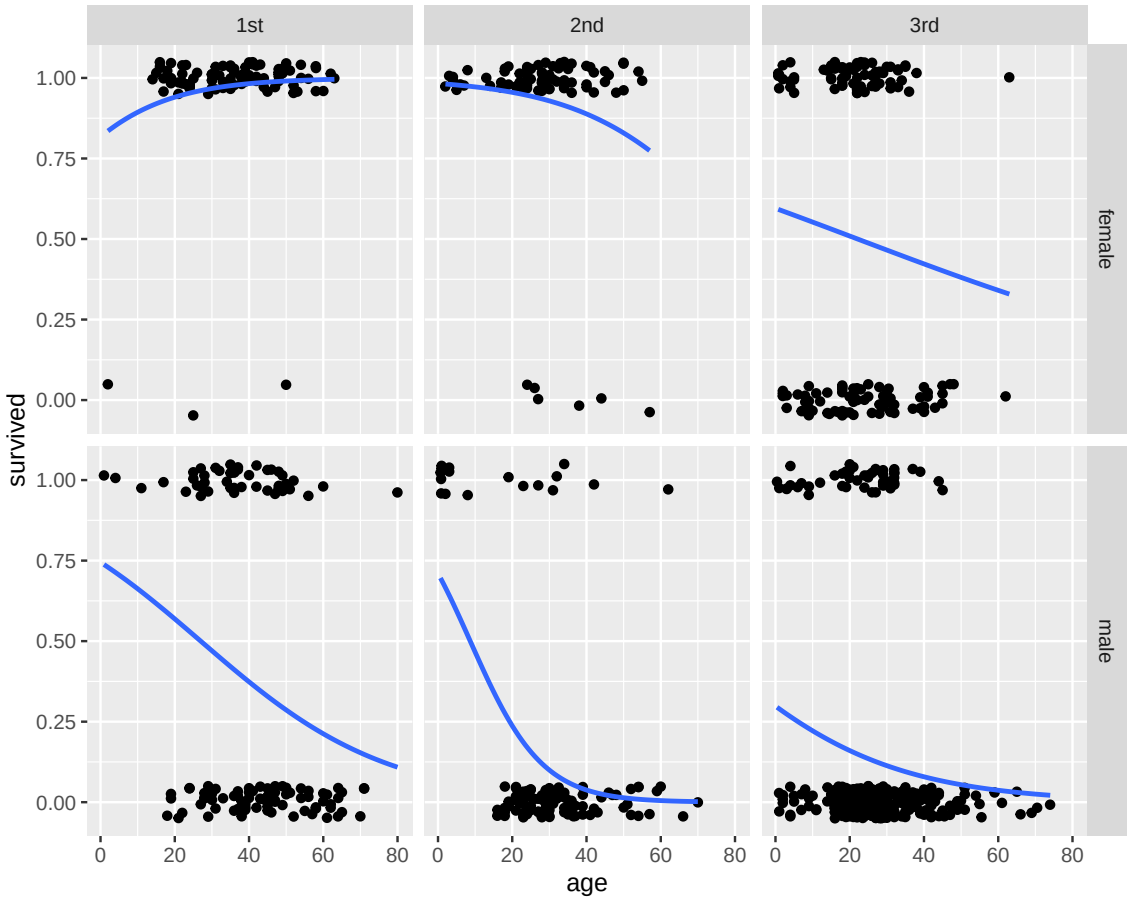
```
(p8 <- ggplot(titanic, aes(age, survived)) +
     geom_jitter(height = 0.05) +
     geom_smooth(method = "glm",
                 method.args = list(family = "binomial"),
                 se = FALSE)
)
```

# GGPlot: Facets



# GGPlot: Facets

```
p8 + facet_grid(vars(sex), vars(class))
```

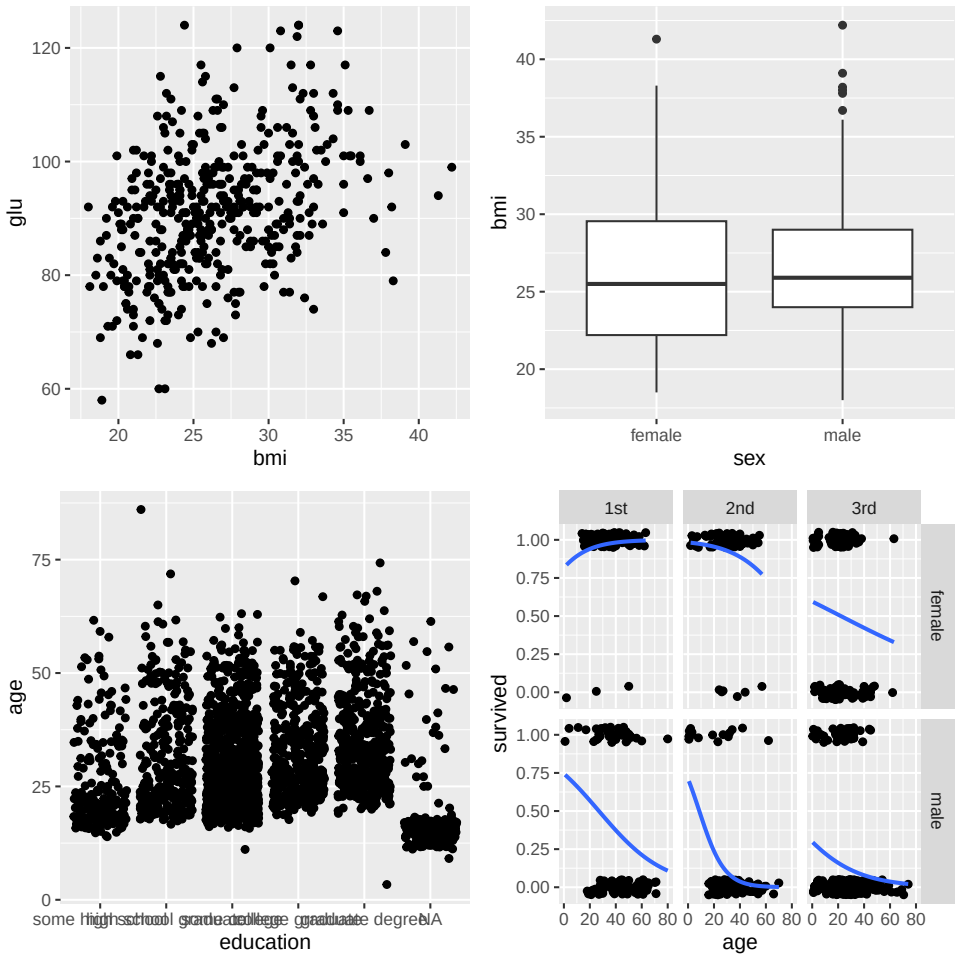


# GGPlot: Joining Multiple Figures

If we want to paste several different plots into a single figure (without faceting), we can use the utilities in the **gridExtra** package.

```
library(gridExtra)

grid.arrange(p1 + geom_point(),
             p3 + geom_boxplot(),
             p4 + geom_jitter(),
             p8 + facet_grid(vars(sex), vars(class)),
             ncol = 2)
```

# GGPlot: Joining Multiple Figures



# Saving Graphics

To save a graphic that we've created in R, we simply redirect the graphical output to a file using an appropriate function.

```
figDir <- "figures/"

## Save as PDF
pdf(paste0(figDir, "example_plot.pdf"))

p7 + facet_wrap(vars(sex))

dev.off()

pdf
  2
```

# Saving Graphics

```
## Save as JPEG
jpeg(paste0(figDir, "example_plot.jpg"))

p7 + facet_wrap(vars(sex))

dev.off()

pdf
  2

## Save as PNG
png(paste0(figDir, "example_plot.png"))

p7 + facet_wrap(vars(sex))

dev.off()

pdf
  2
```

# Saving Graphics

With PDF documents, we can save multiple figures to a single file.

```
pdf(paste0(figDir, "example_plot2.pdf"))

p6.1 + geom_jitter(size = 3, height = 0.1) + geom_smooth()
p7 + facet_wrap(vars(sex))
p8 + facet_grid(vars(sex), vars(class))

dev.off()

pdf
  2
```