

STAT-6494 Advanced Statistical Computing with R – HW 1

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Exercise: Comorbidity Measures

Comorbidity measures are important in health-care research. They can be obtained from hospital discharge records using the diagnosis coding of ICD-9-CM (International Classification of Diseases, Ninth Edition, Clinical Modifications). An influential, widely cited method was proposed by Elixhauser et al. (Comorbidity Measures for Use with Administrative Data. Medical Care, 1998;36:8–27). The method has been refined by the Healthcare Cost and Utilization Project [HCUP](#). Their [implementation](#) is in SAS. Construction of the variables is summarized in a PDF table under the section “Variables Created”. For simplicity, let us ignore the DRG code for this assignment. For real usage, one would need to consider the DRG code. An R implementation is available in package [comorbidities](#). We will focus on the function `ahrq` in this package. The input of the function is a data frame where rows are patients and columns are ICD-9-CM codes. Each patient does not necessarily have all columns filled; some ICD-9-CM codes can be NA or empty. The output of the functions is a list, and we are interested in the data frame where rows are patients and columns are comorbidity measures. This function can be made much more efficient by vectorizing. Please write a function `cmbd`. Its input is the same as `ahrq` and its output is a data frame with only first two comorbidity measures: CHF and VALVE (again, for simplicity). We have a sample input of 100 patients in csv format for your testing. The function will be graded with another sample input randomly selected from my real data. Comment: For real implementation, We had to clean the data: 1) trim the leading and trailing spaces; 2) add zero to the end for codes with length smaller than 5; 3) consider DRG code; and 4) automate the generation of functions.

Implementation: Function `cmbd`

The function body of `cmbd` is shown as follows:

```
cmbd <- function (data) {
  mat <- as.matrix(data)
  numMat <- gsub("^[Vv]", "32", mat)
  numMat <- gsub("^[Ee]", "15", numMat)
  numMat <- as.numeric(numMat)
  dim(numMat) <- dim(mat)
  funList <- codeFun()
  outDat <- sapply(seq_along(funList),
    function (a, numMat) {
      funList[[a]](numMat)
    }, numMat = numMat)
  colnames(outDat) <- c("CHF", "VALVE")
  data.frame(outDat)
}

codeFun <- function () {
  ## internal function for CHF measures
```

```

chf <- function (numMat) {
  indVec1 <- numMat %in% c(39891, 40201, 40211, 40291, 40401,
                          40403, 40411, 40413, 40491, 40493)
  indVec2 <- numMat >= 42800 & numMat <= 42890
  indMat <- indVec1 | indVec2
  dim(indMat) <- dim(numMat)
  as.integer(rowSums(indMat, na.rm = TRUE) > 0)
}
## internal function for VALVE measures
valve <- function (numMat) {
  indVec1 <- numMat >= 9320 & numMat <= 9324
  indVec2 <- numMat >= 39400 & numMat <= 39710
  indVec3 <- numMat >= 42400 & numMat <= 42499
  indVec4 <- numMat >= 74630 & numMat <= 74660
  indVec5 <- numMat %in% c(324220, 324330, 39790)
  indMat <- indVec1 | indVec2 | indVec3 | indVec4 | indVec5
  dim(indMat) <- dim(numMat)
  as.integer(rowSums(indMat, na.rm = TRUE) > 0)
}
list(chf = chf, valve = valve)
}

```

Result of Sample Dataset

By using the function `cmbd` defined in last section, the diagnosed result for each patient by ICD9 code in sample dataset is shown as follows.

```

sampleDat <- read.csv("icd9sample.csv")
(myRes <- cmbd(sampleDat))

```

```

##      CHF VALVE
## 1      0      0
## 2      1      0
## 3      0      0
## 4      0      0
## 5      0      0
## 6      0      0
## 7      0      1
## 8      0      0
## 9      0      0
## 10     0      0
## 11     0      0
## 12     0      0
## 13     0      0
## 14     0      0
## 15     0      0
## 16     0      0
## 17     0      0
## 18     1      0
## 19     0      0
## 20     0      1

```

## 21	0	0
## 22	0	0
## 23	0	0
## 24	0	0
## 25	0	0
## 26	0	0
## 27	0	0
## 28	0	0
## 29	0	1
## 30	0	0
## 31	1	0
## 32	0	0
## 33	0	0
## 34	0	0
## 35	0	0
## 36	0	0
## 37	0	0
## 38	0	0
## 39	0	0
## 40	0	0
## 41	0	0
## 42	0	0
## 43	0	0
## 44	0	0
## 45	0	0
## 46	0	0
## 47	0	0
## 48	0	1
## 49	0	0
## 50	0	0
## 51	0	0
## 52	0	0
## 53	0	0
## 54	0	0
## 55	0	0
## 56	0	0
## 57	1	1
## 58	0	0
## 59	1	1
## 60	0	0
## 61	0	0
## 62	0	0
## 63	0	0
## 64	0	0
## 65	0	0
## 66	0	0
## 67	0	0
## 68	0	0
## 69	0	0
## 70	0	0
## 71	0	0
## 72	1	0
## 73	0	0
## 74	0	0

```
## 75    0    0
## 76    0    0
## 77    0    0
## 78    0    0
## 79    0    0
## 80    0    0
## 81    1    0
## 82    0    0
## 83    0    0
## 84    1    0
## 85    0    0
## 86    0    0
## 87    0    0
## 88    0    0
## 89    0    0
## 90    0    0
## 91    0    0
## 92    0    0
## 93    0    0
## 94    0    0
## 95    1    0
## 96    0    0
## 97    0    0
## 98    0    0
## 99    0    0
## 100   0    0
```

```
## compare the results with the one from package comorbidities
library(comorbidities)
pkgRes <- (ahrq(sampleDat)[[2]])[, 1:2]
all.equal(pkgRes, myRes) # match if TRUE
```

```
## [1] TRUE
```

Performance

Although function `cmbd` only generate the diagnosis result for CHF and VALVE, from the comparison of computing performance by package `microbenchmark`, we may find that the computing speed of `cmbd` is much faster than function `ahrq` in package `comorbidities`.

```
library(microbenchmark)
microbenchmark(ahrq(sampleDat), cmbd(sampleDat), times = 5)
```

```
## Unit: milliseconds
##      expr      min      lq      mean      median
##  ahrq(sampleDat) 10747.527499 10759.559865 10783.141101 10794.797174
##  cmbd(sampleDat)   1.284635   1.306382   1.352108   1.323691
##      uq      max neval cld
## 10795.949809 10817.871157    5  b
##    1.412956    1.432876    5  a
```