

CSC433 Assignment 7
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###PART 1###

#Define a Constructor

```
ChlorReads<-function(theID,theName,theGender,theLdl,theHdl,theTrigl){  
  theObject<-list(id=theID,name=theName,gender=theGender,  
  ldl=theLdl,hd=theHdl,trigl=theTrigl)  
  class(theObject)="ChlorReads"  
  return(theObject)  
}
```

#make an example for testing

```
p1 <- ChlorReads(9876, "Virgil", "M", 248, 45, 148)
```

###PART2###

#Make a print function

```
print.ChlorReads<-function(theObject){
```

```
  #Define symbols to use in printing
```

```
  if(theObject$ldl >= 240){
```

```
    sym1= "*"
```

```
  } else if(theObject$ldl >= 200){
```

```
    sym1="+"
```

```
  } else {
```

```
    sym1=" "
```

```
  }
```

```
  if(theObject$hd >= 60){
```

```
    sym2=" "
```

```
  } else if(theObject$hd >=40){
```

```
    sym2= "+"
```

```
  } else {
```

```
    sym2= "*"
```

```
  }
```

```
  if(theObject$trigl >= 200){
```

```
    sym3= "*"
```

```
  } else if(theObject$trigl >= 150){
```

```
    sym3= "+"
```

```
  } else {
```

```
    sym3= " "
```

```
  }
```

```
#Create new variables using our original variable and the new symbol
```

```
newLDL<-paste0(theObject$ldl,sym1,collapse = NULL)
```

```
newHd<-paste0(theObject$hd,sym2, collapse = NULL)
```

```
newTri<-paste0(theObject$trigl,sym3)
```

```
#return all the things we want
```

```
cat("ID:",theObject$id,"Name:",theObject$name,"Gender:",theObject$gender,"LDL:",newLDL,"HDL:",newHd,"Triglycerides:",newTri,"\n")
}
```

###PART 3###

```
plot.ChlorReads<-function(theObject){
  barplot(height=c(theObject$ldl,theObject$hd,theObject
$trig),names.arg=c("LDL","HDL","TrigI"),main='CHLORESTEROL
READING',sub=paste("Id:",theObject$id,"Name:",theObject$name,"Gender:",theObject$gender)
)
}
```

###PART 4 ###

```
#define default methods and errors
getPatientInfo<-function(theObject){
  UseMethod("getPatientInfo",theObject)
}
getChloresteroI<-function(theObject){
  UseMethod("getChloresteroI",theObject)
}
getPatientInfo.default<-function(theObject){
  warning("Default getPatientInfo method ","called with unrecognized object")
  return(theObject)
}
```

```
getChloresteroI.default<-function(theObject){
  warning("Default getChloresteroIInfo method ","called with unrecognized object")
  return(theObject)
}
```

```
getPatientInfo.ChlorReads3<-function(theObject){
  cat("ID Name Gender","\n",theObject$id,theObject$name,theObject$gender)}
```

```
getChloresteroI.ChlorReads3<-function(theObject){
  cat("LDL HDL TrigI","\n",theObject$ldl,theObject$hd,theObject$trigI)
}
```

#####Part 5#####

```
#Set working directory so I can access my file
```

```
setwd("/Users/sarahcummings/Documents/csc433/RData")
chlor <- read.table("chlor-reads.txt")
#initialize lst

#create a list
lst <- NULL

for(i in 1:nrow(chlor)) {
  lst<- ChlorReads(chlor[i, ]$id, as.character(chlor[i, ]$name),as.character(chlor[i, ]$gender),
  chlor[i, ]$ldl, chlor[i, ]$hdl, chlor[i, ]$trigl)
}

#print all of the items in the list

for(i in lst){
  print.ChlorReads(i)
}

#plot graphs for each item

for(i in lst){
  plot.ChlorReads(i)
}
```