Risk Stratification

Risk stratification of diabetic patients for readmission

EDA and Feature engineering

```
data <- read.csv("data/diabetic_data_original.csv", header=TRUE,
                 na.strings = c("NA","na",""," ","?"), stringsAsFactors = FALSE)
```

Checking structure of data

```
str(data)
```

```
## 'data.frame':    101766 obs. of  50 variables:
##  $ encounter_id            : int  2278392 149190 64410 500364 16680 35754 55842 63
##  $ patient_nbr             : int  8222157 55629189 86047875 82442376 42519267 8263
##  $ race                    : chr  "Caucasian" "Caucasian" "AfricanAmerican" "Cauca
##  $ gender                  : chr  "Female" "Female" "Female" "Male" ...
##  $ age                     : chr  "[0-10)" "[10-20)" "[20-30)" "[30-40)" ...
##  $ weight                  : chr  NA NA NA NA ...
##  $ admission_type_id       : int  6 1 1 1 1 2 3 1 2 3 ...
##  $ discharge_disposition_id: int  25 1 1 1 1 1 1 1 1 3 ...
##  $ admission_source_id     : int  1 7 7 7 7 2 2 7 4 4 ...
##  $ time_in_hospital        : int  1 3 2 2 1 3 4 5 13 12 ...
##  $ payer_code              : chr  NA NA NA NA ...
##  $ medical_specialty       : chr  "Pediatrics-Endocrinology" NA NA NA ...
##  $ num_lab_procedures      : int  41 59 11 44 51 31 70 73 68 33 ...
##  $ num_procedures          : int  0 0 5 1 0 6 1 0 2 3 ...
##  $ num_medications         : int  1 18 13 16 8 16 21 12 28 18 ...
##  $ number_outpatient       : int  0 0 2 0 0 0 0 0 0 0 ...
##  $ number_emergency        : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ number_inpatient        : int  0 0 1 0 0 0 0 0 0 0 ...
##  $ diag_1                  : chr  "250.83" "276" "648" "8" ...
##  $ diag_2                  : chr  NA "250.01" "250" "250.43" ...
##  $ diag_3                  : chr  NA "255" "V27" "403" ...
##  $ number_diagnoses        : int  1 9 6 7 5 9 7 8 8 8 ...
##  $ max_glu_serum           : chr  "None" "None" "None" "None" ...
##  $ A1Cresult               : chr  "None" "None" "None" "None" ...
##  $ metformin               : chr  "No" "No" "No" "No" ...
##  $ repaglinide             : chr  "No" "No" "No" "No" ...
##  $ nateglinide             : chr  "No" "No" "No" "No" ...
##  $ chlorpropamide          : chr  "No" "No" "No" "No" ...
##  $ glimepiride             : chr  "No" "No" "No" "No" ...
##  $ acetohexamide           : chr  "No" "No" "No" "No" ...
##  $ glipizide               : chr  "No" "No" "Steady" "No" ...
##  $ glyburide               : chr  "No" "No" "No" "No" ...
##  $ tolbutamide             : chr  "No" "No" "No" "No" ...
##  $ pioglitazone            : chr  "No" "No" "No" "No" ...
##  $ rosiglitazone           : chr  "No" "No" "No" "No" ...
##  $ acarbose                : chr  "No" "No" "No" "No" ...
##  $ miglitol                : chr  "No" "No" "No" "No" ...
##  $ troglitazone            : chr  "No" "No" "No" "No" ...
##  $ tolazamide              : chr  "No" "No" "No" "No" ...
##  $ examide                 : chr  "No" "No" "No" "No" ...
##  $ citoglipton             : chr  "No" "No" "No" "No" ...
##  $ insulin                 : chr  "No" "Up" "No" "Up" ...
##  $ glyburide.metformin     : chr  "No" "No" "No" "No" ...
##  $ glipizide.metformin     : chr  "No" "No" "No" "No" ...
##  $ glimepiride.pioglitazone: chr  "No" "No" "No" "No" ...
##  $ metformin.rosiglitazone : chr  "No" "No" "No" "No" ...
##  $ metformin.pioglitazone  : chr  "No" "No" "No" "No" ...
##  $ change                  : chr  "No" "Ch" "No" "Ch" ...
##  $ diabetesMed             : chr  "No" "Yes" "Yes" "Yes" ...
##  $ readmitted              : chr  "NO" ">30" "NO" "NO" ...
```

Check for NA

```
sapply(data, function(x) sum(is.na(x)))
```

```
##             encounter_id              patient_nbr                     race
##                        0                        0                     2273
##                   gender                      age                   weight
##                        0                        0                    98569
##        admission_type_id discharge_disposition_id      admission_source_id
##                        0                        0                        0
##         time_in_hospital               payer_code        medical_specialty
##                        0                    40256                    49949
##       num_lab_procedures           num_procedures          num_medications
##                        0                        0                        0
##        number_outpatient         number_emergency         number_inpatient
##                        0                        0                        0
##                   diag_1                   diag_2                   diag_3
##                       21                      358                     1423
##         number_diagnoses            max_glu_serum                A1Cresult
##                        0                        0                        0
##                metformin              repaglinide              nateglinide
##                        0                        0                        0
##           chlorpropamide              glimepiride            acetohexamide
##                        0                        0                        0
##                glipizide                glyburide              tolbutamide
##                        0                        0                        0
##             pioglitazone            rosiglitazone                 acarbose
##                        0                        0                        0
##                 miglitol             troglitazone               tolazamide
##                        0                        0                        0
##                  examide              citoglipton                  insulin
##                        0                        0                        0
##      glyburide.metformin      glipizide.metformin glimepiride.pioglitazone
##                        0                        0                        0
##  metformin.rosiglitazone   metformin.pioglitazone                   change
##                        0                        0                        0
##              diabetesMed               readmitted
##                        0                        0
```

Check variable

```
# encounter_id
length(unique(data$encounter_id))
```

```
## [1] 101766
```

```
# 101766 variable, no duplicate
 #  remove encounterid
data <- subset(data, select=-c(encounter_id))
```

```
# patient_nbr
# Save the patient id to identify the patien after analysis
Patient_Id <- data$patient_nbr
#  remove unwanted variable
data <- subset(data, select=-c(patient_nbr))
```

```
# race
table(data$race)
```

```
##
## AfricanAmerican           Asian       Caucasian        Hispanic
##           19210             641           76099            2037
##           Other
##            1506
```

```
# AfricanAmerican: 19210, Asian: 641, Caucasian: 76099, Hispanic: 2037, Other: 1506
class(data$race)
```

```
## [1] "character"
```

```
data$race <- as.factor(data$race)
class(data$race)
```

```
## [1] "factor"
```

```
# gender
table(data$gender)
```

```
## 
##          Female            Male Unknown/Invalid 
##           54708           47055               3
```

```
#Female : 54708, Male: 47055, Unknown/Invalid: 3
class(data$gender)
```

```
## [1] "character"
```

```
data$gender <- replace(data$gender, data$gender == "Unknown/Invalid", NA)
table(data$gender)
```

```
## 
## Female   Male 
##  54708  47055
```

```
#convert gender to as.numeric
summary(factor(data$gender))
```

```
## Female   Male   NA's 
##  54708  47055      3
```

```
# convert to factor
data$gender <- as.factor(data$gender)
# give values 1 and 0 to the factors
levels(data$gender)<-c(1,0)
#convert to as.numeric
data$gender <- as.numeric(levels(data$gender))[data$gender]
summary(data$gender)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
##  0.0000  0.0000  1.0000  0.5376  1.0000  1.0000       3
```

```
# Age
table(data$age)
```

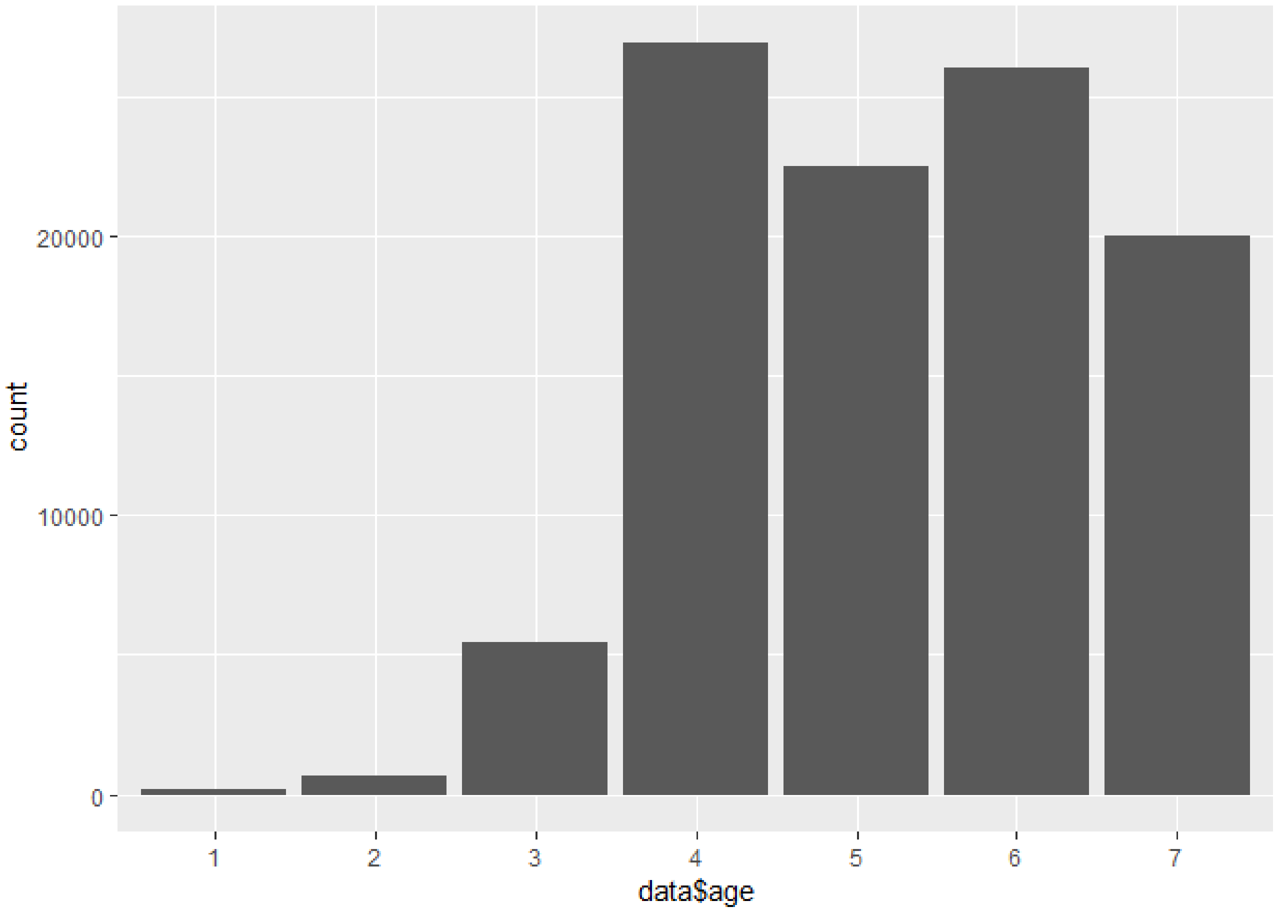
```
## 
##   [0-10)  [10-20)  [20-30)  [30-40)  [40-50)  [50-60)  [60-70)  [70-80) 
##      161      691     1657     3775     9685    17256    22483    26068 
##  [80-90) [90-100) 
##    17197     2793
```

Reducing the levels

```
table(data$age)
```

```
## 
##     1     2     3     4     5     6     7 
##   161   691  5432 26941 22483 26068 19990
```

```
ggplot(data, aes(data$age)) + geom_bar()
```



```
data$age <- as.factor(data$age)
```

```
# weight
table(data$weight)
```

```
## 
##     [0-25) [100-125) [125-150) [150-175) [175-200)    [25-50)    [50-75) 
##         48       625       145        35        11         97        897 
##   [75-100)      >200 
##       1336         3
```

```
summary(data$weight)
```

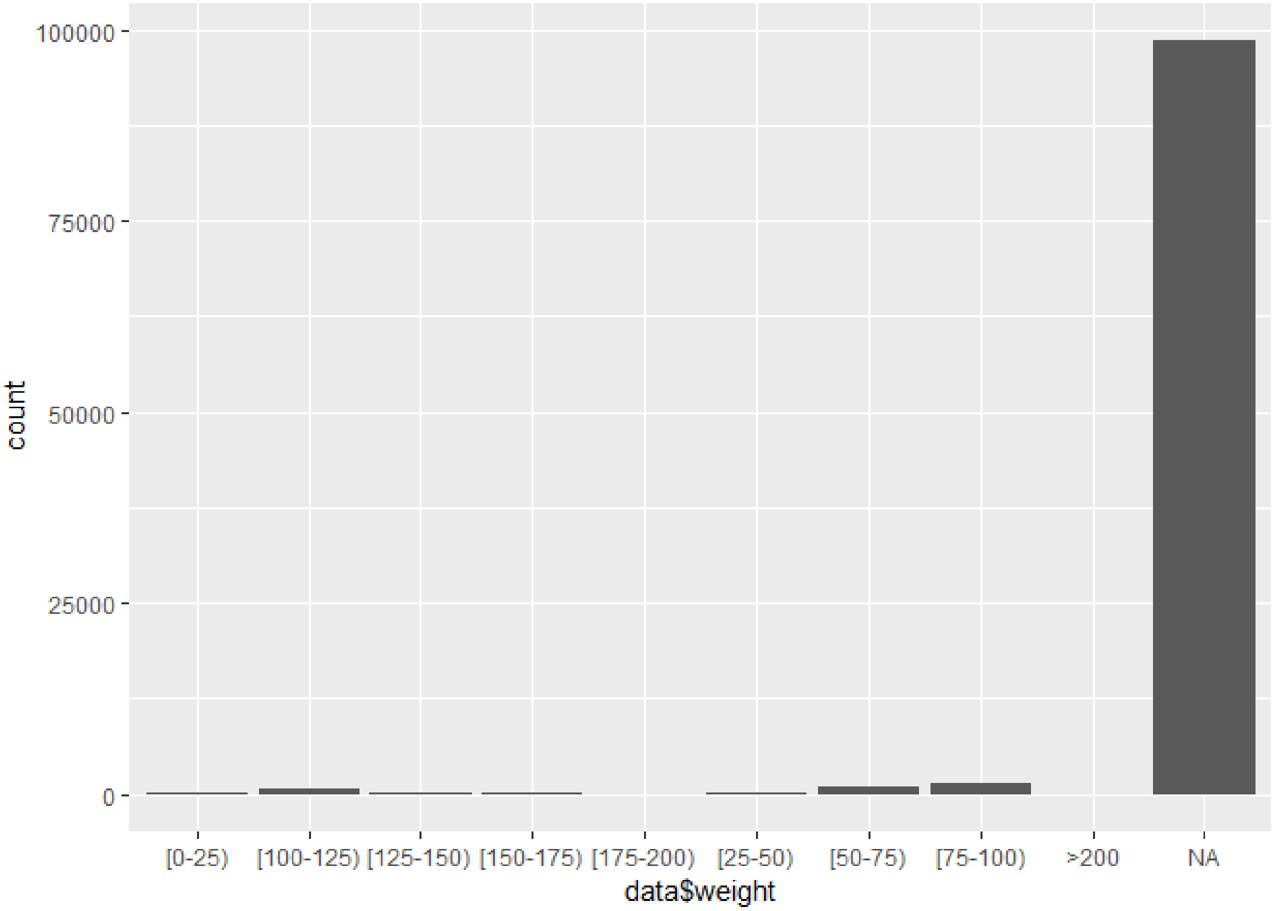
```
##    Length     Class      Mode 
##    101766 character character
```

```
sum(is.na(data$weight))
```

```
## [1] 98569
```

Checking if the data is unbalanced

```
ggplot(data, aes(data$weight)) + geom_bar()
```



```
data <- subset(data, select=-c(weight))
```

```
#admission_type_id
table(data$admission_type_id)
```

```
##
##     1     2     3     4     5     6     7     8
## 53990 18480 18869    10  4785  5291    21   320
```

Reducing the levels

```
table(data$admission_type_id)
```

```
##
##     1     3     4     5     7
## 72470 18869    10 10396    21
```

```
data$admission_type_id <- as.factor(data$admission_type_id)
```

```
# discharge_disposition_id 1 8 16 17 27 30
table(data$discharge_disposition_id)
```

```
##
##     1     2     3     4     5     6     7     8     9    10    11    12
## 60234  2128 13954   815  1184 12902   623   108    21     6  1642     3
##    13    14    15    16    17    18    19    20    22    23    24    25
##   399   372    63    11    14  3691     8     2  1993   412    48   989
##    27    28
##     5   139
```

Reducing the levels, grouping similar discharge dispositions

```
# 11 19 20 21# Few are grouped together
data$discharge_disposition_id <- replace(data$discharge_disposition_id, data$discharg
data$discharge_disposition_id <- replace(data$discharge_disposition_id, data$discharg
data$discharge_disposition_id <- replace(data$discharge_disposition_id, data$discharg
data$discharge_disposition_id <- replace(data$discharge_disposition_id, data$discharg
```

```
table(data$discharge_disposition_id)
```

```
##
##     1     2     3     4
## 60372 34436  5306  1652
```

```
summary(data$discharge_disposition_id)
```

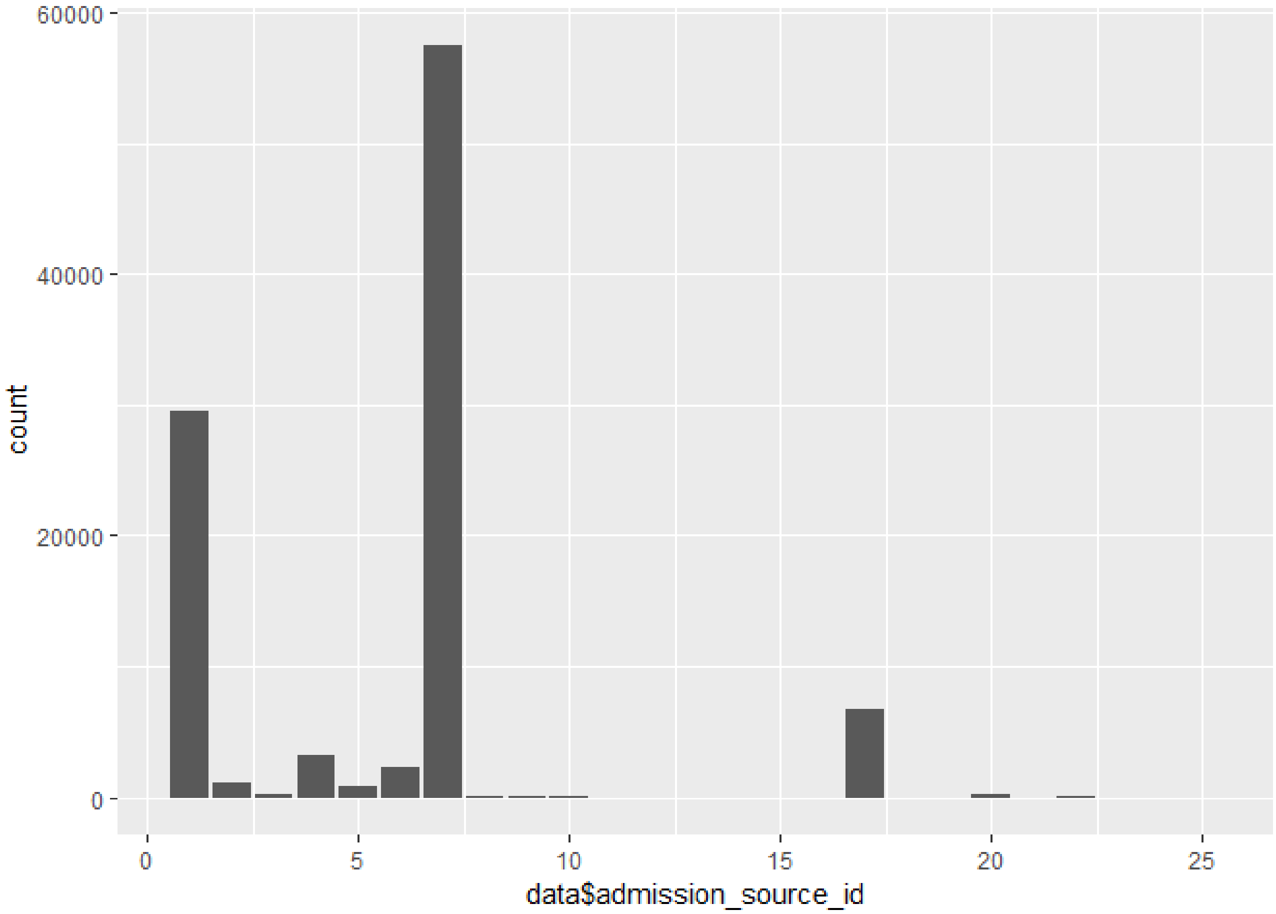
```
##    Length     Class      Mode
##     Length     Class      Mode
##     101766 character character
```

```
data$discharge_disposition_id <- as.factor(data$discharge_disposition_id)
```

```
# admission_source_id
table(data$admission_source_id)
```

```
## 
##     1     2     3     4     5     6     7     8     9    10    11    13 
## 29565  1104   187  3187   855  2264 57494    16   125     8     2     1 
##    14    17    20    22    25 
##     2  6781   161    12     2
```

```
ggplot(data, aes(data$admission_source_id)) + geom_bar()
```



```
table(data$admission_source_id)
```

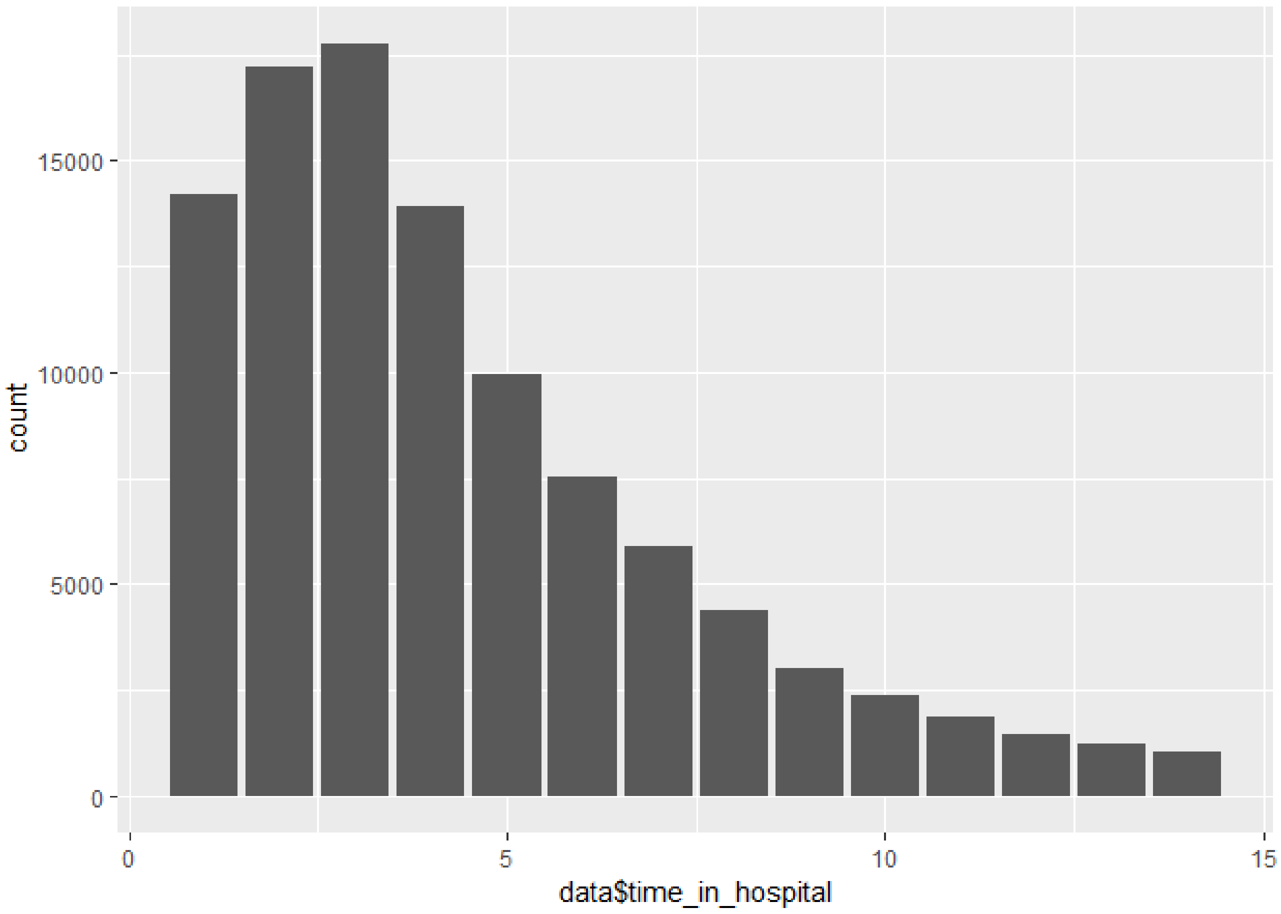
```
##
##     1     2     3     4
## 30872 63822  7067     5
```

```
data$admission_source_id <- as.factor(data$admission_source_id)
```

```
# time_in_hospital
table(data$time_in_hospital)
```

```
##
##     1     2     3     4     5     6     7     8     9    10    11    12
## 14208 17224 17756 13924  9966  7539  5859  4391  3002  2342  1855  1448
##    13    14
##  1210  1042
```

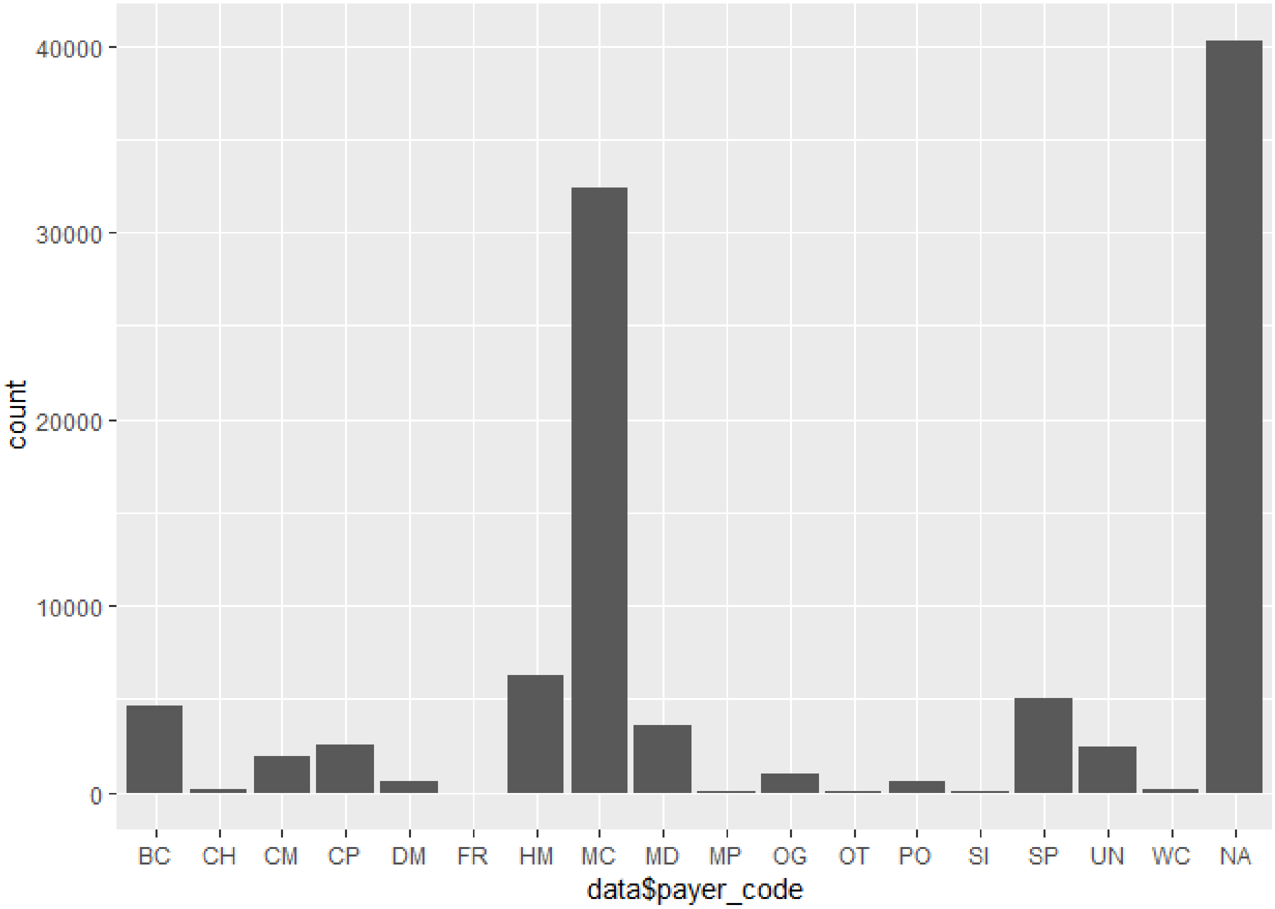
```
ggplot(data, aes(data$time_in_hospital)) + geom_bar()
```



```
str(data$time_in_hospital)
```

```
##  int [1:101766] 1 3 2 2 1 3 4 5 13 12 ...
```

```
# Payercode
ggplot(data, aes(data$payer_code)) + geom_bar()
```

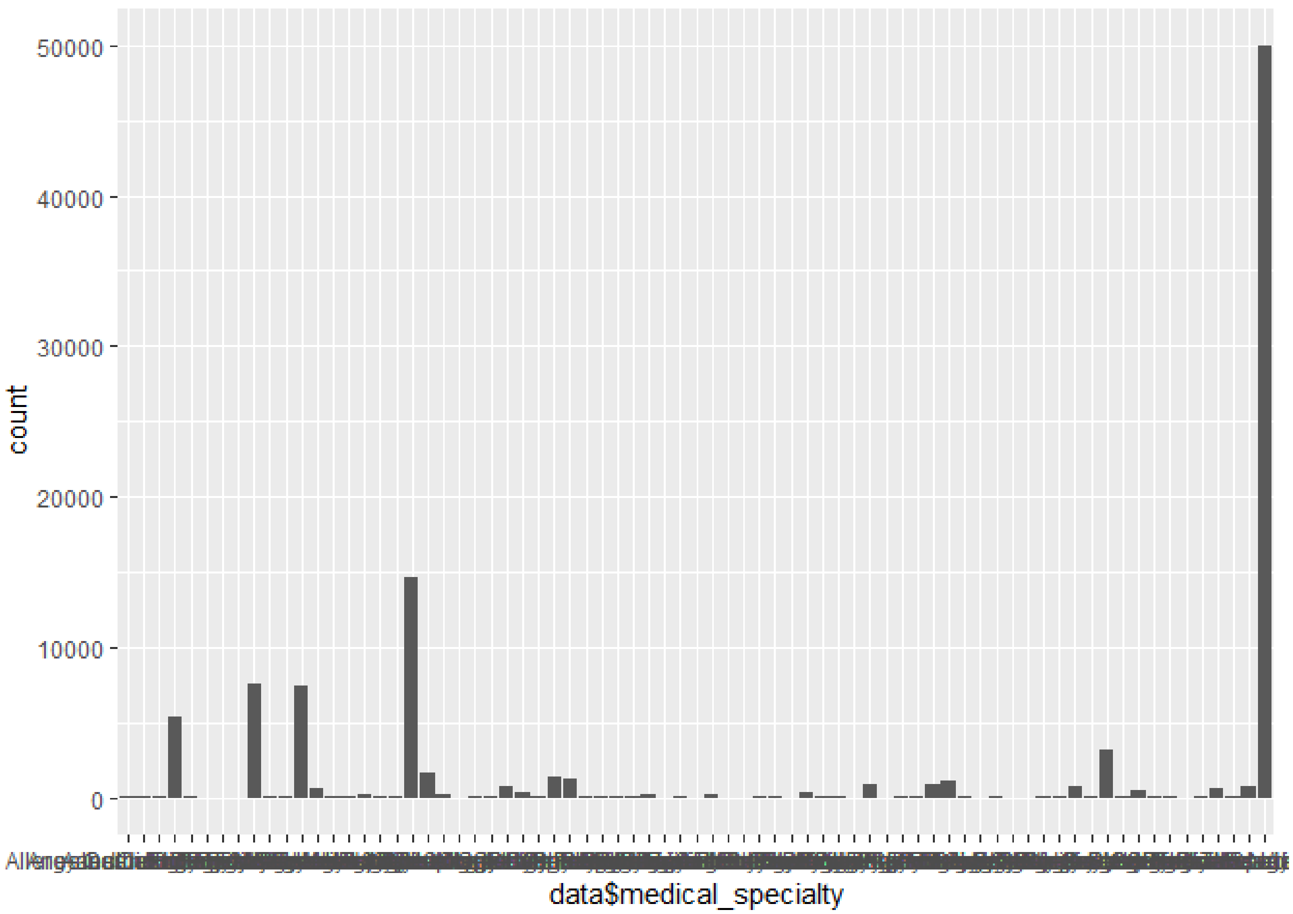


```
 #  remove unwanted variable, not helpful as not patient disease info
data <- subset(data, select=-c(payer_code))
```

```
# medical_specialty
table(data$medical_specialty)
```

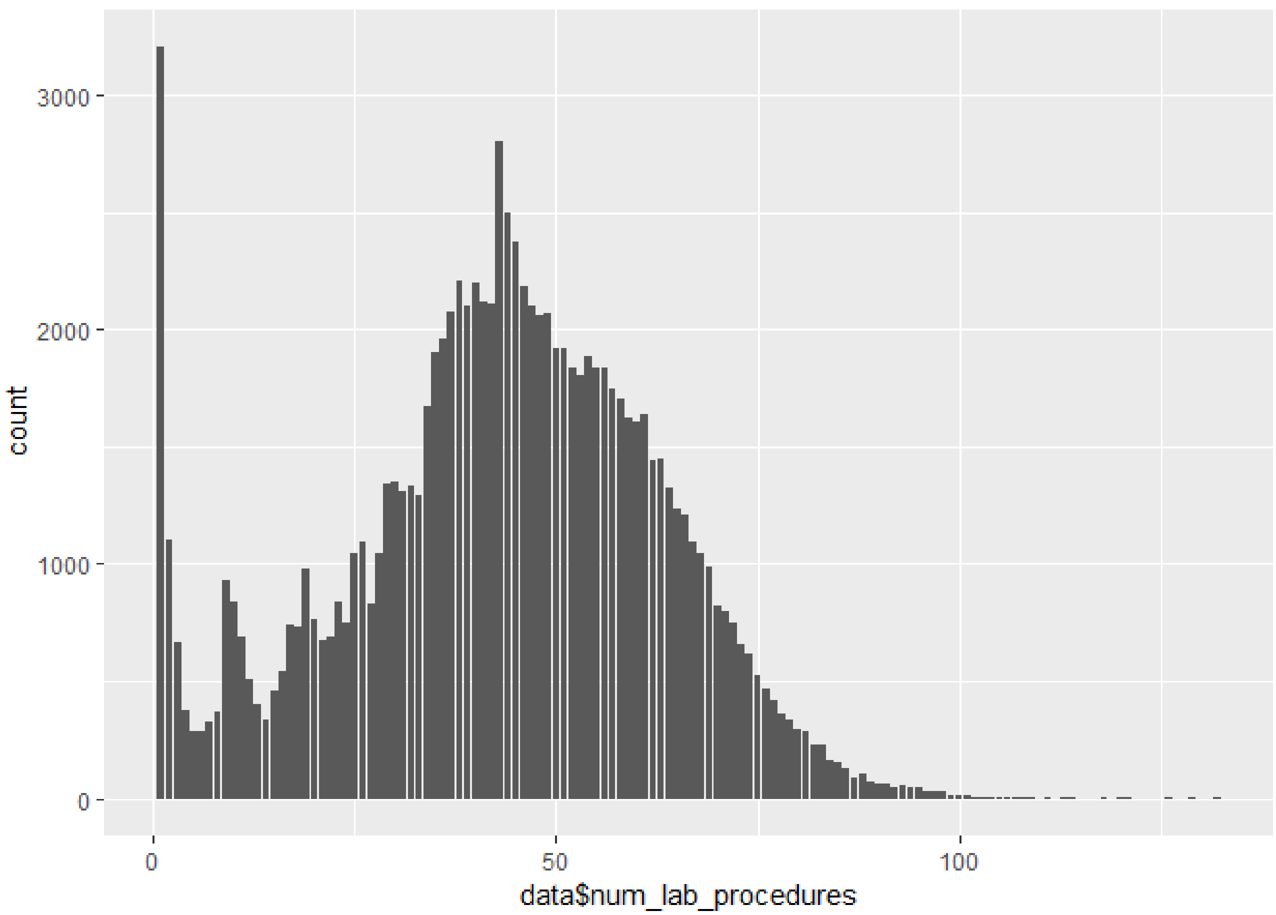
```
## 
##                  AllergyandImmunology                       Anesthesiology
##                                     7                                   12
##              Anesthesiology-Pediatric                           Cardiology
##                                    19                                 5352
##                                   19                                 5352
##                 Cardiology-Pediatric                              DCPTEAM
##                                    7                                    6
##                            Dentistry                          Dermatology
##                                    4                                    1
##                     Emergency/Trauma                        Endocrinology
##                                 7565                                  120
##             Endocrinology-Metabolism               Family/GeneralPractice
##                                    8                                 7440
##                     Gastroenterology                           Gynecology
##                                  564                                   58
##                           Hematology                  Hematology/Oncology
##                                   82                                  207
##                          Hospitalist                   InfectiousDiseases
##                                   57                                   37
##                     InternalMedicine                           Nephrology
##                                14635                                 1613
##                            Neurology                      Neurophysiology
##                                  203                                    1
## Obsterics&Gynecology-GynecologicOnco                           Obstetrics
##                                   25                                   19
##              ObstetricsandGynecology                             Oncology
##                                  671                                  348
##                        Ophthalmology                          Orthopedics
##                                   38                                 1400
##           Orthopedics-Reconstructive                            Osteopath
##                                 1233                                   39
##                       Otolaryngology                     OutreachServices
##                                  125                                   12
##                            Pathology                           Pediatrics
##                                   17                                  254
##      Pediatrics-AllergyandImmunology              Pediatrics-CriticalCare
##                                    3                                   87
##         Pediatrics-EmergencyMedicine             Pediatrics-Endocrinology
##                                    3                                  159
##       Pediatrics-Hematology-Oncology        Pediatrics-InfectiousDiseases
##                                    4                                    1
##                 Pediatrics-Neurology               Pediatrics-Pulmonology
##                                   10                                   25
##                         Perinatology    PhysicalMedicineandRehabilitation
##                                    1                                  391
##                    PhysicianNotFound                             Podiatry
##                                   11                                  100
##                           Proctology                           Psychiatry
##                                    1                                  854
##                 Psychiatry-Addictive          Psychiatry-Child/Adolescent
##                                    1                                    7
##                           Psychology                          Pulmonology
##                                  101                                  871
##                          Radiologist                            Radiology
##                                 1140                                   53
##                             Resident                         Rheumatology
##                             Resident                         Rheumatology
##                                    2                                   17
##                               Speech                       SportsMedicine
##                                    1                                    1
##                              Surgeon               Surgery-Cardiovascular
##                                   45                                   98
##      Surgery-Cardiovascular/Thoracic                 Surgery-Colon&Rectal
##                                  652                                   11
##                      Surgery-General                Surgery-Maxillofacial
##                                 3099                                   11
##                        Surgery-Neuro                    Surgery-Pediatric
##                                  468                                    8
##                      Surgery-Plastic     Surgery-PlasticwithinHeadandNeck
##                                   41                                    1
##                     Surgery-Thoracic                     Surgery-Vascular
##                                  109                                  533
##                    SurgicalSpecialty                              Urology
##                                   33                                  685
```

```
ggplot(data, aes(data$medical_specialty)) + geom_bar()
```



```
#  remove unwanted variable
data <- subset(data, select=-c(medical_specialty))
```

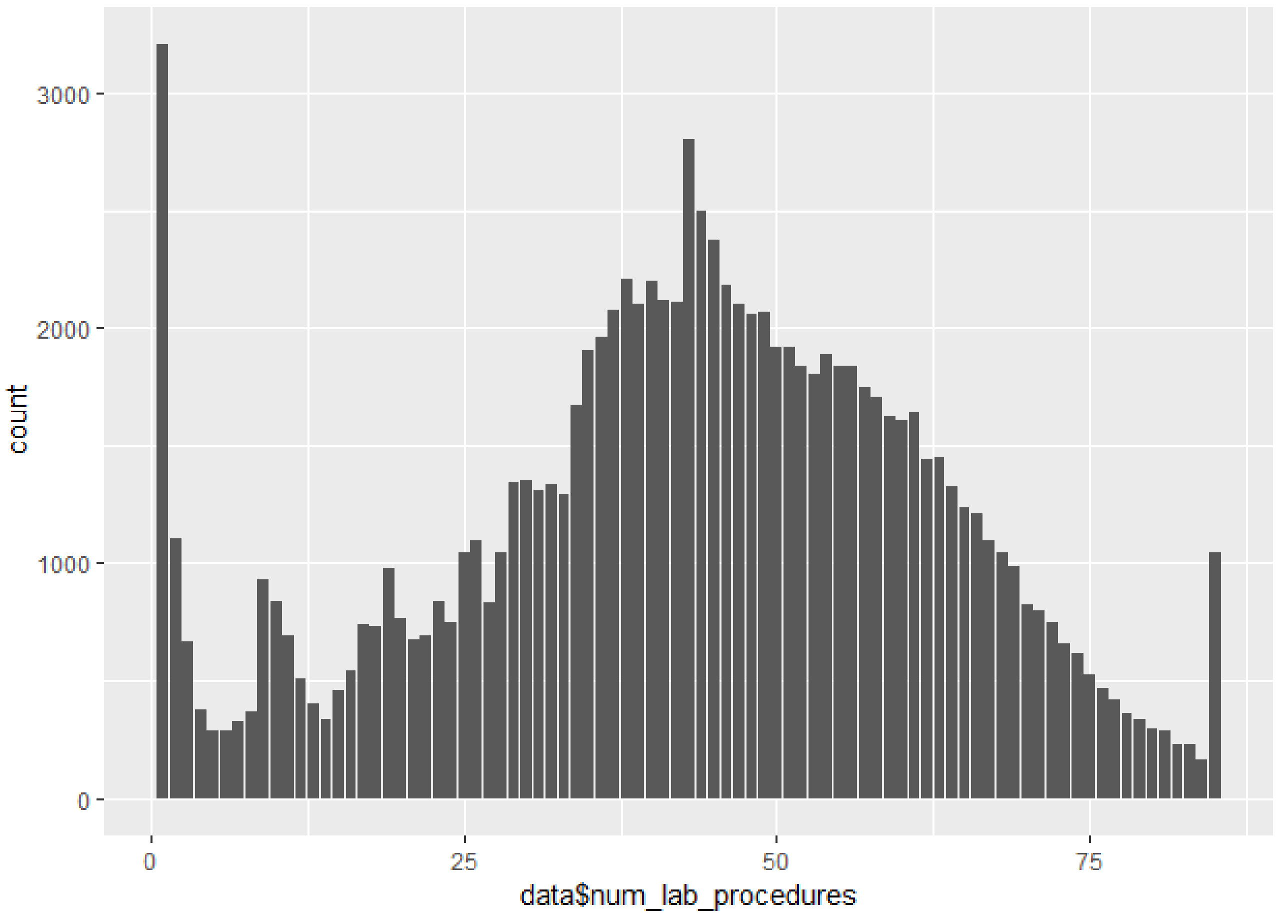
```
ggplot(data, aes(data$num_lab_procedures)) + geom_bar()
```



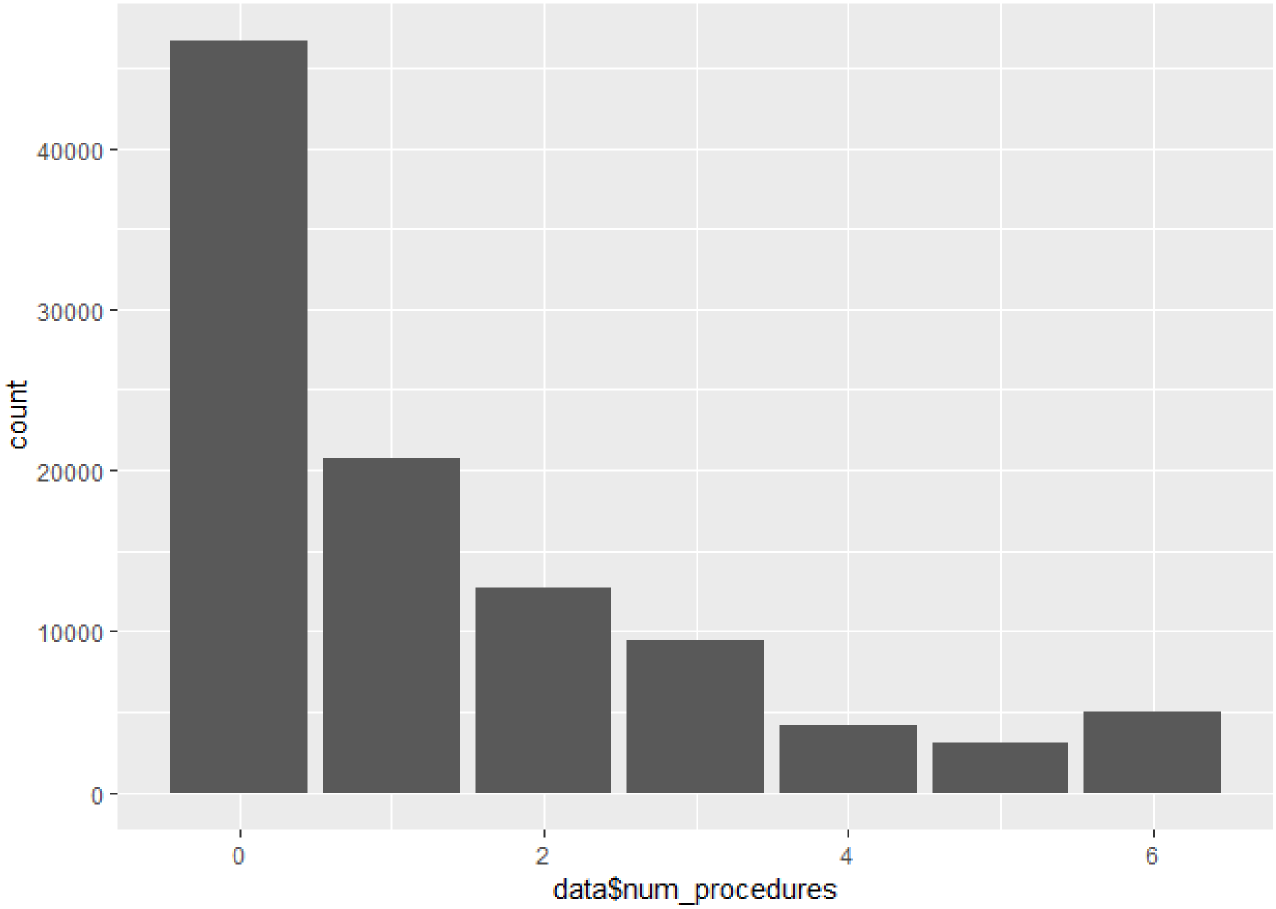
```
quantile(data$num_lab_procedures, seq(0,1, 0.01))
```

```
##   0%   1%   2%   3%   4%   5%   6%   7%   8%   9%  10%  11%  12%  13%  14% 
##    1    1    1    1    2    4    7    9   10   12   14   16   18   19   20 
##  15%  16%  17%  18%  19%  20%  21%  22%  23%  24%  25%  26%  27%  28%  29% 
##   22   23   24   25   26   27   28   29   30   31   31   32   33   34   34 
##  30%  31%  32%  33%  34%  35%  36%  37%  38%  39%  40%  41%  42%  43%  44% 
##   35   35   36   36   37   37   38   38   39   39   40   40   41   41   42 
##  45%  46%  47%  48%  49%  50%  51%  52%  53%  54%  55%  56%  57%  58%  59% 
##   42   43   43   43   44   44   45   45   45   46   46   47   47   48   48 
##  60%  61%  62%  63%  64%  65%  66%  67%  68%  69%  70%  71%  72%  73%  74% 
##   49   49   50   50   51   51   52   52   53   54   54   55   55   56   56 
##  75%  76%  77%  78%  79%  80%  81%  82%  83%  84%  85%  86%  87%  88%  89% 
##   57   57   58   59   59   60   61   61   62   63   63   64   65   66   66 
##  90%  91%  92%  93%  94%  95%  96%  97%  98%  99% 100% 
##   67   68   69   71   72   73   75   77   80   85  132 
##    67    68    69    71    72    73    75    77    80    85   132
```

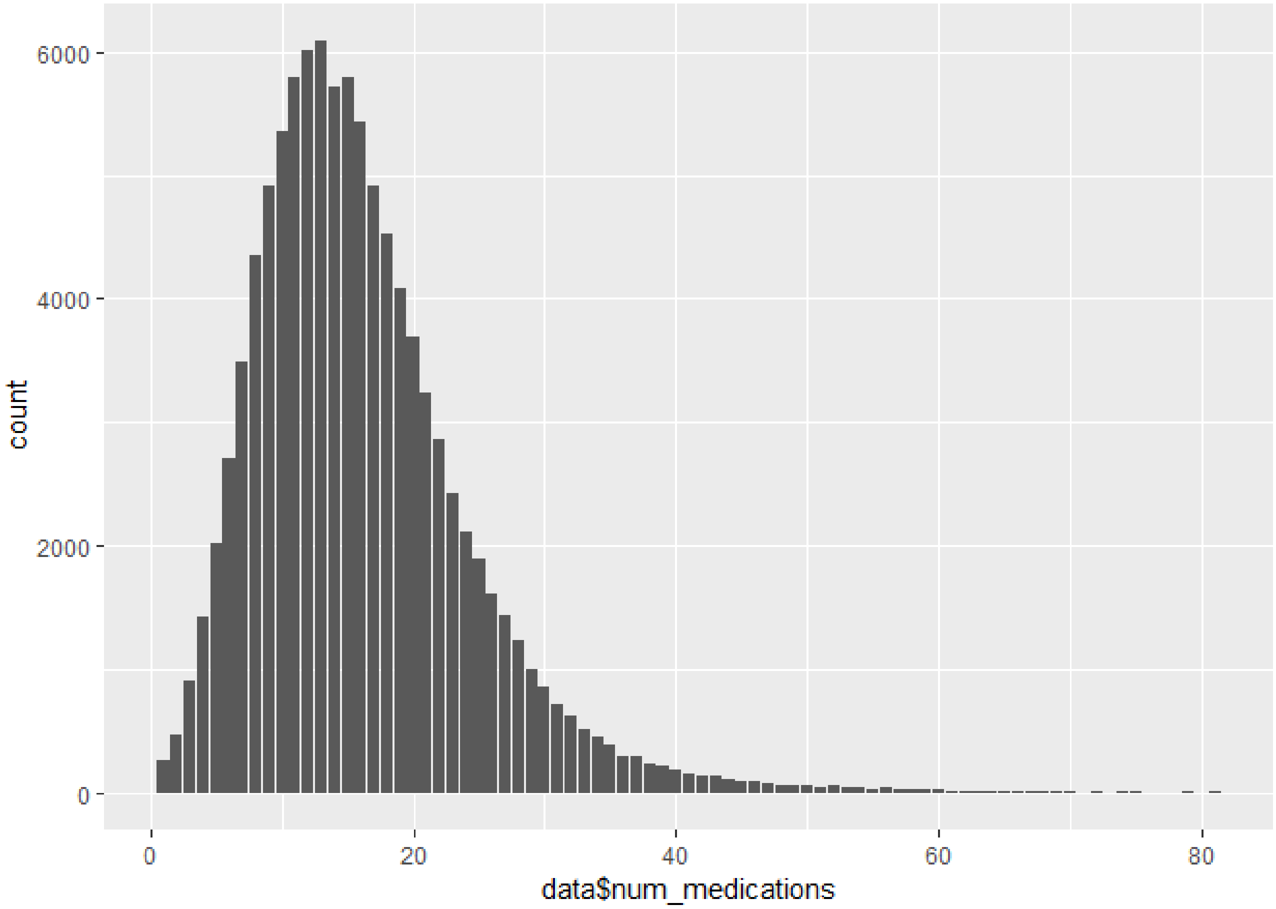
```
data$num_lab_procedures[data$num_lab_procedures > quantile(data$num_lab_procedures, 0
  quantile(data$num_lab_procedures, 0.99)
ggplot(data, aes(data$num_lab_procedures)) + geom_bar()
```



```
ggplot(data, aes(data$num_procedures)) + geom_bar()
```



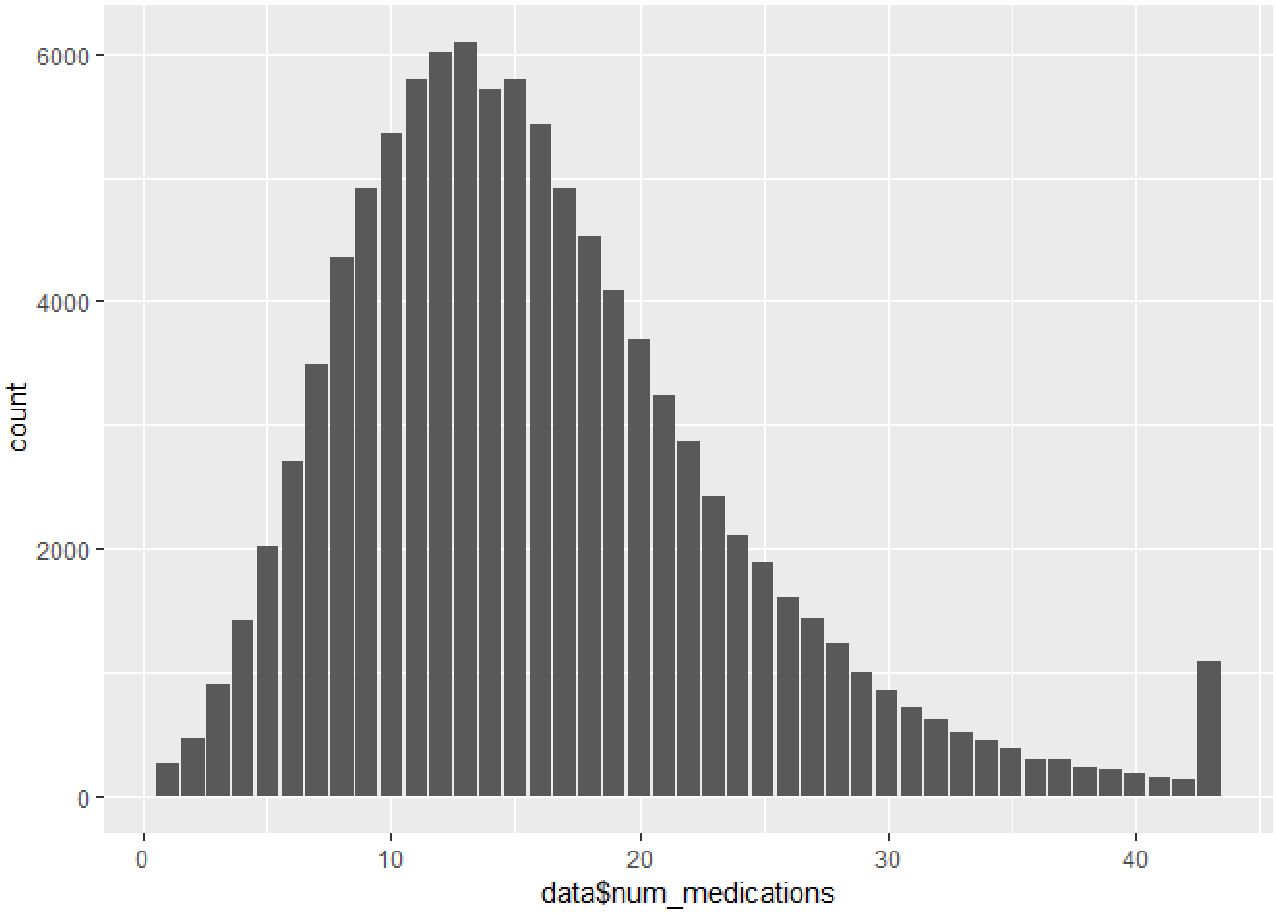
```
ggplot(data, aes(data$num_medications)) + geom_bar()
```



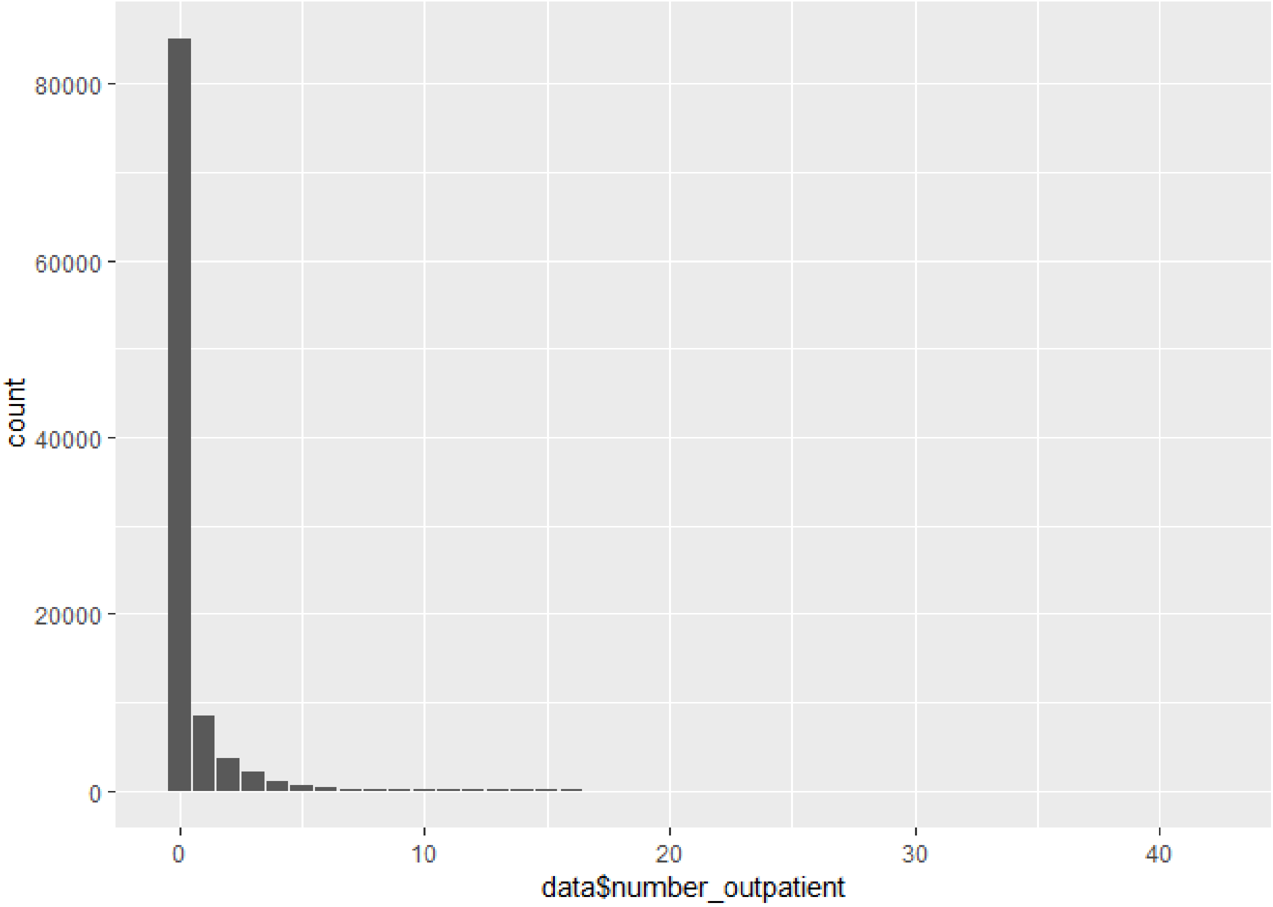
```
quantile(data$num_medications, seq(0,1, 0.01))
```

```
##   0%   1%   2%   3%   4%   5%   6%   7%   8%   9%  10%  11%  12%  13%  14% 
##    1    3    4    5    5    6    6    6    7    7    7    7    8    8    8 
##  15%  16%  17%  18%  19%  20%  21%  22%  23%  24%  25%  26%  27%  28%  29% 
##    8    9    9    9    9    9   10   10   10   10   10   11   11   11   11 
##  30%  31%  32%  33%  34%  35%  36%  37%  38%  39%  40%  41%  42%  43%  44% 
##   11   11   12   12   12   12   12   12   13   13   13   13   13   14   14 
##  45%  46%  47%  48%  49%  50%  51%  52%  53%  54%  55%  56%  57%  58%  59% 
##   14   14   14   14   15   15   15   15   15   15   16   16   16   16   16 
##  60%  61%  62%  63%  64%  65%  66%  67%  68%  69%  70%  71%  72%  73%  74% 
##   17   17   17   17   17   18   18   18   18   19   19   19   19   20   20 
##  75%  76%  77%  78%  79%  80%  81%  82%  83%  84%  85%  86%  87%  88%  89% 
##   20   20   21   21   21   22   22   22   23   23   24   24   25   25   26 
##  90%  91%  92%  93%  94%  95%  96%  97%  98%  99% 100% 
##   26   27   28   28   29   31   32   34   37   43   81
```

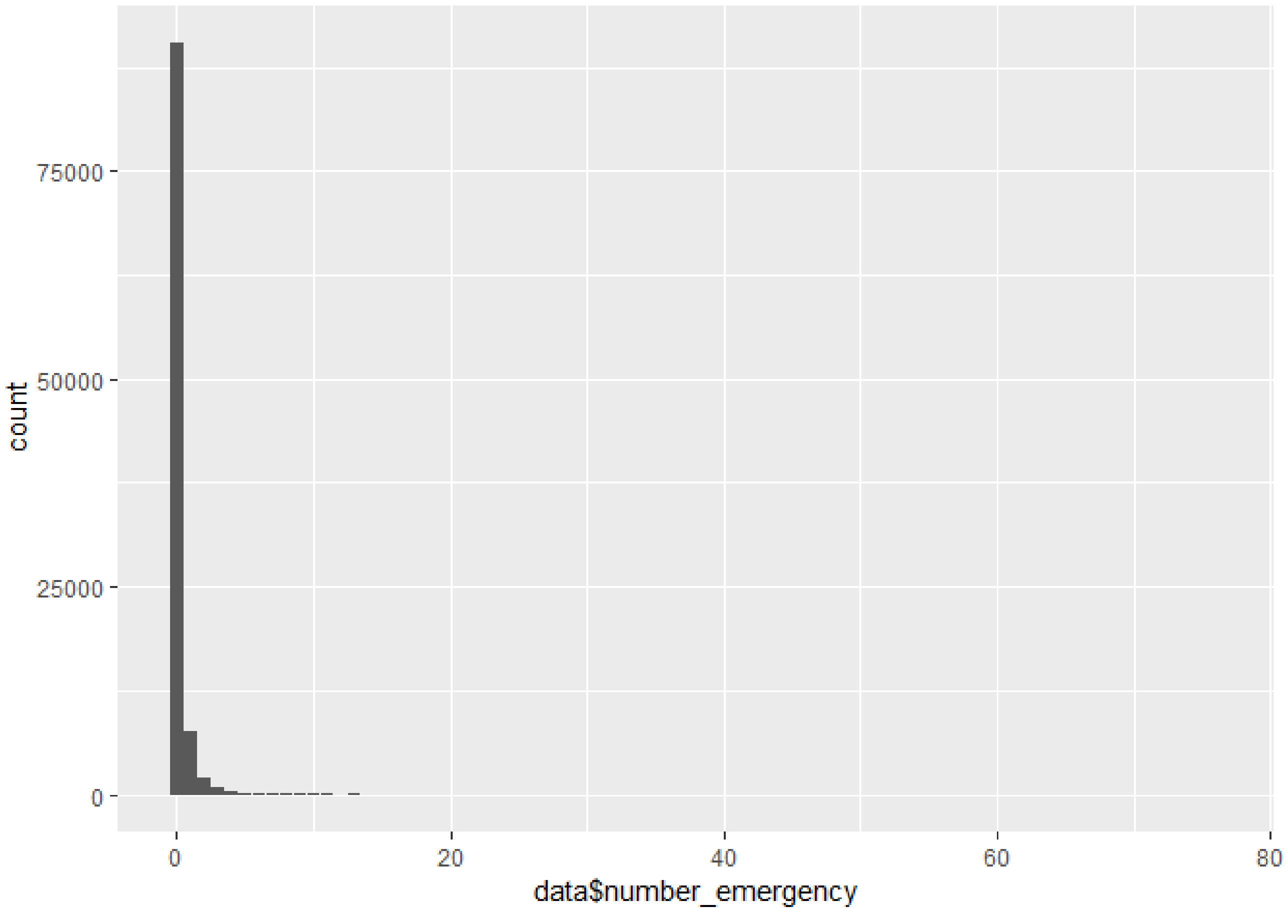
```
data$num_medications[data$num_medications > quantile(data$num_medications, 0.99)] <-
  quantile(data$num_medications, 0.99)
ggplot(data, aes(data$num_medications)) + geom_bar()
```



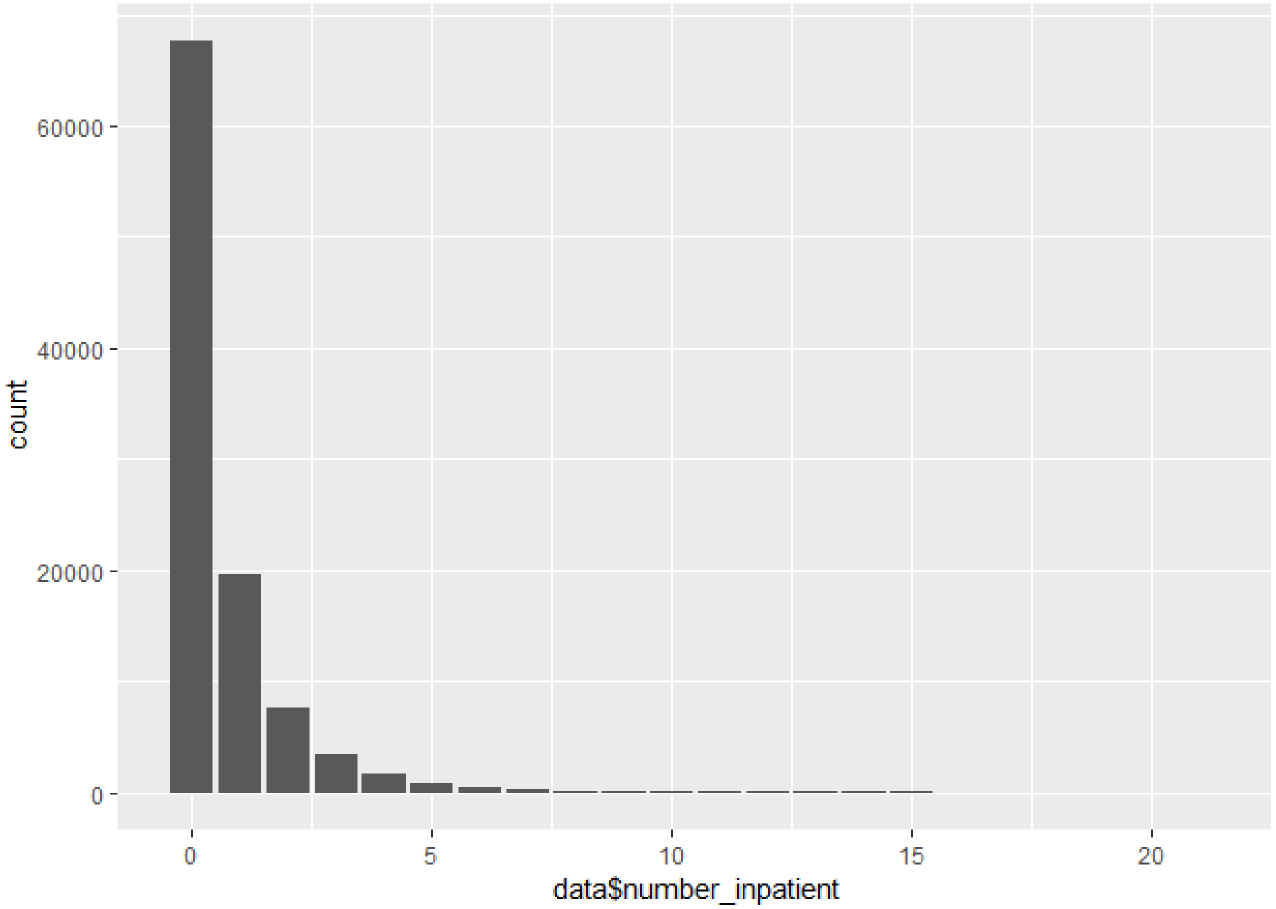
```
ggplot(data, aes(data$number_outpatient)) + geom_bar()
```



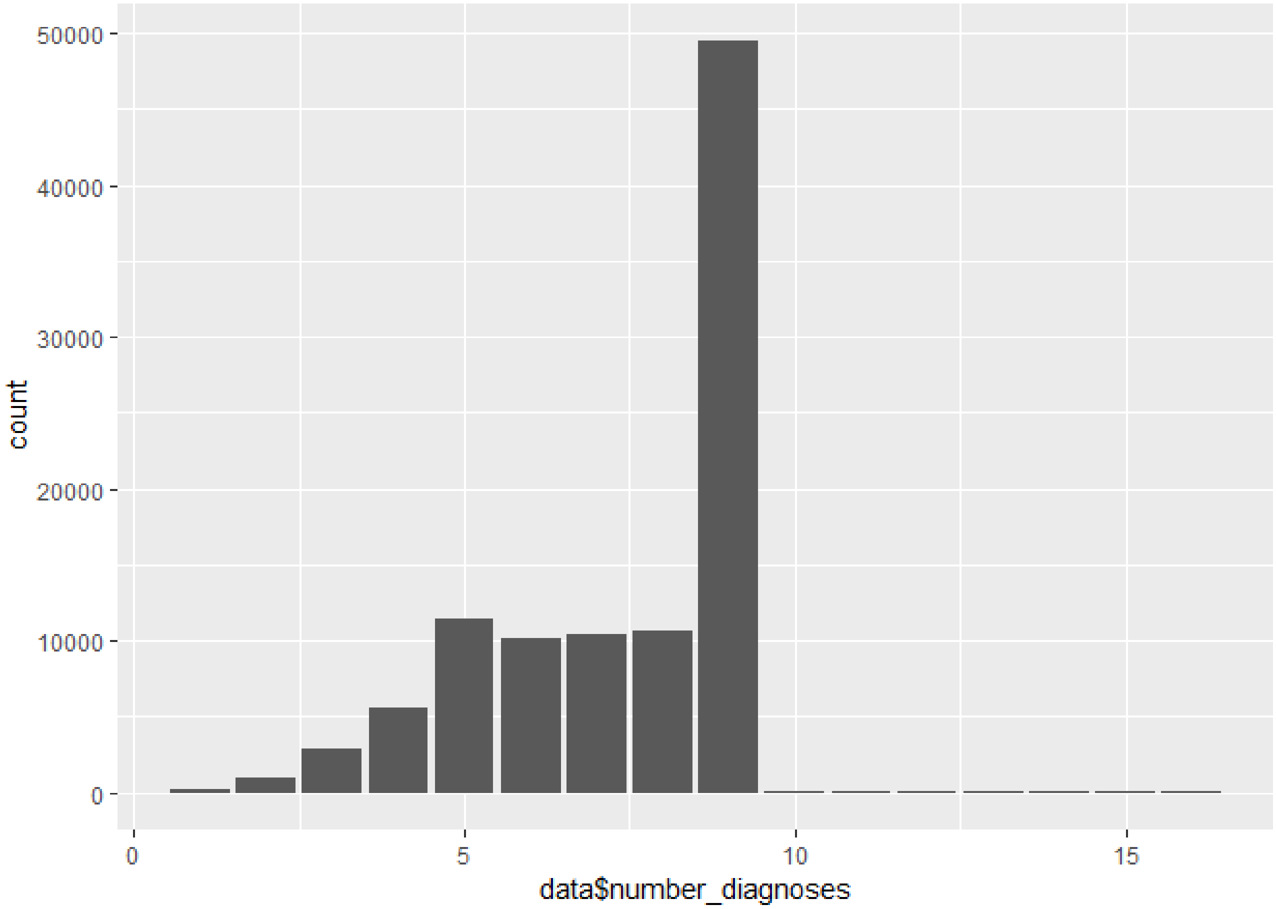
```
ggplot(data, aes(data$number_emergency)) + geom_bar()
```



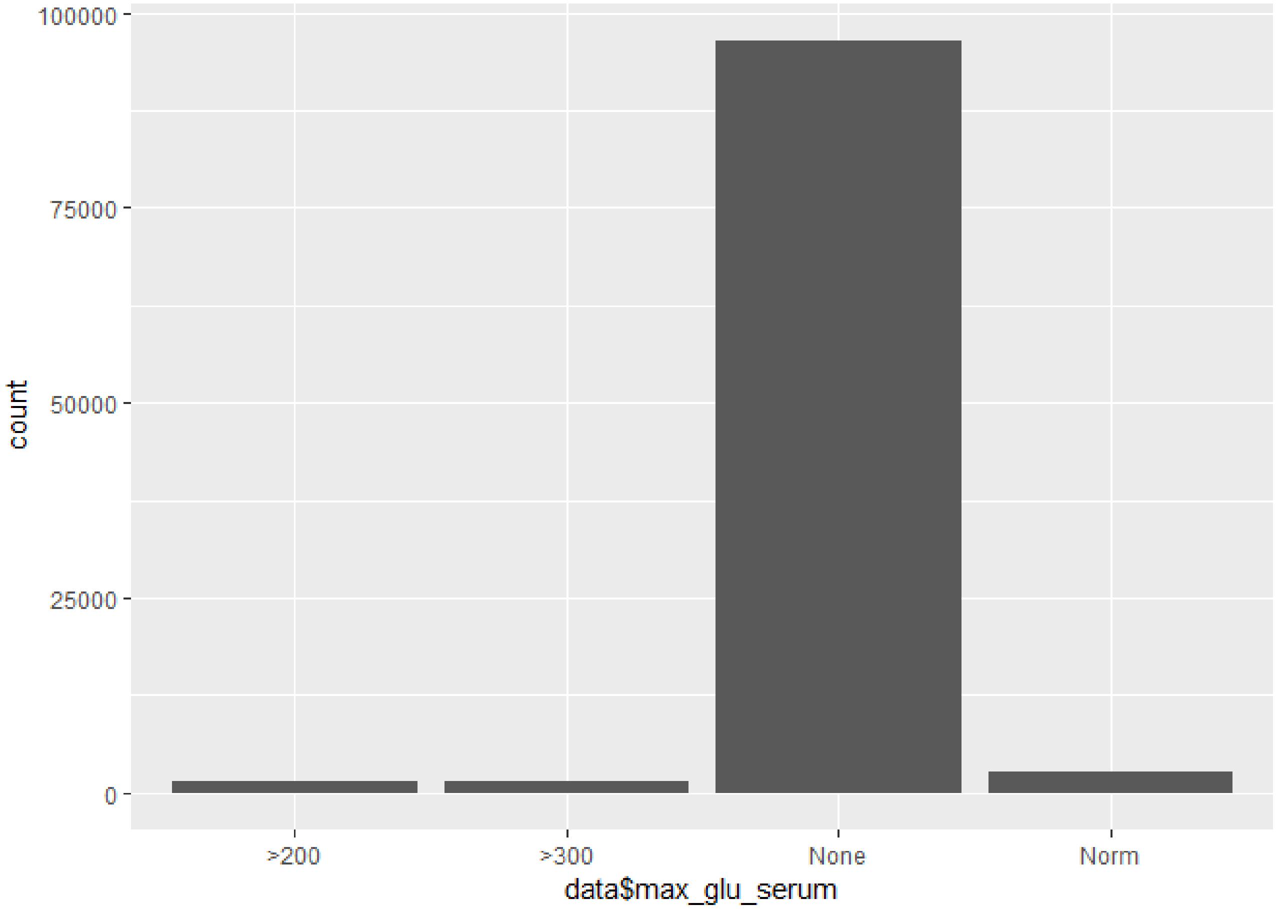
```
ggplot(data, aes(data$number_inpatient)) + geom_bar()
```



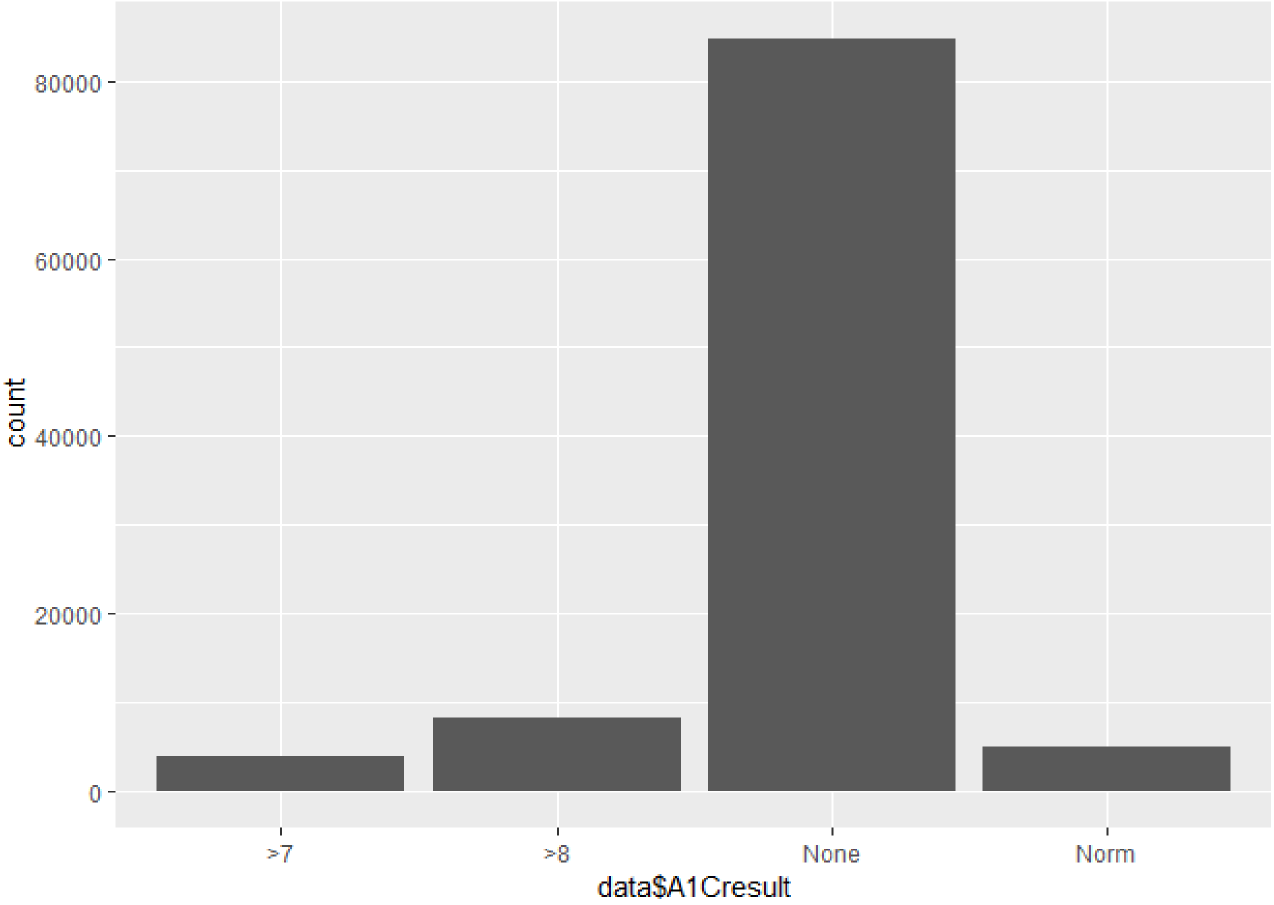
```
ggplot(data, aes(data$number_diagnoses)) + geom_bar()
```



```
ggplot(data, aes(data$max_glu_serum)) + geom_bar()
```



```
# A1Cresult compensate for this column
#  remove unwanted variable
data <- subset(data, select=-c(max_glu_serum))
#A1Cresult
ggplot(data, aes(data$A1Cresult)) + geom_bar()
```



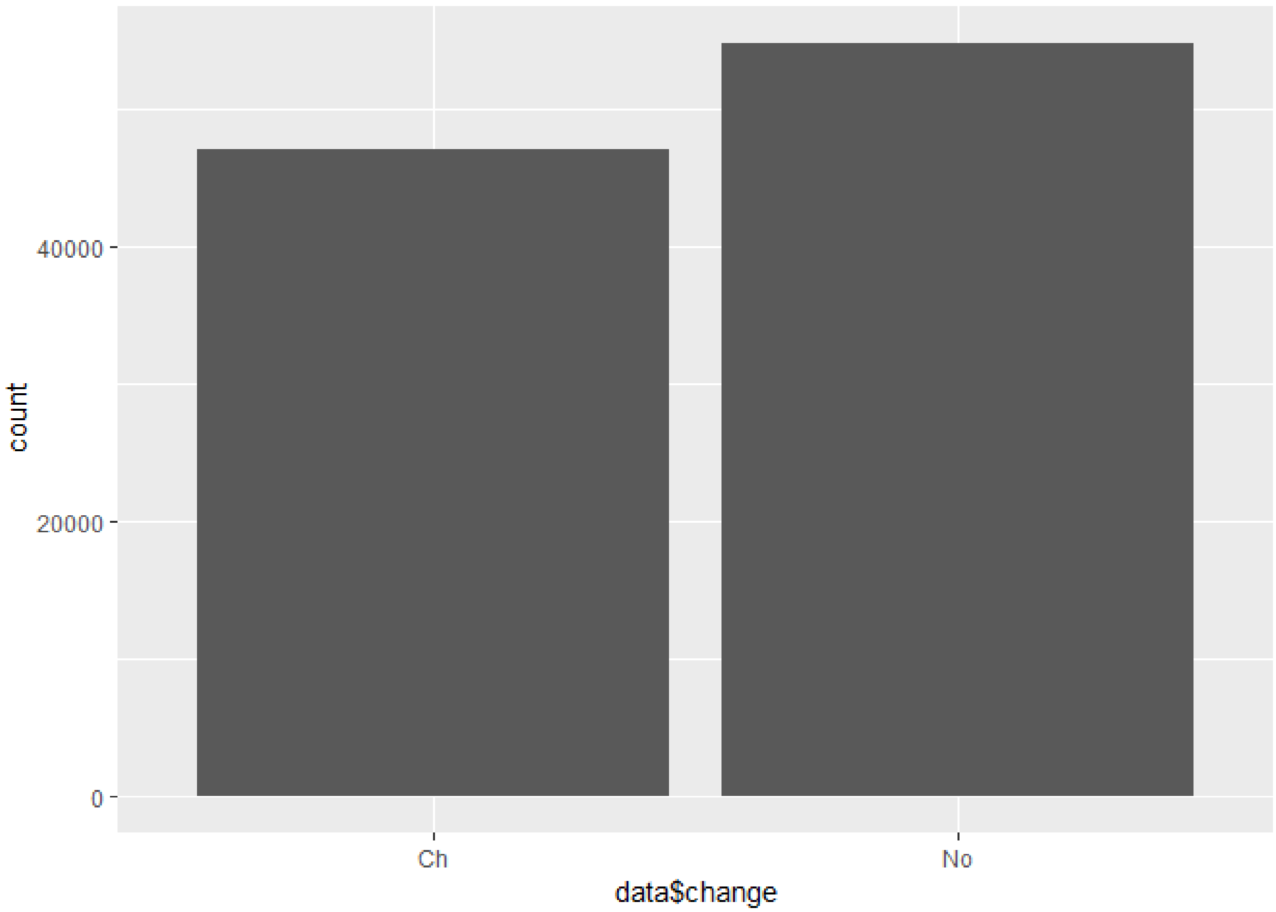
```
ggsave("figs/A1C.png")
```

```
## Saving 7 x 5 in image
```

```
data$A1Cresult <- as.factor(data$A1Cresult)
```

```
# remove unwanted variable as this is not taken in to account in this analysis

data <- subset(data, select=-c(metformin,repaglinide,nateglinide,chlorpropamide,glime
                        acetohexamide,glipizide,glyburide,tolbutamide,pioglitazone,
                        rosiglitazone,acarbose,miglitol,troglitazone,tolazamide,exami
                        citoglipton,glyburide.metformin,glipizide.metformin,
                        glimepiride.pioglitazone,metformin.rosiglitazone,
                        metformin.pioglitazone))
# head(data)
```

```
#change
ggplot(data, aes(data$change)) + geom_bar()
```



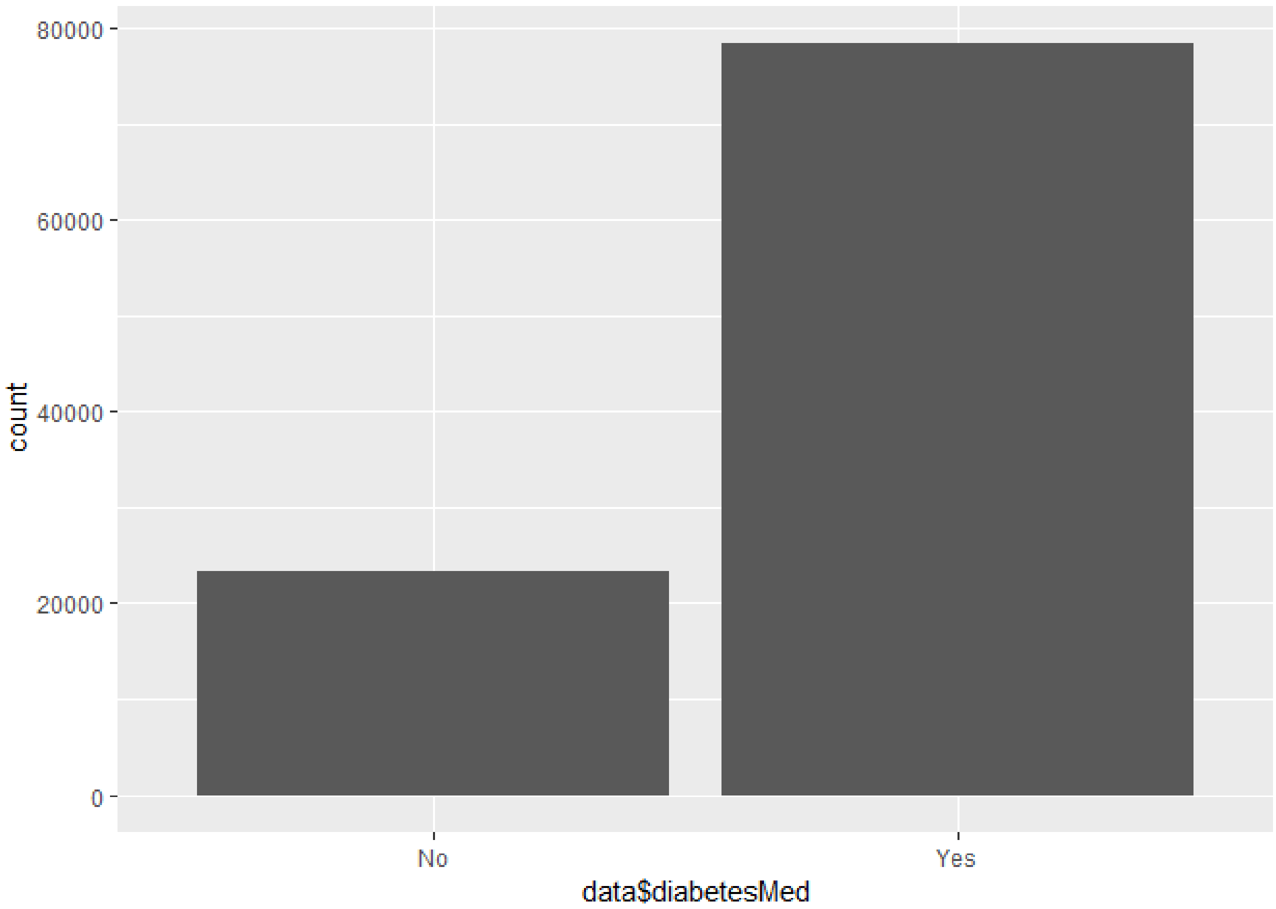
```
data$change <- replace(data$change, data$change == "Ch", "1")
data$change <- replace(data$change, data$change == "No", "0")
# convert to factor
summary(factor(data$change))
```

```
##     0     1
## 54755 47011
```

```
data$change <- as.numeric(data$change)
str(data$change)
```

```
##  num [1:101766] 0 1 0 1 1 0 1 0 1 1 ...
```

```
#diabetesMed
ggplot(data, aes(data$diabetesMed)) + geom_bar()
```



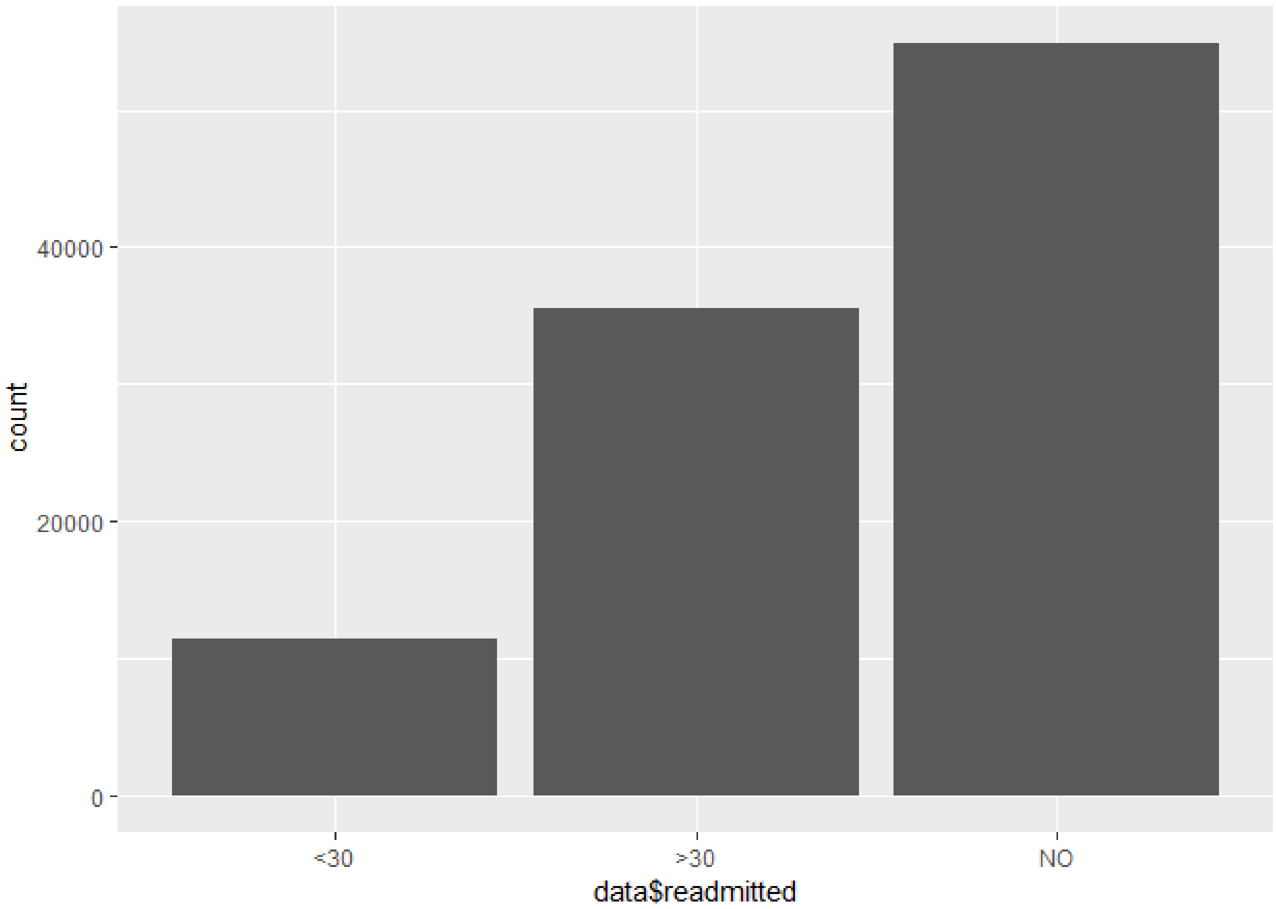
```
data$diabetesMed <- replace(data$diabetesMed, data$diabetesMed == "Yes", "1")
data$diabetesMed <- replace(data$diabetesMed, data$diabetesMed == "No", "0")
#convert gender to as.numeric
summary(factor(data$diabetesMed))
```

```
##     0     1
## 23403 78363
```

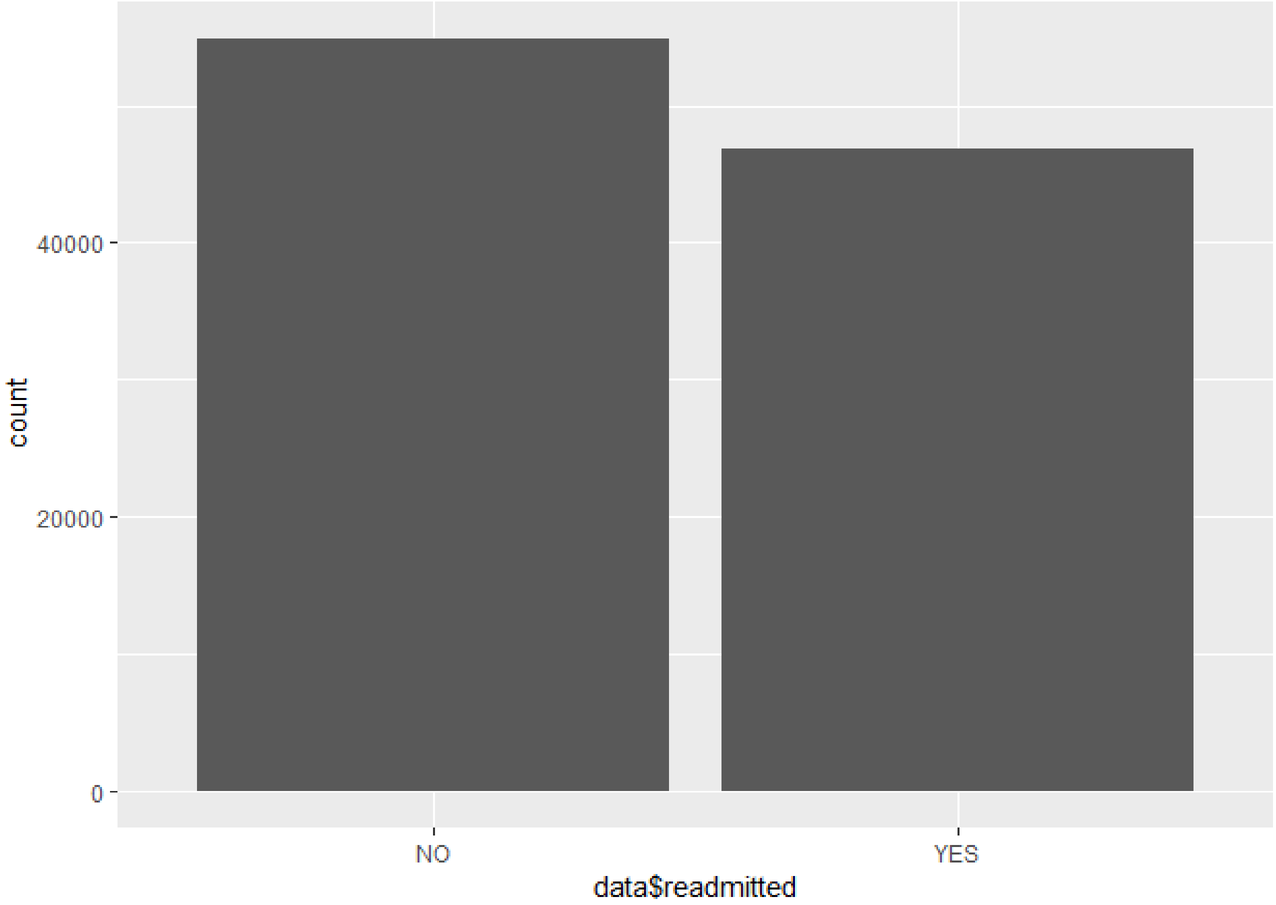
```
data$diabetesMed <- as.numeric(data$diabetesMed)
str(data$diabetesMed)
```

```
##  num [1:101766] 0 1 1 1 1 1 1 1 1 1 ...
```

```
#readmitted
ggplot(data, aes(data$readmitted)) + geom_bar()
```



```
data$readmitted <- replace(data$readmitted, data$readmitted == "<30", "YES")
data$readmitted <- replace(data$readmitted, data$readmitted == ">30", "YES")
ggplot(data, aes(data$readmitted)) + geom_bar()
```



```
summary(factor(data$readmitted))
```

```
##    NO   YES 
## 54864 46902
```

Feature engineering

Converting comorbidity conditions to analyseable format

```
## diab_code <- 250.xx
## circulatory_code <- 390-459, 785
## Not diabetic or have BP=0, diabetic alone=1, BP alone=2, both diabetic and BP=3

diagnosis <- data.frame(diag1 = as.character(data$diag_1),
                        diag2 = as.character(data$diag_2),
                        diag3 = as.character(data$diag_3),
                        stringsAsFactors = F)
str(diagnosis)
```

```
## 'data.frame':    101766 obs. of  3 variables:
```

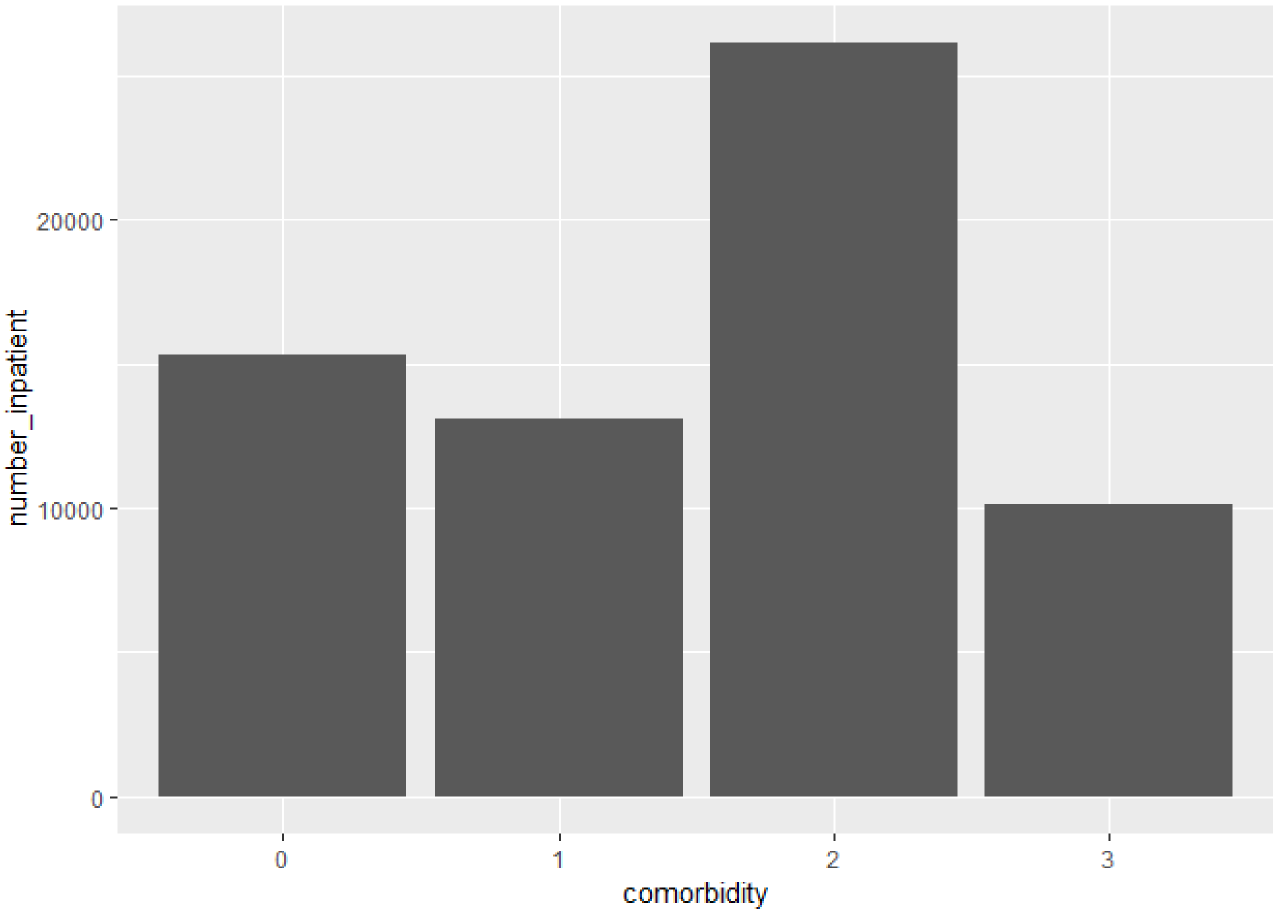
```
##  $ diag1: chr  "250.83" "276" "648" "8" ...
##  $ diag2: chr  NA "250.01" "250" "250.43" ...
##  $ diag3: chr  NA "255" "V27" "403" ...
```

```
diagnosis[is.na(diagnosis) == T] <- 0

make_comorbidity <- function(x){

  comorbidity <- character(length = nrow(data))
  diabetes_code <- "^[2][5][0]"
  circulatory_code <- "^[3][9][0-9]|^[4][0-5][0-9]"

  if((str_detect(x[1], diabetes_code) == F & (str_detect(x[2], circulatory_code) == F
     (str_detect(x[2], diabetes_code) == F & (str_detect(x[1], circulatory_code) == F
     (str_detect(x[3], diabetes_code) == F & (str_detect(x[1], circulatory_code) == F
    comorbidity <- 0
  }

  if((str_detect(x[1], diabetes_code) == T & (str_detect(x[2], circulatory_code) == F
     (str_detect(x[2], diabetes_code) == T & (str_detect(x[1], circulatory_code) == F
     (str_detect(x[3], diabetes_code) == T & (str_detect(x[1], circulatory_code) == F
    comorbidity <- 1
  }

  if((str_detect(x[1], circulatory_code) == T & (str_detect(x[2], diabetes_code) == F
     (str_detect(x[2], circulatory_code) == T & (str_detect(x[1], diabetes_code) == F
     (str_detect(x[3], circulatory_code) == T & (str_detect(x[1], diabetes_code) == F
    comorbidity <- 2
  }

  if((str_detect(x[1], diabetes_code) == T & (str_detect(x[2], circulatory_code) == T
     (str_detect(x[2], diabetes_code) == T & (str_detect(x[1], circulatory_code) == T
     (str_detect(x[3], diabetes_code) == T & (str_detect(x[1], circulatory_code) == T
    comorbidity <- 3
  }
  comorbidity <- ordered(comorbidity, levels = c(0,1,2,3))
  return(comorbidity)
}
data$comorbidity <- apply(diagnosis, 1, make_comorbidity)

# remove diagnosis
data$diag_1 <- NULL
data$diag_2 <- NULL
data$diag_3 <- NULL
```

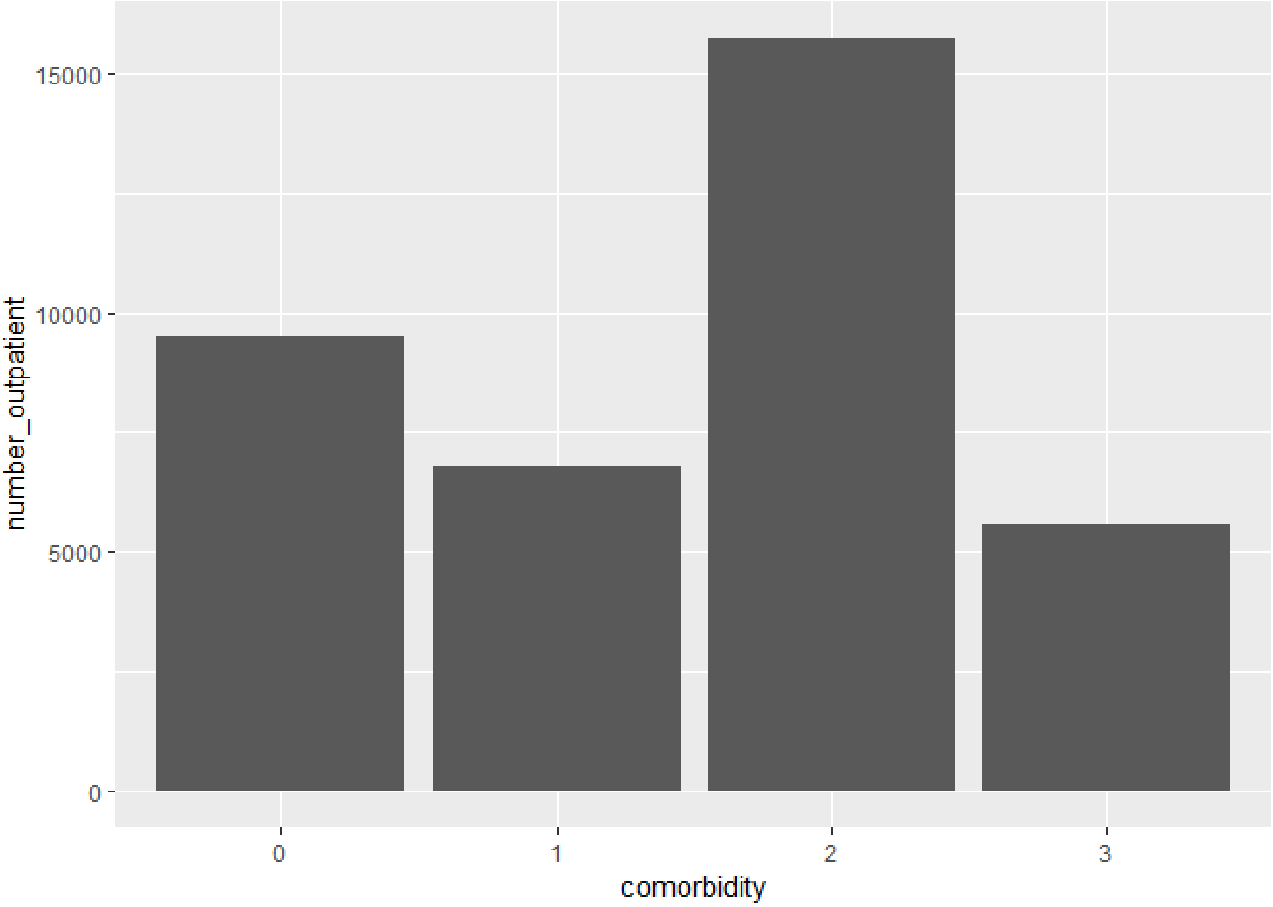
```
# comorbidity and readmission
prop.table(table(data$readmitted, data$comorbidity), margin = 2)
```

```
##
##              0         1         2         3
##   NO  0.5589385 0.5511183 0.5202076 0.5427348
##   YES 0.4410615 0.4488817 0.4797924 0.4572652
```

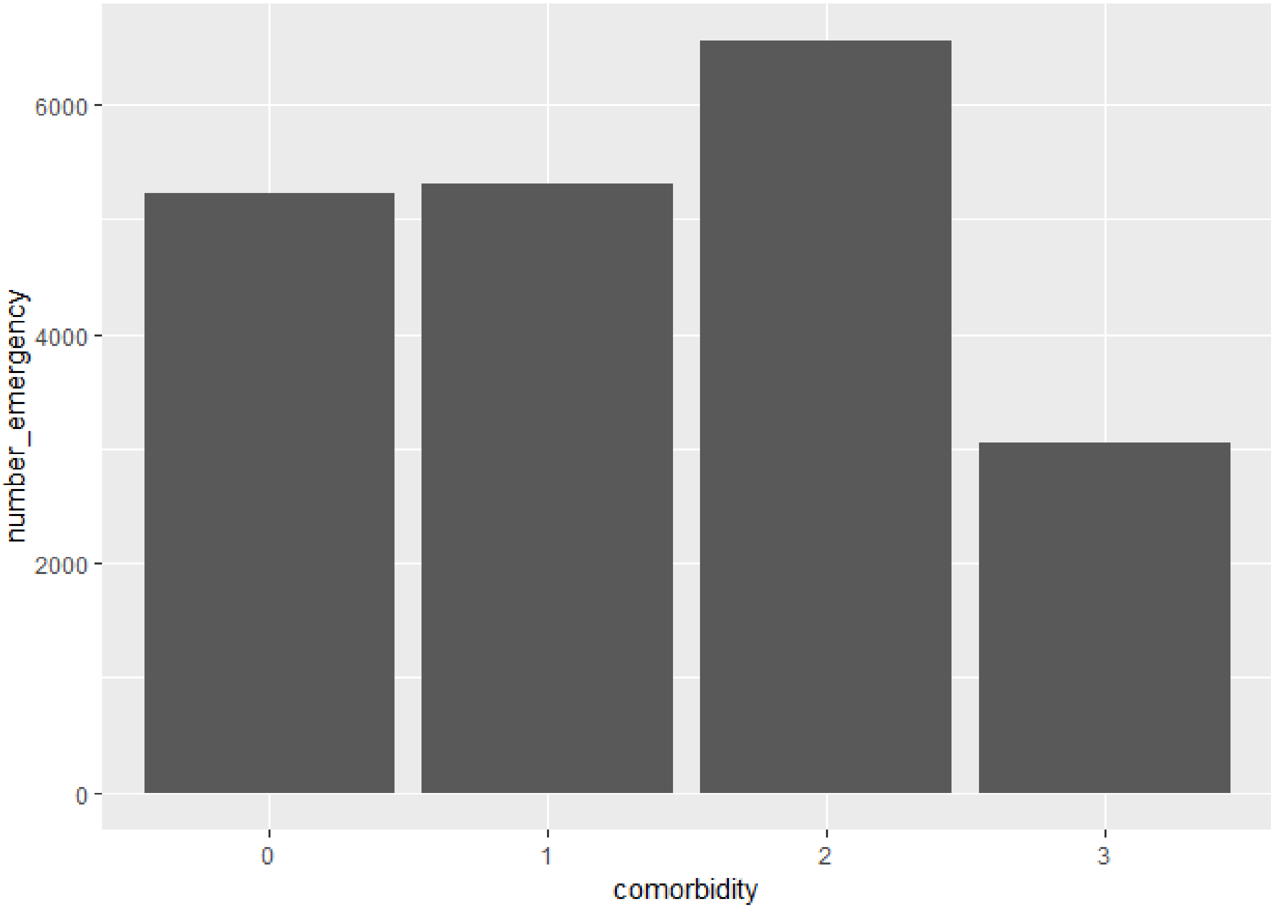
```
# analyse comorbidity
ggplot(data, aes(x=comorbidity, y=number_inpatient)) + geom_bar(stat = "identity")
```



```
ggplot(data, aes(x=comorbidity, y=number_outpatient)) + geom_bar(stat = "identity")
```



```
ggplot(data, aes(x=comorbidity, y=number_emergency)) + geom_bar(stat = "identity")
```



```
tapply(data$number_inpatient, data$comorbidity, mean)
```

```
##         0         1         2         3 
## 0.6565466 0.6623921 0.6461006 0.5561838
```

```
tapply(data$number_emergency, data$comorbidity, mean)
```

```
##         0         1         2         3 
## 0.2243741 0.2682385 0.1620319 0.1668771
```

```
tapply(data$number_outpatient, data$comorbidity, mean)
```

```
##         0         1         2         3 
## 0.4082106 0.3428081 0.3888271 0.3053192
```

```
tapply(data$time_in_hospital, data$comorbidity, mean)
```

```
##        0        1        2        3
## 4.942844 4.106326 4.515091 3.747379
```

```
tapply(data$number_diagnoses, data$comorbidity, mean)
```

```
##        0        1        2        3
## 8.075879 6.397637 7.989173 6.443761
```

```
tapply(data$num_lab_procedures, data$comorbidity, mean)
```

```
##        0        1        2        3
## 44.47503 41.96072 43.70849 40.87671
```

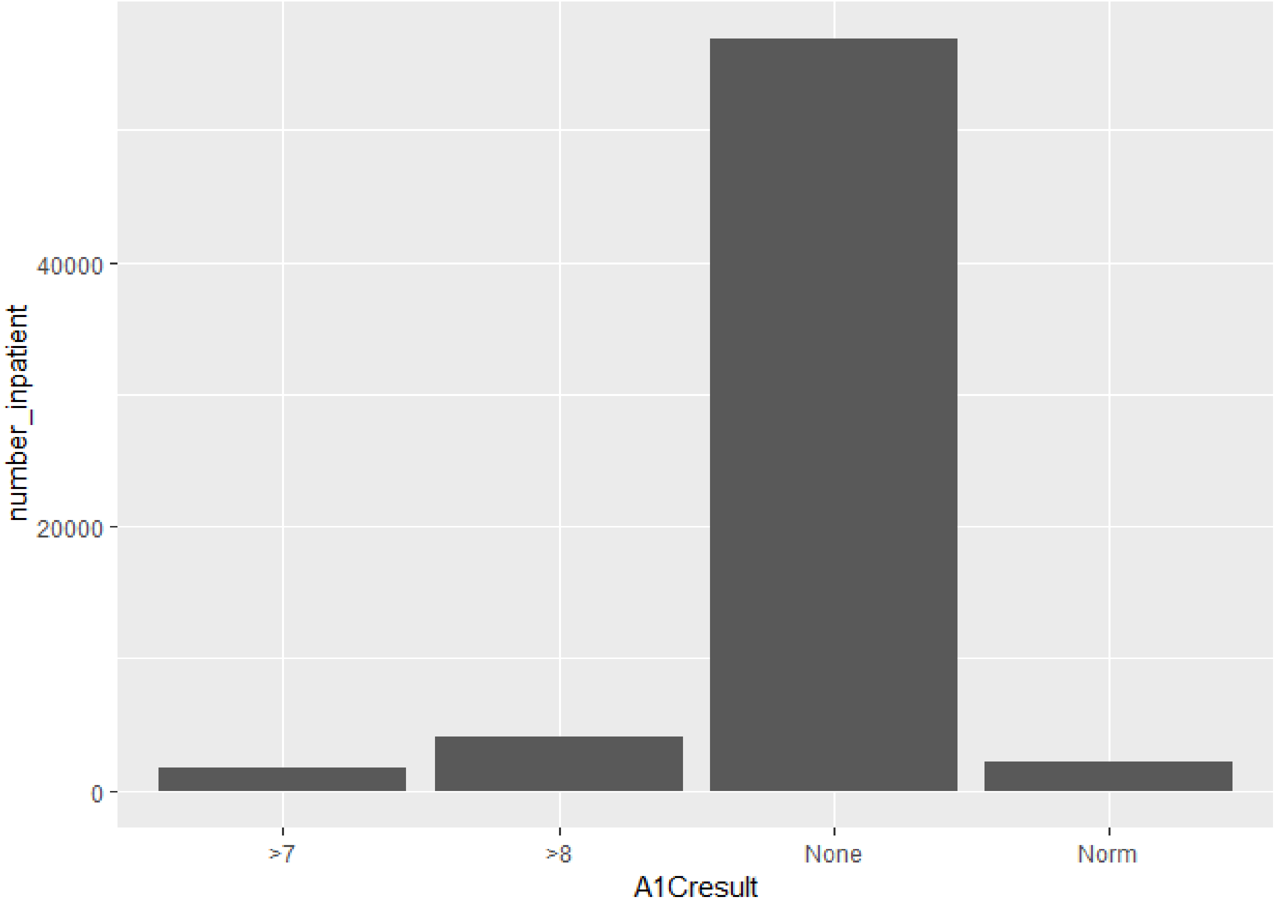
```
tapply(data$num_procedures, data$comorbidity, mean)
```

```
##         0         1         2         3
## 1.2195646 0.9189176 1.5773328 1.4232310
```

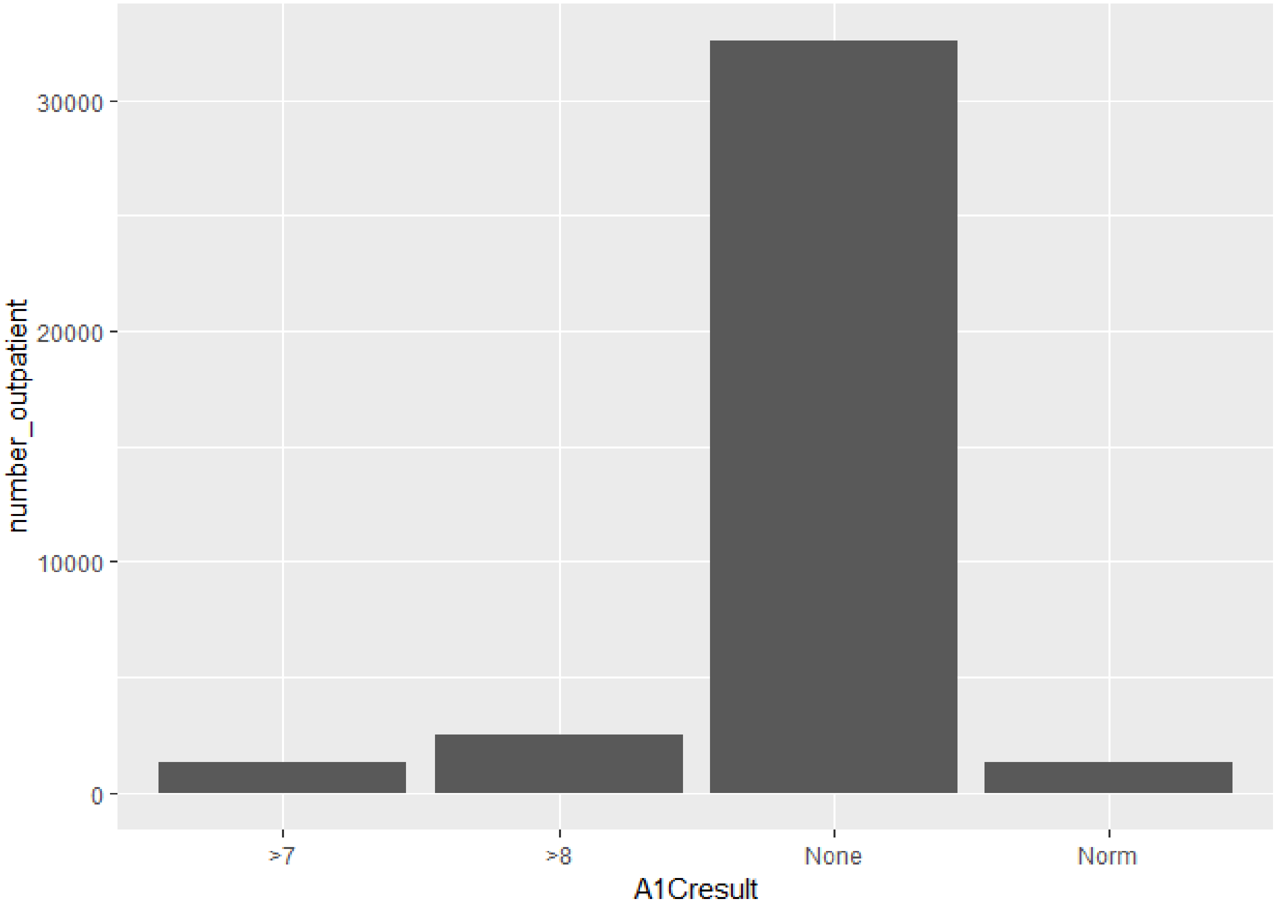
```
tapply(data$num_medications, data$comorbidity, mean)
```

```
##        0        1        2        3
## 16.30596 14.07856 17.04810 15.05588
```

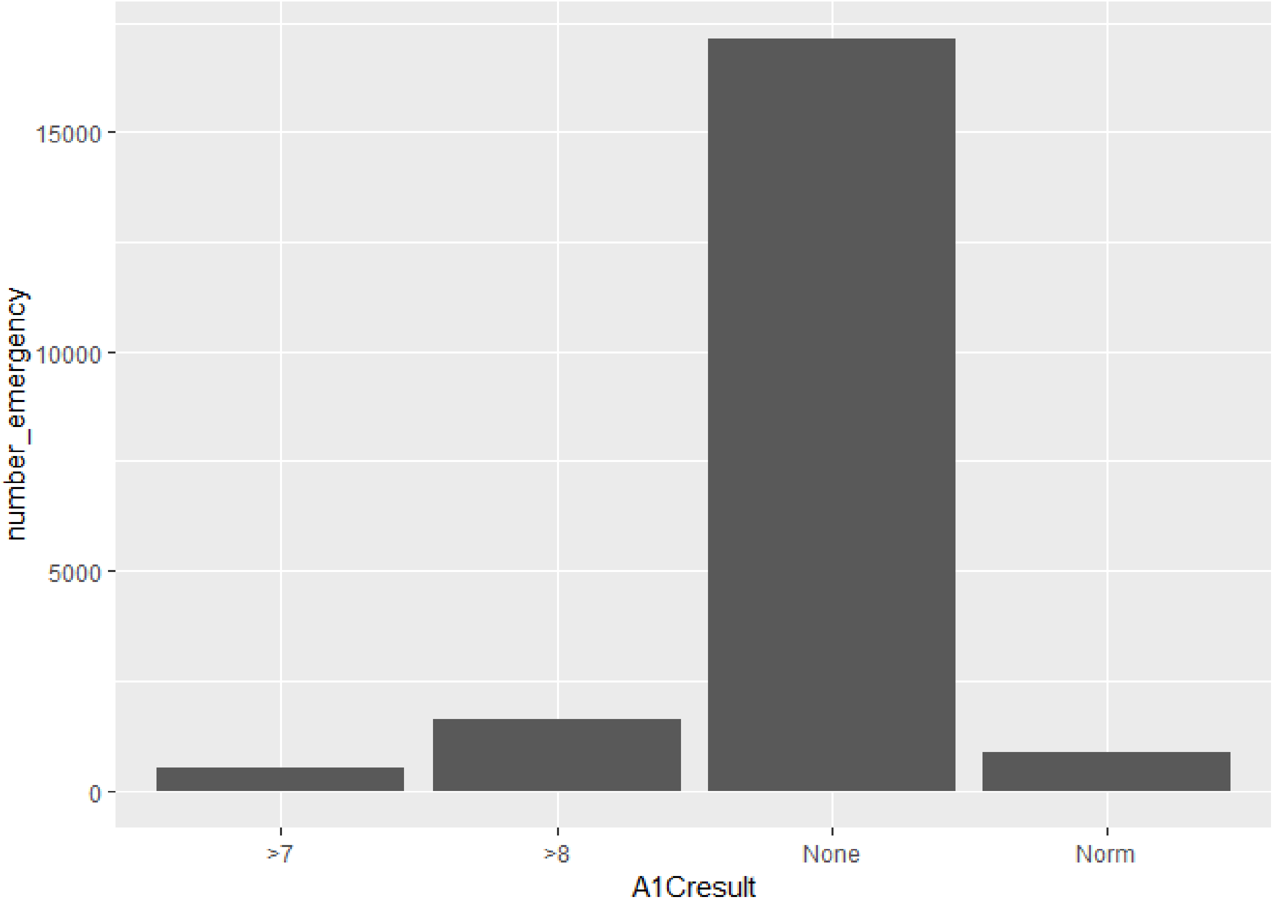
```
# Analyse A1Cresult
ggplot(data, aes(x=A1Cresult, y=number_inpatient)) + geom_bar(stat = "identity")
```



```
ggplot(data, aes(x=A1Cresult, y=number_outpatient)) + geom_bar(stat = "identity")
```



```
ggplot(data, aes(x=A1Cresult, y=number_emergency)) + geom_bar(stat = "identity")
```



```
tapply(data$number_inpatient, data$A1Cresult, mean)
```

```
##        >7        >8      None      Norm
## 0.4296957 0.4905063 0.6713079 0.4246493
```

```
tapply(data$number_outpatient, data$A1Cresult, mean)
```

```
##        >7        >8      None      Norm
## 0.3433893 0.2968598 0.3842451 0.2557114
```

```
tapply(data$number_emergency, data$A1Cresult, mean)
```

```
##        >7        >8      None      Norm
## 0.1343127 0.1970545 0.2020343 0.1763527
```

```
#Missing values
sapply(data, function(x) sum(is.na(x)))
```

```
##                     race                   gender                      age 
##                     2273                        3                        0 
##        admission_type_id discharge_disposition_id      admission_source_id 
##                        0                        0                        0 
##         time_in_hospital       num_lab_procedures           num_procedures 
##                        0                        0                        0 
##          num_medications        number_outpatient         number_emergency 
##                        0                        0                        0 
##         number_inpatient         number_diagnoses                A1Cresult 
##                        0                        0                        0 
##                  insulin                   change              diabetesMed 
##                        0                        0                        0 
##               readmitted              comorbidity 
##                        0                        0
```

```
#Percentage of missing values
colMeans(is.na(data))
```

```
##                     race                   gender                      age 
##             2.233555e-02             2.947939e-05             0.000000e+00 
##        admission_type_id discharge_disposition_id      admission_source_id 
##             0.000000e+00             0.000000e+00             0.000000e+00 
##         time_in_hospital       num_lab_procedures           num_procedures 
##             0.000000e+00             0.000000e+00             0.000000e+00 
##          num_medications        number_outpatient         number_emergency 
##             0.000000e+00             0.000000e+00             0.000000e+00 
##         number_inpatient         number_diagnoses                A1Cresult 
##             0.000000e+00             0.000000e+00             0.000000e+00 
##                  insulin                   change              diabetesMed 
##             0.000000e+00             0.000000e+00             0.000000e+00 
##               readmitted              comorbidity 
##             0.000000e+00             0.000000e+00
```

```
# Removing NAs
# before removing NAs patient ID is joined to the data
data <- cbind(Patient_Id, data)
data<-na.omit(data)
ID <- data$Patient_Id
data <- data[, 2:21]
```

Dummay variables are created

```
# race
#creating dummy variable for race variable
dummy_race <- model.matrix(~race - 1,data=data)
# Removing the 1st dummy variable
dummy_race <- dummy_race[,-1]
# Adding dummy variable of race to data and removing race column
data <- cbind(data[,-1], dummy_race)

#age
#creating dummy variable for age variable
dummy_age <- model.matrix(~age - 1,data=data)
# Removing the 1st dummy variable
dummy_age <- dummy_age[,-1]
# Adding dummy variable of age to data and removing age column
data <- cbind(data[,-2], dummy_age)

#admission_type_id
#creating dummy variable for admission_type_id variable
dummy_admission_type_id <- model.matrix(~admission_type_id - 1,data=data)
# Removing the 1st dummy variable
dummy_admission_type_id <- dummy_admission_type_id[,-1]
# Adding dummy variable of admission_type_id to data and removing admission_type_id c
data <- cbind(data[,-2], dummy_admission_type_id)

#discharge_disposition_id
#creating dummy variable for discharge_disposition_id variable
dummy_discharge_disposition_id <- model.matrix(~discharge_disposition_id - 1,data=dat
# Removing the 1st dummy variable
dummy_discharge_disposition_id <- dummy_discharge_disposition_id[,-1]
# Adding dummy variable of discharge_disposition_id to data and removing discharge_di
data <- cbind(data[,-2], dummy_discharge_disposition_id)

#admission_source_id
#creating dummy variable for admission_source_id variable
dummy_admission_source_id <- model.matrix(~admission_source_id - 1,data=data)
# Removing the 1st dummy variable
dummy_admission_source_id <- dummy_admission_source_id[,-1]
# Adding dummy variable of admission_source_id to data and removing admission_source_
data <- cbind(data[,-2], dummy_admission_source_id)

#A1Cresult
#creating dummy variable for A1Cresult variable
dummy_A1Cresult <- model.matrix(~A1Cresult - 1,data=data)
# Removing the 1st dummy variable
dummy_A1Cresult <- dummy_A1Cresult[,-1]
# Adding dummy variable of A1Cresult to data and removing A1Cresult column
data <- cbind(data[,-10], dummy_A1Cresult)
```

```
#insulin
#creating dummy variable for insulin variable
dummy_insulin <- model.matrix(~insulin - 1,data=data)
# Removing the 1st dummy variable
dummy_insulin <- dummy_insulin[,-1]
# Adding dummy variable of insulin to data and removing insulin column
data <- cbind(data[,-10], dummy_insulin)

#comorbidity
#creating dummy variable for comorbidity variable
dummy_comorbidity <- model.matrix(~comorbidity - 1,data=data)
# Removing the 1st dummy variable
dummy_comorbidity <- dummy_comorbidity[,-1]
# Adding dummy variable of race to data and removing race column
data <- cbind(data[,-13], dummy_comorbidity)
```

```
# Readmitted is separated and added to the first column in the dataset and removed th
readmitted <- data$readmitted
data <- cbind(readmitted, data)
data <- data[,-13]
# All are numerical variable.
```

```
# join the ID of patients
data <- cbind(ID, data)
str(data)
```

```
## 'data.frame':    99492 obs. of  42 variables:
##  $ ID                       : int  8222157 55629189 86047875 82442376 42519267 826
##  $ readmitted               : Factor w/ 2 levels "NO","YES": 1 2 1 1 1 2 1 2 1 1 .
##  $ gender                   : num  1 1 1 0 0 0 0 0 1 1 ...
##  $ time_in_hospital         : num [1:99492, 1] -1.138 -0.468 -0.803 -0.803 -1.138
##   ..- attr(*, "scaled:center")= num 4.4
##   ..- attr(*, "scaled:scale")= num 2.99
##  $ num_lab_procedures       : num [1:99492, 1] -0.103 0.8177 -1.6375 0.0505 0.4085
##   ..- attr(*, "scaled:center")= num 43
##   ..- attr(*, "scaled:scale")= num 19.6
##  $ num_procedures           : num [1:99492, 1] -0.787 -0.787 2.148 -0.2 -0.787 ...
##   ..- attr(*, "scaled:center")= num 1.34
##   ..- attr(*, "scaled:scale")= num 1.7
##  $ num_medications          : num [1:99492, 1] -1.91881 0.26327 -0.37851 0.00656 -
##   ..- attr(*, "scaled:center")= num 15.9
##   ..- attr(*, "scaled:scale")= num 7.79
##  $ number_outpatient        : num [1:99492, 1] -0.292 -0.292 1.274 -0.292 -0.292 .
##   ..- attr(*, "scaled:center")= num 0.373
##   ..- attr(*, "scaled:scale")= num 1.28
##  $ number_emergency         : num [1:99492, 1] -0.214 -0.214 -0.214 -0.214 -0.214
##   ..- attr(*, "scaled:center")= num 0.201
##   ..- attr(*, "scaled:scale")= num 0.94
##  $ number_inpatient         : num [1:99492, 1] -0.506 -0.506 0.281 -0.506 -0.506 .
##   ..- attr(*, "scaled:center")= num 0.643
##   ..- attr(*, "scaled:scale")= num 1.27
##  $ number_diagnoses         : num [1:99492, 1] -3.343 0.81 -0.747 -0.228 -1.266 ..
##   ..- attr(*, "scaled:center")= num 7.44
##   ..- attr(*, "scaled:scale")= num 1.93
##  $ change                   : num  0 1 0 1 1 0 1 0 1 1 ...
##  $ diabetesMed              : num  0 1 1 1 1 1 1 1 1 1 ...
##  $ raceAsian                : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ raceCaucasian            : num  1 1 0 1 1 1 1 1 1 1 ...
##  $ raceHispanic             : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ raceOther                : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ age2                     : num  0 1 0 0 0 0 0 0 0 0 ...
##  $ age3                     : num  0 0 1 1 0 0 0 0 0 0 ...
##  $ age4                     : num  0 0 0 0 1 1 0 0 0 0 ...
##  $ age5                     : num  0 0 0 0 0 0 1 0 0 0 ...
##  $ age6                     : num  0 0 0 0 0 0 0 1 0 0 ...
##  $ age7                     : num  0 0 0 0 0 0 0 0 1 1 ...
##  $ admission_type_id3       : num  0 0 0 0 0 0 1 0 0 1 ...
##  $ admission_type_id4       : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ admission_type_id5       : num  1 0 0 0 0 0 0 0 0 0 ...
##  $ admission_type_id7       : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ discharge_disposition_id2: num  0 0 0 0 0 0 0 0 0 1 ...
##  $ discharge_disposition_id3: num  1 0 0 0 0 0 0 0 0 0 ...
##  $ discharge_disposition_id4: num  0 0 0 0 0 0 0 0 0 0 ...
##  $ admission_source_id2     : num  0 1 1 1 1 0 0 1 1 1 ...
##  $ admission_source_id3     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ admission_source_id4     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ A1Cresult>8              : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ A1CresultNone            : num  1 1 1 1 1 1 1 1 1 1 ...
##  $ A1CresultNorm            : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ insulinNo                : num  1 0 1 0 0 0 0 1 0 0 ...
##  $ insulinSteady            : num  0 0 0 0 1 1 1 0 1 1 ...
##  $ insulinUp                : num  0 1 0 1 0 0 0 0 0 0 ...
##  $ comorbidity1             : num  1 1 1 0 1 0 0 0 0 0 ...
##  $ comorbidity2             : num  0 0 0 0 0 0 1 0 1 1 ...
##  $ comorbidity3             : num  0 0 0 1 0 1 0 1 0 0 ...
```