

# Using R Control Structures

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## Exploring R Control Structures with the PimaIndiansDiabetes2 data

First we load the `mlbench` package and then the diabetes data set. The data has 768 observations of 9 variables, which we can see with the `str()` function. The data was collected from Pima Indian women in the late 1990s.

```
library(mlbench)
data(PimaIndiansDiabetes2)
str(PimaIndiansDiabetes2)

## 'data.frame': 768 obs. of 9 variables:
## $ pregnant: num 6 1 8 1 0 5 3 10 2 8 ...
## $ glucose : num 148 85 183 89 137 116 78 115 197 125 ...
## $ pressure: num 72 66 64 66 40 74 50 NA 70 96 ...
## $ triceps : num 35 29 NA 23 35 NA 32 NA 45 NA ...
## $ insulin : num NA NA NA 94 168 NA 88 NA 543 NA ...
## $ mass : num 33.6 26.6 23.3 28.1 43.1 25.6 31 35.3 30.5 NA ...
## $ pedigree: num 0.627 0.351 0.672 0.167 2.288 ...
## $ age : num 50 31 32 21 33 30 26 29 53 54 ...
## $ diabetes: Factor w/ 2 levels "neg","pos": 2 1 2 1 2 1 2 1 2 2 ...
```

### Look for NAs

The `sapply()` function applies a function to elements of a list. In this case the elements of the list are columns in our data frame. The function is an anonymous function (we didn't name it), and it just sums, ignoring NAs.

```
sapply(PimaIndiansDiabetes2, function(x) sum(is.na(x)==TRUE))

## pregnant glucose pressure triceps insulin mass pedigree age
## 0 5 35 227 374 11 0 0
## diabetes
## 0
```

### Write a function

As an example of how to write a function, we write a function named `fill_NA` that takes two arguments and returns a vector. In R the `return()` statement is often not needed since R will return the last thing evaluated. In this function, the `mean_med` variable is a switch to choose whether to fill NAs with the mean or the median.

After the function is defined, we can call it with different columns. Then we use the `complete.cases()` function to get rid of the remaining rows that have NAs.

```
fill_NA <- function(mean_med, v){
  # fill missing values with either 1=mean or 2=median
  if (mean_med == 1){
```

```

    m <- mean(v, na.rm=TRUE)
  } else {
    m <- median(v, na.rm=TRUE)
  }
  v[is.na(v)] <- m
  v
}

# make a new data set with NA's filled
df <- PimaIndiansDiabetes2
df$triceps <- fill_NA(1, df$triceps)
df$insulin <- fill_NA(1, df$insulin)
df <- df[complete.cases(df),]

```

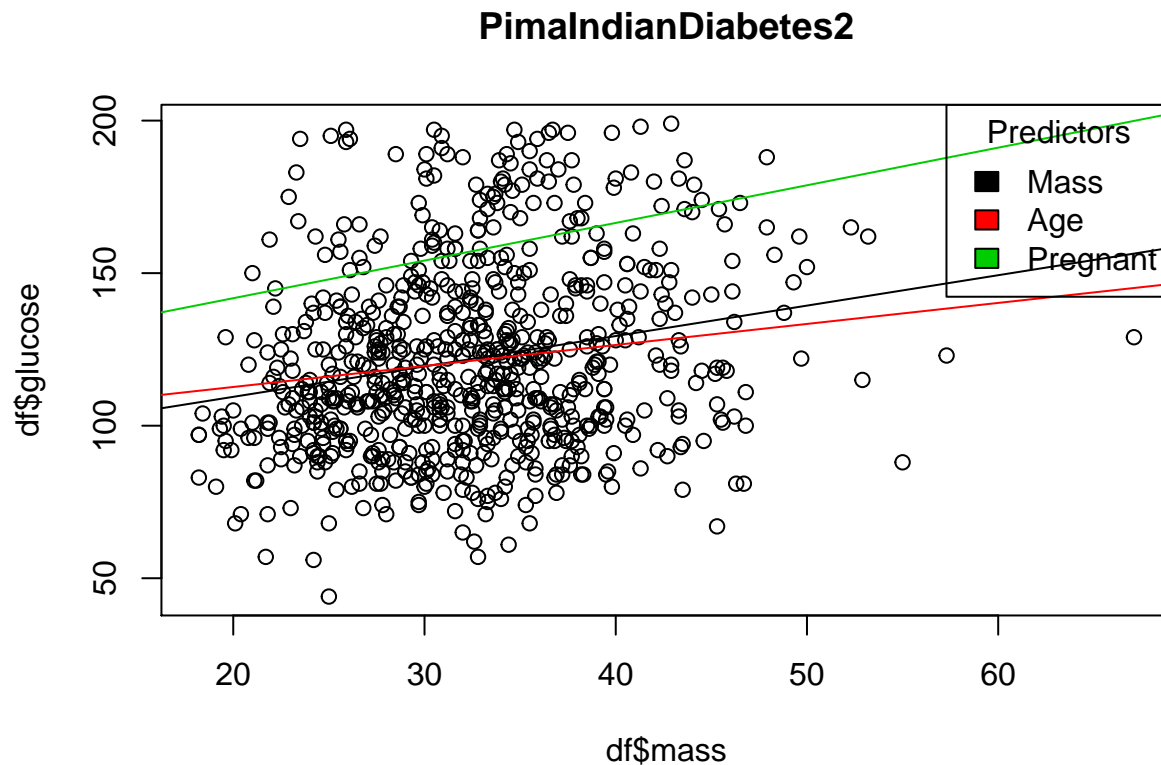
## Plots and for loops

The following plots some data from the data set and 3 ablines which are 3 linear regression lines created by `lm()`. Each regression line is a different color and we added a legend.

```

cols <- c(6,8,1)
plot(df$mass, df$glucose, main="PimaIndianDiabetes2")
for (i in 1:3){
  model <- lm(glucose~df[,cols[i]], data=df)[1]
  abline(model, col=i)
}
legend("topright", title="Predictors", c("Mass", "Age", "Pregnant"), fill=c(1,2,3))

```



### Using ifelse()

We use `ifelse()` to set a variable=1 if insulin is over 155 and 0 otherwise. Then we convert it to a factor, and place it in a new variable.

Then we plot.

```
df$large <- factor(ifelse(df$insulin>155,1,0))  
plot(df$mass, df$glucose, pch=21, bg=c("blue","red")[unclass(df$large)])
```

