

Classification_models_1

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The goal is to help answer whether maternal smoking has an effect on birth weight, applying LDA, QDA, NaiveBayes .

Let's start by loading the data

```
# Load the "infants" dataset
load(url("http://www.stodden.net/StatData/KaiserBabies.rda"))

# Check the data
names(infants)
```

```
## [1] "gestation" "bwt"      "parity"   "age"      "ed"      "ht"
## [7] "wt"        "dage"     "ded"      "dht"      "dwt"     "marital"
## [13] "inc"       "smoke"    "number"
```

```
dim(infants)
```

```
## [1] 1236  15
```

```
## Understand the data
summary(infants)
```

```
##      gestation      bwt      parity      age
## Min.   :148.0   Min.   : 55.0   Min.   : 0.000   Min.   :15.00
## 1st Qu.:272.0   1st Qu.:108.8   1st Qu.: 0.000   1st Qu.:23.00
## Median :280.0   Median :120.0   Median : 1.000   Median :26.00
## Mean   :279.3   Mean   :119.6   Mean   : 1.932   Mean   :27.26
## 3rd Qu.:288.0   3rd Qu.:131.0   3rd Qu.: 3.000   3rd Qu.:31.00
## Max.   :353.0   Max.   :176.0   Max.   :13.000   Max.   :45.00
## NA's    :13                      NA's    :2
##      ed      ht      wt      dage
## No High School : 19   Min.   :53.00   Min.   : 87.0   Min.   :18.00
## Some High School:183   1st Qu.:62.00   1st Qu.:114.8   1st Qu.:25.00
## High School    :444   Median :64.00   Median :125.0   Median :29.00
## Trade          : 65   Mean   :64.05   Mean   :128.6   Mean   :30.35
## Some College   :298   3rd Qu.:66.00   3rd Qu.:139.0   3rd Qu.:34.00
## College        :219   Max.   :72.00   Max.   :250.0   Max.   :62.00
```

```
## Unknown      : 8  NA's :22      NA's :36      NA's :7
##              ded      dht      dwt      marital
## No High School : 33  Min.   :60.0  Min.   :110.0  Married:1208
## Some High School:193 1st Qu.:68.0  1st Qu.:155.0  Once   : 20
## High School    :342 Median :71.0  Median :170.0  Never  : 6
## Trade          : 37 Mean   :70.2  Mean   :171.2  NA's   : 2
## Some College   :265 3rd Qu.:72.0  3rd Qu.:185.0
## College        :347 Max.   :78.0  Max.   :260.0
## Unknown        : 19 NA's   :492  NA's   :499
##              inc      smoke      number
## [2500, 5000) :195  Never      :544  Never   :544
## [6000, 7000) :180  Now        :484  20-29   :195
## [5000, 6000) :179  Until Pregnant: 95  5-9     :167
## [10000, 12500):143 Once, Not Now :103  1-4     :155
## [7000, 8000) :138 Unknown      : 10  10-14   : 75
## [8000, 9000) :126              :    30-39   : 32
## (0ther)      :275              :    (Other): 68
```

According to the objective to examine the effect of maternal smoking on birthweight, I would instead use birth weight to understand the effect and predict maternal smoking because LDA, QDA, and NaiveBayes are classifiers not regression problem.

Data preprocessing

```
## Since dht and dwt have a lot of nulls, fill missing values for dht and dwt with mean of its value
infants$dht[is.na(infants$dht)] <- mean(infants$dht, na.rm = T)
infants$dwt[is.na(infants$dwt)] <- mean(infants$dwt, na.rm = T)
infants$wt[is.na(infants$wt)] <- mean(infants$wt, na.rm = T)

# Remove null from the data
infants = infants[complete.cases(infants), ]

# Recheck the data manipulation
summary(infants)
```

```
##      gestation      bwt      parity      age
## Min.   :181.0  Min.   : 55.0  Min.   : 0.000  Min.   :15.00
## 1st Qu.:272.0  1st Qu.:108.0  1st Qu.: 0.000  1st Qu.:23.00
## Median :280.0  Median :120.0  Median : 1.000  Median :26.00
## Mean   :279.3  Mean   :119.6  Mean   : 1.905  Mean   :27.22
## 3rd Qu.:288.0  3rd Qu.:131.0  3rd Qu.: 3.000  3rd Qu.:31.00
## Max.   :353.0  Max.   :176.0  Max.   :11.000  Max.   :45.00
##
##              ed      ht      wt      dage
## No High School : 19  Min.   :53.00  Min.   : 87.0  Min.   :18.00
## Some High School:174 1st Qu.:62.00  1st Qu.:115.0  1st Qu.:25.00
## High School    :431 Median :64.00  Median :125.0  Median :29.00
## Trade          : 63 Mean   :64.04  Mean   :128.6  Mean   :30.36
## Some College   :285 3rd Qu.:66.00  3rd Qu.:138.2  3rd Qu.:34.00
## College        :213 Max.   :72.00  Max.   :250.0  Max.   :62.00
## Unknown        : 7
```

```
##          ded          dht          dwt          marital
## No High School : 33   Min.   :60.00   Min.   :110.0   Married:1170
## Some High School:183  1st Qu.:70.00   1st Qu.:165.0   Once   : 17
## High School    :329  Median :70.20   Median :171.2   Never  : 5
## Trade          : 37   Mean    :70.23   Mean    :171.2
## Some College   :257  3rd Qu.:71.00   3rd Qu.:175.0
## College        :336  Max.    :78.00   Max.    :260.0
## Unknown        : 17
##          inc          smoke          number
## [2500, 5000) :188   Never           :526   Never   :526
## [6000, 7000) :173   Now             :465   20-29   :187
## [5000, 6000) :171   Until Pregnant: 92   5-9     :162
## [10000, 12500):138  Once, Not Now : 99   1-4     :149
## [7000, 8000) :133   Unknown        : 10   10-14   : 71
## Unknown      :123                      30-39   : 30
## (Other)      :266                      (Other): 67
```

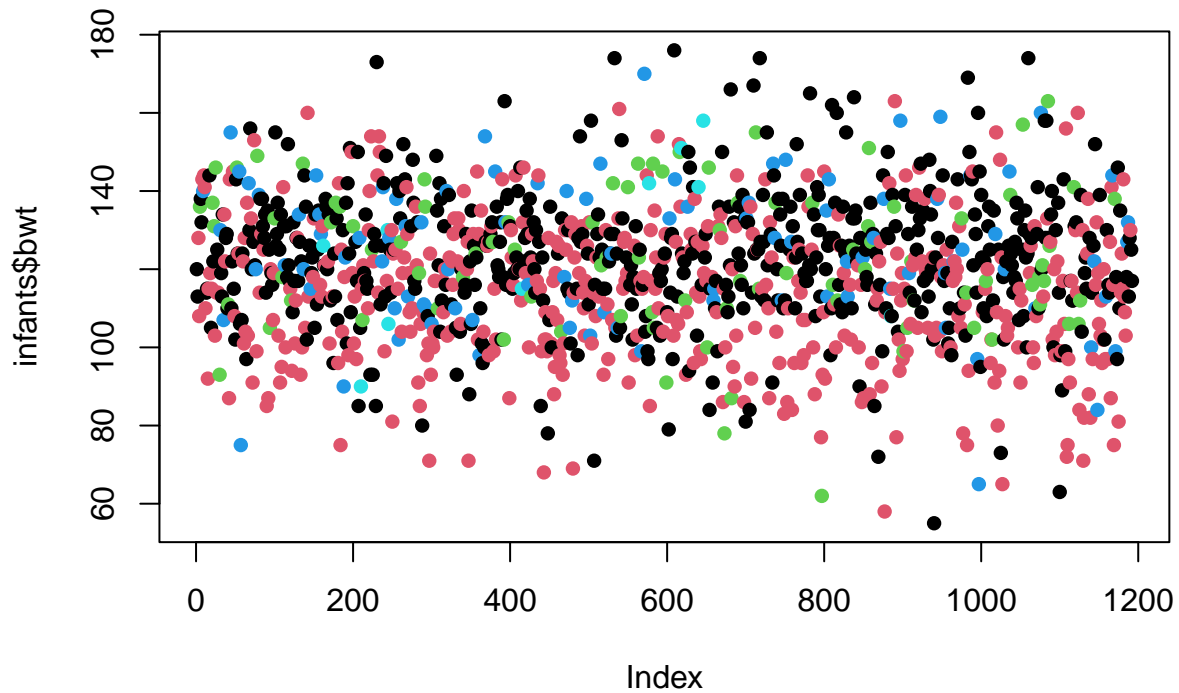
```
dim(infants) # The rows go down from 1236 to 1192
```

```
## [1] 1192 15
```

Now all the NAs are gone

Data understanding

```
# A scatter plot that shows the points in groups according to their "maternal smoke"
plot(infants$bwt,
     pch = 16,
     col = as.numeric(infants$smoke)
)
```



Based on the plot, there is no clear patterns between maternal smoke and birthweight.

Therefore, we need to investigate the relationships using other statistical methods and models.

```
# Correlation plot with qualitative data removal
coorelation = cor(infants[, -c(5, 9, 12, 13, 14, 15)])
coorelation
```

```
##          gestation      bwt      parity      age      ht
## gestation  1.000000000  0.42279626 -0.10584995 -0.0569947688  0.072589084
## bwt        0.422796257  1.000000000  0.02522582  0.0290861580  0.201689082
## parity     -0.105849955  0.02522582  1.000000000  0.5307818279 -0.028562995
## age        -0.056994769  0.02908616  0.53078183  1.00000000000 -0.006682069
## ht         0.072589084  0.20168908 -0.02856300 -0.0066820692  1.000000000
## wt         0.027338316  0.15805223  0.18862310  0.1484914054  0.430845238
## dage       -0.032252953  0.03914802  0.47678154  0.8199498962 -0.029637908
## dht         0.003283079  0.08231169 -0.05045843 -0.0457083338  0.268630217
## dwt         0.003303946  0.11110868  0.05956771 -0.0002038911  0.198270487
##          wt      dage      dht      dwt
## gestation 0.02733832 -0.03225295  0.003283079  0.0033039456
## bwt       0.15805223  0.03914802  0.082311686  0.1111086765
## parity    0.18862310  0.47678154 -0.050458427  0.0595677133
## age       0.14849141  0.81994990 -0.045708334 -0.0002038911
## ht        0.43084524 -0.02963791  0.268630217  0.1982704870
## wt        1.00000000  0.18205187  0.105631547  0.1512449825
```

```
## dage      0.18205187  1.00000000 -0.114784637 -0.0245753234
## dht       0.10563155 -0.11478464  1.000000000  0.5351696900
## dwt       0.15124498 -0.02457532  0.535169690  1.0000000000
```

According to the correlation of the quantitative data, age and dage with a correlation value of 0.82 and dht and dwt with a correlation value of 0.54 have significant correlation values, therefore I will choose only age and dht as representatives because I can randomly pick one from the group.

Initially, we need to split the data into 10-folds cross validation since this k neither suffers from excessively high bias nor very high variance compared to LOOCV.

```
library(caret) # I'll use the caret package to slice the dataset into 10 folds
```

```
## Loading required package: lattice
```

```
set.seed(1)
infants_folds = createFolds(infants$smoke, k = 10)
# From the data of 1,192 rows, I will split the data into 10 training and test dataset
# when k = 10. Each training dataset has 1111 datapoints, and test dataset has 120 datapoints.

infants_folds[1:3] # Note that the values of this list is index, not the actual values.
```

```
## $Fold01
## [1] 1 10 28 40 59 62 81 83 106 111 123 146 147 152 196
## [16] 202 208 229 248 263 277 300 310 321 328 341 350 355 375 407
## [31] 415 418 424 431 440 442 454 468 478 479 484 490 502 510 532
## [46] 544 561 573 579 583 585 590 599 600 609 622 630 643 645 652
## [61] 656 662 672 693 702 728 736 754 762 763 767 771 779 784 802
## [76] 803 804 810 812 819 822 828 834 836 837 839 846 850 869 876
## [91] 877 905 930 933 938 944 953 967 970 982 998 1012 1014 1024 1031
## [106] 1037 1045 1054 1065 1067 1073 1085 1089 1092 1095 1097 1112 1129 1172 1178
##
## $Fold02
## [1] 32 38 39 46 60 68 77 95 97 101 107 148 158 168 169
## [16] 181 193 204 207 209 211 241 244 246 253 269 270 280 286 291
## [31] 301 302 303 312 320 340 343 345 390 391 393 395 396 398 399
## [46] 401 411 417 420 425 428 444 445 475 488 508 511 515 524 538
## [61] 539 546 553 556 565 614 619 651 655 659 667 680 687 690 716
## [76] 718 721 731 756 760 764 793 809 811 816 849 860 865 873 874
## [91] 895 901 910 931 936 955 964 971 985 992 1013 1018 1041 1100 1105
## [106] 1117 1136 1141 1144 1145 1151 1157 1160 1161 1168 1179 1182 1185 1186
##
## $Fold03
## [1] 21 25 56 65 67 104 119 125 127 142 150 157 159 163 170
## [16] 175 180 185 186 189 213 214 224 240 242 245 247 249 257 262
## [31] 274 276 288 293 344 346 361 374 380 404 430 458 467 480 481
## [46] 487 492 496 517 520 521 531 549 552 555 558 563 574 578 581
## [61] 598 626 637 642 648 654 668 682 713 715 726 733 734 739 740
## [76] 742 744 778 782 801 821 843 875 887 914 927 929 934 946 976
## [91] 980 1001 1002 1004 1007 1020 1021 1038 1040 1048 1052 1056 1058 1066 1098
## [106] 1113 1114 1119 1120 1127 1162 1167 1171 1173 1175 1188 1189 1190
```

1. LDA

Implement a function for LDA that uses the K-fold dataset.

```
library(MASS)
## Create a function that takes the index of each fold, fit and predict using LDA
cV.LDA = function(complete_data, i){

  # Training data: not in fold indices
  train = complete_data[-i, ]

  # Test data: all data in the fold indices
  test = complete_data[i, ]

  # fit all variables except dage and dwt due to high correlation
  # ded and ed are very similar so I pick one of them
  lda.fit = lda(smoke ~ . - dage - dwt - ded, data = train)

  # apply the model to the test dataset and obtain predicted classes
  lda.class = predict(lda.fit, test)$class

  # return a data.frame with two columns containing the cross-validated
  # predictions for the fold and the corresponding reference observations
  return(data.frame(Prediction = lda.class,
                    Actual = test$smoke)) # Obtain actual class from the test dataset
}
```

```
# Check test errors for only one class
cV_one_fold = cV.LDA(infants, infants_folds[[1]])
```

```
## Warning in lda.default(x, grouping, ...): variables are collinear
```

```
# Show a confusion matrix and compute test errors
table(cV_one_fold$Prediction, cV_one_fold$Actual)
```

```
##
##               Never Now Until Pregnant Once, Not Now Unknown
##  Never           53   0               0           0         0
##  Now              0  40               6           6         0
##  Until Pregnant   0   4               2           1         0
##  Once, Not Now    0   3               1           2         0
##  Unknown          0   0               0           1         1
```

```
mean(cV_one_fold$Prediction != cV_one_fold$Actual) # Error rate
```

```
## [1] 0.1833333
```

Calculate test errors for all cross validation dataset with $k = 10$

```
# create empty data.frame
lda.cV_all_folds = data.frame(Prediction = numeric(0), Reference = numeric(0))

for(i in infants_folds){
  # add the rows of the fold
  lda.cV_all_folds = rbind(lda.cV_all_folds, cV.LDA(infants, i))
}
```

```
## Warning in lda.default(x, grouping, ...): variables are collinear
## Warning in lda.default(x, grouping, ...): variables are collinear
## Warning in lda.default(x, grouping, ...): variables are collinear
## Warning in lda.default(x, grouping, ...): variables are collinear
## Warning in lda.default(x, grouping, ...): variables are collinear
## Warning in lda.default(x, grouping, ...): variables are collinear
## Warning in lda.default(x, grouping, ...): variables are collinear
## Warning in lda.default(x, grouping, ...): variables are collinear
## Warning in lda.default(x, grouping, ...): variables are collinear
## Warning in lda.default(x, grouping, ...): variables are collinear
```

```
# Show a confusion matrix and compute test errors
table(lda.cV_all_folds$Prediction, lda.cV_all_folds$Actual)
```

```
##
##               Never Now Until Pregnant Once, Not Now Unknown
##   Never           526   5              3              5      0
##   Now              0 397              60              54      0
##   Until Pregnant   0  43              20              19      0
##   Once, Not Now    0  17              8              15      0
##   Unknown          0   3              1              6     10
```

```
mean(lda.cV_all_folds$Prediction != lda.cV_all_folds$Actual) # Error rate
```

```
## [1] 0.1879195
```

2. QDA

Implement a function for QDA that uses the K-fold dataset.

```
## Create a function that takes the index of each fold, fit and predict using QDA
cV.QDA = function(complete_data, i){

  # Training data: not in fold indices
```

```

train = complete_data[-i, ]

# Test data: all data in the fold indices
test = complete_data[i, ]

# fit a model using the training dataset
# I choose to remove all qualitative variables because the QDA model gives an error
qda.fit = qda(smoke ~ . - dage - dwt -ed -ded -marital -inc -number, data = train)

# apply the model to the test dataset and obtain predicted classes
qda.class = predict(qda.fit, test)$class

# return a data.frame with two columns containing the cross-validated
# predictions for the fold and the corresponding reference observations
return(data.frame(Prediction = qda.class,
                  Actual = test$smoke)) # Obtain actual class from the test dataset
}

# Call the above function, train, and predict using QDA

# create empty data.frame
qda.cV_all_folds = data.frame(Prediction = numeric(0), Reference = numeric(0))

for(i in infants_folds){
  # add the rows of the fold
  qda.cV_all_folds = rbind(qda.cV_all_folds, cV.QDA(infants, i))
}

# Show a confusion matrix and compute test errors
table(qda.cV_all_folds$Prediction, qda.cV_all_folds$Actual)

```

```

##
##           Never Now Until Pregnant Once, Not Now Unknown
##  Never           344 213           61           63         8
##  Now             174 248           31           34         2
##  Until Pregnant    2   1           0           0         0
##  Once, Not Now     4   3           0           1         0
##  Unknown           2   0           0           1         0

```

```

mean(qda.cV_all_folds$Prediction != qda.cV_all_folds$Actual) # Error rate

```

```

## [1] 0.5025168

```

3.

Implement a function for NaiveBayes that uses the K-fold dataset.

```

library(e1071)
## Create a function that takes the index of each fold, fit and predict using NaiveBayes

cV.NB = function(complete_data, i){

```



```

# Training data: not in fold indices
train = complete_data[-i, ]

# Test data: all data in the fold indices
test = complete_data[i, ]

# fit all variables except dage and dwt due to high correlation
# ded and ed are very similar so I pick one of them
nb.fit = naiveBayes(smoke ~ . - dage - dwt -ded, data = train)

# apply the model to the test dataset and obtain predicted classes
nb.class = predict(nb.fit, test)

# return a data.frame with two columns containing the cross-validated
# predictions for the fold and the corresponding reference observations
return(data.frame(Prediction = nb.class,
                  Actual = test$smoke)) # Obtain actual class from the test dataset
}

# Call the above function to train and predict using NaiveBayes

# create empty data.frame
nb.cV_all_folds = data.frame(Prediction = numeric(0), Reference = numeric(0))

for(i in infants_folds){
  # add the rows of the fold
  nb.cV_all_folds = rbind(nb.cV_all_folds, cV.NB(infants, i))
}

# Show a confusion matrix and compute test errors
table(nb.cV_all_folds$Prediction, nb.cV_all_folds$Actual)

```

```
##
##               Never Now Until Pregnant Once, Not Now Unknown
##   Never           526   0              0              0      0
##   Now              0 426              75              70      1
##   Until Pregnant   0  16              9               6      0
##   Once, Not Now    0  22              7              22      4
##   Unknown          0   1              1              1      5

```

```
mean(nb.cV_all_folds$Prediction != nb.cV_all_folds$Actual) # Error rate
```

```
## [1] 0.1711409
```

Interpretation

```

# These are the test errors of the methods.
#           Test errors
# 1. LDA  0.1879195

```

```

# Interpretation: the overall accuracy of this model is about 81%, which is quite decent.
# Therefore, according to this model, birthweight together with additional factors
# perform well in predicting and explaining maternal smoking.
# Similarly, we can infer that maternal smoking has an impact on birthweight because of
# a reverse effect.

#          Test errors
# 2. QDA  0.5025168
# Interpretation: the overall accuracy of this model is about 50%, which is closed to
# random chance. According to this model, birthweight together with additional factors do not have
# significant effects on maternal smoking, and therefore maternal smoking does not have
# an impact on birthweight with non-linear relationship.

#          Test errors
# 3. NB   0.1711409
# Interpretation: the overall accuracy of this model is about 83%, which is slightly better
# Therefore, according to this model, birthweight together with additional factors
# perform well in predicting and explaining maternal smoking.
# Similarly, we can infer that maternal smoking has an impact on birthweight because of
# a reverse effect.

```

To compare the performance of these models, I would use test errors as a measurement.

NaiveBayes is the most accurate model of these three because it has the lowest test errors of 0.1711409, following by LDA which has test errors of 0.1879195 and QDA that performs poorly with test errors of 0.5025168.

What make differences between these models are the assumptions that each model holds. To be more specific, LDA assumes that each class from 1...K has a common covariance and that the observations are drawn from a multivariate Gaussian distribution, leading to potentially high bias and low variance trade-off. Even though QDA assumes that the observations are drawn from a multivariate Gaussian distribution, unlike LDA, it does not each class has its own covariance. Finally, NaiveBayes only assumes that within the kth class, the p predictors are independent. As far as I'm concerned, these methods work well when their assumptions hold true, which is, in this case, each class seems to has its own covariance and the predictors are independent.

However, I am of the opinion that the performance of LDA and NaiveBayes models is quite decent, except only the QDA method. As of now, I include only numerical data into the model because it gives errors "some group is too small for 'qda'". Therefore, I am going to improve only qda by using dummy variables to represent qualitative predictors. Hopefully, it will solve the error.

I am going to use 'fastDummies' to handle the work.

```

library('fastDummies')

infants.tranf <- dummy_cols(infants, select_columns = c('ed', 'marital', 'inc' , 'number'),
                             remove_selected_columns = TRUE)

head(infants.tranf)

```

##	gestation	bwt	parity	age	ht	wt	dage	ded	dht	dwt
## 1	284	120	1	27	62	100	31	College	65.0000	110.0000
## 2	282	113	2	33	64	135	38	College	70.0000	148.0000
## 3	279	128	1	28	64	115	32	Some High School	70.2043	171.2008
## 4	282	108	1	23	67	125	24	College	70.2043	171.2008
## 5	286	136	4	25	62	93	28	High School	64.0000	130.0000

```

## 6      244 138      4 33 62 178 37      Some College 70.2043 171.2008
##      smoke ed_No High School ed_Some High School ed_High School ed_Trade
## 1      Never      0      0      0      0
## 2      Never      0      0      0      0
## 3      Now      0      0      1      0
## 4      Now      0      0      0      0
## 5 Until Pregnant 0      0      1      0
## 6      Never      0      0      1      0
##      ed_Some College ed_College ed_Unknown marital_Married marital_Once
## 1      0      1      0      1      0
## 2      0      1      0      1      0
## 3      0      0      0      1      0
## 4      0      1      0      1      0
## 5      0      0      0      1      0
## 6      0      0      0      1      0
##      marital_Never inc_< 2500 inc_[2500, 5000) inc_[5000, 6000) inc_[6000, 7000)
## 1      0      0      1      0      0
## 2      0      0      0      0      0
## 3      0      0      0      1      0
## 4      0      0      1      0      0
## 5      0      0      0      0      0
## 6      0      0      0      0      0
##      inc_[7000, 8000) inc_[8000, 9000) inc_[9000, 10000) inc_[10000, 12500)
## 1      0      0      0      0
## 2      1      0      0      0
## 3      0      0      0      0
## 4      0      0      0      0
## 5      1      0      0      0
## 6      0      0      0      0
##      inc_[12500, 15000) inc_15000+ inc_Unknown number_Never number_1-4 number_5-9
## 1      0      0      0      1      0      0
## 2      0      0      0      1      0      0
## 3      0      0      0      0      1      0
## 4      0      0      0      0      0      0
## 5      0      0      0      0      0      1
## 6      0      0      1      1      0      0
##      number_10-14 number_15-19 number_20-29 number_30-39 number_40-60 number_60+
## 1      0      0      0      0      0      0
## 2      0      0      0      0      0      0
## 3      0      0      0      0      0      0
## 4      0      0      1      0      0      0
## 5      0      0      0      0      0      0
## 6      0      0      0      0      0      0
##      number_Unknown
## 1      0
## 2      0
## 3      0
## 4      0
## 5      0
## 6      0

```

Redefine variables in QDA with the dummy variables

```
## Create a function that takes the index of each fold, fit and predict using QDA
cV.QDA = function(complete_data, i){

  # Training data: not in fold indices
  train = complete_data[-i, ]

  # Test data: all data in the fold indices
  test = complete_data[i, ]

  # fit a model using the training dataset
  # I choose to remove all qualitative variables except smoke because the QDA model gives an error
  qda.fit = qda(smoke ~ . - dage - dwt -ded, data = train)

  # apply the model to the test dataset and obtain predicted classes
  qda.class = predict(qda.fit, test)$class

  # return a data.frame with two columns containing the cross-validated
  # predictions for the fold and the corresponding reference observations
  return(data.frame(Prediction = qda.class,
                    Actual = test$smoke)) # Obtain actual class from the test dataset
}

# Call the above function, train, and predict using QDA

# create empty data.frame
#qda.cV_all_folds = data.frame(Prediction = numeric(0), Reference = numeric(0))

#for(i in infants_folds){
  # add the rows of the fold
  #qda.cV_all_folds = rbind(qda.cV_all_folds, cV.QDA(infants.transf, i))
#}

# Show a confusion matrix and compute test errors
#table(qda.cV_all_folds$Prediction, qda.cV_all_folds$Actual)
#mean(qda.cV_all_folds$Prediction != qda.cV_all_folds$Actual) # Error rate

## I still get this error so I need to comment the code above.
# Error in qda.default(x, grouping, ...) :
# some group is too small for 'qda'
```

Unfortunately, I still get the same errors, meaning the dummy variables did not help solve the error. Therefore, I would recommend to use other methods instead of qda to fit the data in order to improve the model performance.