Bios 6301: Assignment 8

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Due Tuesday, 16 November, 1:00 PM

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

30 points total.

Submit a single knitr file (named homework8.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 homework8.rmd or include author name may result in 5 points taken off.

Question 1

15 points

Install the readxl package and run the following

```
fn <- 'icd10.xlsx'
if(file.access(fn, mode = 4) == -1) {
    url <- "https://www.cdc.gov/nhsn/xls/icd10-pcs-pcm-nhsn-opc.xlsx"
    download.file(url, destfile = fn, mode = 'wb')
}
dat <- readxl::read_excel(fn, sheet = 2)</pre>
```

1. Show the class of dat. (1 point)

class(dat)

```
## [1] "tbl df" "tbl" "data.frame"
```

2. Show the methods available for objects of the given class (if there are multiple classes, show methods for all classes). (3 points)

```
for(i in 1:length(class(dat))){
  print(methods(class=class(dat)[i]))
}
```

```
##
    [1] [
                       [[<-
                                                     [<-
                                                                   $
##
    [6] $<-
                       as.data.frame coerce
                                                     initialize
                                                                   names<-
                                                     slotsFromS3
  [11] Ops
                       row.names<-
                                      show
                                                                   str
  see '?methods' for accessing help and source code
                                 $<-
    [1] [[<-
                     [<-
                                              coerce
                                                           format
                                                                        initialize
                                 show
##
    [7] Ops
                     print
                                              slotsFromS3
## see '?methods' for accessing help and source code
                                                                   $<-
    [1] [
                                      [[<-
                                                    as.data.frame as.list
                       anyDuplicated anyNA
    [6] aggregate
## [11] as.matrix
                       by
                                      cbind
                                                    coerce
                                                                   dim
## [16] dimnames
                       dimnames<-
                                      droplevels
                                                    duplicated
                                                                   edit
```

```
## [21] format
                        formula
                                       head
                                                       initialize
                                                                      is.na
## [26] Math
                        merge
                                       na.exclude
                                                      na.omit
                                                                      Ops
## [31] plot
                        print
                                       prompt
                                                       rbind
                                                                      row.names
## [36] row.names<-
                                                       slotsFromS3
                        rowsum
                                       show
                                                                      split
## [41] split<-
                        stack
                                       str
                                                       subset
                                                                      summary
## [46] Summary
                                                      transform
                                       tail
                                                                      type.convert
                        t
## [51] unique
                        unstack
                                       within
## see '?methods' for accessing help and source code
  3. If you call print(dat), what print method is being dispatched? (1 point)
findMethod <- function(generic, ...) {</pre>
  ch <- deparse(substitute(generic))</pre>
  f <- X <- function(x, ...) UseMethod("X")</pre>
  for(m in methods(ch)) assign(sub(ch, "X", m, fixed = TRUE), "body<-"(f, value = m))</pre>
  X(\ldots)
}
findMethod(print, dat)
## [1] "print.tbl"
  4. Set the class of dat to be a data frame. (1 point)
class(dat) <- "data.frame"</pre>
  5. If you call print(dat) again, what print method is being dispatched? (1 point)
findMethod(print, dat)
## [1] "print.data.frame"
Define a new generic function nUnique with the code below.
nUnique <- function(x) {
    UseMethod('nUnique')
}
  6. Write a default method for nUnique to count the number of unique values in an element. (2 points)
nUnique.default <- function(x) {
  length(unique(x))
  7. Check your function (2 points)
nUnique(letters) # should return 26
## [1] 26
nUnique(sample(10, 100, replace = TRUE)) # should return 10 (probably)
## [1] 10
  8. Write a data frame method for nUnique to operate on data frame objects. This version should return
     counts for each column in a data.frame. (2 points)
nUnique.data.frame <- function(x) {
data <- c()
for(i in 1: ncol(x)){
  data <-c(data, length(sapply(x, unique)[[i]]))</pre>
```

```
}
names(data) <- colnames(x)
print(data)
}</pre>
```

9. Check your function (2 points)

```
nUnique(dat)
```

Question 2

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, gender, dob, doa, pulse, temp, fluid)
}</pre>
```

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)

```
## $name
## [1] "Yes"
##
## $gender
## [1] male
## Levels: female male
##
## $date_of_birth
## [1] "1977-05-03"
```

```
##
## $date_of_admission
  [1] "2013-06-09" "2013-07-02"
##
## $pulse
## [1] 79 78
##
## $temperature
## [1] 98.07 97.50
##
## $fluid_intake
## [1] 0.28 0.52
## attr(,"class")
## [1] "medicalRecord"
attributes(patient)
## $names
                             "gender"
## [1] "name"
                                                   "date_of_birth"
## [4] "date_of_admission" "pulse"
                                                   "temperature"
## [7] "fluid_intake"
## $class
## [1] "medicalRecord"
  2. Write a medicalRecord method for the generic function mean, which returns averages for pulse,
     temperature and fluids. Also write a medical Record 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)
library(dplyr)
##
```

```
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
##
       intersect, setdiff, setequal, union
mean.medicalRecord <- function(x) {</pre>
  vector <- c(mean(x$pulse), mean(x$temperature), mean(x$fluid_intake))</pre>
  names(vector) <- c("pulse", "temperature", "fluid_intake")</pre>
  print(vector)
}
print.medicalRecord <- function(x) {</pre>
  data <- data.frame(matrix(NA, length(x$date_of_admission), length(x)))</pre>
  for(i in 1:length(x)){
  data[,i] <- x[[i]]
  colnames(data) <- names(x)</pre>
  data <- arrange(data,date_of_admission)</pre>
```

```
data
}
plot.medicalRecord <- function(x) {</pre>
  par(mfrow = c(1,3))
  plot(x$date_of_admission, x$pulse, col = 'red')
  plot(x$date_of_admission, x$temperature, col = 'red')
  plot(x$date_of_admission, x$fluid_intake, col = 'red')
mean(patient)
##
            pulse
                     temperature fluid_intake
##
           78.500
                           97.785
                                            0.400
print(patient)
##
      name gender date_of_birth date_of_admission pulse temperature fluid_intake
## 1
                        1977-05-03
                                               2013-06-09
                                                                79
                                                                           98.07
## 2
      Yes
               male
                        1977-05-03
                                               2013-07-02
                                                                78
                                                                           97.50
                                                                                            0.52
plot(patient)
    79.0
                                                                              0.50
                                         98.0
    78.8
                                                                              0.45
                                         97.9
    78.6
                                    x$temperature
                                                                         x$fluid_intake
x$pulse
                                         \infty
                                                                              0.40
                                         97.
    78.4
                                         97.7
    78.2
                                         9.76
                                                                              0.30
    78.0
                                         97.5
       Jun 10
                    Jun 24
                                            Jun 10
                                                         Jun 24
                                                                                 Jun 10
                                                                                              Jun 24
           x$date_of_admission
                                                x$date_of_admission
                                                                                    x$date_of_admission
```

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)

```
set.seed(8)
cohort <- list()</pre>
```

```
for(i in 1:10) {
patient <- makePatient()</pre>
names(patient) <- c("name", "gender", "date_of_birth", "date_of_admission",</pre>
                        "pulse", "temperature", "fluid_intake")
# class(patient) <- "medicalRecord"</pre>
cohort[[i]] <- patient</pre>
}
class(cohort) <- "medicalCohort"</pre>
mean.medicalCohort <- function(x){</pre>
 mat <- matrix(NA, 10, 3)</pre>
  for(i in 1:10) {
    mat[i,] <- mean.medicalRecord(x[[i]])</pre>
  colMeans(mat)
}
mean(cohort)
##
          pulse temperature fluid_intake
##
         78.500
                       97.785
                                      0.400
          pulse temperature fluid_intake
##
##
     86.3333333
                   98.3966667
                                  0.4133333
##
          pulse temperature fluid_intake
##
        77.0000
                      98.6475
                                     0.5200
          pulse temperature fluid_intake
##
##
     83.1666667
                   98.4850000
                                  0.2966667
##
          pulse temperature fluid_intake
##
        83.5000
                      98.4500
                                     0.4525
##
          pulse temperature fluid_intake
##
         84.400
                       98.484
##
          pulse temperature fluid_intake
##
        76.5000
                      98.3800
                                     0.3975
##
          pulse temperature fluid_intake
                      98.3675
##
        75.0000
                                     0.5225
##
          pulse
                  temperature fluid_intake
##
          73.00
                        98.36
                                       0.15
##
          pulse
                 temperature fluid_intake
##
          77.00
                        98.54
                                       0.15
## [1] 79.44000 98.38957 0.38245
print.medicalCohort <- function(x) {</pre>
  dat <- data.frame()</pre>
  for(i in 1:10) {
    dat <- rbind(dat, print.medicalRecord(cohort[[i]]))</pre>
  }
  dat
}
print(cohort)
      name gender date_of_birth date_of_admission pulse temperature fluid_intake
                                         2013-06-09
                                                        79
## 1
      Yes male
                      1977-05-03
                                                                  98.07
```

##	2	Yes	male	1977-05-03	2013-07-02	78	97.50	0.52
##	3	Fal	male	1988-05-24	2010-11-16	76	98.23	0.18
##	4	Fal	male	1988-05-24	2013-03-24	87	98.21	0.10
##	5	Fal	male	1988-05-24	2013-09-12	96	98.75	0.96
##	6	Zog	male	1988-12-14	2010-02-24	84	98.54	0.40
##	7	Zog	male	1988-12-14	2013-03-25	69	98.49	0.81
##	8	Zog	male	1988-12-14	2013-07-29	75	98.82	0.59
##	9	Zog	male	1988-12-14	2013-10-27	80	98.74	0.28
##	10	Yol	male	1986-03-11	2010-02-22	84	98.87	0.39
##	11	Yol	male	1986-03-11	2011-12-27	89	98.27	0.97
##	12	Yol	male	1986-03-11	2012-03-10	87	98.78	0.12
##	13	Yol	male	1986-03-11	2012-11-26	92	98.26	0.14
##	14	Yol	male	1986-03-11	2013-03-24	78	98.44	0.13
##	15	Yol	male	1986-03-11	2014-01-28	69	98.29	0.03
##	16	Yak	female	1983-09-15	2011-07-19	75	98.58	0.60
##	17	Yak	female	1983-09-15	2012-04-07	88	97.53	0.29
##	18	Yak	female	1983-09-15	2012-07-11	81	99.11	0.66
##	19	Yak	female	1983-09-15	2012-08-30	90	98.58	0.26
	20	Gaf	female	1978-04-27	2010-07-19	91	98.01	0.47
##	21		female	1978-04-27	2011-05-03	90	98.61	0.36
	22		female	1978-04-27	2012-04-24	89	98.32	0.42
##	23		female	1978-04-27	2012-08-06	77	98.96	0.74
	24		female	1978-04-27	2013-08-21	75	98.52	0.62
	25		female	1980-11-07	2010-10-03	82	98.49	0.12
	26		female	1980-11-07	2010-10-29	81	98.17	0.93
	27		female	1980-11-07	2011-09-16	72	98.21	0.29
	28		female	1980-11-07	2012-07-10	71	98.65	0.25
	29		female	1989-07-16	2010-02-08	66	97.95	0.79
	30		female	1989-07-16	2010-04-19	88	98.00	0.50
	31		female	1989-07-16	2010-06-11	83	98.45	0.79
	32		female	1989-07-16	2012-03-02	63	99.07	0.01
	33	Fel	male	1985-08-16	2010-09-26	81	98.51	0.24
	34	Fel	male	1985-08-16	2012-06-24	65	98.21	0.06
##	35	Say	female	1974-09-22	2010-03-14	77	98.54	0.15