ISYE 6501 HW9

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Question 12.1

Describe a situation or problem from your job, everyday life, current events, etc., for which a design of experiments approach would be appropriate.

Suppose we are the record company running the hip-hop show Rhythm and Flow, we may want to know which candidate of the champion can bring greater benefits to the company, so that the record company will be able to cheat and manipulate the results of the competition behind the scenes.

Since we may have many potential championship candidates, and other candidates may also bring profit to the company, we don't want to lose value. In this case, we can use the Multi Armed Bandit approach. During the last episode before the final, the company can randomly ask an audience to buy virtual currency in order to show his or her support to one of the candidates. Then we can renew the score of this particular candidate, and ask another audience rating another candidate. First, every candidate has equal probability of selecting. But as we keep renewing each candidate's score, the probability of appearance of an individual candidate changes. Finally we are able to have the result of who is likely to be the best. Moreover, if every candidate have an equal probability of appearing, people are less likely to buy virtual currency to support a less popular candidate. Thus we successfully prevent losing money.

Question 12.2

To determine the value of 10 different yes/no features to the market value of a house (large yard, solar roof, etc.), a real estate agent plans to survey 50 potential buyers, showing a fictitious house with different combinations of features. To reduce the survey size, the agent wants to show just 16 fictitious houses. Use R's FrF2 function (in the FrF2 package) to find a fractional factorial design for this experiment: what set of features should each of the 16 fictitious houses have? Note: the output of FrF2 is "1" (include) or "-1" (don't include) for each feature.

We use the FrF2 function to choose 16 different combinations among 10 factors

```
#First, we should load the FrF2 Package
library(FrF2)

## Loading required package: DoE.base

## Loading required package: grid

## Loading required package: conf.design

## Registered S3 method overwritten by 'DoE.base':
##   method           from
##   factorize.factor conf.design

##
## Attaching package: 'DoE.base'

## The following objects are masked from 'package:stats':
##
##     aov, lm

## The following object is masked from 'package:graphics':
##
##     plot.design

## The following object is masked from 'package:base':
##
##     lengths

set.seed(123)
#We choose 10 different factors that affects the value of a house
featureNames=c("A","B","C","D","E","F","G","H","J","K")
#We have 10 different features and we want to test 16 different combina
tions
conbination <- FrF2(nruns = 16,nfactors = 10,factor.names = featureName
s)
#Finally we have the results: in the following chart, 1 means we choose
 that factor, and -1 refers to not included of a certain factor. We can
 use the following 16 combinations:
conbination

##     A  B  C  D  E  F  G  H  J  K
## 1  -1  1  1  1 -1 -1  1 -1  1 -1
## 2   1  1  1  1  1  1  1  1  1  1
## 3  -1  1 -1 -1 -1  1 -1  1  1 -1
## 4   1 -1  1  1 -1  1 -1  1 -1 -1
## 5   1 -1 -1  1 -1 -1  1  1  1  1
## 6   1 -1 -1 -1 -1 -1  1 -1 -1 -1
## 7   1 -1  1 -1 -1  1 -1 -1  1  1
## 8  -1 -1  1 -1  1 -1 -1  1  1 -1
## 9   1  1 -1 -1  1 -1 -1 -1  1  1
## 10  1  1 -1  1  1 -1 -1  1 -1 -1
## 11 -1  1  1 -1 -1 -1  1  1 -1  1
## 12 -1 -1 -1 -1  1  1  1  1 -1  1
## 13 -1  1 -1  1 -1  1 -1 -1 -1  1
## 14 -1 -1  1  1  1 -1 -1 -1 -1  1
## 15  1  1  1 -1  1  1  1 -1 -1 -1
## 16 -1 -1 -1  1  1  1  1 -1  1 -1
## class=design, type= FrF2
```

In this fractional factorial design, each factor is included 8 times, which is half of the total number of conbinations.

```
featureTimes=data.frame(nrow=10,ncol=2)
featureNames=c("A","B","C","D","E","F","G","H","J","K")
for (i in seq(1,10)) {
  name=featureNames[i]
  featureTimes[i,1]=name
  featureTimes[i,2]=nrow(conbination[conbination[,name]==1,name])
}
colnames(featureTimes)=c("Feature id","Included times")
featureTimes

##    Feature id Included times
## 1           A              8
## 2           B              8
## 3           C              8
## 4           D              8
## 5           E              8
## 6           F              8
## 7           G              8
## 8           H              8
## 9           J              8
## 10          K              8
```

And half of the combinations (8 our of 16) include 5 factors. One includes all of the ten factors and oneincludes two factors. Then four include four factors and two include six factors.

```
featureIn=data.frame(nrow=16,ncol=2)
for (i in seq(1,16)) {
  featureIn[i,1]=i
  featureIn[i,2]=ncol(conbination[i,conbination[i,]==1])
}
colnames(featureIn)=c("House No.","Number of included features")
featureIn

##    House No. Number of included features
## 1          1                           5
## 2          2                          10
## 3          3                           4
## 4          4                           5
## 5          5                           6
## 6          6                           2
## 7          7                           5
## 8          8                           4
## 9          9                           5
## 10        10                           5
## 11        11                           5
## 12        12                           5
## 13        13                           4
## 14        14                           4
## 15        15                           6
## 16        16                           5
```

```
cat("frequency:\n");table(featureIn[,2])
```

```
## frequency:
```

```
##
##  2  4  5  6 10
##  1  4  8  2  1
```

Question 14.1

The breast cancer data set breast-cancer-wisconsin.data.txt from http://archive.ics.uci.edu/ml/machine-learning-databases/breast-cancer-wisconsin/ (description at http://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+%28Original%29) has missing values. 1. Use the mean/mode imputation method to impute values for the missing data. 2. Use regression to impute values for the missing data. 3. Use regression with perturbation to impute values for the missing data. 4. (Optional) Compare the results and quality of classification models (e.g., SVM, KNN) build using (1) the data sets from questions 1,2,3; (2) the data that remains after data points with missing values are removed; and (3) the data set when a binary variable is introduced to indicate missing values.

To explore the missing data, we firstly run a frequency table for each column(excluding column 1 which is the ID of each data point). The results show that only one column has missing data and the missing data are represented by “?”.

```
rawData = read.csv("breast-cancer-wisconsin.data.txt",header=F)
for (i in seq(2,ncol(rawData))) {
  print(table(rawData[,i]))
  print(sum(table(rawData[,i])))
}
```

```
##
##   1   2   3   4   5   6   7   8   9  10
## 145  50 108  80 130  34  23  46  14  69
## [1] 699
## 
##   1   2   3   4   5   6   7   8   9  10 
## 384  45  52  40  30  27  19  29   6  67 
## [1] 699
## 
##   1   2   3   4   5   6   7   8   9  10 
## 353  59  56  44  34  30  30  28   7  58 
## [1] 699
## 
##   1   2   3   4   5   6   7   8   9  10 
## 407  58  58  33  23  22  13  25   5  55 
## [1] 699
## 
##   1   2   3   4   5   6   7   8   9  10 
##  47 386  72  48  39  41  12  21   2  31 
## [1] 699
## 
##   ?   1  10   2   3   4   5   6   7   8   9 
##  16 402 132  30  28  19  30   4   8  21   9 
## [1] 699
## 
##   1   2   3   4   5   6   7   8   9  10 
## 152 166 165  40  34  10  73  28  11  20 
## [1] 699
## 
##   1   2   3   4   5   6   7   8   9  10 
## 443  36  44  18  19  22  16  24  16  61 
## [1] 699
## 
##   1   2   3   4   5   6   7   8  10 
## 579  35  33  12   6   3   9   8  14 
## [1] 699
## 
##   2   4 
## 458 241 
## [1] 699
```

So we import the data again and set "?" as missing data. To summary, there are 16 missing data points in column *Bare Nuclei*.

```
rawData = read.csv("breast-cancer-wisconsin.data.txt",header=F,na.strin
g="?")
colnames(rawData)=c("ID","ClumpThickness","UniformityofCellSize",
                    "UniformityofCellShape","MarginalAdhesion",
                    "SingleEpithelialCellSize","BareNuclei",
                    "BlandChromatin","NormalNucleoli",
                    "Mitoses","Class")
rawData[rawData[,"Class"]==2,"Class"]="benign"
rawData[rawData[,"Class"]==4,"Class"]="malignant"
```

```r
rawData$Class=as.factor(rawData$Class)
summary(rawData)
```

```
##        ID           ClumpThickness   UniformityofCellSize
##  Min.   :   61634   Min.   : 1.000   Min.   : 1.000
##  1st Qu.:  870688   1st Qu.: 2.000   1st Qu.: 1.000
##  Median : 1171710   Median : 4.000   Median : 1.000
##  Mean   : 1071704   Mean   : 4.418   Mean   : 3.134
##  3rd Qu.: 1238298   3rd Qu.: 6.000   3rd Qu.: 5.000
##  Max.   :13454352   Max.   :10.000   Max.   :10.000
##
##  UniformityofCellShape MarginalAdhesion SingleEpithelialCellSize
##  Min.   : 1.000        Min.   : 1.000   Min.   : 1.000
##  1st Qu.: 1.000        1st Qu.: 1.000   1st Qu.: 2.000
##  Median : 1.000        Median : 1.000   Median : 2.000
##  Mean   : 3.207        Mean   : 2.807   Mean   : 3.216
##  3rd Qu.: 5.000        3rd Qu.: 4.000   3rd Qu.: 4.000
##  Max.   :10.000        Max.   :10.000   Max.   :10.000
##
##    BareNuclei     BlandChromatin   NormalNucleoli      Mitoses
##  Min.   : 1.000   Min.   : 1.000   Min.   : 1.000   Min.   : 1.000
##  1st Qu.: 1.000   1st Qu.: 2.000   1st Qu.: 1.000   1st Qu.: 1.000
##  Median : 1.000   Median : 3.000   Median : 1.000   Median : 1.000
##  Mean   : 3.545   Mean   : 3.438   Mean   : 2.867   Mean   : 1.589
##  3rd Qu.: 6.000   3rd Qu.: 5.000   3rd Qu.: 4.000   3rd Qu.: 1.000
##  Max.   :10.000   Max.   :10.000   Max.   :10.000   Max.   :10.000
##  NA's   :16
##        Class
##  benign   :458
##  malignant:241
##
##
##
##
##
```

1.Use the mean/mode imputation method to impute values for the missing data.

We use both mean and mode to impute values. But according to the frequency table below, the distribution of *Bare Nuclei* is heavily bi-polared. Most of the data points equal to 1 or 10. We propose that using mode instead of mean seems to be a better option to impute values for the missing data. In question4, we will do further comparation towards mean and mode imputation method.

```r
cat("frequency:");table(rawData[,"BareNuclei"])
```

```
## frequency:

##
##   1   2   3   4   5   6   7   8   9  10
## 402  30  28  19  30   4   8  21   9 132
```

```
# use mode
dataMode=rawData
dataMode[is.na(dataMode[,"BareNuclei"])==T,"BareNuclei"]=1
summary(dataMode[,"BareNuclei"])
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##   1.000   1.000   1.000   3.486   5.000  10.000
```

```
# use mean
dataMean=rawData
dataMean[is.na(dataMean[,"BareNuclei"])==T,"BareNuclei"]=
  mean(dataMean[,"BareNuclei"], na.rm=TRUE)
summary(dataMean[,"BareNuclei"])
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##   1.000   1.000   1.000   3.545   5.000  10.000
```

2.Use regression to impute values for the missing data.

We use *mice* package to impute values using regression. We use all the variables(excluding *BareNuclei* and *ID*) as predicting variables in the regressiong model to predict the value of *BareNuclei*. Results are showed below. And all the predicting values are in the feasible range of *BareNuclei's* value(1 to 10).

```
library(mice)
```

```
## Loading required package: lattice

## 
## Attaching package: 'mice'

## The following object is masked from 'package:DoE.base':
## 
##     make.formulas

## The following objects are masked from 'package:base':
## 
##     cbind, rbind
```

```
dataReg=rawData
model1=mice(dataReg[,2:11], method="norm.predict", m=1, maxit=1, seed=1
234)
```

```
## 
##  iter imp variable
##   1   1  BareNuclei
```

```
model1$imp$BareNuclei
```

```
##            1
## 24  7.201509
## 41  3.412194
## 140 1.200127
## 146 1.588095
## 159 1.271663
## 165 1.444743
## 236 1.960806
## 250 1.407689
## 276 1.625150
## 293 6.343076
## 295 1.219350
## 298 1.000995
## 316 2.005965
## 322 1.407689
## 412 1.200127
## 618 1.048844

dataReg[,2:11]=complete(model1)
```

3.Use regression with perturbation to impute values for the missing data.

We also use *mice* package to impute values using regression with pertrbation. We use all the variables(excluding *BareNuclei* and *ID*) as predicting variables in the regressiong model and add random error terms to the predicted value. Results are showed below. We draw a scatter plot to compare the values from regression and values from regression with perturbation. Most of the points are located away from 45 degree line, which indicates the perturbation.

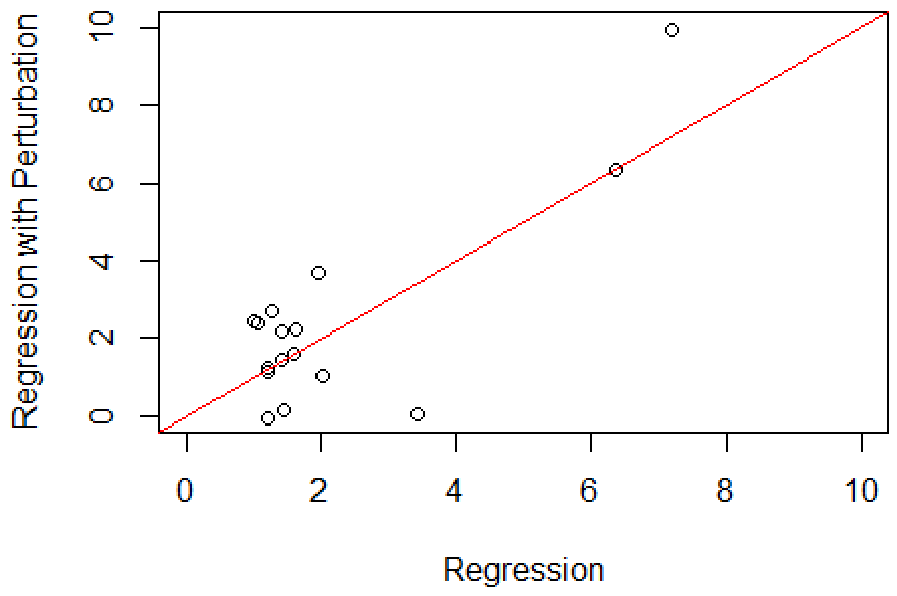
```
library(mice)
dataRegPer=rawData
model2=mice(dataRegPer[,2:11], method="norm.nob", m=1, maxit=1, seed=12
34)

##
##  iter imp variable
##   1   1  BareNuclei

model2$imp$BareNuclei

##                 1
## 24   9.94371380
## 41   0.03484965
## 140 -0.05574598
## 146  1.62475788
## 159  2.68327455
## 165  0.14967372
## 236  3.69855214
## 250  2.15955873
## 276  2.24616931
## 293  6.35309746
## 295  1.14402987
## 298  2.45010184
## 316  1.01169507
## 322  1.43049705
## 412  1.21986249
## 618  2.40646790

plot(model1$imp$BareNuclei[,1], model2$imp$BareNuclei[,1],
     xlim=c(0,10), ylim=c(0,10),
     xlab="Regression", ylab="Regression with Perturbation")
abline(a=0, b=1, col="red")
```



On the other hand, we notice that there are three values out of the feasible range of *BareNuclei*. We search some literatures and two common ways to deal with such issue are: 1) retaining the values, 2) post-imputation rounding(https://bmcmedresmethodol.biomedcentral.com/articles/10.1186/1471-2288-14-57). So we use these two method to deal with the imputed values and compare them in question4.

```
cat("out of range values:\n");sum(model2$imp$BareNuclei<1 | model2$imp
$BareNuclei>10)

## out of range values:

## [1] 3

dataRegPer[,2:11]=complete(model2)
dataRegPerRetain=dataRegPer
dataRegPerRound=dataRegPer
dataRegPerRound[dataRegPerRound$BareNuclei<1,"BareNuclei"]=1
dataRegPerRound[dataRegPerRound$BareNuclei>10,"BareNuclei"]=10
```

4. Compare the results and quality of classification models (e.g., SVM, KNN) build using (1) the data sets from questions 1,2,3; (2) the data that remains after data points with missing values are removed; and (3) the data set when a binary variable is introduced to indicate missing values.

We firstly creat a data set by removing the missing values. Then we introduce the binary variable to indicate missing values in another data set *dataBinary*. We also introduce the interaction terms between the binary variable with all other independent variable into the data set.

```
dataRemove=rawData
dataRemove=na.omit(dataRemove)

dataBinary=rawData
dataBinary$Missing=rep(1,nrow(dataBinary)) # 0=missing, 1=not
dataBinary[is.na(dataBinary$BareNuclei)==T, "Missing"]=0

dependents=c("ClumpThickness","UniformityofCellSize",
          "UniformityofCellShape","MarginalAdhesion",
          "SingleEpithelialCellSize","BlandChromatin",
          "NormalNucleoli","Mitoses")

for (col in dependents) {
  newCol=paste(col,"Interact",sep="")
  dataBinary[,newCol]=dataBinary[,col]*dataBinary$Missing
}

dataBinary[is.na(dataBinary$BareNuclei)==T, "BareNuclei"]=0
```

So to summarize, the approach of dealing with missing data and the corresponding data set we use are:
1). Replace by mode: dataMode
2). Replace by mean: dataMean
3). Use regression to impute values for the missing data: dataReg
4). Use regression with perturbation to impute values for the missing data: dataRegPerRetain
5). Use regression with perturbation to impute values for the missing data and round the values that is out of range to the nearest bound: dataRegPerRound
6). Remove data points with missing values: dataRemove
7). Intordunce binary variable to indicate missing values: dataBinary

We use KNN model to compare the results and quality of these approaches. We split the data into training set and test set. To ensure the results is comparable, the rows of data point in training and in test among different data set is identical. The only exception is *dataRemove*, in which several rows are removed. Our method is to split the data set according to *ID*. For *dataRemove*, the way to split it is also to check whether the *ID* is in training list or test list.

```
# sampling ID for training set
trainingSize=floor(0.75*nrow(rawData))
set.seed(1234)
trainRows=sample(x=rawData[,"ID"],size=trainingSize,replace=F)
```

We use *train.kknn* function to train our KNN model, which apply leave-one-out approach to find the best combination of k and kernel. We build a function upon *train.kknn*, using data set as input and outputing best k and kernel and model quality evaluation via test set (predicting accuracy).

```
library(kknn)
knnRun = function(data) {
  trainset=data[data$ID %in% trainRows==T,2:ncol(data)]
  testset=data[data$ID %in% trainRows==F,2:ncol(data)]
  modelTrain=train.kknn(Class~., trainset, kmax=15,
                        kernel= c("rectangular", "triangular", "epanech
nikov",
                                  "gaussian", "rank", "optimal"))
  testResults=predict(modelTrain, testset)
  return (list("k"=modelTrain$best.parameters$k,
               "kernel"=modelTrain$best.parameters$kernel,
               "accuracy"=sum(testResults==testset$Class)/nrow(testse
t)))
}

# use different data set and make comparison
r=data.frame(ncol=4,nrow=7)

r[1,1]="dataMode"
r[1,2]=knnRun(dataMode)$k
r[1,3]=knnRun(dataMode)$kernel
r[1,4]=knnRun(dataMode)$accuracy

r[2,1]="dataMean"
r[2,2]=knnRun(dataMean)$k
r[2,3]=knnRun(dataMean)$kernel
r[2,4]=knnRun(dataMean)$accuracy

r[3,1]="dataReg"
r[3,2]=knnRun(dataReg)$k
r[3,3]=knnRun(dataReg)$kernel
r[3,4]=knnRun(dataReg)$accuracy

r[4,1]="dataRegPerRetain"
r[4,2]=knnRun(dataRegPerRetain)$k
r[4,3]=knnRun(dataRegPerRetain)$kernel
r[4,4]=knnRun(dataRegPerRetain)$accuracy

r[5,1]="dataRegPerRound"
```

```r
r[5,2]=knnRun(dataRegPerRound)$k
r[5,3]=knnRun(dataRegPerRound)$kernel
r[5,4]=knnRun(dataRegPerRound)$accuracy

r[6,1]="dataRemove"
r[6,2]=knnRun(dataRemove)$k
r[6,3]=knnRun(dataRemove)$kernel
r[6,4]=knnRun(dataRemove)$accuracy

r[7,1]="dataBinary"
r[7,2]=knnRun(dataBinary)$k
r[7,3]=knnRun(dataBinary)$kernel
r[7,4]=knnRun(dataBinary)$accuracy

colnames(r)=c("dataset", "best k", "best kernel", "accuracy")

r

##            dataset best k best kernel  accuracy
## 1         dataMode     15 rectangular 0.9679487
## 2         dataMean      7 rectangular 0.9615385
## 3          dataReg     15 rectangular 0.9679487
## 4 dataRegPerRetain     15 rectangular 0.9679487
## 5  dataRegPerRound     15 rectangular 0.9679487
## 6       dataRemove     11 rectangular 0.9610390
## 7       dataBinary      9 rectangular 0.9487179
```

According to the results above, generally the difference between every missing data imputing approach is small based on our raw data set. We believe it's plausible because there are only 16 missing values in one predictor, which is really a small proportion of the whole data set (699 observations with 9 predictors). If we want to compare between different imputation approaches, a data set with a bit more missing values maybe useful. But we can also recognize two meaningful points in the results. The accuracy of imputing by mean is relatively lower comparing to other approaches. Because the distribution of *BareNuclei* is bi-polar with 402 ones and 132 tens. Mean value is not a good representive of the variable. Second, removing data points with missing values also generates a lower results. We check all independent variables' mean values as well as the distribution of response variable *Class* between missing-value group and none-missing gourp. From the table below we can see that the mean values in missing-value group are relatively low. Besides, the distribution among *Class Benigh* and *Class Malignant* is different. So the data points with missing values may not be random. There seems existing some systematic difference between observations with missing values and other observations. Removing them directly may not be a good choice.

```r
groupcompare=data.frame(nrow=11, ncol=3)
var=c("ClumpThickness","UniformityofCellSize","UniformityofCellShape",
      "MarginalAdhesion","SingleEpithelialCellSize", "BareNuclei",
      "BlandChromatin","NormalNucleoli","Mitoses")
```

```
for (i in seq(1,length(var))){
  groupcompare[i,1]=var[i]
  groupcompare[i,2]=mean(rawData[is.na(rawData$BareNuclei)==T,var[i]])
  groupcompare[i,3]=mean(rawData[is.na(rawData$BareNuclei)==F,var[i]])
}

groupcompare[10,1]="Num.of benigh"
groupcompare[10,2]=sum(rawData[is.na(rawData$BareNuclei)==T,"Class"]=="
benign")
groupcompare[10,3]=sum(rawData[is.na(rawData$BareNuclei)==F,"Class"]=="
benign")

groupcompare[11,1]="Num.of malignant"
groupcompare[11,2]=sum(rawData[is.na(rawData$BareNuclei)==T,"Class"]=="
malignant")
groupcompare[11,3]=sum(rawData[is.na(rawData$BareNuclei)==F,"Class"]=="
malignant")

colnames(groupcompare)=c("variables", "missing-value group", "none-miss
ing group")

groupcompare
```

```
##                   variables missing-value group none-missing group
## 1            ClumpThickness              3.3750           4.442167
## 2      UniformityofCellSize              2.4375           3.150805
## 3     UniformityofCellShape              2.8750           3.215227
## 4          MarginalAdhesion              1.8125           2.830161
## 5  SingleEpithelialCellSize              2.4375           3.234261
## 6                BareNuclei                  NA           3.544656
## 7            BlandChromatin              3.1250           3.445095
## 8            NormalNucleoli              2.7500           2.869693
## 9                   Mitoses              1.0000           1.603221
## 10            Num.of benigh             14.0000         444.000000
## 11         Num.of malignant              2.0000         239.000000
```