

final_hi2021

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R Markdown

```
stroke_dt <- read.csv("stroke.csv")
colnames(stroke_dt)
```

```
[1] "id"           "gender"       "age"
[4] "hypertension" "heart_disease" "ever_married"
[7] "work_type"    "Residence_type" "avg_glucose_level"
[10] "bmi"         "smoking_status" "stroke"
```

```
# PART 1: CLEANING, PROCESSING, and PREPARING THE DATA
# Exploratory Data Analysis
library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

```
filter, lag
```

The following objects are masked from 'package:base':

```
intersect, setdiff, setequal, union
```

```
stroke_dt %>% count(gender)
```

```
gender      n
1 Female 2994
2  Male 2115
3  Other    1
```

```
stroke_dt %>% count(smoking_status)
```

```
smoking_status      n
1      Unknown 1544
2 formerly smoked  885
3   never smoked 1892
4         smokes  789
```

```
stroke_dt %>% count(Residence_type)
```

```
Residence_type      n
1      Rural 2514
2      Urban 2596
```

```
stroke_dt %>% count(work_type)
```

```

  work_type    n
1   Govt_job  657
2 Never_worked  22
3    Private 2925
4 Self-employed  819
5    children  687

```

```
# Handle Missing Data
```

```

library(dplyr)
stroke_dt1 <- stroke_dt %>%
  mutate_all(~replace(., . == 'N/A', NA))

```

```
# Imputing missing data
```

```

missing_dt <- apply(stroke_dt1, MARGIN = 2, function(x){sum(is.na(x))/length(x)*100})
missing_dt # shows the percentage of missing data in each column, bmi missing 3.9%

```

```

      id      gender      age      hypertension
0.000000  0.000000  0.000000  0.000000
heart_disease ever_married work_type Residence_type
0.000000  0.000000  0.000000  0.000000
avg_glucose_level      bmi      smoking_status      stroke
0.000000  3.933464  0.000000  0.000000

```

```

new_stroke <- stroke_dt1[,missing_dt < 20] # blank before the comma because we want to keep all rows
apply(new_stroke, 2, function(x){sum(is.na(x))/length(x)*100})

```

```

      id      gender      age      hypertension
0.000000  0.000000  0.000000  0.000000
heart_disease ever_married work_type Residence_type
0.000000  0.000000  0.000000  0.000000
avg_glucose_level      bmi      smoking_status      stroke
0.000000  3.933464  0.000000  0.000000

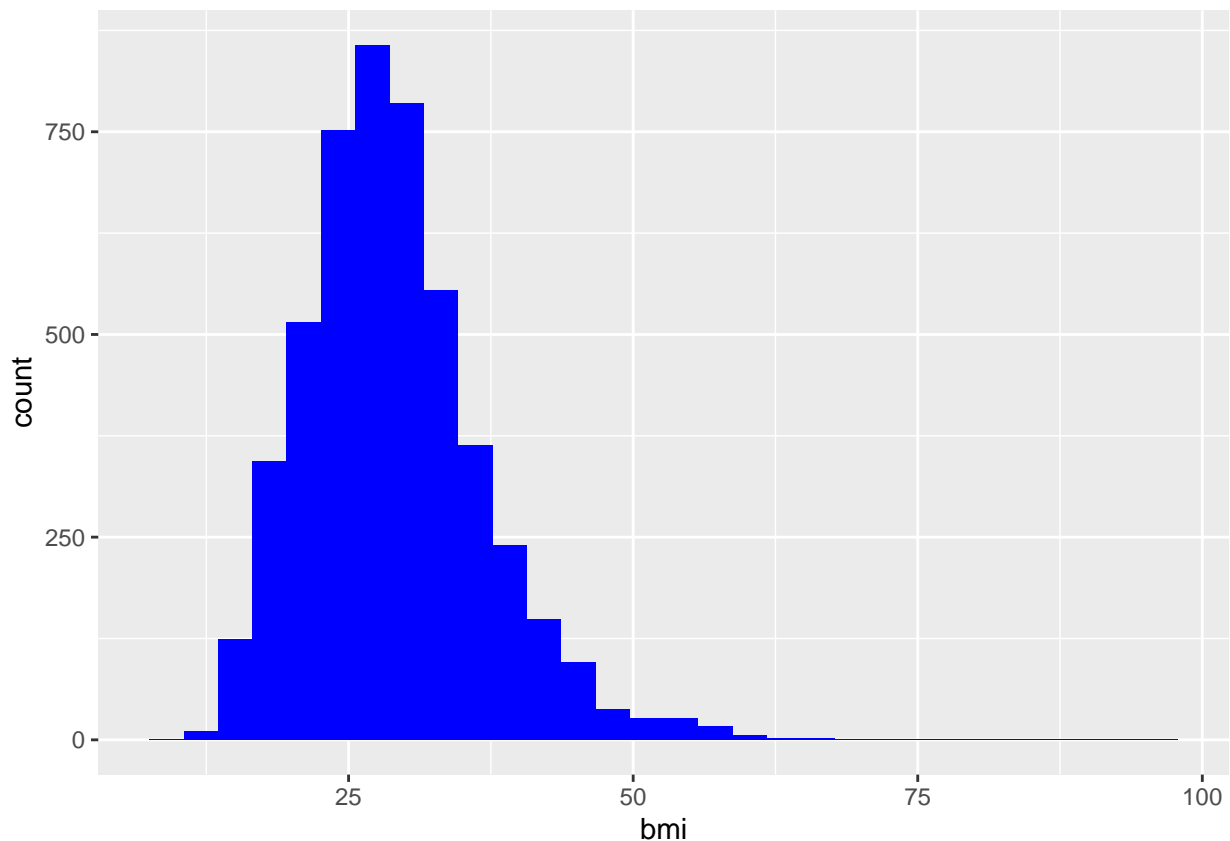
```

```

library(ggplot2) # determine if normal distribution before imputing data
stroke_dt1$bmi <- as.numeric(stroke_dt1$bmi) # convert BMI to numeric
ggplot(data=subset(stroke_dt1, !is.na(bmi)), aes(x=bmi)) +
  geom_histogram(fill = 'blue')

```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
# Imputing data with the mean
imputed_bmi <- data.frame(
  original = stroke_dt1$bmi,
  bmi_imputed = replace(stroke_dt1$bmi, is.na(stroke_dt1$bmi), mean(stroke_dt1$bmi, na.rm = TRUE))
)

# Combining the imputed data with the original dataframe, use cbind()
stroke_dt2 <- cbind(stroke_dt1, imputed_bmi)

stroke_dt3 <- stroke_dt2[ -c(10,13) ] # remove ID, ever_married, old BMI columns

prop.table(table(stroke_dt3$stroke)) # see ratio of stroke and non stroke patients
```

```
      0      1
0.95127202 0.04872798
```

```
stroke_pos <- subset(stroke_dt3, stroke == '1') # creating separate df for + stroke and - stroke
summary(stroke_pos)
```

id	gender	age	hypertension
Min. : 210	Length:249	Min. : 1.32	Min. :0.0000
1st Qu.:17013	Class :character	1st Qu.:59.00	1st Qu.:0.0000
Median :36706	Mode :character	Median :71.00	Median :0.0000
Mean :37115		Mean :67.73	Mean :0.2651
3rd Qu.:56669		3rd Qu.:78.00	3rd Qu.:1.0000
Max. :72918		Max. :82.00	Max. :1.0000
heart_disease	ever_married	work_type	Residence_type

Min. :0.0000	Length:249	Length:249	Length:249
1st Qu.:0.0000	Class :character	Class :character	Class :character
Median :0.0000	Mode :character	Mode :character	Mode :character
Mean :0.1888			
3rd Qu.:0.0000			
Max. :1.0000			

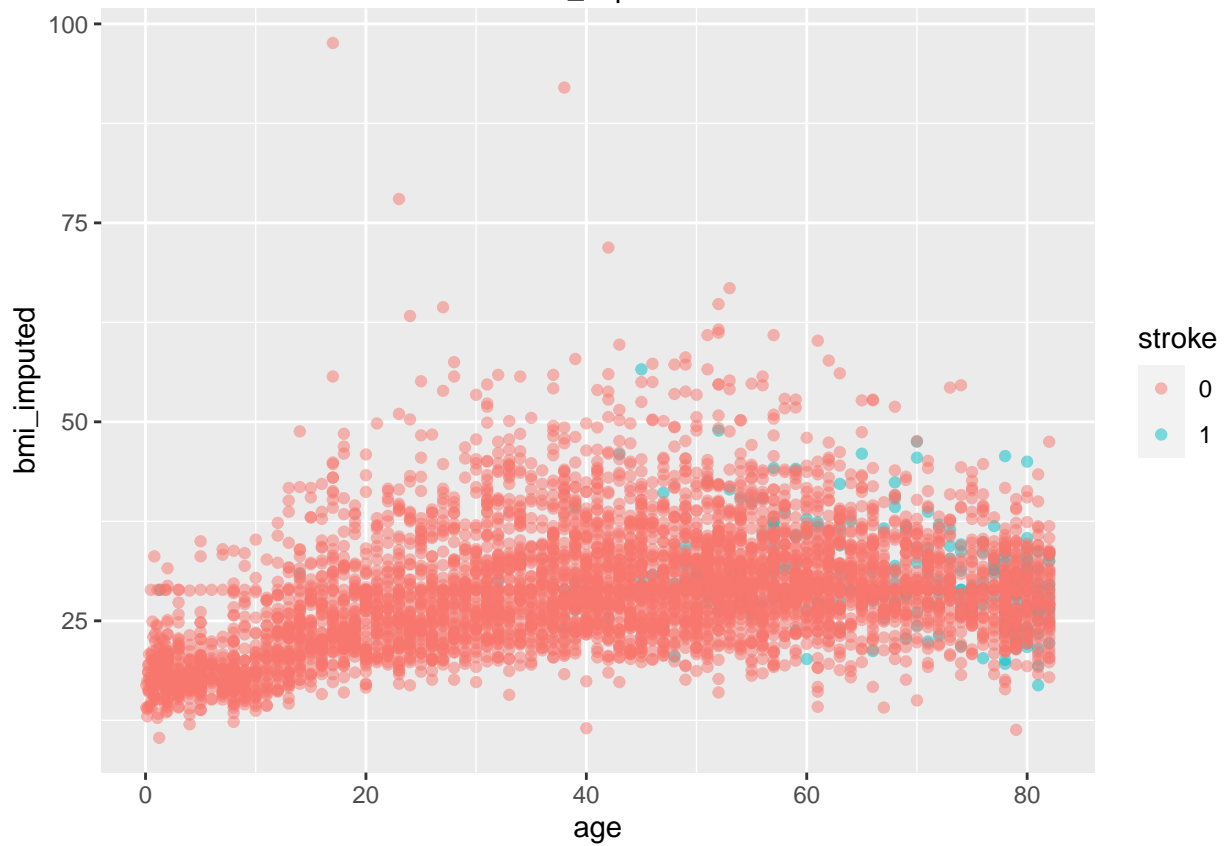
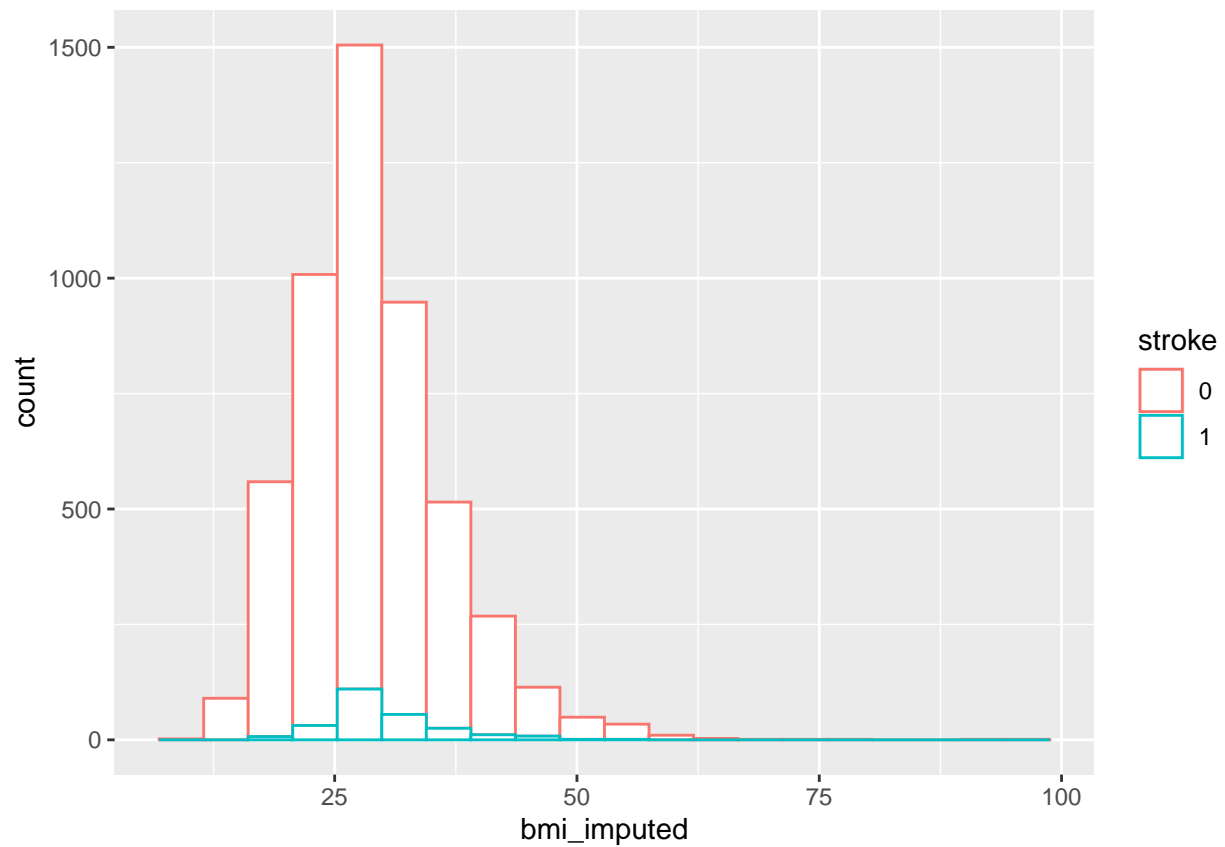
avg_glucose_level	smoking_status	stroke	bmi_imputed
Min. : 56.11	Length:249	Min. :1	Min. :16.90
1st Qu.: 79.79	Class :character	1st Qu.:1	1st Qu.:27.00
Median :105.22	Mode :character	Median :1	Median :28.89
Mean :132.54		Mean :1	Mean :30.22
3rd Qu.:196.71		3rd Qu.:1	3rd Qu.:32.50
Max. :271.74		Max. :1	Max. :56.60

```
stroke_neg <- subset(stroke_dt3, stroke == '0')
summary(stroke_neg)
```

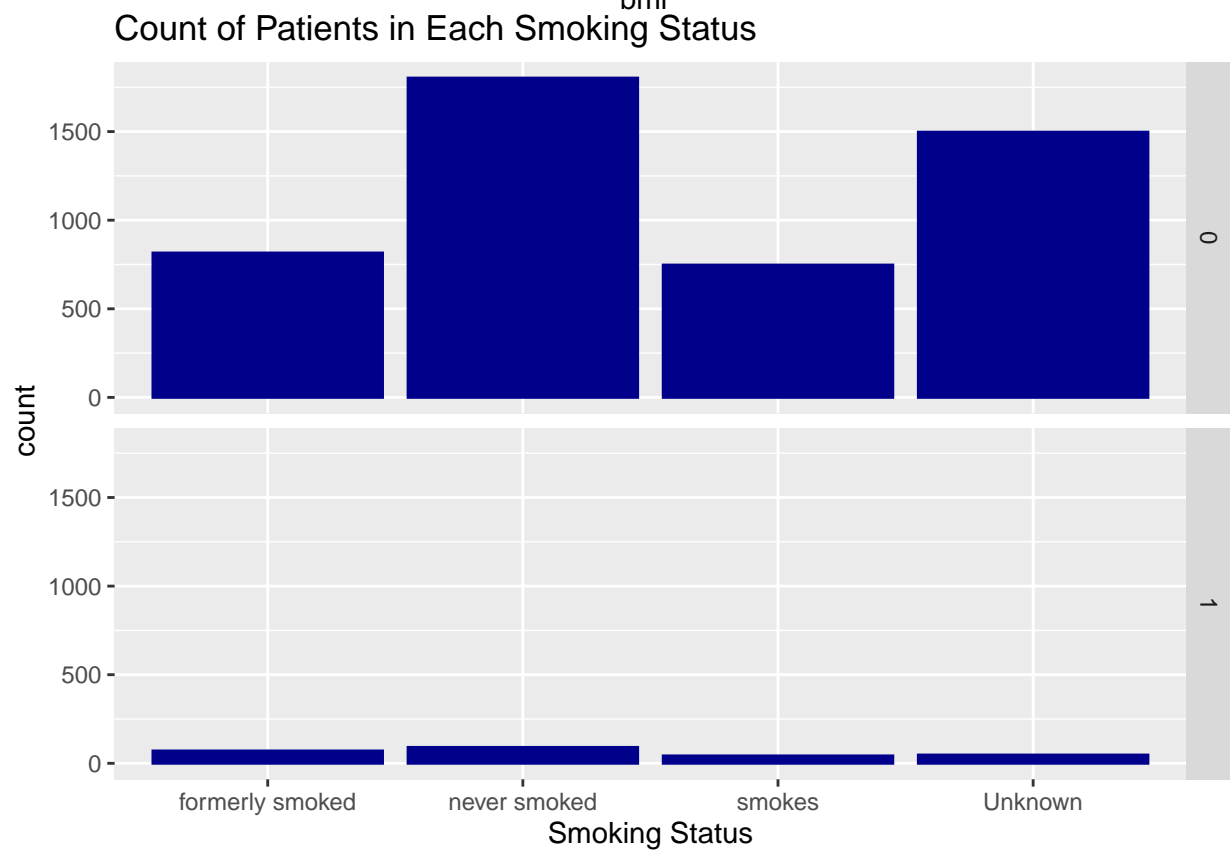
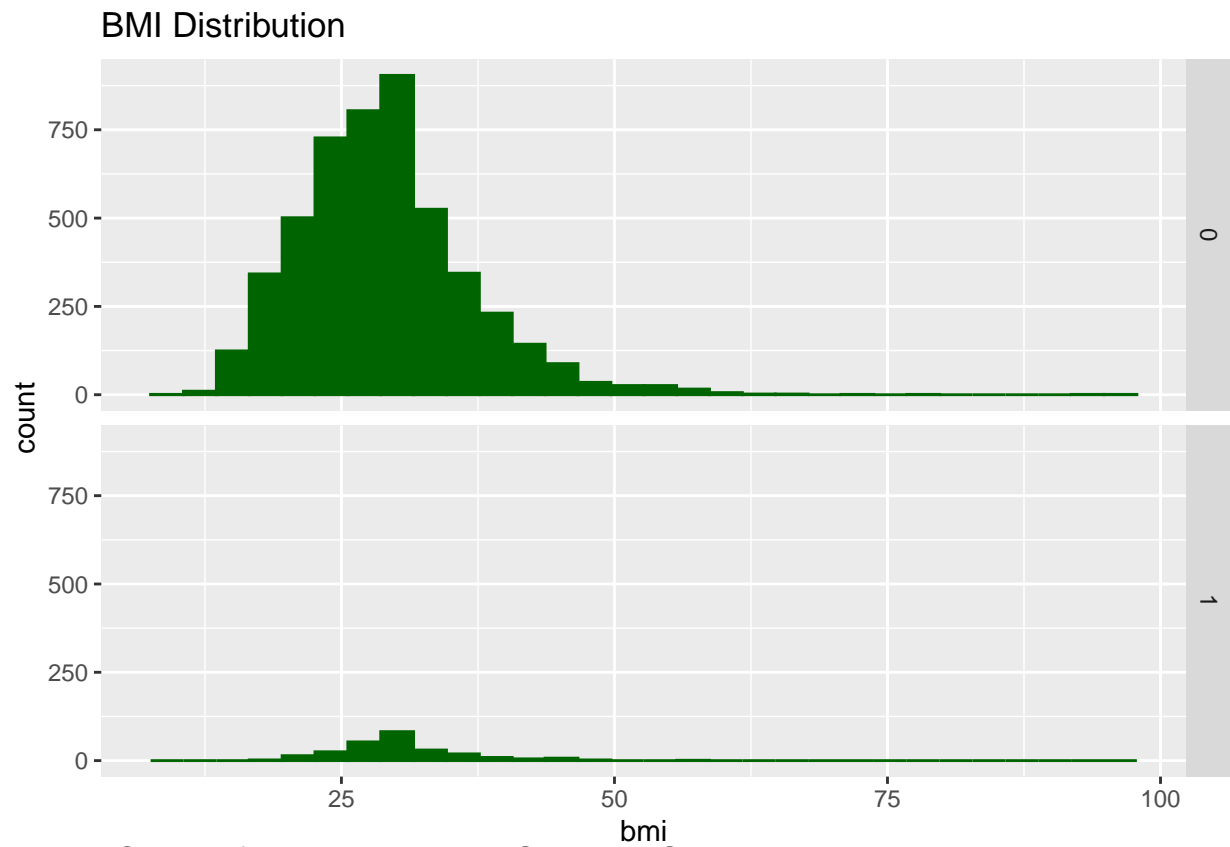
id	gender	age	hypertension
Min. : 67	Length:4861	Min. : 0.08	Min. :0.00000
1st Qu.:17762	Class :character	1st Qu.:24.00	1st Qu.:0.00000
Median :36958	Mode :character	Median :43.00	Median :0.00000
Mean :36487		Mean :41.97	Mean :0.08887
3rd Qu.:54497		3rd Qu.:59.00	3rd Qu.:0.00000
Max. :72940		Max. :82.00	Max. :1.00000

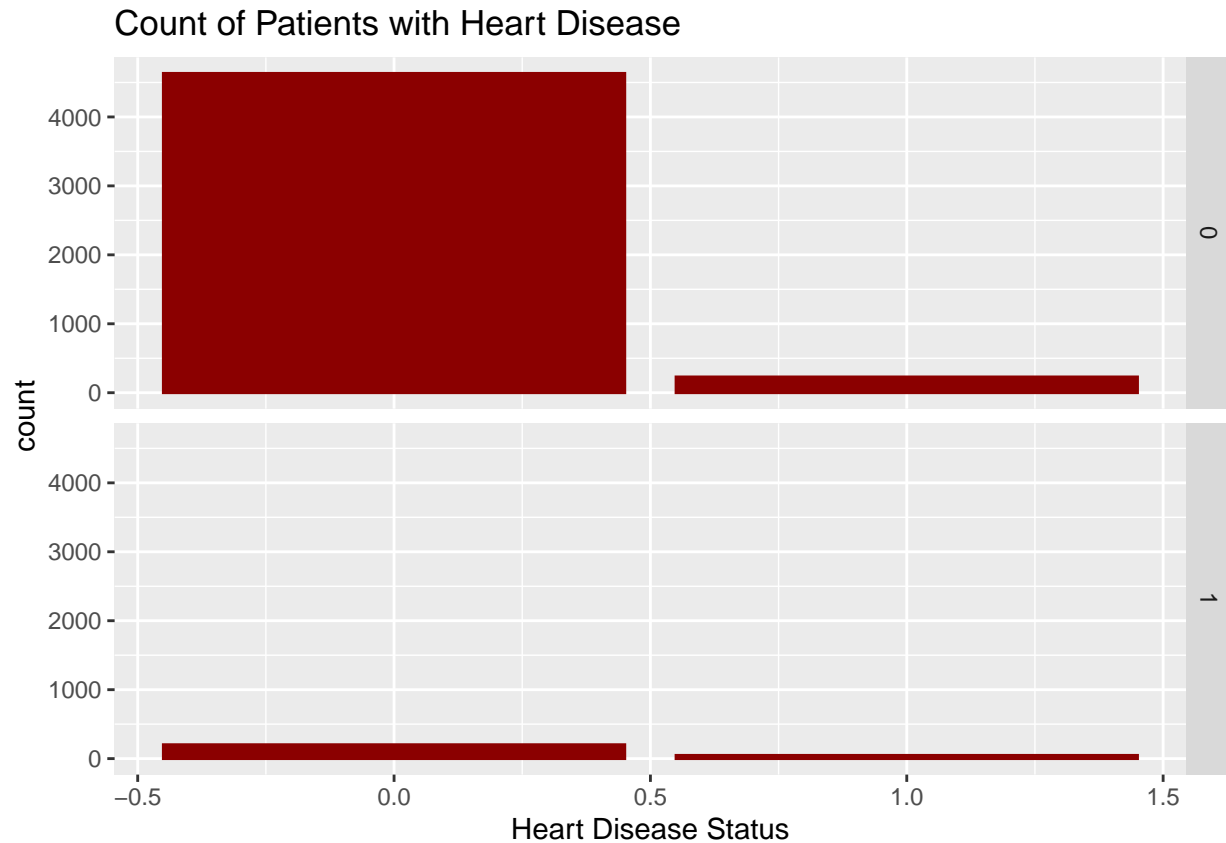
heart_disease	ever_married	work_type	Residence_type
Min. :0.00000	Length:4861	Length:4861	Length:4861
1st Qu.:0.00000	Class :character	Class :character	Class :character
Median :0.00000	Mode :character	Mode :character	Mode :character
Mean :0.04711			
3rd Qu.:0.00000			
Max. :1.00000			

avg_glucose_level	smoking_status	stroke	bmi_imputed
Min. : 55.12	Length:4861	Min. :0	Min. :10.30
1st Qu.: 77.12	Class :character	1st Qu.:0	1st Qu.:23.60
Median : 91.47	Mode :character	Median :0	Median :28.30
Mean :104.80		Mean :0	Mean :28.83
3rd Qu.:112.83		3rd Qu.:0	3rd Qu.:32.80
Max. :267.76		Max. :0	Max. :97.60



``stat_bin()`` using ``bins = 30``. Pick better value with ``binwidth``.





Welch Two Sample t-test

```
data:  stroke_dt3$bmi_imputed by stroke_dt3$stroke
t = -3.6104, df = 295.21, p-value = 0.0003591
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
95 percent confidence interval:
 -2.1513954 -0.6334067
sample estimates:
mean in group 0 mean in group 1
    28.82539      30.21779
```

Welch Two Sample t-test

```
data:  stroke_dt3$avg_glucose_level by stroke_dt3$stroke
t = -6.9824, df = 260.89, p-value = 2.401e-11
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
95 percent confidence interval:
 -35.57474 -19.92371
sample estimates:
mean in group 0 mean in group 1
    104.7955      132.5447
```

Welch Two Sample t-test

```
data:  stroke_dt3$age by stroke_dt3$stroke
```

t = -29.686, df = 331.65, p-value < 2.2e-16
 alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
 95 percent confidence interval:
 -27.4634 -24.0499

sample estimates:

mean in group 0 mean in group 1
 41.97154 67.72819

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
bmi_imputed	1	0.36	0.359	7.878	0.00502 **
hypertension	1	3.60	3.599	78.905	< 2e-16 ***
Residuals	5107	232.91	0.046		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
bmi_imputed	1	0.36	0.359	7.90	0.00496 **
hypertension	1	3.60	3.599	79.13	< 2e-16 ***
bmi_imputed:hypertension	1	0.70	0.697	15.33	9.15e-05 ***
Residuals	5106	232.21	0.045		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1