Bios 6301: Assignment 6

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Thursday, 1 December

Due Thursday, 1 December, 1:00 PM

$5^{n=day}$ points taken off for each day late.

50 points total.

Submit a single knitr file (named `homework6.rmd`), along with a valid PDF output file. Inside the file, clearly indicate which parts of your responses go with which problems (you may use the original homework document as a template). Add your name as `author` to the file's metadata section. Raw R code/output or word processor files are not acceptable.

Failure to name file `homework6.rmd` or include author name may result in 5 points taken off.

Question 1

15 points

Consider the following very simple genetic model (*very* simple – don't worry if you're not a geneticist!). A population consists of equal numbers of two sexes: male and female. At each generation men and women are paired at random, and each pair produces exactly two offspring, one male and one female. We are interested in the distribution of height from one generation to the next. Suppose that the height of both children is just the average of the height of their parents, how will the distribution of height change across generations?

Represent the heights of the current generation as a dataframe with two variables, m and f, for the two sexes. We can use `rnorm` to randomly generate the population at generation 1:

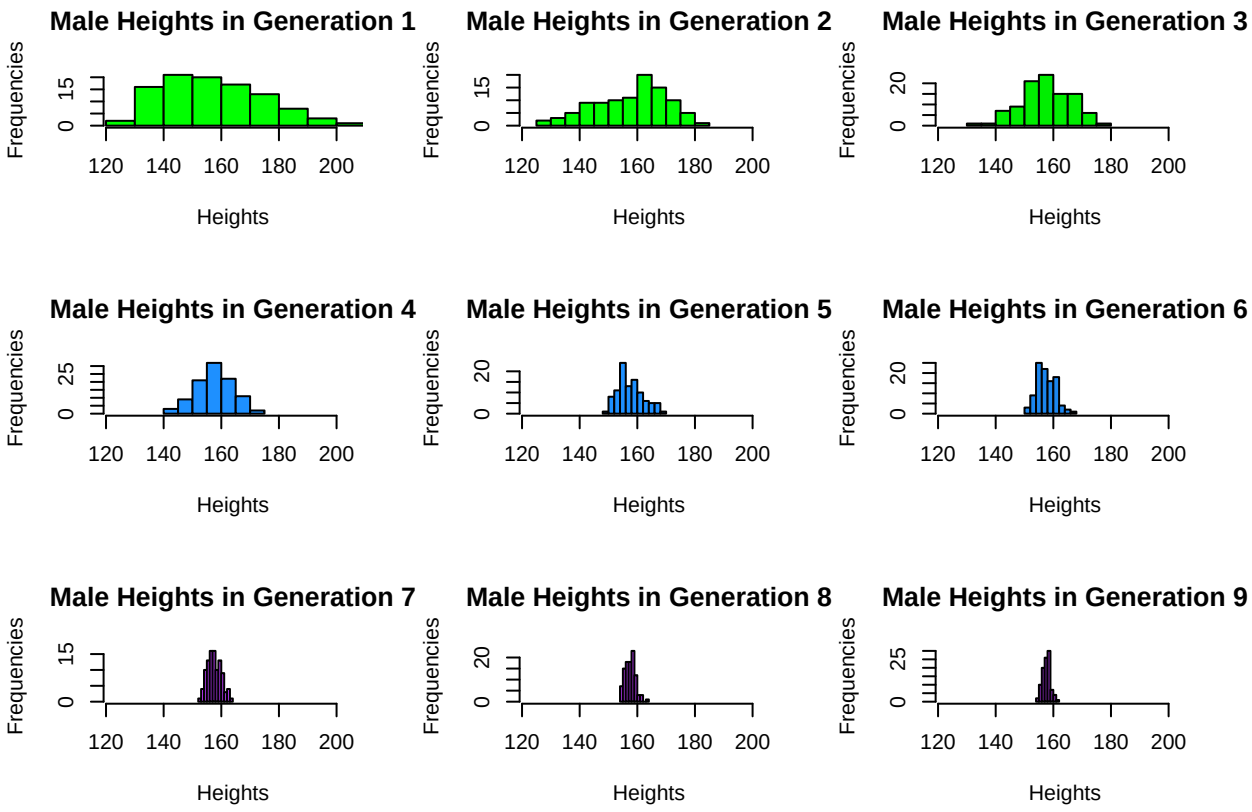
```
set.seed(280)
pop <- data.frame(m = rnorm(100, 160, 20), f = rnorm(100, 160, 20))
```

The following function takes the data frame `pop` and randomly permutes the ordering of the men. Men and women are then paired according to rows, and heights for the next generation are calculated by taking the mean of each row. The function returns a data frame with the same structure, giving the heights of the next generation.

```
next_gen <- function(pop) {
    pop$m <- sample(pop$m)
    pop$m <- rowMeans(pop)
    pop$f <- pop$m
    pop
}
```

Use the function `next_gen` to generate nine generations (you already have the first), then use the function `hist` to plot the distribution of male heights in each generation (this will require multiple calls to `hist`). The phenomenon you see is called regression to the mean. Provide (at least) minimal decorations such as title and x-axis labels.

```
gens2 <- data.frame(m=rep(NA,900),f=rep(NA,900),gen=rep(1:9,each=100))
gens2[1:100,1:2] <- pop
for(i in 2:9){
  start <- (i-2)*100+1
  end <- (i-1)*100
  data <- gens2[start:end,1:2]
  assign.start <- ((i-1)*100+1)
  assign.end <- i*100
  gens2[assign.start:assign.end,1:2] <- next_gen(data)
}

par(mfrow=c(3,3))
palette <- c("green","green1","green2","dodgerblue","dodgerblue1",
             "dodgerblue2","darkorchid1","darkorchid2","darkorchid3")
for(i in 1:9){
  title <- paste("Male Heights in Generation ", i, sep="")
  hist(gens2$m[which(gens2$gen==i)],main=title,xlab="Heights",ylab="Frequencies",col=palette[i],
       xlim = c(min(gens2$m[which(gens2$gen==1)]),max(gens2$m[which(gens2$gen==1)])))
}
```

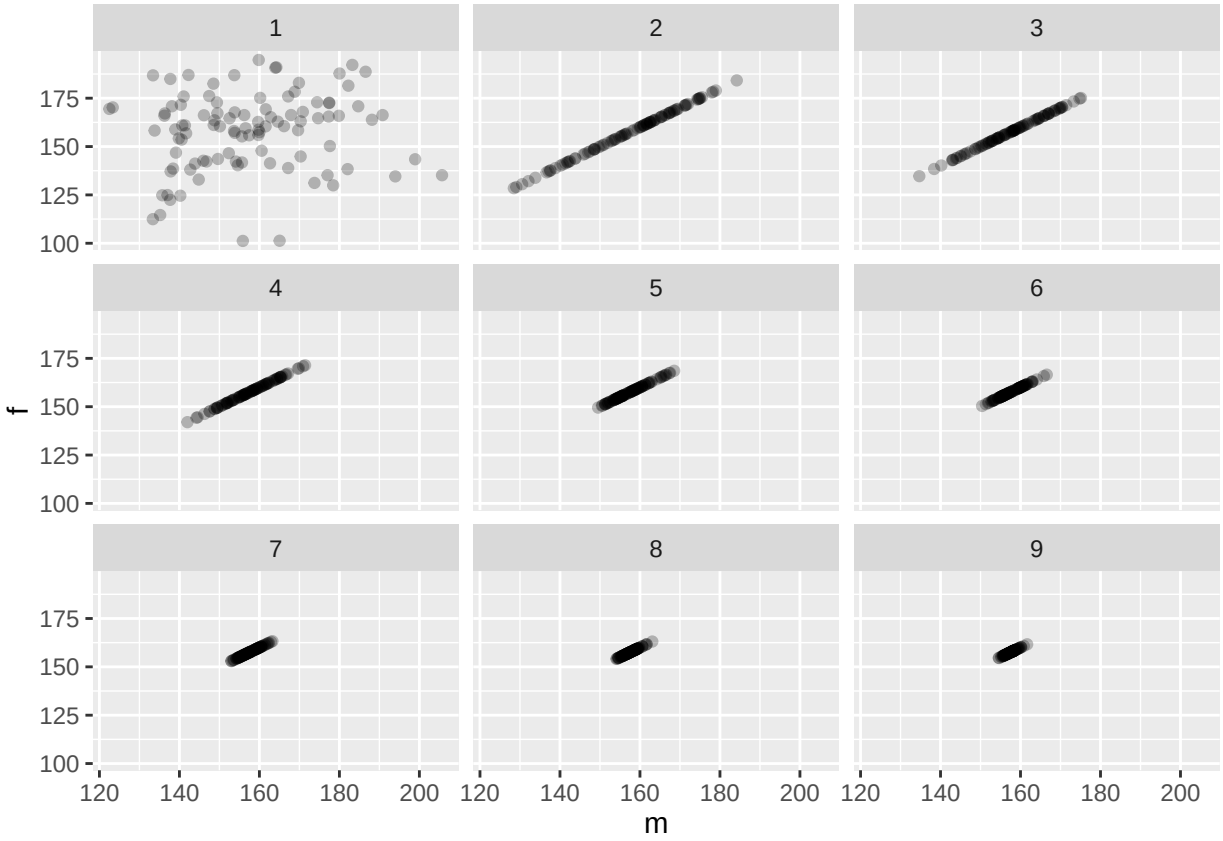


Question 2

10 points

Use the simulated results from question 1 to reproduce (as closely as possible) the following plot in ggplot2.

```
library(ggplot2)
p <- ggplot(data = gens2, aes(x=m,y=f)) + facet_wrap(~gen,nrow=3)
g <- p + geom_point(alpha=.25) +
  scale_x_continuous(limits = c(min(gens2$m[which(gens2$gen==1)]),max(gens2$m[which(gens2$gen==1)]))) +
  scale_y_continuous(limits = c(min(gens2$f[which(gens2$gen==1)]),max(gens2$f[which(gens2$gen==1)])))
g
```



Question 3

10 points

You calculated the power of a study design in question #2 of assignment 3. The study has two variables, treatment group and outcome. There are two treatment groups (0, 1) and they should be assigned randomly with equal probability. The outcome should be a random normal variable with a mean of 60 and standard deviation of 20. If a patient is in the treatment group, add 5 to the outcome.

Starting with a sample size of 250, create a 95% bootstrap percentile interval for the mean of each group. Then create a new bootstrap interval by increasing the sample size by 250 until the sample is 2500. Thus you will create a total of 10 bootstrap intervals. Each bootstrap should create 1000 bootstrap samples. (4 points)

```
set.seed(496)
base.sample <- function(n){
  start.sample <- data.frame(Treatment=rbinom(n,1,.5))
  start.sample$Outcome <- rnorm(n,60,20)
  for (j in 1:n) {
    if (start.sample$Treatment[j]==1) {
```

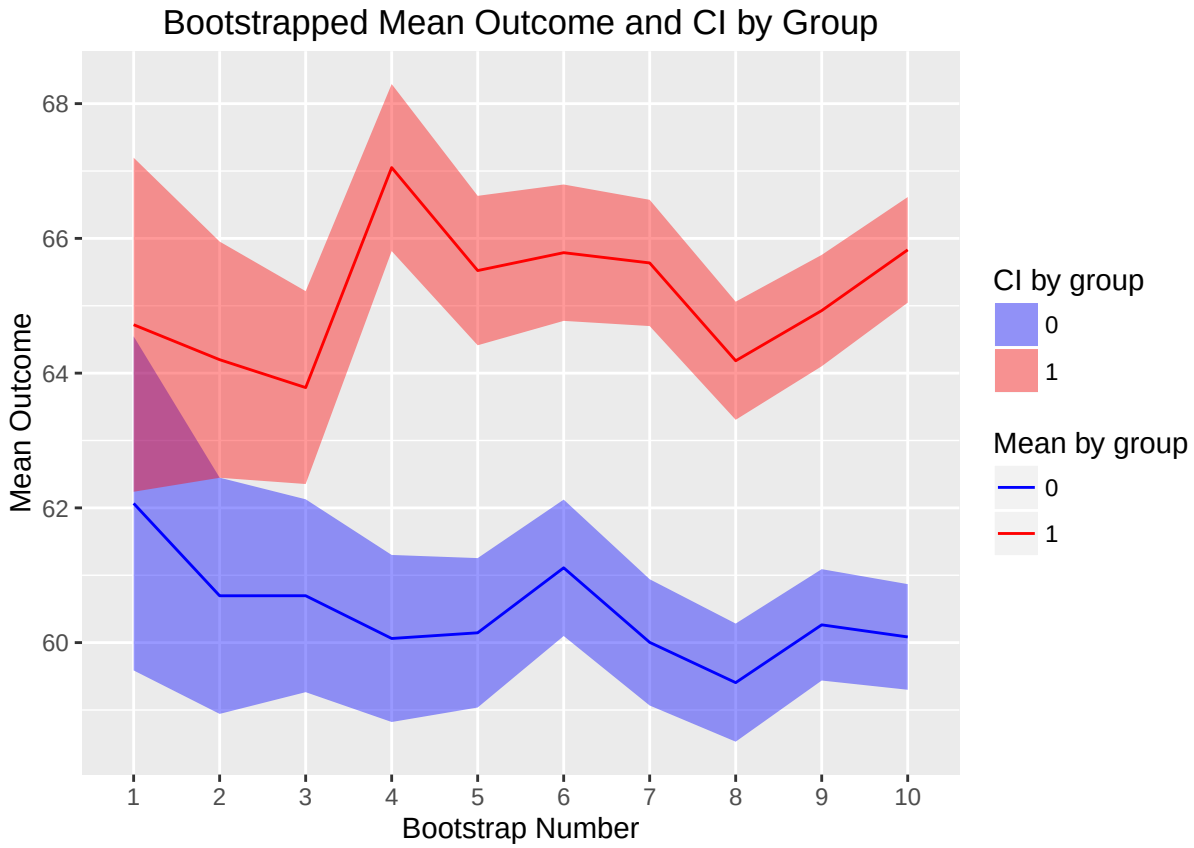
```
      start.sample$Outcome[j] <- start.sample$Outcome[j] + 5
    }
  }
  return(start.sample)
}

bootstrap.mean <- function(data,n){
  means.0 <- vector()
  means.1 <- vector()
  for(i in 1:1000){
    test.sample <- data[sample(nrow(data),250,replace=TRUE),]
    means <- aggregate(test.sample[,2],list(test.sample$Treatment),mean)
    means.0[i] <- means[1,2]
    means.1[i] <- means[2,2]
  }
  total.0 <- mean(means.0)
  total.1 <- mean(means.1)
  dev.0 <- sd(means.0)
  dev.1 <- sd(means.1)
  lb.0 <- total.0 - 1.96*(20/sqrt(n))
  ub.0 <- total.0 + 1.96*(20/sqrt(n))
  lb.1 <- total.1 - 1.96*(20/sqrt(n))
  ub.1 <- total.1 + 1.96*(20/sqrt(n))
  results.0 <- data.frame(mean=total.0,lower=lb.0,upper=ub.0,n)
  results.1 <- data.frame(mean=total.1,lower=lb.1,upper=ub.1,n)
  final <- rbind(results.0,results.1)
  return(final)
}

straps <- data.frame()
for(i in 1:10){
  size <- 250*i
  strap <- cbind(strap=as.factor(c(i,i)),group=c(0,1),bootstrap.mean(base.sample(size),size))
  straps <- rbind(straps,strap)
}

straps
```

```
##    strap group     mean    lower    upper    n
## 1      1     0 62.06658 59.58735 64.54581  250
## 2      1     1 64.71846 62.23924 67.19769  250
## 3      2     0 60.69528 58.94220 62.44835  500
## 4      2     1 64.19968 62.44661 65.95276  500
## 5      3     0 60.69614 59.26475 62.12752  750
## 6      3     1 63.78546 62.35408 65.21684  750
## 7      4     0 60.06159 58.82198 61.30120 1000
## 8      4     1 67.05116 65.81155 68.29077 1000
## 9      5     0 60.14599 59.03724 61.25473 1250
## 10     5     1 65.52253 64.41378 66.63127 1250
## 11     6     0 61.11046 60.09832 62.12260 1500
## 12     6     1 65.78783 64.77569 66.79997 1500
## 13     7     0 60.00362 59.06656 60.94068 1750
## 14     7     1 65.63553 64.69847 66.57258 1750
```

```
## 15      8      0 59.40611 58.52957 60.28264 2000
## 16      8      1 64.18384 63.30730 65.06038 2000
## 17      9      0 60.26381 59.43740 61.09022 2250
## 18      9      1 64.92870 64.10229 65.75511 2250
## 19     10      0 60.08429 59.30029 60.86829 2500
## 20     10      1 65.82973 65.04573 66.61373 2500
```

Produce a line chart that includes the bootstrapped mean and lower and upper percentile intervals for each group. Add appropriate labels and a legend. (6 points)

```
p <- ggplot(data=straps, aes(x=strap, y=mean)) +
  scale_fill_manual(values=c("blue","red"),name="CI by group") +
  scale_colour_manual(values=c("blue","red"),name="Mean by group") +
  geom_ribbon(aes(ymin=straps$lower, ymax=straps$upper,group=factor(group),
                  fill=factor(group)), alpha=0.4) +
  geom_line(aes(group=factor(group), colour=factor(group))) +
  ylab("Mean Outcome") +
  xlab("Bootstrap Number") +
  ggtitle("Bootstrapped Mean Outcome and CI by Group")
p
```



Question 4

15 points

Programming with classes. The following function will generate random patient information.

```
makePatient <- function() {
  vowel <- grep("[aeiou]", letters)
  cons <- grep("[^aeiou]", letters)
  name <- paste(sample(LETTERS[cons], 1), sample(letters[vowel], 1), sample(letters[cons], 1), sep='')
  gender <- factor(sample(0:1, 1), levels=0:1, labels=c('female','male'))
  dob <- as.Date(sample(7500, 1), origin="1970-01-01")
  n <- sample(6, 1)
  doa <- as.Date(sample(1500, n), origin="2010-01-01")
  pulse <- round(rnorm(n, 80, 10))
  temp <- round(rnorm(n, 98.4, 0.3), 2)
  fluid <- round(runif(n), 2)
  list(name=name, gender=gender, date_of_birth=dob, date_of_admission=doa,
       pulse=pulse, temperature=temp, fluid_intake=fluid)
}
```

1. Create an S3 class `medicalRecord` for objects that are a list with the named elements `name`, `gender`, `date_of_birth`, `date_of_admission`, `pulse`, `temperature`, `fluid_intake`. Note that an individual patient may have multiple measurements for some measurements. Set the RNG seed to `8` and create a medical record by taking the output of `makePatient`. Print the medical record, and print the class of the medical record. (5 points)

```
set.seed(8)
record <- makePatient()
class(record) <- "medicalRecord"
print.default(record)
```

```
## $name
## [1] "Mev"
##
## $gender
## [1] male
## Levels: female male
##
## $date_of_birth
## [1] "1976-08-09"
##
## $date_of_admission
## [1] "2011-03-14" "2013-10-30" "2013-02-27" "2012-08-23" "2011-11-16"
##
## $pulse
## [1] 67 81 95 74 81
##
## $temperature
## [1] 98.33 98.16 99.00 98.49 98.67
##
## $fluid_intake
## [1] 0.62 0.93 0.18 0.39 0.34
##
## attr(,"class")
## [1] "medicalRecord"
```

```
class(record)
```

```
## [1] "medicalRecord"
```

2. Write a `medicalRecord` method for the generic function `mean`, which returns averages for pulse, temperature and fluids. Also write a `medicalRecord` method for `print`, which employs some nice formatting, perhaps arranging measurements by date, and `plot`, that generates a composite plot of measurements over time. Call each function for the medical record created in part 1. (5 points)

```
mean.medicalRecord <- function(x){
  pulse <- mean(x$pulse)
  temperature <- mean(x$temperature)
  fluids <- mean(x$fluid_intake)
  results <- list(mean_pulse = pulse, mean_temperature = temperature, mean_fluids = fluids)
  return(results)
}

print.medicalRecord <- function(x){
  n_obs <- length(x$date_of_admission)
  chart <- data.frame(Name=rep(x$name,n_obs),Gender=rep(x$gender,n_obs),
                      dob=rep(x$date_of_birth,n_obs),doa=x$date_of_admission,
                      Pulse=x$pulse,Temperature=x$temperature,Fluids=x$fluid_intake)
  chart <- chart[order(chart$doa),]
  return(chart)
}

plot.medicalRecord <- function(x){
  chart <- print.medicalRecord(x)
  par(mfrow=c(1,3))
  plot(x=chart$doa,y=chart$Pulse,main="Pulse by Admission",
       xlab="Date of Admission",ylab="Pulse",type="l",lwd=2,col="red")
  plot(x=chart$doa,y=chart$Temperature,main="Temperature by Admission",
       xlab="Date of Admission",ylab="Temperature",type="l",lwd=2,col="green")
  plot(x=chart$doa,y=chart$Fluids,main="Fluid Intake by Admission",
       xlab="Date of Admission",ylab="Temperature",type="l",lwd=2,col="purple")
}

mean(record)
```

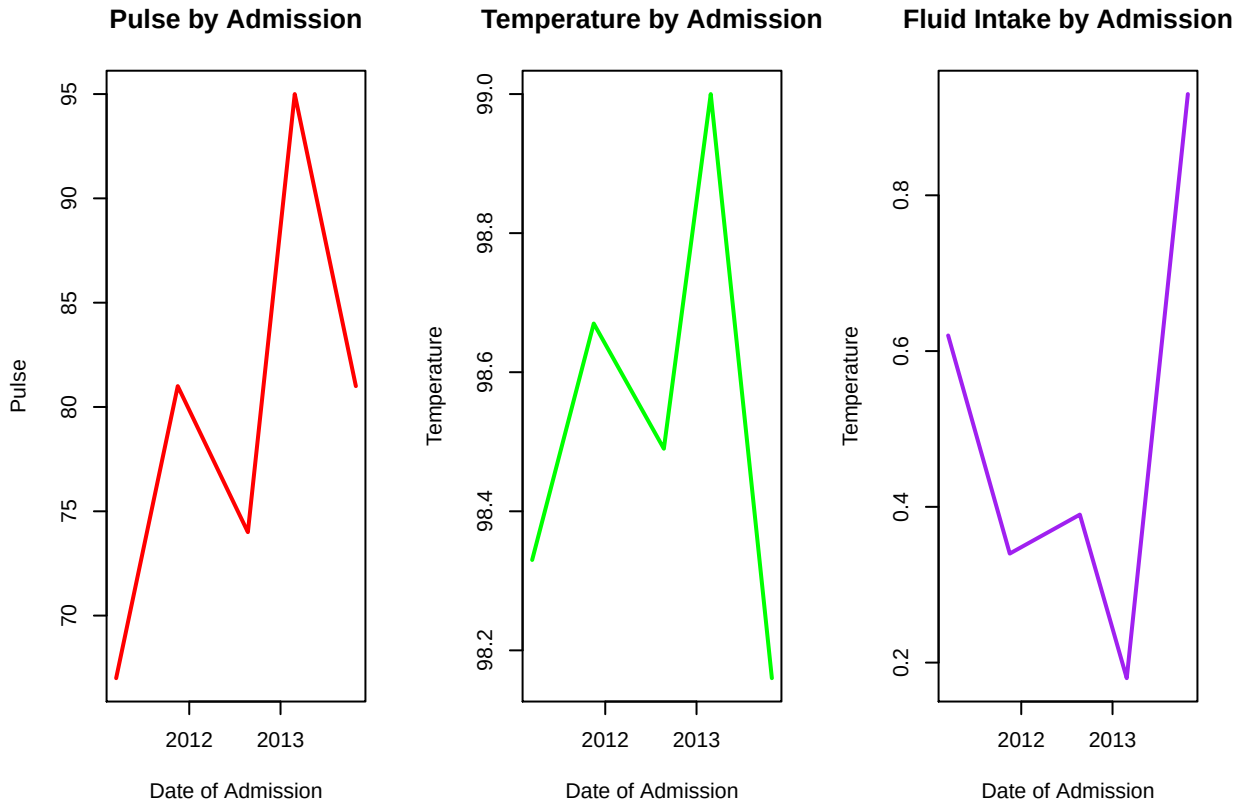
```
## $mean_pulse
## [1] 79.6
##
## $mean_temperature
## [1] 98.53
##
## $mean_fluids
## [1] 0.492
```

```
print(record)
```

```
##   Name Gender        dob        doa Pulse Temperature Fluids
```

```
## 1  Mev   male 1976-08-09 2011-03-14    67       98.33   0.62
## 5  Mev   male 1976-08-09 2011-11-16    81       98.67   0.34
## 4  Mev   male 1976-08-09 2012-08-23    74       98.49   0.39
## 3  Mev   male 1976-08-09 2013-02-27    95       99.00   0.18
## 2  Mev   male 1976-08-09 2013-10-30    81       98.16   0.93
```

```
plot(record)
```



3. Create a further class for a cohort (group) of patients, and write methods for `mean` and `print` which, when applied to a cohort, apply mean or print to each patient contained in the cohort. Hint: think of this as a "container" for patients. Reset the RNG seed to 8 and create a cohort of ten patients, then show the output for `mean` and `print`. (5 points)

```
mean.cohort <- function(x){
  names <- vector()
  pulses <- vector()
  temps <- vector()
  fluids <- vector()
  for(i in 1:ncol(x)){
    names[i] <- x[,i]$name
    pulses[i] <- mean(x[,i]$pulse)
    temps[i] <- mean(x[,i]$temperature)
    fluids[i] <- mean(x[,i]$fluid_intake)
  }
  results <- data.frame(Name=names,Mean_Pulse=pulses,Mean_Temperature=temps,Mean_Fluid_Intake=fluids)
  return(results)
}
```

```
print.cohort <- function(x){
  cohort.chart <- data.frame()
  for(i in 1:ncol(x)){
    n_obs <- length(x[,i]$date_of_admission)
    chart <- data.frame(Name=rep(x[,i]$name,n_obs),Gender=rep(x[,i]$gender,n_obs),
                        dob=rep(x[,i]$date_of_birth,n_obs),doa=x[,i]$date_of_admission,
                        Pulse=x[,i]$pulse,Temperature=x[,i]$temperature,Fluids=x[,i]$fluid_intake)
    chart <- chart[order(chart$doa),]
    cohort.chart <- rbind(cohort.chart,chart)
  }
  return(cohort.chart)
}
set.seed(8)
cohort <- replicate(10,makePatient())
class(cohort) <- "cohort"
mean(cohort)
```

```
##    Name Mean_Pulse Mean_Temperature Mean_Fluid_Intake
## 1   Mev   79.60000         98.53000         0.4920000
## 2   Yul   78.00000         98.49500         0.2450000
## 3   Zet   81.50000         98.44000         0.4033333
## 4   Qih   78.00000         98.60000         0.6500000
## 5   Wut   88.33333         98.05000         0.5866667
## 6   Juy   83.50000         98.45000         0.4525000
## 7   God   83.00000         98.01000         0.9700000
## 8   Fut   77.50000         98.14833         0.3366667
## 9   Pet   77.00000         98.83000         0.4450000
## 10  Yed   79.33333         98.30000         0.6583333
```

```
print(cohort)
```

```
##    Name Gender        dob        doa Pulse Temperature Fluids
## 1   Mev   male 1976-08-09 2011-03-14    67       98.33   0.62
## 5   Mev   male 1976-08-09 2011-11-16    81       98.67   0.34
## 4   Mev   male 1976-08-09 2012-08-23    74       98.49   0.39
## 3   Mev   male 1976-08-09 2013-02-27    95       99.00   0.18
## 2   Mev   male 1976-08-09 2013-10-30    81       98.16   0.93
## 11  Yul   male 1988-06-28 2012-01-16    76       98.92   0.14
## 21  Yul   male 1988-06-28 2013-08-07    80       98.07   0.35
## 6   Zet female 1970-06-13 2010-03-21    79       98.58   0.22
## 51  Zet female 1970-06-13 2010-04-01    73       98.32   0.61
## 41  Zet female 1970-06-13 2012-08-29    88       98.47   0.59
## 31  Zet female 1970-06-13 2013-06-01    84       98.22   0.25
## 12  Zet female 1970-06-13 2013-11-03    72       98.54   0.03
## 22  Zet female 1970-06-13 2014-02-05    93       98.51   0.72
## 13  Qih female 1987-08-30 2011-06-22    78       98.60   0.65
## 32  Wut   male 1974-06-28 2010-04-12    76       98.05   0.65
## 14  Wut   male 1974-06-28 2011-02-16    93       98.26   0.97
## 23  Wut   male 1974-06-28 2012-04-12    96       97.84   0.14
## 42  Juy   male 1983-06-09 2010-03-10    81       99.11   0.66
## 15  Juy   male 1983-06-09 2010-03-25    90       98.58   0.26
## 33  Juy   male 1983-06-09 2010-04-18    75       98.58   0.60
```

```
## 24  Juy   male 1983-06-09 2010-06-10    88       97.53   0.29
## 16  God female 1990-02-12 2010-03-12    83       98.01   0.97
## 52  Fut   male 1970-01-11 2011-04-07    80       97.87   0.36
## 43  Fut   male 1970-01-11 2011-04-14    83       97.91   0.00
## 25  Fut   male 1970-01-11 2011-08-16    66       98.49   0.13
## 17  Fut   male 1970-01-11 2013-03-15    74       98.38   0.31
## 61  Fut   male 1970-01-11 2013-06-20    74       98.41   0.49
## 34  Fut   male 1970-01-11 2013-11-12    88       97.83   0.73
## 18  Pet   male 1979-01-01 2010-10-30    85       98.84   0.60
## 26  Pet   male 1979-01-01 2012-05-10    69       98.82   0.29
## 44  Yed   male 1977-11-11 2010-01-28    63       97.95   0.94
## 35  Yed   male 1977-11-11 2010-03-06    81       98.45   0.67
## 19  Yed   male 1977-11-11 2010-07-10    98       98.65   0.79
## 62  Yed   male 1977-11-11 2010-08-27    66       97.68   0.36
## 53  Yed   male 1977-11-11 2011-06-18    83       98.00   0.69
## 27  Yed   male 1977-11-11 2013-01-06    85       99.07   0.50
```