# S3 and S4 Objects

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# Motivations

The plot function is very "talented". Explain the following behavior.

```
# This gives us a scatterplot

plot(mtcars$wt,mtcars$mpg)

# We create a table and plot somehow knows how to deal with. How ?

mytable <- table(mtcars$am,mtcars$cyl)
plot(mytable)

# We create a Linear Modeling object and plot knows how to
# plot it. How ?

mylm <- lm(mpg~wt, data=mtcars)
plot(mylm)
```

# Motivations

And the mystery continues.....

```
# This gives us a pairs plot

plot(mtcars)

# This will plot a histogram

myhisto <- hist(mtcars$mpg)
plot(myhisto)

# We create a pincipal components object

myprcomp <- prcomp(~ Murder + Assault + Rape,
                   data = USArrests, scale = TRUE)
plot(myprcomp)
```

# Objects

How does it do all of this ? First. Let's go back to some basics. Everything in R is an object. Functions are objects and functions can return objects. These objects belong to a class.

```
mylm <- lm(mpg~wt,data=mtcars)
class(mylm)
[1] "lm"

#

mytable <- table(mtcars$am, mtcars$cyl)
class(mytable)
[1] "table"

#

class(mtcars)
[1] "data.frame"
```

# S3 Objects

It turns out that the plot function is not just one command. It's an **S3 class**. Usually if we type a function's name at the prompt we can see the source code but in this case we don't get that.

```
plot
function (x, y, ...)
UseMethod("plot")
<bytecode: 0x7f861b133228>
<environment: namespace:graphics>
```

```
> methods(plot)
 [1] plot.acf*           plot.data.frame*    plot.decomposed.ts*
 [4] plot.default        plot.dendrogram*    plot.density*
 [7] plot.ecdf           plot.factor*        plot.formula*
[10] plot.function       plot.hclust*        plot.histogram*
[13] plot.HoltWinters*   plot.infant         plot.isoreg*
[16] plot.lm*            plot.medpolish*     plot.mlm*
[19] plot.ppr*           plot.prcomp*        plot.princomp*
[22] plot.profile.nls*   plot.spec*          plot.stepfun
[25] plot.stl*           plot.table*         plot.ts
[28] plot.tskernel*      plot.TukeyHSD*

   Non-visible functions are asterisked
```

# S3 Objects and Methods

Plot is actually an S3 object that has many "methods" at it's disposal. Notice that there is a plot method for many scenarios.

```
plot
function (x, y, ...)
UseMethod("plot")
<bytecode: 0x7f861b133228>
<environment: namespace:graphics>

> methods(plot)
 [1] plot.acf*           plot.data.frame*    plot.decomposed.ts*
 [4] plot.default        plot.dendrogram*    plot.density*
 [7] plot.ecdf           plot.factor*        plot.formula*
[10] plot.function       plot.hclust*        plot.histogram*
[13] plot.HoltWinters*   plot.infant         plot.isoreg*
[16] plot.lm*            plot.medpolish*     plot.mlm*
[19] plot.ppr*           plot.prcomp*        plot.princomp*
[22] plot.profile.nls*   plot.spec*          plot.stepfun
[25] plot.stl*           plot.table*         plot.ts
[28] plot.tskernel*      plot.TukeyHSD*

   Non-visible functions are asterisked
```

# S3 Objects and Methods

Note that the **summary** function is similar. It can handle a large number of objects.

```
summary
function (object, ...)
UseMethod("summary")
<bytecode: 0x7f861bf83708>
<environment: namespace:base>

> methods(summary)
 [1] summary.aov             summary.aovlist*        summary.aspell*
 [4] summary.connection      summary.data.frame      summary.Date
 [7] summary.default         summary.ecdf*           summary.factor
[10] summary.glm             summary.infl*           summary.lm
[13] summary.loess*          summary.manova          summary.matrix
[16] summary.mlm*            summary.nls*            summary.packageStatus*
[19] summary.PDF_Dictionary* summary.PDF_Stream*     summary.POSIXct
[22] summary.POSIXlt         summary.ppr*            summary.prcomp*
[25] summary.princomp*       summary.proc_time       summary.srcfile
[28] summary.srcref          summary.stepfun         summary.stl*
[31] summary.table           summary.tukeysmooth*

   Non-visible functions are asterisked
```

# S3 Objects and Methods

So if we use the **summary** function on the mtcars dataframe we are actually using the **summary.data.drame** function. We could call the **summary.data.frame** function directly if we wanted to.

```
grep("data.frame",methods(summary),value=TRUE)
[1] "summary.data.frame"

summary(mtcars)

# Same as

summary.data.frame(mtcars)

# Check to see if they are identical

identical(summary(mtcars), summary.data.frame(mtcars))
[1] TRUE
```

# S3 Objects and Methods

So if we have an object of class "lm" does plot know how to deal with it ? We already know it can.

```
mylm <- lm(mpg~wt, data=mtcars)
class(mylm)
[1] "lm"

methods(plot)
 [1] plot.acf*           plot.data.frame*    plot.decomposed.ts*
 [4] plot.default        plot.dendrogram*    plot.density*
 [7] plot.ecdf           plot.factor*        plot.formula*
[10] plot.function       plot.hclust*        plot.histogram*
[13] plot.HoltWinters*   plot.infant         plot.isoreg*
[16] plot.lm*            plot.medpolish*     plot.mlm*
[19] plot.ppr*           plot.prcomp*        plot.princomp*
[22] plot.profile.nls*   plot.spec*          plot.stepfun
[25] plot.stl*           plot.table*         plot.ts
[28] plot.tskernel*      plot.TukeyHSD*

grep("lm",methods(plot),value=T)
[1] "plot.lm"      "plot.mlm"     "plot.ridgelm"
```

# S3 Objects and Methods

- When we give the **plot()** function an object of a certain type, the **generic** plot function will then try to find a plot method that knows how to deal with that object type.
- It does this for you. In this case it finds the command **plot.lm()** method (which is a function) to do the work.
- You don't know what's going on and in most cases don't need to unless of course you are writing your own objects.

```
mylm <- lm(mpg~wt, data=mtcars)
class(mylm)
[1] "lm"

plot(mylm)    # Plot finds the right method based on the class of the object
```

# Object Oriented Programming - OOP

OOP is a very popular and useful idea in computer science although the implementation of OOP can de different across various languages. Some things to keep in mind:

- Objects represent structured data (e.g. data frames, vectors, lists)
- We build objects using class definitions (implicit and/or explicit)
- Classes can have well defined attributes or in R 'slots'
- Classes can ususally inherit from other classes
- R has three OOP implementations: S3, S4, and Reference Classes
- The base installation of R has many S3 classes
- Some say S4 is the best OOP to use (BioConductor requires it)
- Yet many developers continue to develop using S3

# Object Oriented Programming - OOP

- Everything in R is a self describing object

```
class(23)
[1] "numeric"

x <- matrix(1:16,4,4)
class(x)
[1] "matrix"

class(mtcars)
[1] "data.frame"
```

- You can say that every object in R belongs to a class
- Sometimes we use objects and classes as synonyms but technically that's not true
- Objects represent an **instance** of a class
- Functions that operate on Class Objects are called **methods**

# Object Oriented Programming - OOP

- Classes allow us to combine data and structure into a single idea
- Objects are realizations of a Class definition
- Consider **Homo Sapiens** as a class definition
- You and I are specific instances of that class

```
John <- HomoSapien(name="John",age=33,height=72,weight=170,race="caucasian")

Mary <- HomeSapien(name="Mary",age=22,height=62,weight=132,race="american_indi
```

- Note that name, age, height, weight, and race are **properties** or **attributes** of the Homo Sapien class.
- There are others of course but we restrict our attention to just a few of them
- The **race** attribute won't ever change whereas weight, height, and age will

# Object Oriented Programming - OOP

- Every class has a **Constructor** - a way to make an instance of a class
- In R we use functions to help us create instances of a class
- Using a constructor function helps create a valid object

```
aHomoSapien <- function(name,age,height,weight,race) {
     human <- list(name=name,age=age,height=height,weight=weight,race=race)
     class(human) <- "homosapien"
     return(human)
}

john <- aHomoSapien(name="John",age=33,height=72,weight=190,race="caucasian")
class(john)
[1] "homosapien"
```

- So **john** is an object of class **homosapien**
- So what do we do with john ? Well not much at this point

# Object Oriented Programming - OOP

How do we **access** values in the object. It's easy. We can use the **$** symbol:

```
john$name
[1] "John"

john$age
[1] 33

john$race
[1] "caucasian"

john[1:2]   # John is actually a list so we can do this
$name
[1] "John"

$age
[1] 33
```

However it is generally recommended to use an **Accessor** function to retrieve or set object values. This makes it easier for the user and easier for the developer to make changes to the underlying object structure.

# Object Oriented Programming - OOP

Consider a more interesting class where we track John's age and weight over time:

```
age <- c(33,35,37,39,41,43,45)
weight <- c(172,178,181,185,192,200,205)

aHomoSapien <- function(name,age,height,weight,race) {
     human <- list(name=name,info=data.frame(age=age,weight=weight),
                   height=height,race=race)
     class(human) <- "homosapien"
     return(human)
}

john <- aHomoSapien(name="John",age=age,height=72,
                    weight=weight,race="caucasian")

class(john)
[1] "homosapien"
```

# Object Oriented Programming - OOP

- Let's do the same for Mary

```
age <- c(33,35,37,39,41,43,45)
weight <- c(118,121,132,119,111,128,132)


mary <- aHomoSapien(name="Mary",age=age,height=62,
                    weight=weight,race="caucasian")

class(mary)
[1] "homosapien"
```

# Object Oriented Programming - OOP

- Now we could develop some interesting **methods** for analyzing this instance or any like it.
- Some common generic methods involve plotting, summarizing, or printing.
- In R the **plot**, **summary**, and **print** commands are **generic** functions that behave differently based on the class of the arguement(s) passed

```
> plot
function (x, y, ...)
UseMethod("plot")
<bytecode: 0x7f9251b80828>
<environment: namespace:graphics>

> summary
function (object, ...)
UseMethod("summary")
<bytecode: 0x7f9252e08468>
<environment: namespace:base>
```

# Object Oriented Programming - OOP

```
> methods(plot)
 [1] plot.acf*            plot.data.frame*
 [3] plot.decomposed.ts*  plot.default
 [5] plot.dendrogram*     plot.density*
 [7] plot.ecdf            plot.factor*
 [9] plot.formula*        plot.function
[11] plot.hclust*         plot.histogram*
[13] plot.HoltWinters*    plot.isoreg*
[15] plot.lm*             plot.medpolish*
[17] plot.mlm*            plot.newnorm
[19] plot.ppr*            plot.prcomp*
[21] plot.princomp*       plot.profile.nls*
[23] plot.shingle*        plot.spec*
[25] plot.stepfun         plot.stl*
[27] plot.table*          plot.tree
[29] plot.trellis*        plot.ts
[31] plot.tskernel*       plot.TukeyHSD*

   Non-visible functions are asterisked
```

# Object Oriented Programming - OOP

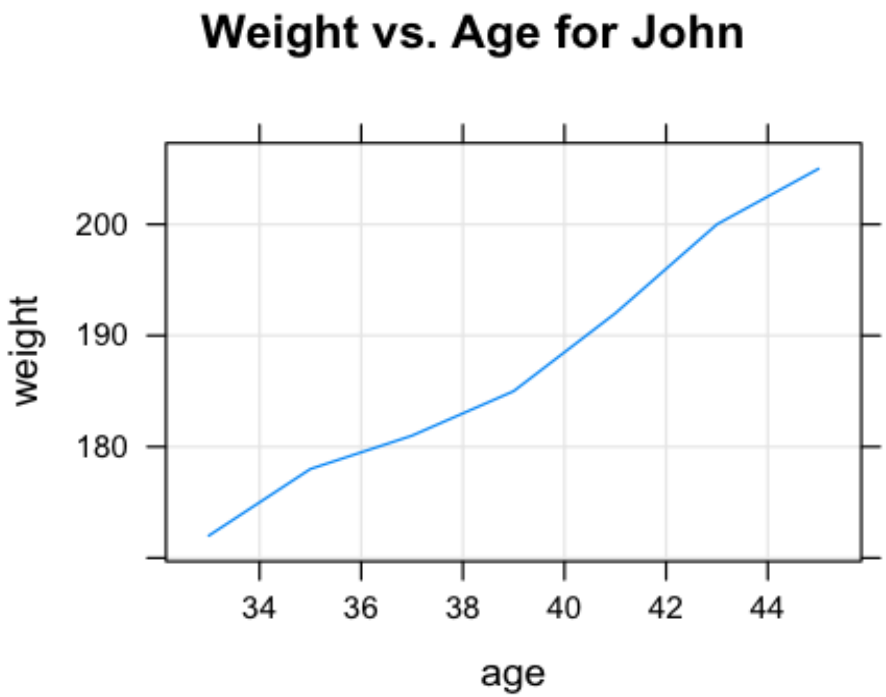
Why is this useful ?

- Well R users are familiar with the plot function so for the non-programmer they can count on the plot function working with objects of class homosapien
- We can alter the underlying **plot.homosapien** without our end users knowing about it.
- We can extend any of the common generic functions including **summary** and **print**

# Object Oriented Programming - OOP

Let's write a plot function specific to objects of class **homosapien**

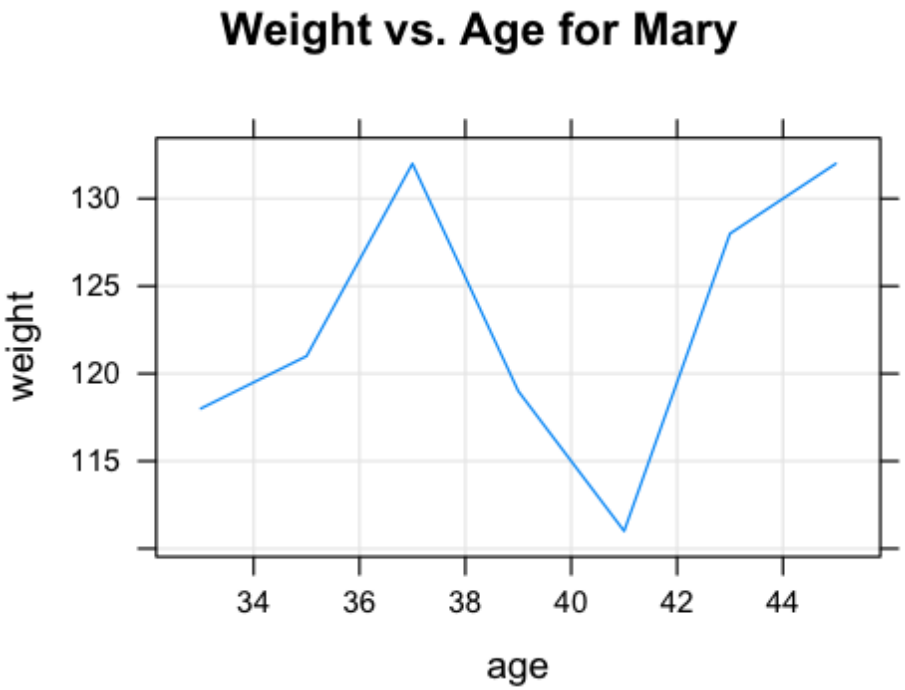
```
plot.homosapien <- function(obj) {
   library(lattice)
   hold <- obj$info
   title <- paste("Weight vs. Age for",obj$name,sep=" ")
   xyplot(weight~age,data=hold,main=title,type=c("l","g"))
}

plot(john)
```



# Object Oriented Programming - OOP

This function will work for Mary also since she too is of class homosapien. Note that we do NOT have to explicitly call **plot.homosapien** since **plot** is a generic function that will **dispatch** the work to the plot function defined for handling objects of type **homosapien**

```
plot(mary)
```



# Object Oriented Programming - OOP

Let's define a **summary** method. This is common for most R objects.

```
summary.homosapien <- function(obj) {
   str <- paste(obj$name,"had a mean weight of",
                round(mean(obj$info$weight),2),"lbs over a period of",
                max(obj$info$age)-min(obj$info$age),"years",sep=" ")
   print(str)
}

summary(john)
[1] "John had a mean weight of 187.57 lbs over a period of 12 years"

summary(mary)
[1] "Mary had a mean weight of 123 lbs over a period of 12 years"
```

# S3 Objects and Methods - generic functions

- We can create a generic function that can then handle a variety of objects based on a given object's type. (We still have to create the functions for a specific type)
- Like with the **plot()** and **summary()** functions.
- Think of plot and summary as a generic function that handles specific objects based on their class by **dispatching** the work to more specific functions

```
mylm <- lm(mpg~wt, data=mtcars)
class(mylm)
[1] "lm"

plot(mylm)    # Plot finds the right method based on the class of the object
```

# Object Oriented Programming - OOP

We can define our own generic function. For example let's come up with a function that extracts a specified range of age and weight information from the object.

```
getRange <- function(obj,start,end,...) {
   UseMethod("getRange")
}


getRange.homosapien <- function(obj,start,end,...) {
    holdf <- obj$info
    retdf <- holdf[holdf$age >= start & holdf$age <= end,]
    return(retdf)
}

getRange(john,35,41)
  age weight
2  35    178
3  37    181
4  39    185
5  41    192
```

# S3 Classes

So I've gotten pretty far into this without any formal definitions. There are three types of classes in R: S3, S4, and Reference Classes.

- S3 has been around for quite a while and there are many S3 classes that come with R. It's said to be "quick and dirty"
- To create an S3 class we setup an object and set it's class attribute to reflect the new class name
- We then define a generic function (if it hasn't already been done) of the form **generic.class**.
- If it's **plot, print**, or **summary** then the generic has already been defined for us. We just write the **generic.class** function

# S3 Classes

- We can conveniently extend the capabilities of an existing function that users know (e.g. plot or getHist) without the user even knowing about it.
- That generic function can grow over time to include related types of data much in the same way the plot and summary functions grew over time to handle objects of different types (e.g. tables, lm, glm, prcomp, etc)
- If desired, users themslves can locally extend a generic function to accommodate new objects of their own making (though generally they don't). I did just to show you that it could be done.
- If you anticipate turning over your functions to a user unfamiliar with R programming they will greatly appreciate the existence of your generic function so they don't have to remember which function to call for what class of data.

# S3 Classes

- S3 Classes are easy to create and use but they lack error checking. We can create a new S3 class and populate it with junk and get away with it.

```
age <- c(33,35,37,39,41,43,45)
weight <- c(172,178,181,185,192,200,205)

aHomoSapien <- function(name,age,height,weight,race) {
     human <- list(name=name,info=data.frame(age=age,weight=weight),
                   height=height,race=race)
     class(human) <- "homosapien"
     return(human)
}

john <- aHomoSapien(name="John",age=age,height="XX",
                    weight=weight,race=23)
```

- No errors were generated despite the fact that **height** should be numeric and **race** should be a character string

# S3 Classes

| Function Name | Purpose |
|---|---|
| str(object) | Display internal object structure |
| is(obj) | Test relationship between object and class |
| is(obj,“class”) | Is obj in “class” ? |
| class(x) | Show classes that x belongs to |
| methods(class=“class”) | Show all methods for “class” |
| unclass(x) | Remove all classes for x |

Table: Important S3 Functions

# An S3 Crime Class

- Okay let's read in the Chicago crime data from the vizualization lecture and use it to build an object of type "crime".

```
url <- "http://steviep42.bitbucket.org/YOUTUBE.DIR/chi_crimes.csv")

download.file(url,"chi_crimes.csv")
```

- So now we make an object/instance of "crime"

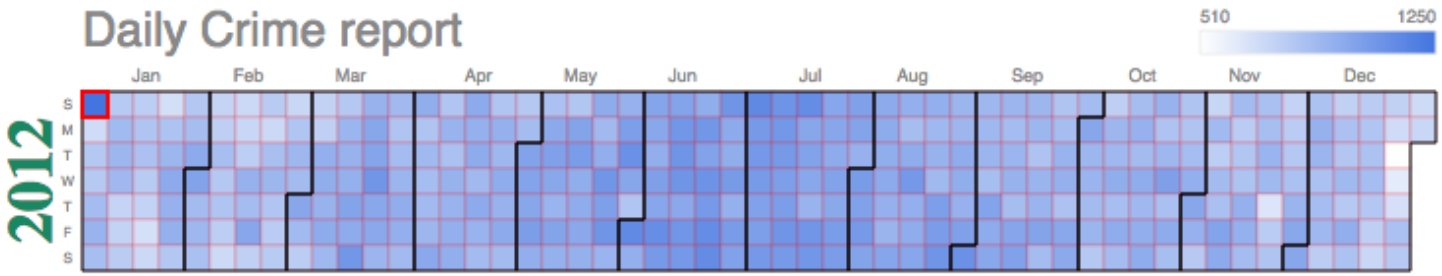
```
makecrime <- function(x,y,z) {
    stopifnot(require(lubridate))
    tmp <- read.csv(z,header=T,sep=",",stringsAsFactors=FALSE)
    tmp <- tmp[complete.cases(tmp),]
    tmp$Date <- parse_date_time(tmp$Date,'%m/%d/%Y %I:%M:%S %p')
    crimes <- list(id=x, source=y, data=tmp)
    class(crimes) <- "crime"
    return(crimes)
}

chicrimes <- makecrime("Chicago,IL","https://data.cityofchicago.org/",chi)
```

# An S3 Crime Class

```
print.crime <- function(object) {
   header <- paste("CITY,STATE:",object$id,"SOURCE:",object$source,sep=" ")
   cat(header,"\n\n")
   str(object$data,0)
}

plot.crime <- function(object,...) {
  stopifnot(require(dplyr))
  stopifnot(suppressPackageStartupMessages(require(googleVis)))
  df <- object$data
  df$Date <- as.Date(df$Date,format="%m/%d/%Y") # We need only the day of year
  df %>% group_by(Date) %>% summarize(count=n()) -> dfout

  Cal <- gvisCalendar(dfout, datevar="Date", numvar="count",
            options=list(width=900,height=600,
                    title="Daily Crime report", height=320,
                    calendar="{yearLabel: { fontName: 'Times-Roman',
                    fontSize: 32, color: '#1A8763', bold: true},
                    cellSize: 13,
                    cellColor: { stroke: 'red', strokeOpacity: 0.2 },
                    focusedCellColor: {stroke:'red'}}"))
  plot(Cal)
}
```

# An S3 Crime Class

```
print(chicrimes)
CITY,STATE: Chicago,IL SOURCE: https://data.cityofchicago.org/

'data.frame':  331980 obs. of  22 variables:


# Now plot

plot(chicrimes)
```



# S4 Classes

- S4 classes attempts to provide more rigor.
- We define our classes with an associated representation that must be adhered to so we can validate new instances of that class.
- Of course this means we have to go to more effort when creating classes and associated methods.
- We create a new S4 class by using the **setClass** function:

```
setClass("homosapien", representation(name="character",
                                      info="data.frame",
                                      height="numeric",
                                      race="character") )
```

```
getSlots("homosapien")
        name          info        height          race
 "character" "data.frame"     "numeric"  "character"
```

# S4 Classes

We create a new S4 class by using the **setClass** function:

```
age <- c(33,35,37,39,41,43,45)

weight <- c(172,178,181,185,192,200,205)

john <- new("homosapien",name="John",
                         info=data.frame(age=age,weight=weight),
                         race="caucasian")
slotNames(john)
[1] "name"   "info"   "height" "race"

john@name
[1] "John"

john@info
  age weight
1  33    172
2  35    178
3  37    181
4  39    185
5  41    192
6  43    200
7  45    205
```

# S4 Classes

The S4 equivalent to S3's **print** method is the **show** method

```
setMethod(f = "show", signature = "homosapien",
          definition = function(object) {
                              cat("Name: ",object@name,"\n")
                              print(object@info)
          })

[1] "show"

> john
Name:  John
  age weight
1  33    172
2  35    178
3  37    181
4  39    185
5  41    192
6  43    200
7  45    205
```

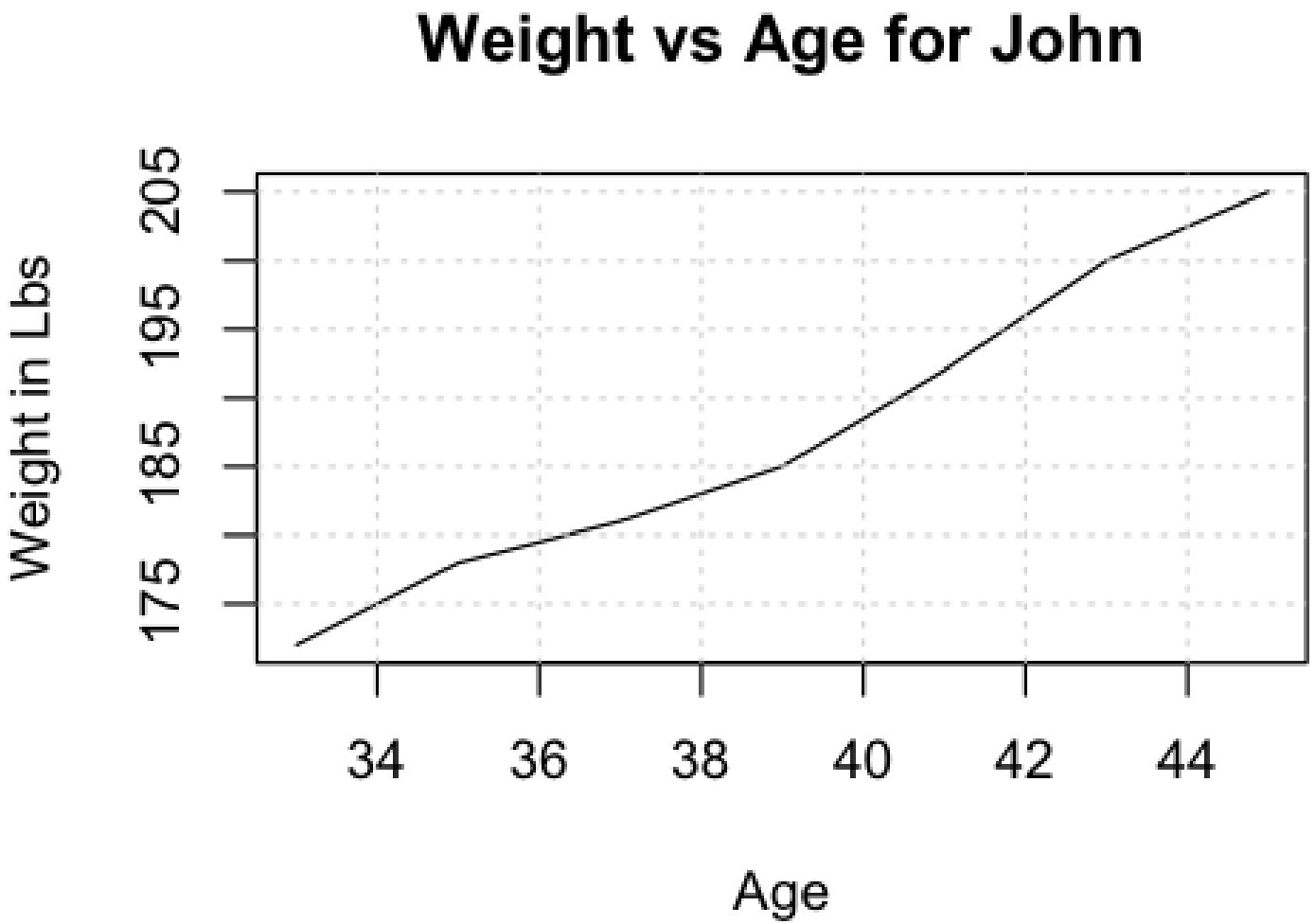
# S4 Classes

Let's define an S4 plot method to handle the plotting of a Homo Sapien object. As with S3 if we are extending the capability of an existing generic function which is in this case the **plot** function. In S4 we use the **setMethod** function to add in our own definition of **plot**

```
setMethod(f = "plot", signature = "homosapien",
          definition = function(x,y,...) {
             main <- "Weight vs Age"
             xlab <- "Age"
             ylab <- "Weight in Lbs"
             name <- x@name
             hold <- x@info
             x <- hold$age
             y <- hold$weight
             main <- paste(main,"for",name,sep=" ")
             plot(x,y,main=main,type="l",xlab=xlab,ylab=ylab)
             grid()
          })
```

# S4 Classes

```
plot(john)
```



# S4 Classes

- So let's define our own generic function. We'll create an **Accessor** function called **getRange()** just as we did with the S3 Homo Sapien object above.
- It's considered a best practice to provide users with an accessor function because they then do not have to memorize the underlying details of the object - we might decide to change the slotnames for example.
- As the developers of the class we can change the underlying class implementation without distrubing the users.
- As long as users are using the accessor function (and we keep it updated to match any changes we make to the object) then all will be well.

# S4 Classes

```
setGeneric("getRange",function(object,start,end) standardGeneric("getRange") )

setMethod("getRange","homosapien",
                      function(object,start,end) {
                         holdf <- object@info
                         retdf <- holdf[holdf$age >= start & holdf$age <= end,]
                         return(retdf)
                      })

getRange(john,35,41)
  age weight
2  35    178
3  37    181
4  39    185
5  41    192
```

# S4 Classes

That was okay but why not return an object of type **homosapien** so we can take advantage of the **plot** function we created ?

```
setGeneric("getRange",function(object,start,end) standardGeneric("getRange") )

setMethod("getRange","homosapien",
                      function(object,start,end) {
                         holdf <- object@info
                         retdf <- holdf[holdf$age >= start & holdf$age <= end,]
                         newhs <- new("homosapien",name="John",
                                      info=retdf,race="caucasian")
                         return(newhs)
                      })

plot(getRange(john,35,41))
```

# S4 Classes

With S3 classes we could give data of most any type and it would not complain. This is a weakness of S3. S4 objects use what is in the **representation** argument to check input types.

```
setClass("homosapien", representation(name="character",
                                      info="data.frame",
                                      height="numeric",
                                      race="character") )

age <- c(33,35,37,39,41,43,45)
weight <- c(172,178,181,185,192,200,205)

john <- new("homosapien",name="John",
                         info=data.frame(age=age,weight=weight),
                         race="caucasian")

# That was okay but check this out:

john <- new("homosapien", name=23,
             info=data.frame(age=age,weight=weight),race="caucasian")

Error in validObject(.Object) :
invalid class ``homosapien'' object: 1: invalid object for slot ``name'' in class
''homosapien'': got class ``numeric'', should be or extend class ''character''
```

# S4 Classes

We saw earlier that if we try to create an instance of an S4 class and we don't match what is in the **representation** field then it throws out an error. Actually we should create our own validation function.

```
setClass("homosapien", representation(name="character",
                                      info="data.frame",
                                      height="numeric",
                                      race="character") )

setValidity("homosapien",
            function(object) {
               retval <- TRUE
               if (!is.character(object@name)) {
                     print("Name should be character")
                     retval <- FALSE
               }
               if ( length(names(object@info)) != 2 ) {
                     print("Data frame is not valid")
                     retval <- FALSE
               }
               return(retval)
            }
  )

plot(tree1)
```