chronic kidney disease

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chronic kidney disease dataset analysis

data preparation

```
library(caret)
library(ggplot2)
library(corrplot)
library(dplyr)
library(reshape2)
library(glmnet)
```

```
file_path <- '/Users/apple/Desktop/me/WCM/semester/fall1/biosta1/final/kidney_disease.
df <- read.csv(file_path)
#str(df)
head(df)
```

```
  Patient.ID Age.of.the.patient Blood.Pressure Specific.Gravity..urine.
1       id,k                age             bp                       sg
2          0                 48             80                     1.02
3          1                  7             50                     1.02
4          2                 62             80                     1.01
5          3                 48             70                    1.005
6          4                 51             80                     1.01
  Albumin.in.urine Sugar.in.urine Red.Blood.Cells.in.urine Pus.Cells.in.urine
1               al             su                      rbc                 pc
2                1              0                                      normal
3                4              0                                      normal
4                2              3                   normal             normal
5                4              0                   normal           abnormal
6                2              0                   normal             normal
  Pus.Cell.Clumps Bacteria.in.urine Blood.Glucose.Random Blood.Urea
1             pcc                ba                  bgr         bu
2      notpresent        notpresent                  121         36
3      notpresent        notpresent                              18
4      notpresent        notpresent                  423         53
5         present        notpresent                  117         56
6      notpresent        notpresent                  106         26
  Serum.Creatinine Sodium.in.blood Potassium.in.blood Hemoglobin.level
1               sc             sod                pot             hemo
2              1.2                                                15.4
3              0.8                                                11.3
4              1.8                                                 9.6
5              3.8             111                2.5             11.2
6              1.4                                                11.6
  Packed.Cell.Volume..Hematocrit. White.Blood.Cell.Count Red.Blood.Cell.Count
```

```
1                            pcv                    wc                   rc
2                             44                  7800                  5.2
3                             38                  6000
4                             31                  7500
5                             32                  6700                  3.9
6                             35                  7300                  4.6
  Hypertension Diabetes.Mellitus Coronary.Artery.Disease Appetite
1          htn                dm                     cad    appet
2          yes               yes                      no     good
3           no                no                      no     good
4           no               yes                      no     poor
5          yes                no                      no     poor
6           no                no                      no     good
  Pedal.Edema..swelling.of.legs. Anemia Diagnosis.label
1                             pe    ane  classification
2                             no     no             ckd
3                             no     no             ckd
4                             no    yes             ckd
5                            yes    yes             ckd
6                             no     no             ckd
```

First check duplicated rows.

```
#check duplicated rows
sum(duplicated(df))
```

```
[1] 0
```

```
#df[duplicated(df),]
```

Delete extra columns, such as the ID column. Classify the numerical and categorical data.

```
df <- subset(df, select = -Patient.ID)#please run this for one first time
#df <- df[, !names(df) %in% c("id")]
#str(df)
#colnames(df)

#name the numerical and categorical data
num_cols <- c(
  "Age.of.the.patient",
  "Blood.Pressure",
  "Specific.Gravity..urine.",
  "Blood.Glucose.Random",
  "Blood.Urea",
  "Serum.Creatinine",
  "Sodium.in.blood",
  "Potassium.in.blood",
  "Hemoglobin.level",
  "Packed.Cell.Volume..Hematocrit.",
  "White.Blood.Cell.Count",
  "Red.Blood.Cell.Count"
)

df[num_cols] <- lapply(df[num_cols], function(x) as.numeric(x))
```

```
str(df)
```

```
'data.frame':	401 obs. of  25 variables:
 $ Age.of.the.patient             : num  NA 48 7 62 48 51 60 68 24 52 ...
 $ Blood.Pressure                 : num  NA 80 50 80 70 80 90 70 NA 100 ...
 $ Specific.Gravity..urine.       : num  NA 1.02 1.02 1.01 1 ...
 $ Albumin.in.urine               : chr  "al" "1" "4" "2" ...
 $ Sugar.in.urine                 : chr  "su" "0" "0" "3" ...
 $ Red.Blood.Cells.in.urine       : chr  "rbc" "" "" "normal" ...
 $ Pus.Cells.in.urine             : chr  "pc" "normal" "normal" "normal" ...
 $ Pus.Cell.Clumps                : chr  "pcc" "notpresent" "notpresent" "notpresent" 
...
 $ Bacteria.in.urine              : chr  "ba" "notpresent" "notpresent" "notpresent" 
...
 $ Blood.Glucose.Random           : num  NA 121 NA 423 117 106 74 100 410 138 ...
 $ Blood.Urea                     : num  NA 36 18 53 56 26 25 54 31 60 ...
 $ Serum.Creatinine               : num  NA 1.2 0.8 1.8 3.8 1.4 1.1 24 1.1 1.9 ...
 $ Sodium.in.blood                : num  NA NA NA NA 111 NA 142 104 NA NA ...
 $ Potassium.in.blood             : num  NA NA NA NA 2.5 NA 3.2 4 NA NA ...
 $ Hemoglobin.level               : num  NA 15.4 11.3 9.6 11.2 11.6 12.2 12.4 12.4 
10.8 ...
 $ Packed.Cell.Volume..Hematocrit.: num  NA 44 38 31 32 35 39 36 44 33 ...
 $ White.Blood.Cell.Count         : num  NA 7800 6000 7500 6700 7300 7800 NA 6900 9600 
...
 $ Red.Blood.Cell.Count           : num  NA 5.2 NA NA 3.9 4.6 4.4 NA 5 4 ...
 $ Hypertension                   : chr  "htn" "yes" "no" "no" ...
 $ Diabetes.Mellitus              : chr  "dm" "yes" "no" "yes" ...
 $ Coronary.Artery.Disease        : chr  "cad" "no" "no" "no" ...
 $ Appetite                       : chr  "appet" "good" "good" "poor" ...
 $ Pedal.Edema..swelling.of.legs. : chr  "pe" "no" "no" "no" ...
 $ Anemia                         : chr  "ane" "no" "no" "yes" ...
 $ Diagnosis.label                : chr  "classification" "ckd" "ckd" "ckd" ...
```

```
cat_cols <- names(df)[sapply(df, is.character) | sapply(df, is.factor)]
#num_col <- names(df)[!(sapply(df, is.character) | sapply(df, is.factor))]
#
cat_cols
```

```
 [1] "Albumin.in.urine"               "Sugar.in.urine"
 [3] "Red.Blood.Cells.in.urine"       "Pus.Cells.in.urine"
 [5] "Pus.Cell.Clumps"                "Bacteria.in.urine"
 [7] "Hypertension"                   "Diabetes.Mellitus"
 [9] "Coronary.Artery.Disease"        "Appetite"
[11] "Pedal.Edema..swelling.of.legs." "Anemia"
[13] "Diagnosis.label"
```

```
#num_col

#summary(df)
```

Deal with “tab”.

```
df <- df[-1,]
#delete the first row:  df <- df[-1, ]
#delete the first two rows: df <- df[-c(1,2), ]
#delete the i th row:   df <- df[-i, ]
#remain 2 to all rows   df <- df[2:nrow(df), ]
#head(df)

df$`Diabetes.Mellitus` <- gsub("\\\tno", "no", df$`Diabetes.Mellitus`)
df$`Diabetes.Mellitus` <- gsub("\\\tyes", "yes", df$`Diabetes.Mellitus`)

df$`Coronary.Artery.Disease` <- gsub("\\\tno", "no", df$`Coronary.Artery.Disease`)
df$`Coronary.Artery.Disease` <- gsub("\\\tyes", "yes", df$`Coronary.Artery.Disease`)

df$Diagnosis.label  <- gsub("ckd\\\t", "ckd", df$Diagnosis.label )
#summary(df)
```

Deal with NAs.

```
colSums(is.na(df))
```

```
                Age.of.the.patient                     Blood.Pressure 
                                 9                                 12 
          Specific.Gravity..urine.                   Albumin.in.urine 
                                47                                  0 
                    Sugar.in.urine            Red.Blood.Cells.in.urine 
                                 0                                  0 
                Pus.Cells.in.urine                    Pus.Cell.Clumps 
                                 0                                  0 
                 Bacteria.in.urine                Blood.Glucose.Random 
                                 0                                 44 
                       Blood.Urea                   Serum.Creatinine 
                                19                                 17 
                   Sodium.in.blood                 Potassium.in.blood 
                                87                                 88 
                  Hemoglobin.level Packed.Cell.Volume..Hematocrit. 
                                52                                 71 
           White.Blood.Cell.Count              Red.Blood.Cell.Count 
                               106                                131 
                      Hypertension                  Diabetes.Mellitus 
                                 0                                  0 
           Coronary.Artery.Disease                           Appetite 
                                 0                                  0 
 Pedal.Edema..swelling.of.legs.                              Anemia 
                                 0                                  0 
                   Diagnosis.label 
                                 0 
```

Missing value imputation methods:

1. For numerical variables (e.g., age, blood pressure, blood sugar): Randomly select some values from the known non-missing values of the column and replace the missing values. • If the mean or median is used for imputation, all missing values will be replaced with the same number, which will reduce the variance of the variable and cause the data to be “oversmoothed”. Random

imputation allows the imputed values to maintain the true distribution characteristics of the data (e.g., the probability that people with high blood sugar will take higher values and people with low blood sugar will take lower values is still preserved). After this processing, the model training will not lose information diversity due to a large number of identical values.

2. For categorical variables: We replace missing values with the value that appears most frequently (mode). These variables have no continuous relationship (they cannot be averaged or randomly selected), and mode imputation is the most natural choice because it preserves the main distribution of the data; it does not introduce invalid categories; and it has the least impact on model bias.

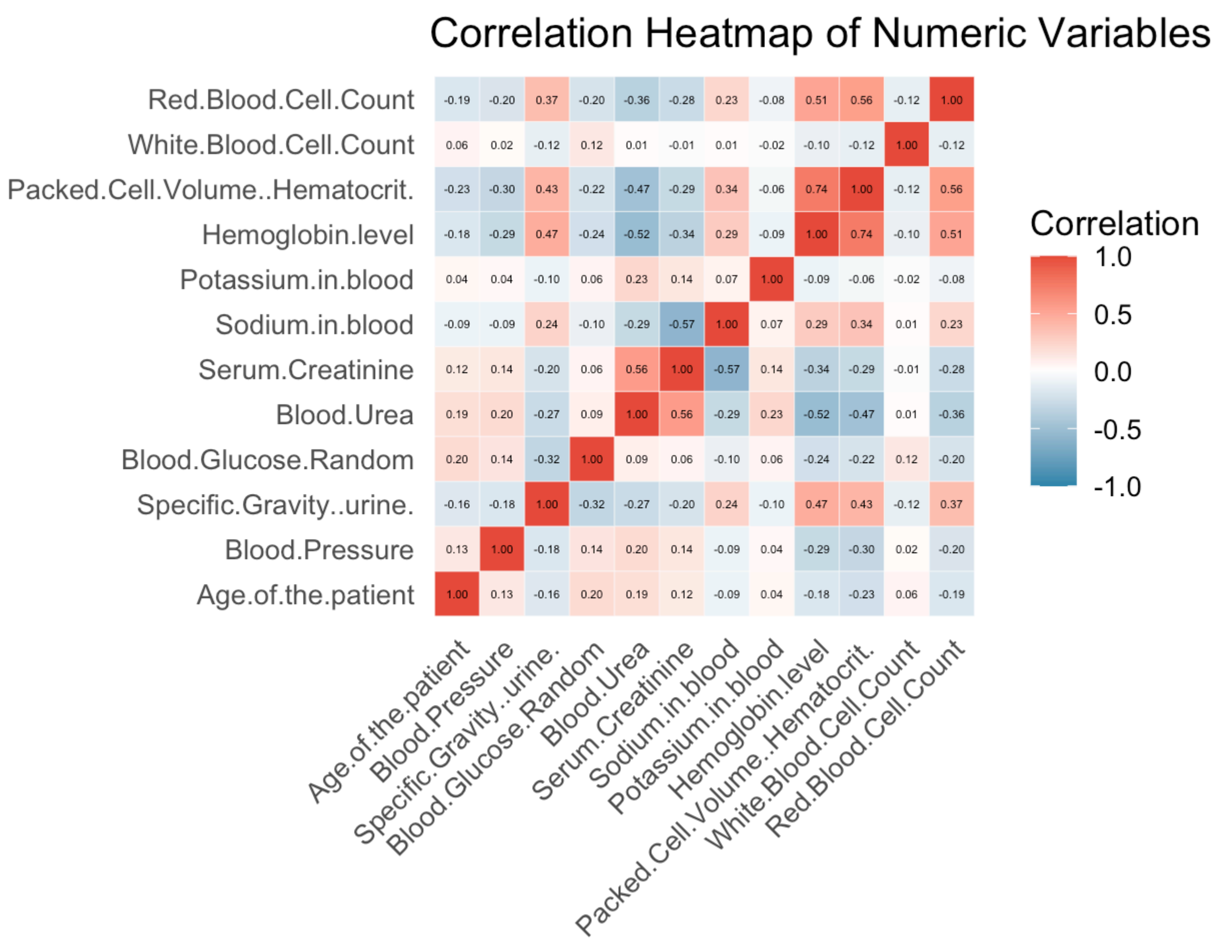
```
#random -- NA--numeric
Random_value_Imputation <- function(x, seed=42) {
  set.seed(seed)
  na_index <- is.na(x)
  x[na_index] <- sample(x[!na_index], sum(na_index), replace=TRUE)
  return(x)
}# "Albumin.in.urine"                "Sugar.in.urine"

#mode -- NA--cate
impute_mode <- function(x, seed=42) {
  set.seed(seed)
  mode_val <- names(sort(table(x), decreasing = TRUE))[1]
  x[is.na(x)] <- mode_val
  return(x)
}

#num_cols
#cat_cols
for (col in num_cols) {
  df[[col]] <- Random_value_Imputation(df[[col]], seed=203)
}
for (col in cat_cols) {
  df[[col]] <- impute_mode(df[[col]], seed=203)
}
```

Draw a heatmap.

Drawing a correlation plot is essential: If a high correlation is found (|r| > 0.8), it is recommended to remove one of the variables; If there are many variables, run vif() first and then delete them; Variable selection is best done after cleaning and before modeling; If you want to predict (rather than explain), you can use penalized regression for automatic selection.

```
num_data <- df[, num_cols]

#make sure it's all numeric
num_data <- mutate_all(num_data, function(x) as.numeric(as.character(x)))

#complete.obs omits NA
corr_matrix <- cor(num_data, use = "complete.obs")
#turn it into matrix
corr_melt <- melt(corr_matrix)
```

```r
ggplot(corr_melt, aes(x = Var1, y = Var2, fill = value)) +
  geom_tile(color = "white") +
  scale_fill_gradient2(low = "#2E86AB", mid = "white", high = "#E74C3C",
                       midpoint = 0, limit = c(-1, 1), name = "Correlation") +
  theme_minimal(base_size = 13) +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust = 1),
        panel.grid = element_blank(),
        axis.title = element_blank()) +
  coord_fixed() +
  geom_text(aes(label = sprintf("%.2f", value)), size = 1.5, color = "black") +
  labs(title = "Correlation Heatmap of Numeric Variables")
```



Perform label encoding for categorical variables

```r
summary(df)
```

```
Age.of.the.patient Blood.Pressure   Specific.Gravity..urine.
Min.   : 2.00      Min.   : 50.00   Min.   :1.005
1st Qu.:42.00      1st Qu.: 70.00   1st Qu.:1.010
Median :54.00      Median : 80.00   Median :1.020
Mean   :51.56      Mean   : 76.53   Mean   :1.017
3rd Qu.:64.25      3rd Qu.: 80.00   3rd Qu.:1.020
Max.   :90.00      Max.   :180.00   Max.   :1.025
Albumin.in.urine   Sugar.in.urine     Red.Blood.Cells.in.urine
Length:400         Length:400         Length:400
Class :character   Class :character   Class :character
```

```
 Mode  :character   Mode  :character   Mode  :character  



 Pus.Cells.in.urine Pus.Cell.Clumps    Bacteria.in.urine  Blood.Glucose.Random
 Length:400         Length:400         Length:400         Min.   : 22.0       
 Class :character   Class :character   Class :character   1st Qu.:100.0       
 Mode  :character   Mode  :character   Mode  :character   Median :122.0       
                                                          Mean   :149.9       
                                                          3rd Qu.:169.0       
                                                          Max.   :490.0       
   Blood.Urea     Serum.Creatinine Sodium.in.blood Potassium.in.blood
 Min.   :  1.50   Min.   : 0.400   Min.   :  4.5   Min.   : 2.500    
 1st Qu.: 27.00   1st Qu.: 0.900   1st Qu.:135.0   1st Qu.: 3.800    
 Median : 44.00   Median : 1.300   Median :138.0   Median : 4.400    
 Mean   : 58.65   Mean   : 3.100   Mean   :137.6   Mean   : 4.774    
 3rd Qu.: 68.00   3rd Qu.: 2.825   3rd Qu.:142.0   3rd Qu.: 4.900    
 Max.   :391.00   Max.   :76.000   Max.   :163.0   Max.   :47.000    
 Hemoglobin.level Packed.Cell.Volume..Hematocrit. White.Blood.Cell.Count
 Min.   : 3.10    Min.   : 9.00                   Min.   : 2200         
 1st Qu.:10.30    1st Qu.:32.75                   1st Qu.: 6400         
 Median :12.60    Median :40.00                   Median : 8000         
 Mean   :12.47    Mean   :38.92                   Mean   : 8357         
 3rd Qu.:15.00    3rd Qu.:45.00                   3rd Qu.: 9800         
 Max.   :17.80    Max.   :54.00                   Max.   :26400         
 Red.Blood.Cell.Count Hypertension       Diabetes.Mellitus 
 Min.   :2.100        Length:400         Length:400        
 1st Qu.:3.900        Class :character   Class :character  
 Median :4.700        Mode  :character   Mode  :character  
 Mean   :4.709                                             
 3rd Qu.:5.400                                             
 Max.   :8.000                                             
 Coronary.Artery.Disease   Appetite         Pedal.Edema..swelling.of.legs.
 Length:400              Length:400         Length:400                    
 Class :character        Class :character   Class :character              
 Mode  :character        Mode  :character   Mode  :character              



    Anemia          Diagnosis.label   
 Length:400         Length:400        
 Class :character   Class :character  
 Mode  :character   Mode  :character  
```

```
#colSums(is.na(df))
head(df)
```

```
  Age.of.the.patient Blood.Pressure Specific.Gravity..urine. Albumin.in.urine
2                 48             80                    1.020                1
3                  7             50                    1.020                4
```

```
4                 62             80                      1.010                 2
5                 48             70                      1.005                 4
6                 51             80                      1.010                 2
7                 60             90                      1.015                 3
  Sugar.in.urine Red.Blood.Cells.in.urine Pus.Cells.in.urine Pus.Cell.Clumps
2              0                                      normal      notpresent
3              0                                      normal      notpresent
4              3                   normal             normal      notpresent
5              0                   normal           abnormal         present
6              0                   normal             normal      notpresent
7              0                                                  notpresent
  Bacteria.in.urine Blood.Glucose.Random Blood.Urea Serum.Creatinine
2        notpresent                  121         36              1.2
3        notpresent                  230         18              0.8
4        notpresent                  423         53              1.8
5        notpresent                  117         56              3.8
6        notpresent                  106         26              1.4
7        notpresent                   74         25              1.1
  Sodium.in.blood Potassium.in.blood Hemoglobin.level
2             144                5.0             15.4
3             140                3.5             11.3
4             140                4.0              9.6
5             111                2.5             11.2
6             147                4.1             11.6
7             142                3.2             12.2
  Packed.Cell.Volume..Hematocrit. White.Blood.Cell.Count Red.Blood.Cell.Count
2                              44                   7800                  5.2
3                              38                   6000                  5.8
4                              31                   7500                  3.7
5                              32                   6700                  3.9
6                              35                   7300                  4.6
7                              39                   7800                  4.4
  Hypertension Diabetes.Mellitus Coronary.Artery.Disease Appetite
2          yes               yes                      no     good
3           no                no                      no     good
4           no               yes                      no     poor
5          yes                no                      no     poor
6           no                no                      no     good
7          yes               yes                      no     good
  Pedal.Edema..swelling.of.legs. Anemia Diagnosis.label
2                             no     no             ckd
3                             no     no             ckd
4                             no    yes             ckd
5                            yes    yes             ckd
6                             no     no             ckd
7                            yes     no             ckd
```

```r
#df<-subset(df,select = -Patient.ID)
cat_cols <- setdiff(cat_cols, "Patient.ID")


# Perform label encoding for categorical variables
df$Hypertension <- as.integer(factor(df$Hypertension))
df$Diabetes.Mellitus <- as.integer(factor(df$Diabetes.Mellitus))
```

```
df$Coronary.Artery.Disease <- as.integer(factor(df$Coronary.Artery.Disease))
df$Appetite <- as.integer(factor(df$Appetite))
df$Pedal.Edema..swelling.of.legs. <- as.integer(factor(df$Pedal.Edema..swelling.of.leg
df$Anemia <- as.integer(factor(df$Anemia))
df$Red.Blood.Cells.in.urine <- as.integer(factor(df$Red.Blood.Cells.in.urine))
df$Albumin.in.urine <- as.integer(factor(df$Albumin.in.urine))
df$Sugar.in.urine <- as.integer(factor(df$Sugar.in.urine))
df$Pus.Cells.in.urine <- as.integer(factor(df$Pus.Cells.in.urine))
df$Pus.Cell.Clumps <- as.integer(factor(df$Pus.Cell.Clumps))
df$Bacteria.in.urine <- as.integer(factor(df$Bacteria.in.urine))
df$ Diagnosis.label <- as.integer(factor(df$ Diagnosis.label))
cat_cols
```

```
 [1] "Albumin.in.urine"                "Sugar.in.urine"
 [3] "Red.Blood.Cells.in.urine"        "Pus.Cells.in.urine"
 [5] "Pus.Cell.Clumps"                 "Bacteria.in.urine"
 [7] "Hypertension"                    "Diabetes.Mellitus"
 [9] "Coronary.Artery.Disease"         "Appetite"
[11] "Pedal.Edema..swelling.of.legs."  "Anemia"
[13] "Diagnosis.label"
```

```
#str(df)

sapply(df, is.numeric)
```

```
             Age.of.the.patient                  Blood.Pressure
                           TRUE                            TRUE
      Specific.Gravity..urine.                Albumin.in.urine
                           TRUE                            TRUE
                 Sugar.in.urine        Red.Blood.Cells.in.urine
                           TRUE                            TRUE
             Pus.Cells.in.urine                 Pus.Cell.Clumps
                           TRUE                            TRUE
              Bacteria.in.urine             Blood.Glucose.Random
                           TRUE                            TRUE
                     Blood.Urea                Serum.Creatinine
                           TRUE                            TRUE
                Sodium.in.blood              Potassium.in.blood
                           TRUE                            TRUE
               Hemoglobin.level Packed.Cell.Volume..Hematocrit.
                           TRUE                            TRUE
        White.Blood.Cell.Count             Red.Blood.Cell.Count
                           TRUE                            TRUE
                   Hypertension               Diabetes.Mellitus
                           TRUE                            TRUE
        Coronary.Artery.Disease                        Appetite
                           TRUE                            TRUE
 Pedal.Edema..swelling.of.legs.                          Anemia
                           TRUE                            TRUE
                Diagnosis.label
                           TRUE
```

```r
index <- createDataPartition(df$ Diagnosis.label, p = 0.8, list = FALSE)
train_data <- df[index, ]
test_data <- df[-index, ]

#Convert tags to binary; machine learning models typically require binary tags.
train_data$ Diagnosis.label <- ifelse(train_data$ Diagnosis.label == 2, 1, 0)
test_data$ Diagnosis.label <- ifelse(test_data$ Diagnosis.label == 2, 1, 0)

#split X / y
X_train <- as.matrix(train_data[, -which(names(train_data) == "Diagnosis.label")])
X_test  <- as.matrix(test_data[, -which(names(test_data) == "Diagnosis.label")])
y_train <- train_data$ Diagnosis.label
y_test  <- test_data$ Diagnosis.label

#summary(train_data)
```

GLM Modeling

```r
log_model <- glm( Diagnosis.label ~ ., data = train_data, family = binomial)
y_pred_prob <- predict(log_model, test_data, type = "response")
y_pred <- ifelse(y_pred_prob > 0.5, 1, 0)

acc <- mean(y_pred == test_data$ Diagnosis.label)

print(acc)
```

```
[1] 1
```

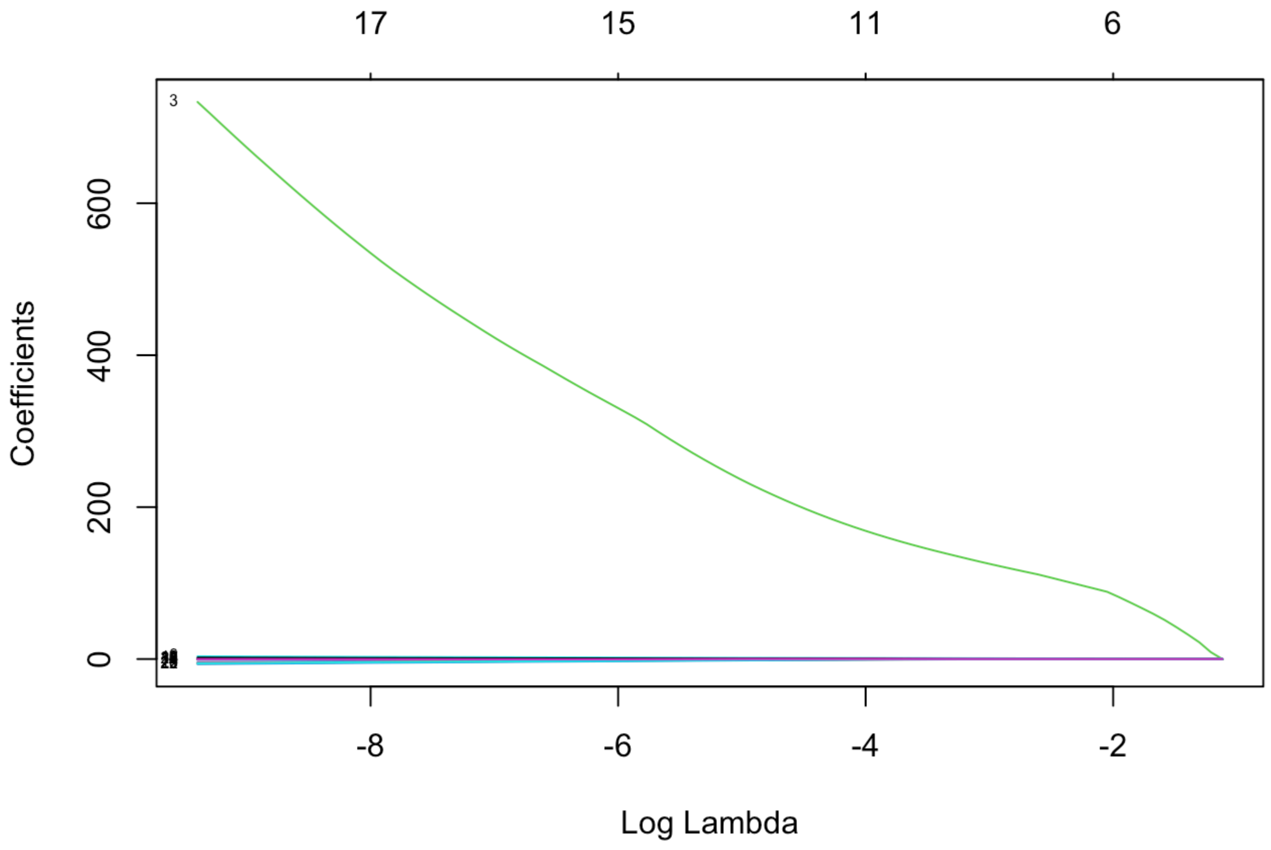
CKD data is typical: indicators like urine protein (albumin-in-urine), urine glucose, and pus cells in urine, once they reach a certain level, almost always indicate CKD; while normal levels almost never indicate CKD. This is the worst-case scenario for logistic regression: one or two variables that can almost separate 0 and 1.

The simplest approach to this type of problem is to use glmnet, not the bare glm(). This is because the penalty term prevents the coefficients from going to infinity.

```r
#make matrix
x_train <- model.matrix(Diagnosis.label ~ ., data = train_data)[, -1]
y_train <- train_data$Diagnosis.label

fit <- glmnet(x_train, y_train, family = "binomial")

#predict
x_test <- model.matrix(Diagnosis.label ~ ., data = test_data)[, -1]
y_pred_prob <- predict(fit, newx = x_test, s = 0.01, type = "response")
y_pred <- ifelse(y_pred_prob > 0.5, 1, 0)
mean(y_pred == test_data$Diagnosis.label)
```

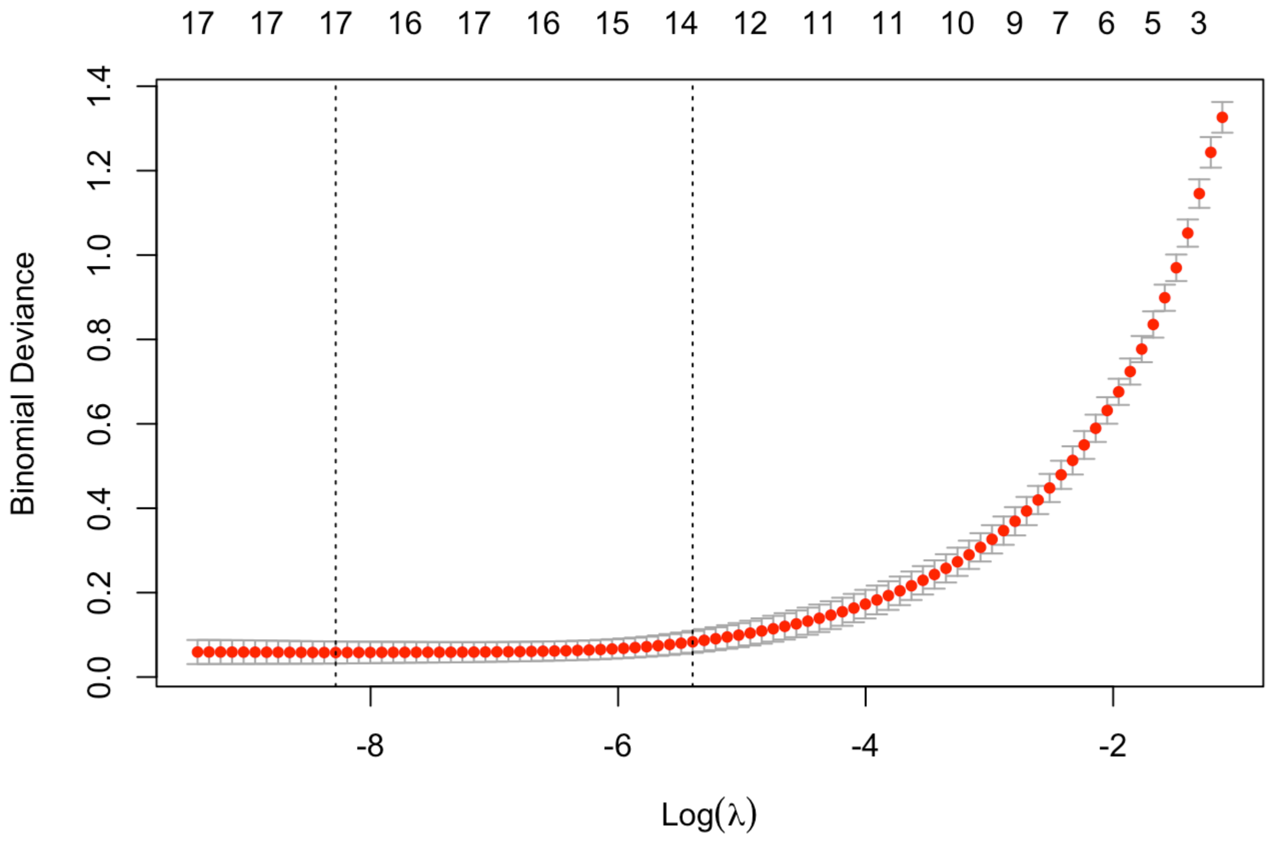
```
[1] 1
```

```r
plot(fit, xvar = "lambda", label = TRUE)
```



About glm choosing lambda.

```
set.seed(50)
cvfit <- cv.glmnet(x_train, y_train, family = "binomial", alpha = 1)

plot(cvfit)
```



```
cvfit$lambda.min   #best λ
```

```
[1] 0.0002530825
```

```
cvfit$lambda.1se   #stable λ
```

```
[1] 0.004526759
```

left → lambda.min (λ with the smallest error) right → lambda.1se (easiest and stable λ)

Linear regression

```
dat <- df
cat_cols
```

```
 [1] "Albumin.in.urine"                "Sugar.in.urine"
 [3] "Red.Blood.Cells.in.urine"        "Pus.Cells.in.urine"
 [5] "Pus.Cell.Clumps"                 "Bacteria.in.urine"
 [7] "Hypertension"                    "Diabetes.Mellitus"
 [9] "Coronary.Artery.Disease"         "Appetite"
[11] "Pedal.Edema..swelling.of.legs." "Anemia"
[13] "Diagnosis.label"
```

```
#split(num_cols,f = ",",sep = "+")
#find names
```

```r
paste(cat_cols, collapse = "+")
```

```
[1]
"Albumin.in.urine+Sugar.in.urine+Red.Blood.Cells.in.urine+Pus.Cells.in.urine+Pus.Cell.
Clumps+Bacteria.in.urine+Hypertension+Diabetes.Mellitus+Coronary.Artery.Disease+Appeti
te+Pedal.Edema..swelling.of.legs.+Anemia+Diagnosis.label"
```

```r
#independent variables
lm_fit <- lm(Diagnosis.label ~  Hemoglobin.level+Albumin.in.urine+Sugar.in.urine+Red.B

             data = dat)

summary(lm_fit)
```

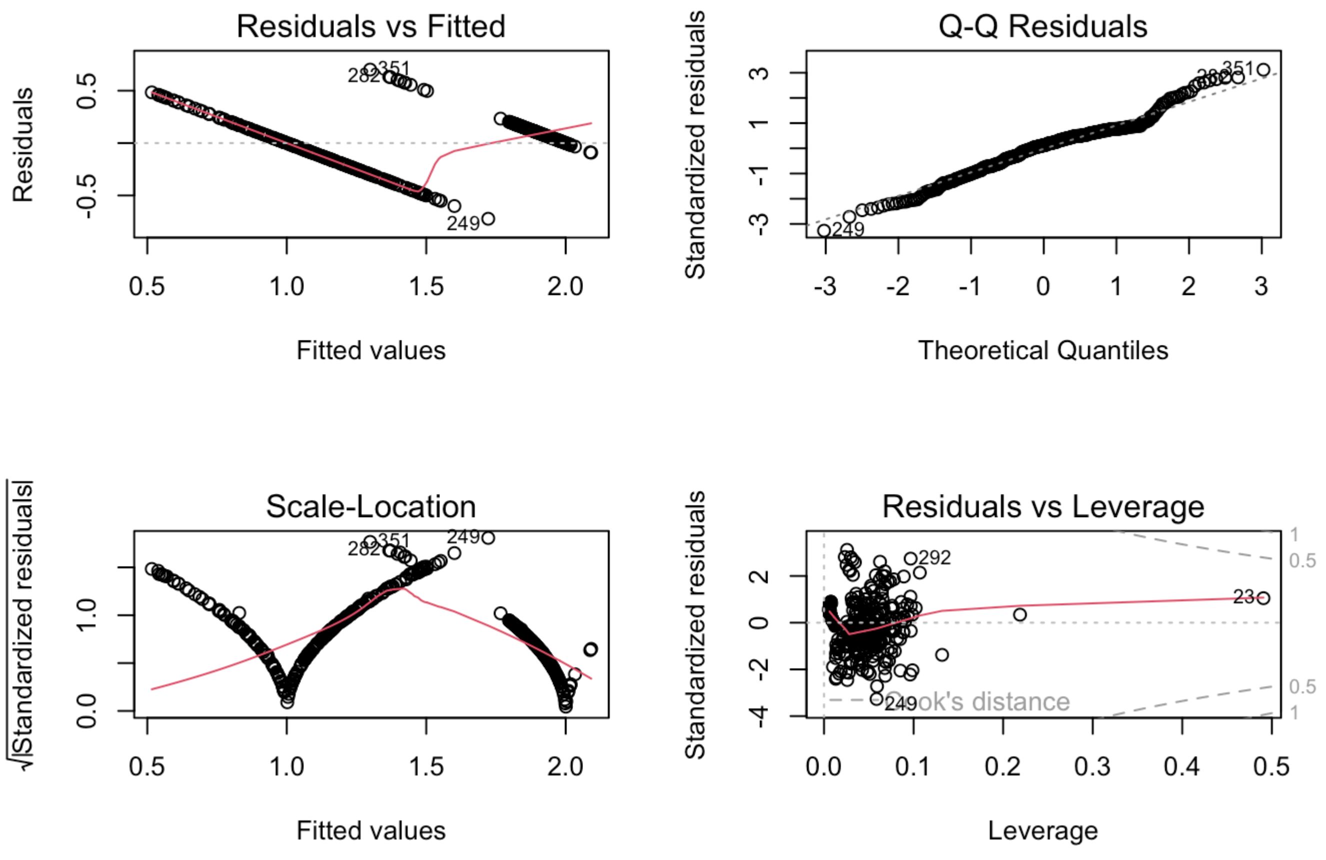
```
Call:
lm(formula = Diagnosis.label ~ Hemoglobin.level + Albumin.in.urine + 
    Sugar.in.urine + Red.Blood.Cells.in.urine + Pus.Cells.in.urine + 
    Pus.Cell.Clumps + Bacteria.in.urine + Hypertension + Diabetes.Mellitus + 
    Coronary.Artery.Disease + Appetite + Pedal.Edema..swelling.of.legs. + 
    Anemia + Serum.Creatinine, data = dat)

Residuals:
     Min       1Q   Median       3Q      Max 
-0.72222 -0.14429  0.02754  0.13604  0.70115 

Coefficients:
                                Estimate Std. Error t value Pr(>|t|)    
(Intercept)                     1.161819   0.234891   4.946 1.13e-06 ***
Hemoglobin.level                0.045430   0.005536   8.206 3.48e-15 ***
Albumin.in.urine               -0.100269   0.010891  -9.207  < 2e-16 ***
Sugar.in.urine                 -0.021568   0.011912  -1.811  0.07098 .  
Red.Blood.Cells.in.urine        0.245296   0.014398  17.037  < 2e-16 ***
Pus.Cells.in.urine              0.037811   0.018470   2.047  0.04132 *  
Pus.Cell.Clumps                -0.049330   0.041120  -1.200  0.23101    
Bacteria.in.urine              -0.042472   0.051083  -0.831  0.40625    
Hypertension                   -0.089461   0.033887  -2.640  0.00863 ** 
Diabetes.Mellitus              -0.071411   0.031744  -2.250  0.02504 *  
Coronary.Artery.Disease         0.069109   0.043929   1.573  0.11650    
Appetite                       -0.062216   0.032872  -1.893  0.05915 .  
Pedal.Edema..swelling.of.legs. -0.013195   0.034795  -0.379  0.70474    
Anemia                          0.016579   0.037287   0.445  0.65684    
Serum.Creatinine               -0.004483   0.002192  -2.045  0.04156 *  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.2278 on 385 degrees of freedom
Multiple R-squared:  0.787,	Adjusted R-squared:  0.7792 
F-statistic: 101.6 on 14 and 385 DF,  p-value: < 2.2e-16
```

```r
car::vif(lm_fit)#whether there is a multicollinearity
```

```
             Hemoglobin.level                 Albumin.in.urine 
                     2.088912                         1.855492 
               Sugar.in.urine         Red.Blood.Cells.in.urine 
                     1.403951                         1.386586 
           Pus.Cells.in.urine                  Pus.Cell.Clumps 
                     1.511873                         1.381603 
           Bacteria.in.urine                     Hypertension 
                     1.267104                         2.134647 
            Diabetes.Mellitus          Coronary.Artery.Disease 
                     1.983162                         1.243940 
                     Appetite Pedal.Edema..swelling.of.legs. 
                     1.387175                         1.468771 
                       Anemia                 Serum.Creatinine 
                     1.401583                         1.193711 
```

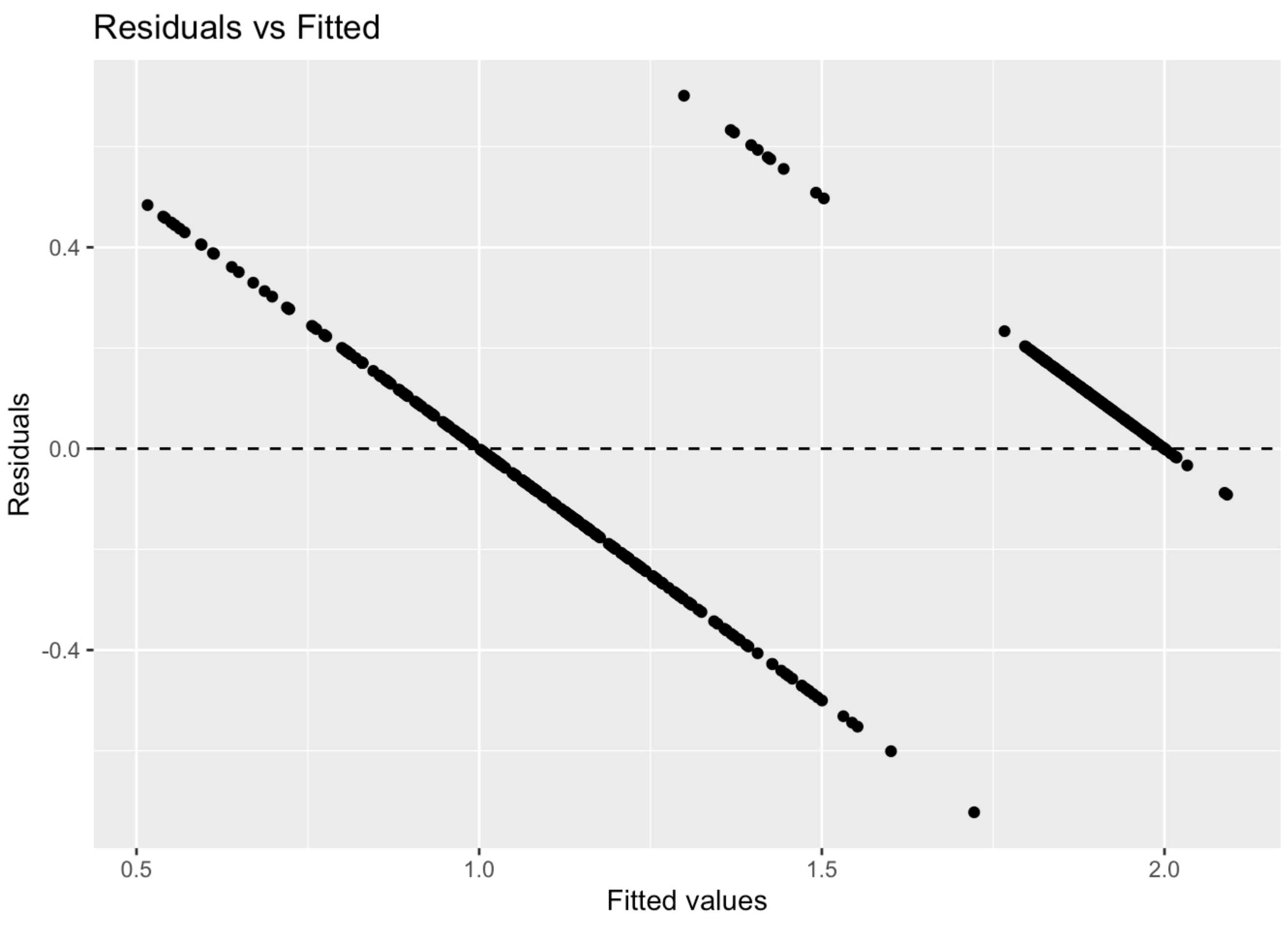
```
#VIF > 10: Severe collinearity;

#5 < VIF ≤ 10: Moderate;

#VIF < 5: Acceptable.
```

```
par(mfrow = c(2, 2))
plot(lm_fit)
```

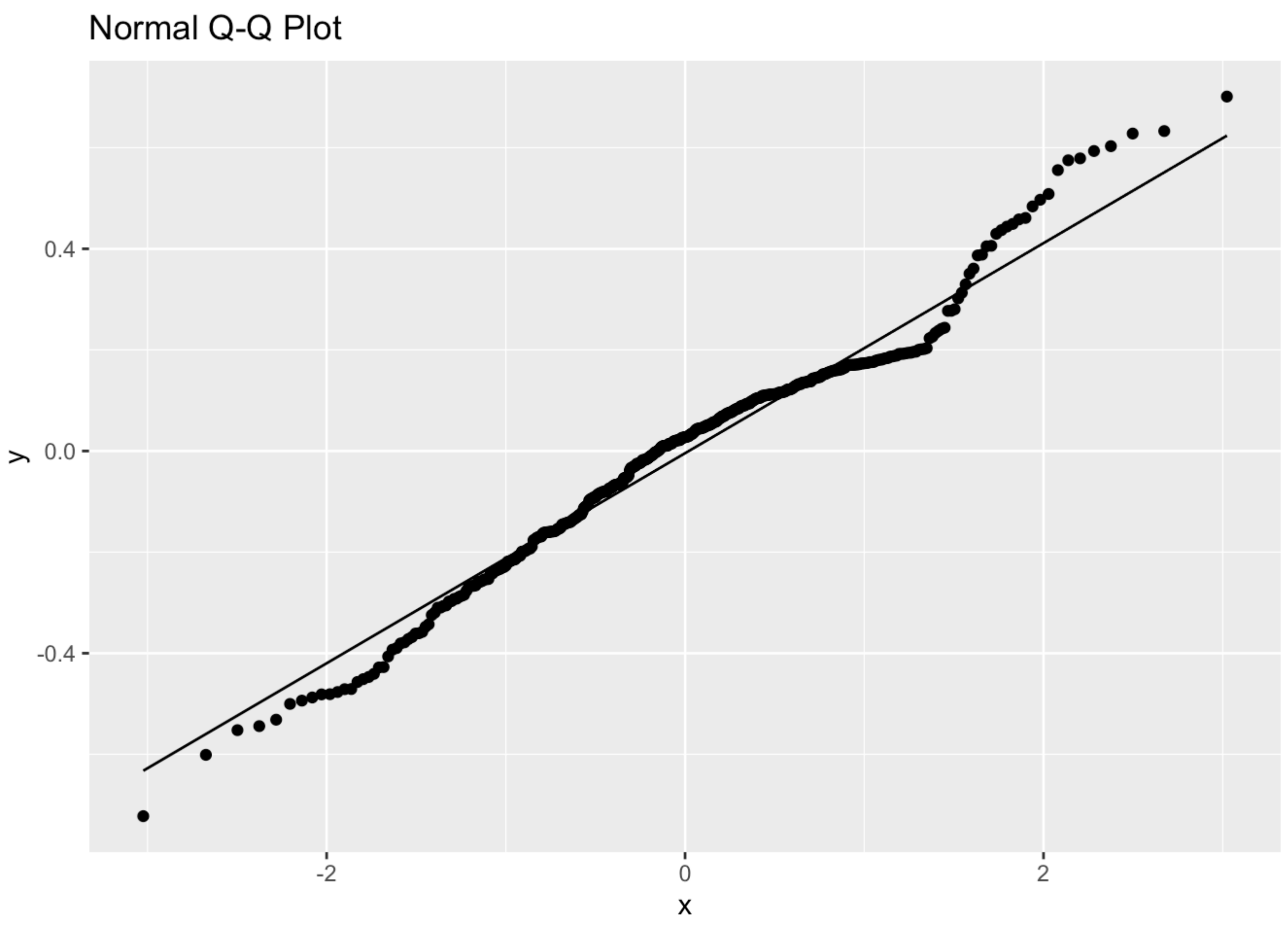


```
par(mfrow = c(1, 1))
```

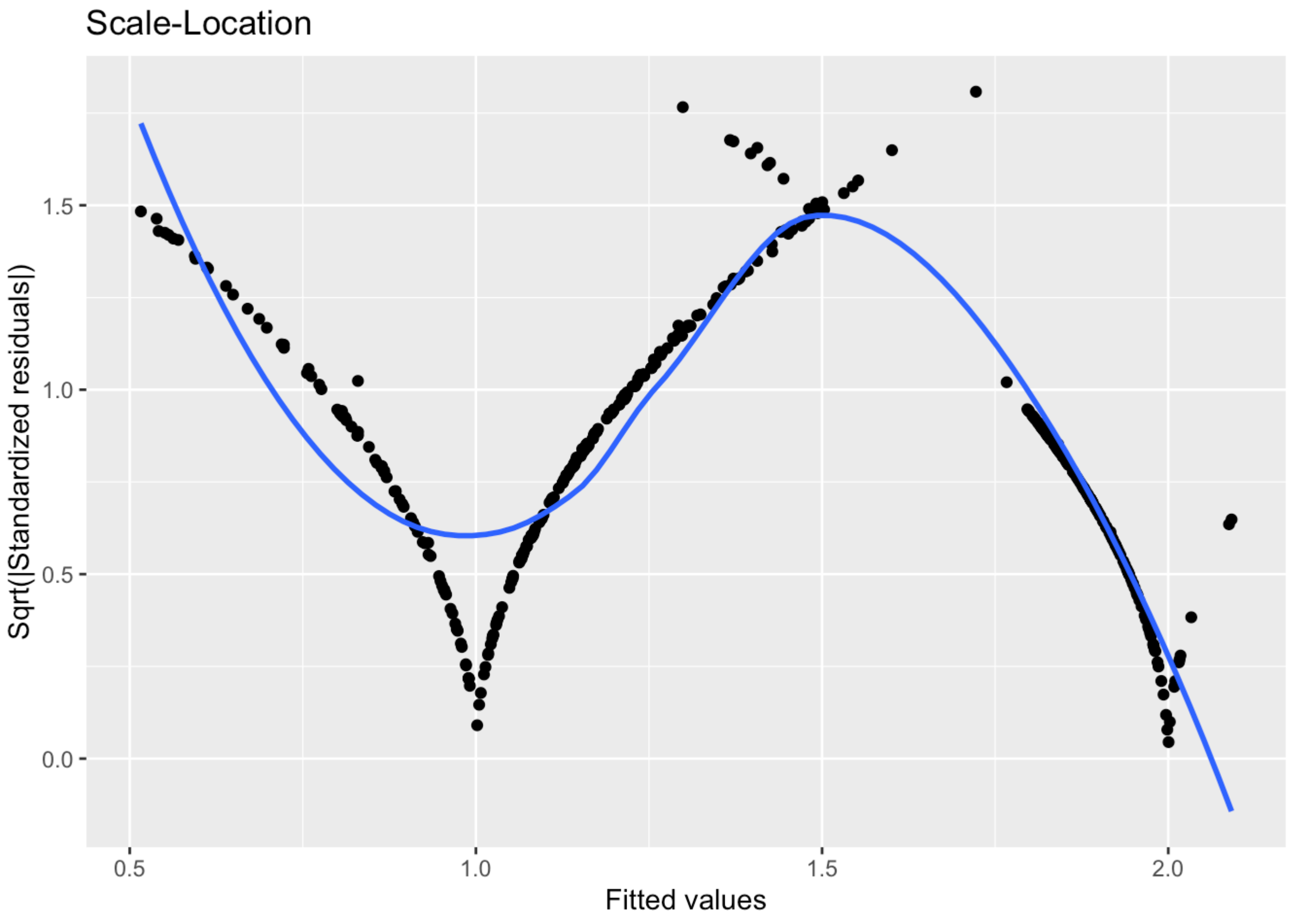
```
diag_df <- data.frame(
  fitted = fitted(lm_fit),
  resid  = resid(lm_fit),
  std_resid = rstandard(lm_fit)
)

#1) Residuals vs Fitted
ggplot(diag_df, aes(x = fitted, y = resid)) +
  geom_point() +
  geom_hline(yintercept = 0, linetype = "dashed") +
  labs(title = "Residuals vs Fitted",
       x = "Fitted values",
       y = "Residuals")
```



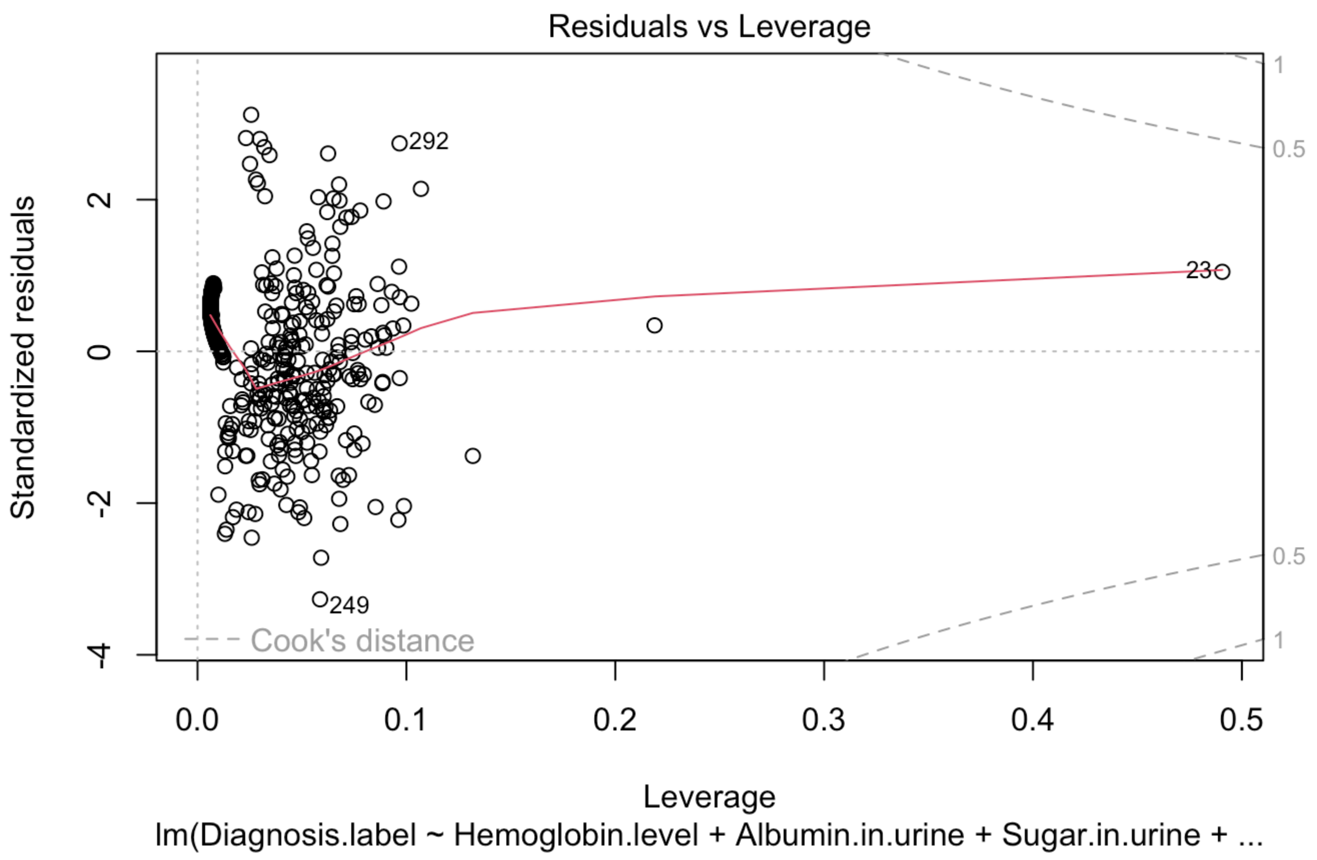
```
#2) QQ Plot
ggplot(diag_df, aes(sample = resid)) +
  stat_qq() +
  stat_qq_line() +
  labs(title = "Normal Q-Q Plot")
```



```
#3) Scale-Location (sqrt |resid|)
ggplot(diag_df, aes(x = fitted, y = sqrt(abs(std_resid)))) +
  geom_point() +
  geom_smooth(se = FALSE) +
  labs(title = "Scale-Location",
       x = "Fitted values",
       y = "Sqrt(|Standardized residuals|)")
```



```r
plot(lm_fit, which = 5)
```


Residuals vs Leverage
Standardized residuals
Cook's distance
Leverage
lm(Diagnosis.label ~ Hemoglobin.level + Albumin.in.urine + Sugar.in.urine + ...