Stroke dataset

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October 6, 2024

```
##
## Adjuntando el paquete: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union

##
## Adjuntando el paquete: 'agricolae'

## The following objects are masked from 'package:e1071':
##
##     kurtosis, skewness
```

Introduction

This dataset is a data obtain from *kaggle* and is used to predict if a pacient will probably get a stroke based on characteristic of them like gender, age, bmi, glucose levels.

The stroke variable have a 4.8% of people have had one. We want to check the distributions of the variables and possibles explanations of which variable can make an impact to get a stroke before creating a model to proved or been proved wrong about it.

The data have the follow variables:

1) id: unique identifier
2) gender: "Male", "Female" or "Other"
3) age: age of the patient
4) hypertension: 0 if the patient doesn't have hypertension, 1 if the patient has hypertension
5) heart_disease: 0 if the patient doesn't have any heart diseases, 1 if the patient has a heart disease
6) ever_married: "No" or "Yes"
7) work_type: "children", "Govt_jov", "Never_worked", "Private" or "Self-employed"
8) Residence_type: "Rural" or "Urban"
9) avg_glucose_level: average glucose level in blood

10) bmi: body mass index
11) smoking_status: “formerly smoked”, “never smoked”, “smokes” or “Unknown”*
12) stroke: 1 if the patient had a stroke or 0 if not

The next is a summary of the data.

```
summary(data)
```

```
##        id           gender          age        hypertension heart_disease
##  Min.   :   67   Female:2994   Min.   : 0.08   0:4612       0:4834
##  1st Qu.:17741   Male  :2115   1st Qu.:25.00   1: 498       1: 276
##  Median :36932   Other :   1   Median :45.00
##  Mean   :36518                 Mean   :43.23
##  3rd Qu.:54682                 3rd Qu.:61.00
##  Max.   :72940                 Max.   :82.00
##
##  ever_married         work_type    Residence_type avg_glucose_level
##  No :1757     children     : 687   Rural:2514     Min.   : 55.12
##  Yes:3353     Govt_job     : 657   Urban:2596     1st Qu.: 77.25
##               Never_worked :  22                  Median : 91.89
##               Private      :2925                  Mean   :106.15
##               Self-employed: 819                  3rd Qu.:114.09
##                                                   Max.   :271.74
##
##       bmi                smoking_status stroke
##  Min.   :10.30   formerly smoked: 885   0:4861
##  1st Qu.:23.50   never smoked   :1892   1: 249
##  Median :28.10   smokes         : 789
##  Mean   :28.89   Unknown        :1544
##  3rd Qu.:33.10
##  Max.   :97.60
##  NA's   :201
```

Dataset

We will star the analysis with the categorical variables.

Categorical Variables

Gender

This variable has 2 categories Male and Female (there’s one person who is Other but it’s only one so we can’t make any assumptions about this data).

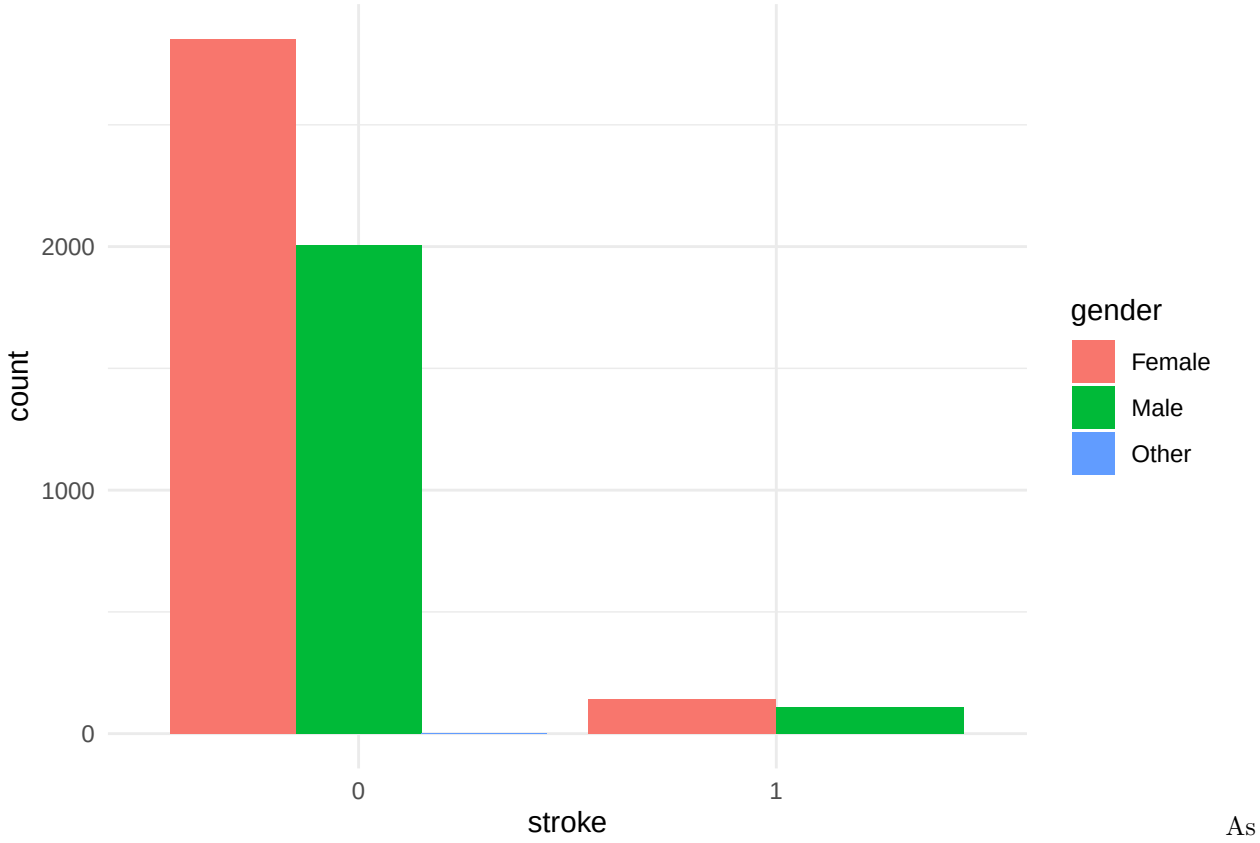
The next table shows a summary of the quantity of people getting a stroke by gender and the corresponding percentage.

```
stroke_gender = data %>% group_by(stroke,gender) %>% summarise(n = n(),.groups = "drop") %>% group_by(g

pander(stroke_gender)
```

stroke	gender	n	percent
0	Female	2853	95.29
0	Male	2007	94.89
0	Other	1	100
1	Female	141	4.709
1	Male	108	5.106

```
ggplot(data)+aes(x=stroke,fill=gender) + geom_bar(position=position_dodge())+theme_minimal()
```



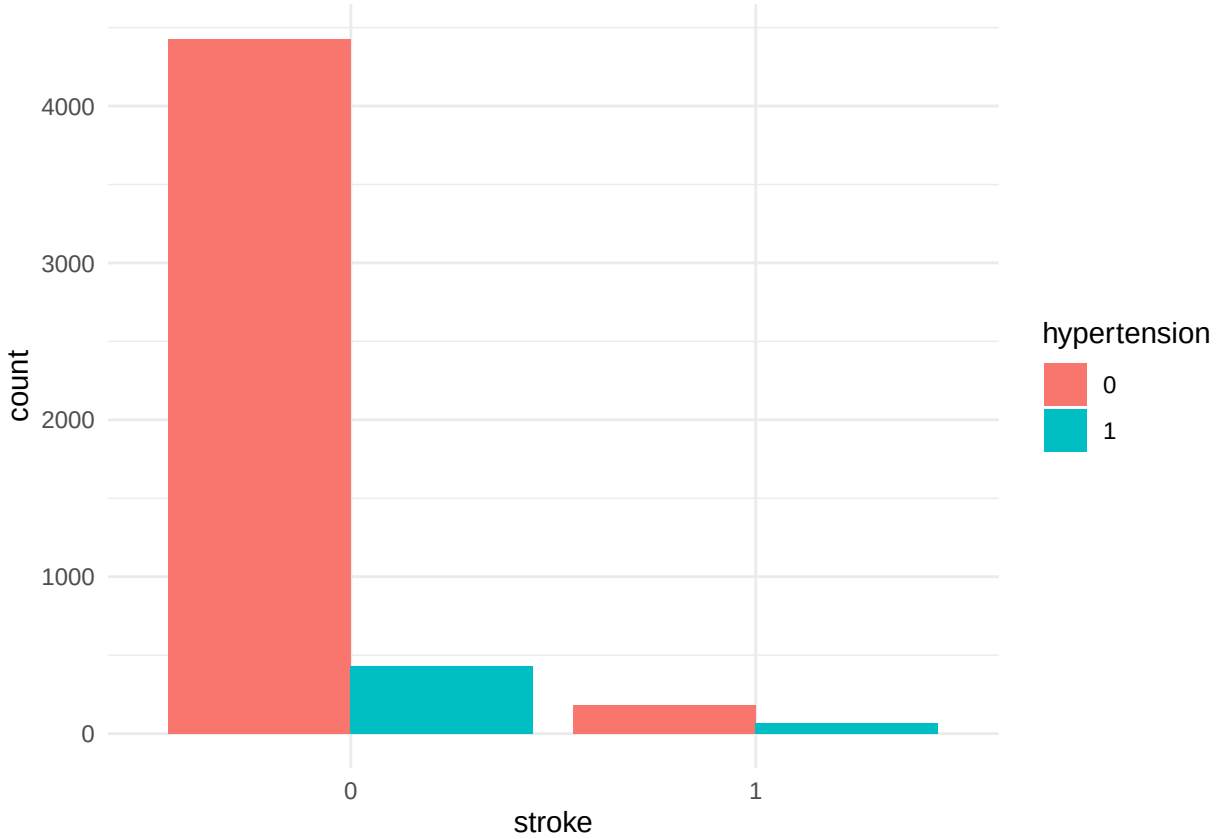
As you can see there's a higher % of male that have had a stroke in the data. This number is a little bit higher than the population so we don't think this would have a great impact in the future model.

Hypertension

```
pander(data %>% group_by(stroke,hypertension) %>% summarise(n = n(),.groups = "drop")%>%
  group_by(hypertension) %>% mutate(percent = n/sum(n)*100))
```

stroke	hypertension	n	percent
0	0	4429	96.03
0	1	432	86.75
1	0	183	3.968
1	1	66	13.25

```
ggplot(data)+aes(x=stroke,fill=hypertension) + geom_bar(position=position_dodge())+theme_minimal()
```

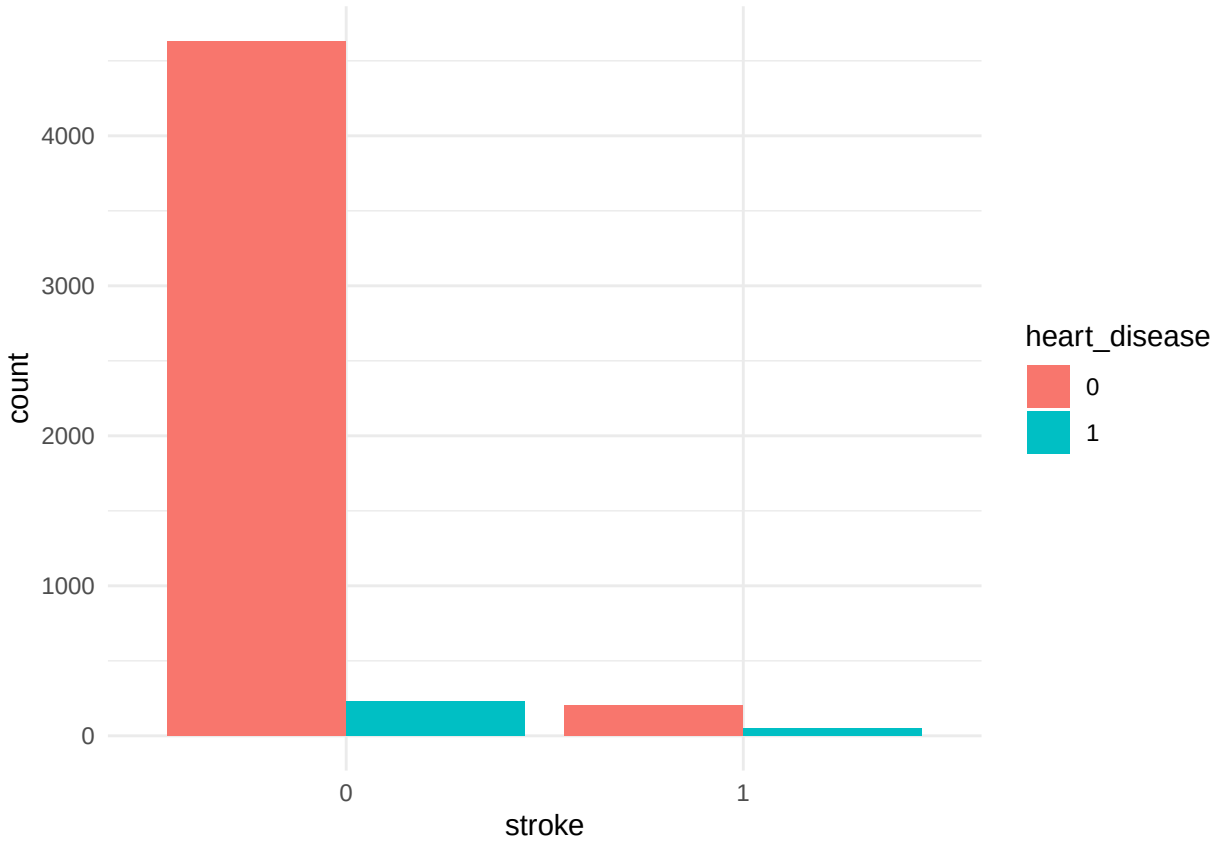


The % of people who have had a stroke and have hypertension are significantly highier than the population. There's a difference approx. 9%. This could mean that if you have hypertension you could be more likely to get a stroke. ### Heart disease

```
pander(data %>% group_by(stroke,heart_disease) %>% summarise(n = n(),.groups = "drop")%>%
  group_by(heart_disease) %>% mutate(percent = n/sum(n)*100))
```

stroke	heart_disease	n	percent
0	0	4632	95.82
0	1	229	82.97
1	0	202	4.179
1	1	47	17.03

```
ggplot(data)+aes(x=stroke,fill=heart_disease) + geom_bar(position=position_dodge())+theme_minimal()
```



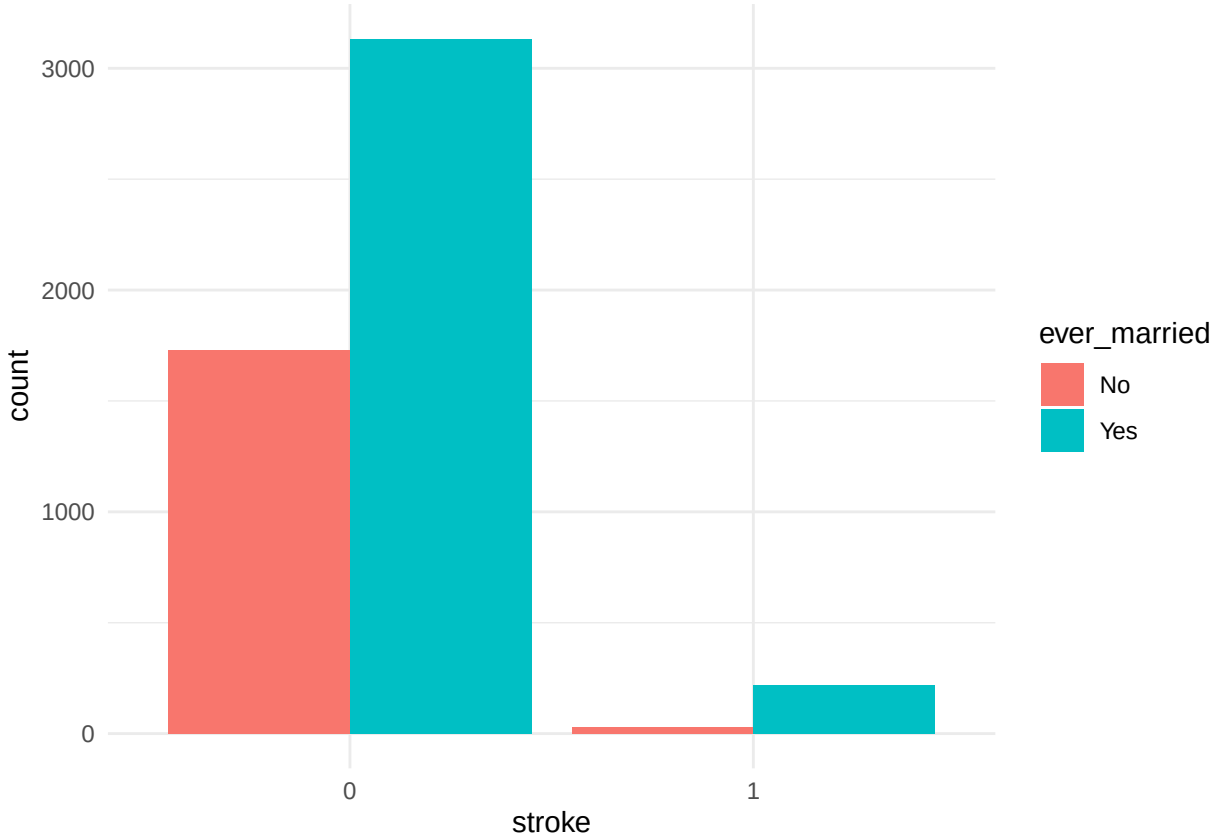
The data of the people who have a heart diseased look even more likely to get a stroke than the ones who have hypertension. Maybe there's a relation between hypertension and having a heart diseased. Heart diseased is a variable to check for more details.

Ever Married

```
pander(data %>% group_by(stroke,ever_married) %>% summarise(n = n(),.groups = "drop")%>%
  group_by(ever_married) %>% mutate(percent = n/sum(n)*100))
```

stroke	ever_married	n	percent
0	No	1728	98.35
0	Yes	3133	93.44
1	No	29	1.651
1	Yes	220	6.561

```
ggplot(data)+aes(x=stroke,fill=ever_married) + geom_bar(position=position_dodge())+theme_minimal()
```

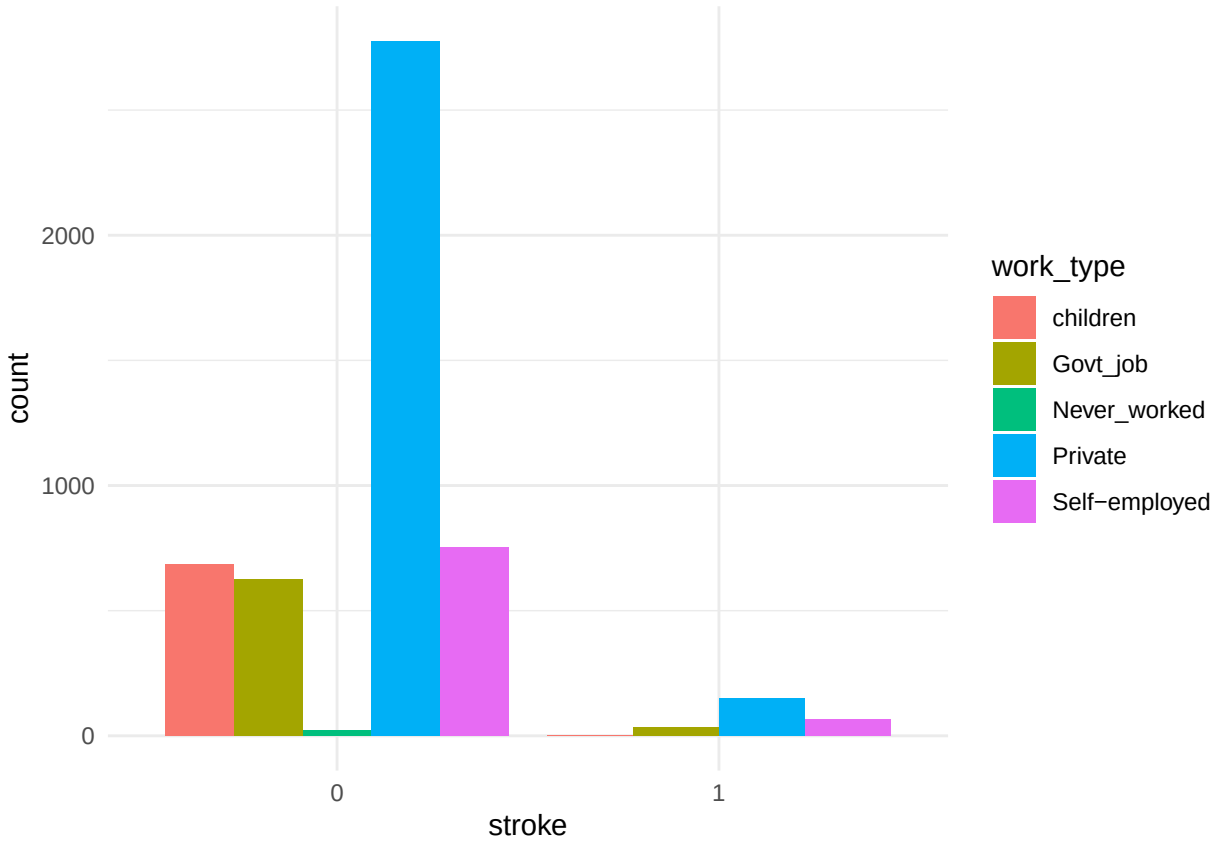


there's more people that have had a stroke you have been married than not been married. The difference with the population is big but with the ones that never married maybe not get married lower your changes or getting a stroke. ### Work Type

```
pander(data %>% group_by(stroke,work_type) %>% summarise(n = n(),.groups = "drop")%>%
  group_by(work_type) %>% mutate(percent = n/sum(n)*100))
```

stroke	work_type	n	percent
0	children	685	99.71
0	Govt_job	624	94.98
0	Never_worked	22	100
0	Private	2776	94.91
0	Self-employed	754	92.06
1	children	2	0.2911
1	Govt_job	33	5.023
1	Private	149	5.094
1	Self-employed	65	7.937

```
ggplot(data)+aes(x=stroke,fill=work_type) + geom_bar(position=position_dodge())+theme_minimal()
```

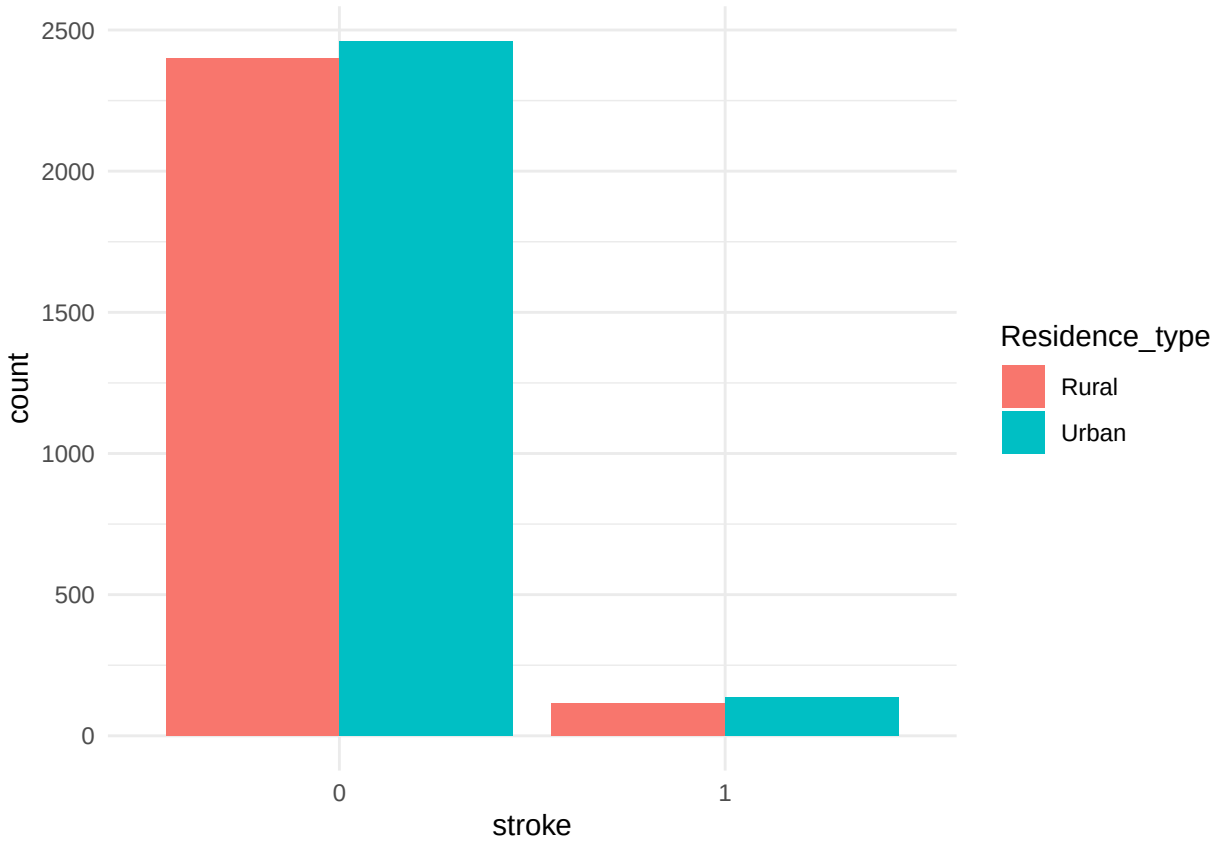


Clairly the self employed have the highest % of people who have han a stroke. This could be because of stress and the people who work with children have the lowest. Hope that working with children reduces your chances. ### Resident Type

```
pander(data %>% group_by(stroke,Residence_type) %>% summarise(n = n(),.groups = "drop")%>%
  group_by(Residence_type) %>% mutate(percent = n/sum(n)*100))
```

stroke	Residence_type	n	percent
0	Rural	2400	95.47
0	Urban	2461	94.8
1	Rural	114	4.535
1	Urban	135	5.2

```
ggplot(data)+aes(x=stroke,fill=Residence_type) + geom_bar(position=position_dodge())+theme_minimal()
```



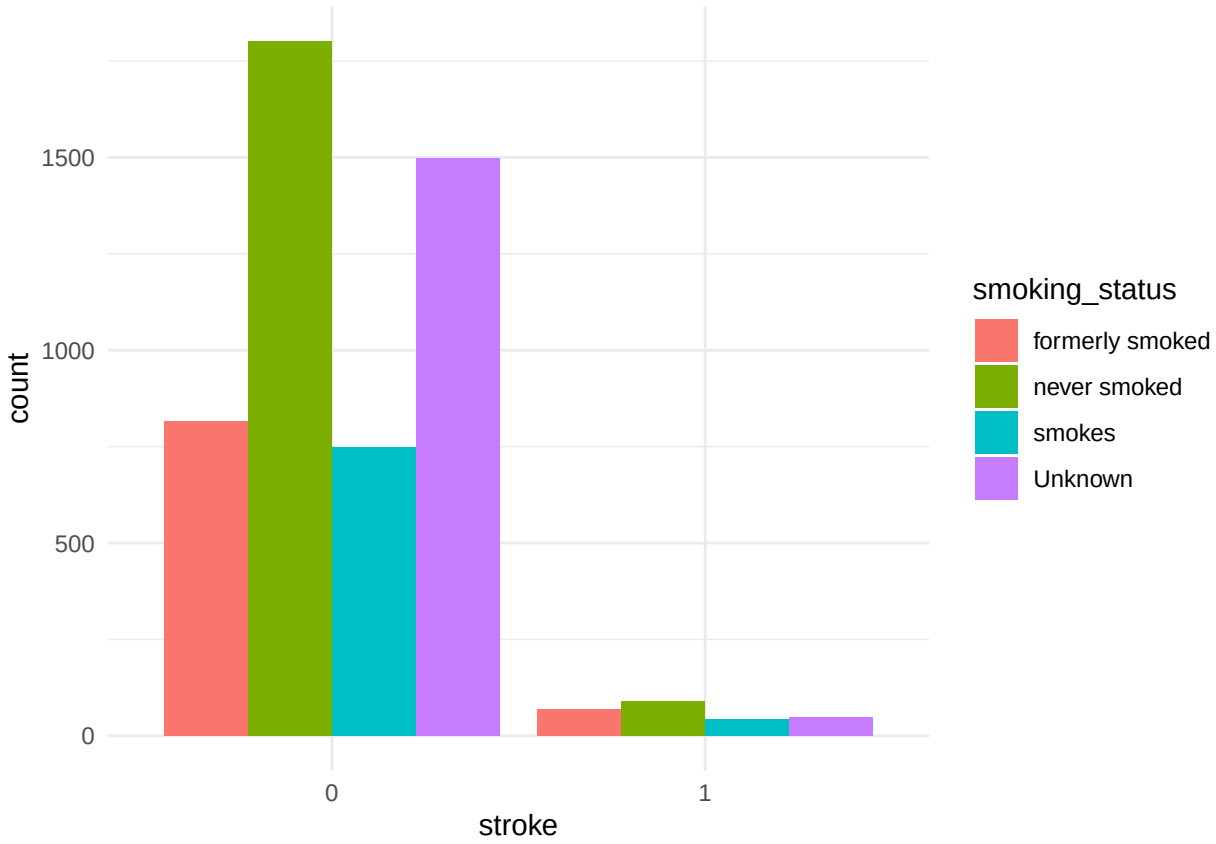
The part of the city that you live looks like it doesn't matter because the % of stroke is very similar to the population and almost the same between the types of resident. This could mean something

Smoking Status

```
pander(data %>% group_by(stroke,smoking_status) %>% summarise(n = n(),.groups = "drop")%>%
  group_by(smoking_status) %>% mutate(percent = n/sum(n)*100))
```

stroke	smoking_status	n	percent
0	formerly smoked	815	92.09
0	never smoked	1802	95.24
0	smokes	747	94.68
0	Unknown	1497	96.96
1	formerly smoked	70	7.91
1	never smoked	90	4.757
1	smokes	42	5.323
1	Unknown	47	3.044

```
ggplot(data)+aes(x=stroke,fill=smoking_status) + geom_bar(position=position_dodge())+theme_minimal()
```



This results call the attention because the people you formerly smoked have 3% higher than the population but obe who smokes or never have similar numbers. This could be a multivariate problem because this type of data probably mix more than one variable at a time. It's very clear that this variable should be important in the model ## Numeric Variables

BMI

The first variable to evaluate will be the *bmi*. This variable is a metric that represent the relation between height and weight of a person. As you can see we have 3.9334638 % percentage of NA. However this is less than 5% so to treat this variable we will deleted all the rows with the NA in *bmi*

```
summary(data$bmi)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##   10.30   23.50   28.10   28.89   33.10   97.60     201
```

Next, we will check the frecquency of the data using the cut between (0-18.5] as underweight, (18.5-24.9] as normal, (24.9-29.9] as overweight, (29.9-34.9] as obese and over this as extremely obese. This value leaves over 50% of our population in normal and overweight and almost 40% in the largest side in obese and extremely obese.

```
data = na.omit(data)
frec_table <- cut(data$bmi, breaks = c(0, 18.5, 24.9, 29.9, 34.9, Inf),
                  labels = c("Underweight", "Normal", "Overweight", "Obese", "Extremely Obese"))
data$cat_weight = frec_table
```

```r
# Create frequency table
bmi_freq_table <- table(frec_table)
print(bmi_freq_table)
```

```
## frec_table
##     Underweight          Normal      Overweight           Obese Extremely Obese
##             349            1231            1409            1000             920
```

```r
bmi_rel_freq <- prop.table(bmi_freq_table)*100
print(bmi_rel_freq)
```

```
## frec_table
##     Underweight          Normal      Overweight           Obese Extremely Obese
##        7.109391       25.076390       28.702383       20.370748       18.741088
```

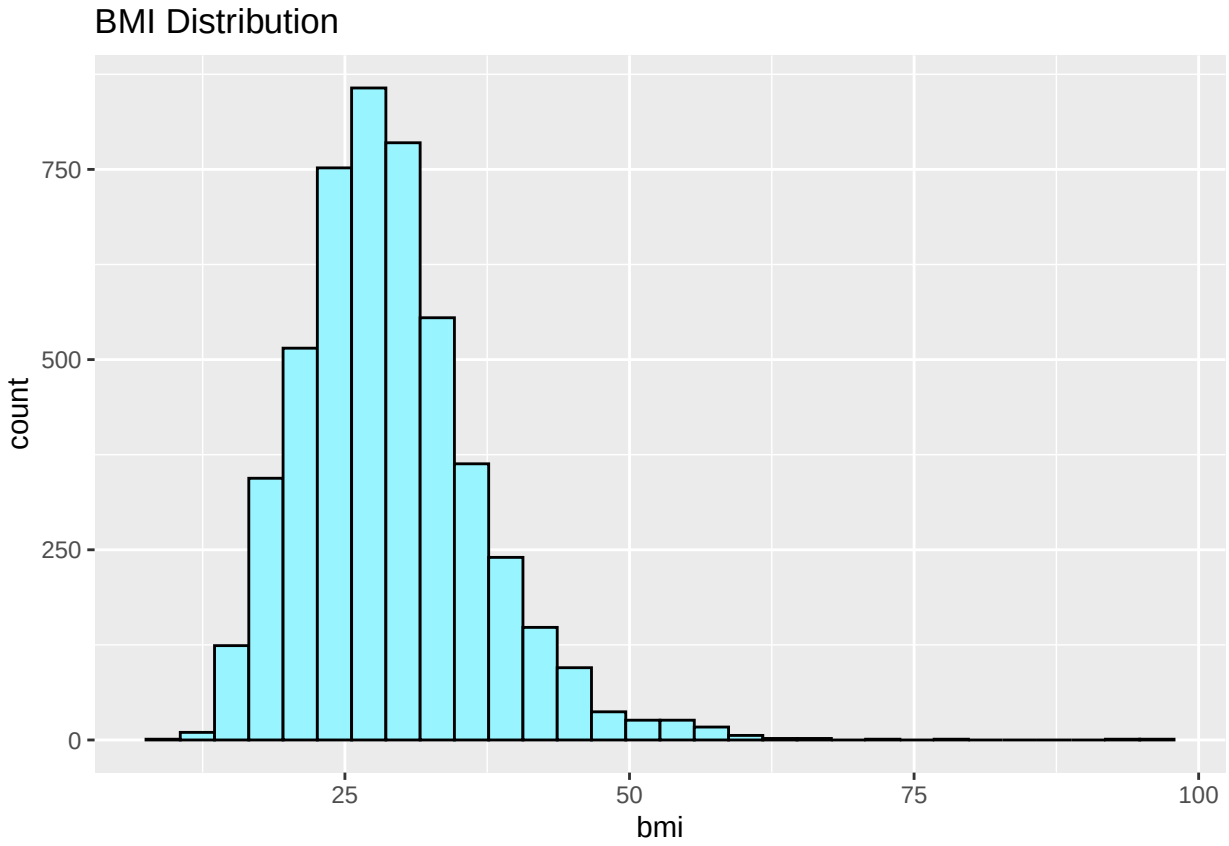
If we check this with a graph we can see that the graph looks a bit symetrical with an inclination to the right. This could it mean that the distribution is not a normal like could it seem. We are going to check the kurtosis and skewness shape to check if there´s a problem.

```r
stat.freq(aux_bmi)
```

```
## $variance
## [1] 63.33058
##
## $mean
## [1] 28.84447
##
## $median
## [1] 28.00745
##
## $mode
##      [- -]     mode
## [1,] 25 30 27.22149
```

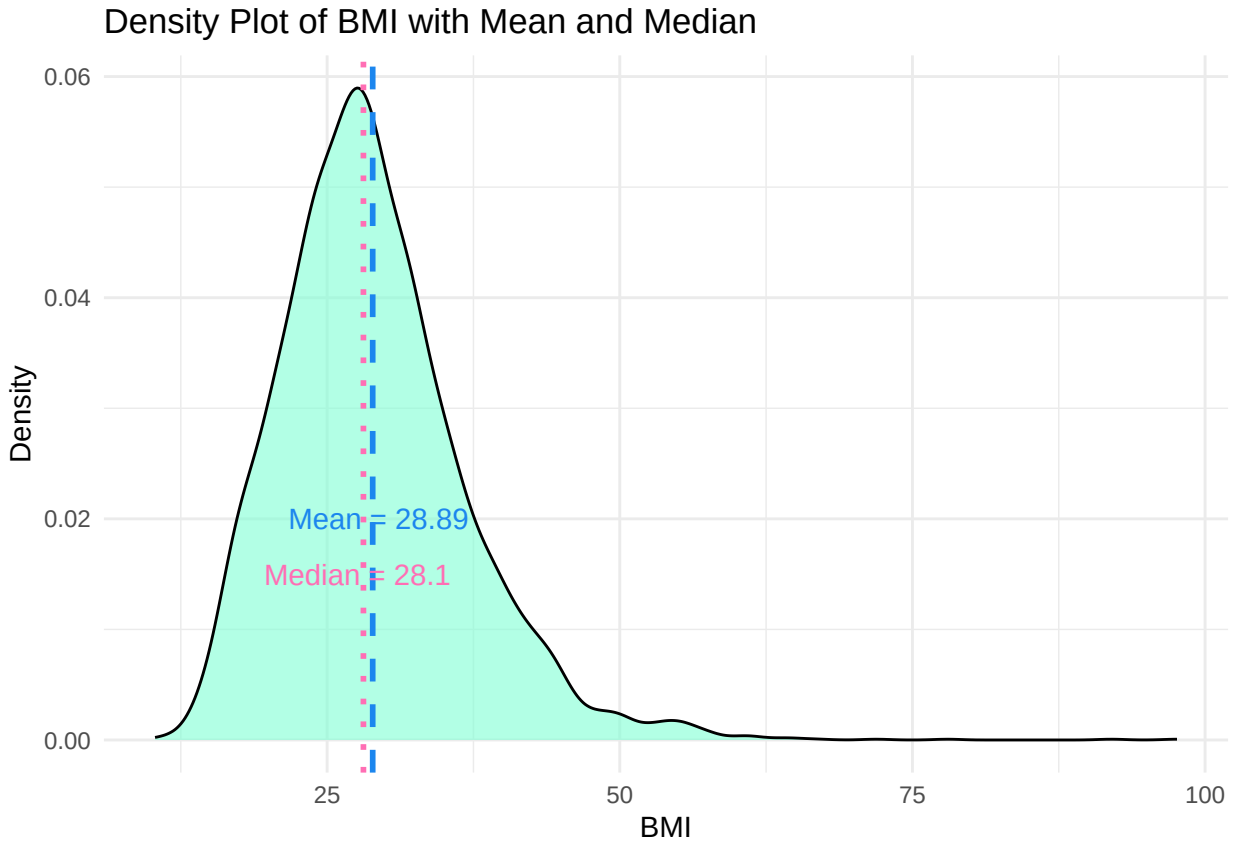
```r
ggplot(data, aes(x=bmi)) +
  geom_histogram(color="black", fill="cadetblue1")+
  labs(title = "BMI Distribution")
```

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




```r
bmi_mean <- mean(data$bmi)
bmi_median <- median(data$bmi)

# Density plot with a vertical line at the mean
ggplot(data, aes(x = data$bmi)) +
  geom_density(fill = "aquamarine1", alpha = 0.6) +
  geom_vline(aes(xintercept = bmi_mean), color = "dodgerblue2", linetype = "dashed", size = 1) +
  geom_vline(aes(xintercept = bmi_median), color = "hotpink1", linetype = "dotted", size = 1) +
  labs(title = "Density Plot of BMI with Mean and Median", x = "BMI", y = "Density") +
  annotate("text", x = bmi_mean + 0.5, y = 0.02, label = paste("Mean =", round(bmi_mean, 2)), color = "
  annotate("text", x = bmi_median - 0.5, y = 0.015, label = paste("Median =", round(bmi_median, 2)), col
  theme_minimal()
```




```
skewness(data$bmi)
```

```
## [1] 1.05534
```

```
kurtosis(data$bmi)
```

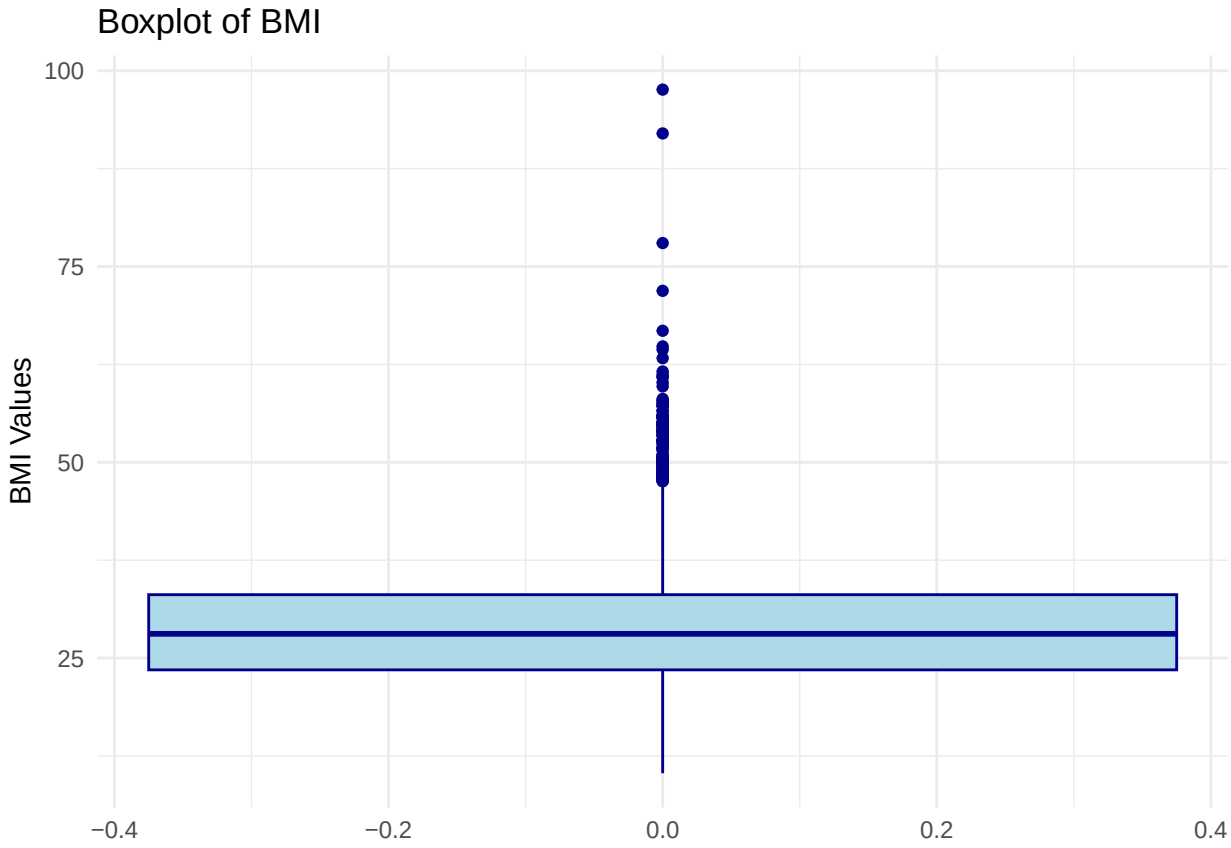
```
## [1] 3.362659
```

The values of the shape tell us that this is not a normal distribution. There's a lot ot people in the center of the data but the quantity of people with a extremely high BMI that change the weigh of the tail in the distribution.

Looking only at the graph we expected that the Kurtosis was close to 3 but a 3.35 shows that this data have a heavier tail than a normal distribution. This means that we have outliers in the data. In this case there's a lot of values over 30. If we combined the Skewness value of 1.05 and the Kurtosis this tell us that the the distribution in skewed to the right and that the heavier tails is to this side explaining the outliers.

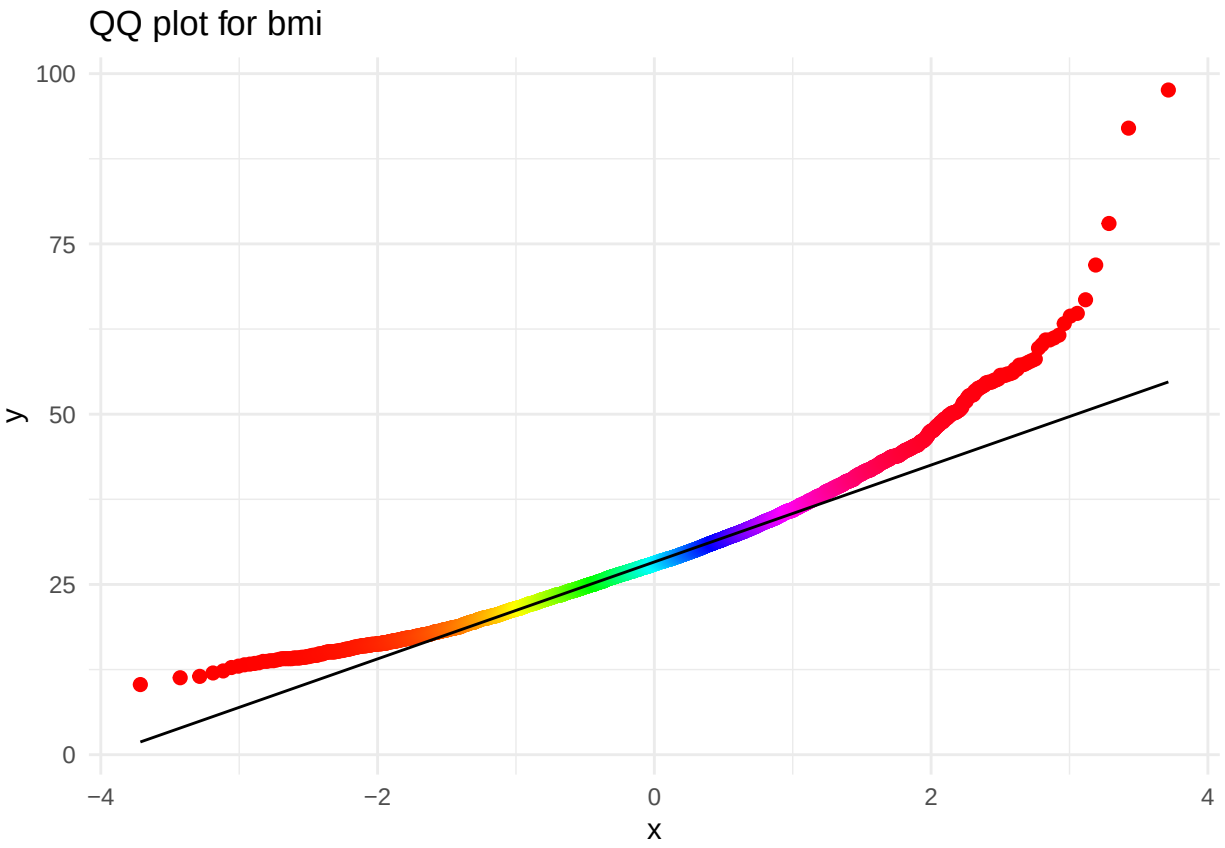
To see if the outliers are correctly in the heavier side we can check the boxplot of the *bmi*

```
ggplot(data, aes(y = data$bmi)) +
  geom_boxplot(fill = "lightblue", color = "darkblue") + # Change box and border color
  labs(title = "Boxplot of BMI", y = "BMI Values") + # Custom title and labels
  theme_minimal()
```



As you can see with the boxplot we can make sure that the *bmi* data have outliers within the largest values. The problem with this data is that we can not be sure if this is a mistake in the part of measure or maybe exist people with those values. YOu can see this in the qqplot next.

```
ggplot(data, aes(sample=bmi)) + stat_qq(size=2,color=rainbow(4909))+stat_qq_line()+theme_minimal()+
  labs(title = "QQ plot for bmi")
```

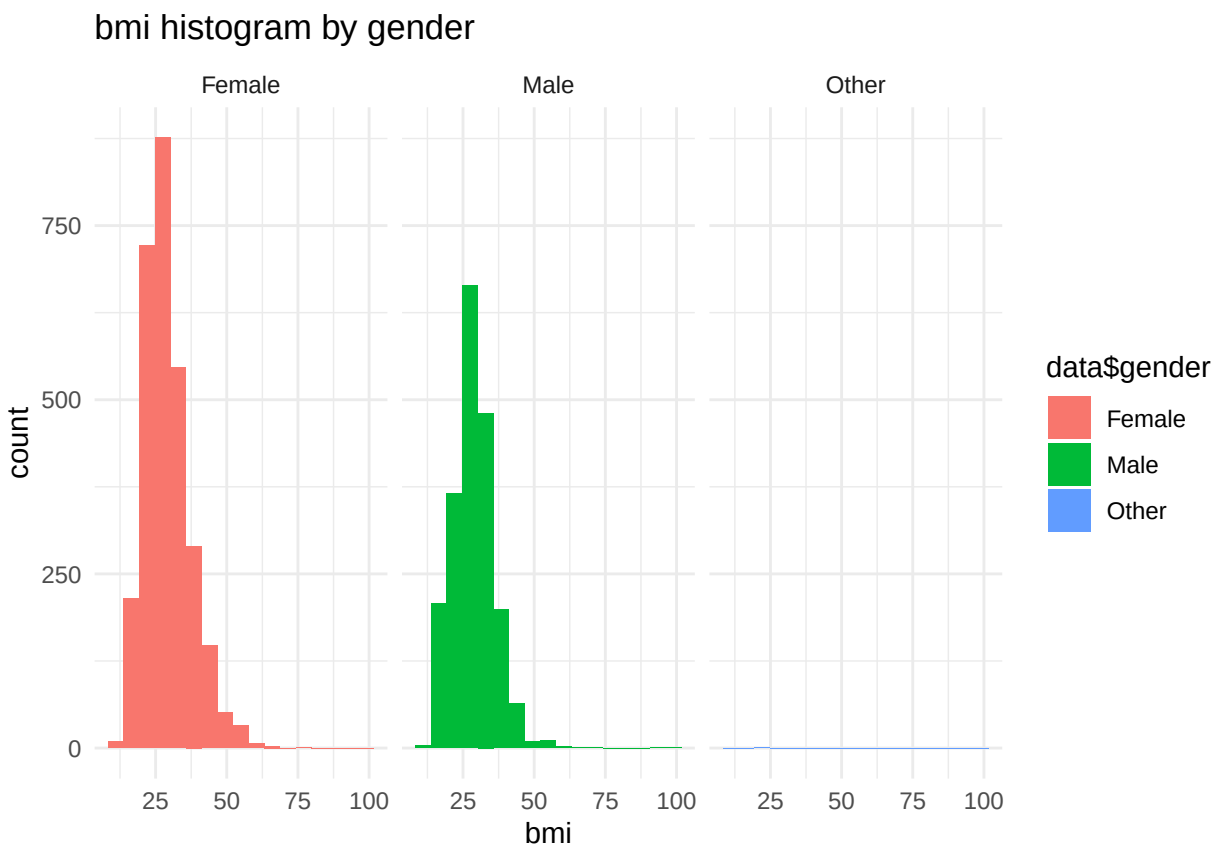



```
data_sub_bmi_gender= data %>% group_by(gender,stroke) %>% summarise(mean = mean(bmi),.groups = "drop")
print(data_sub_bmi_gender)
```

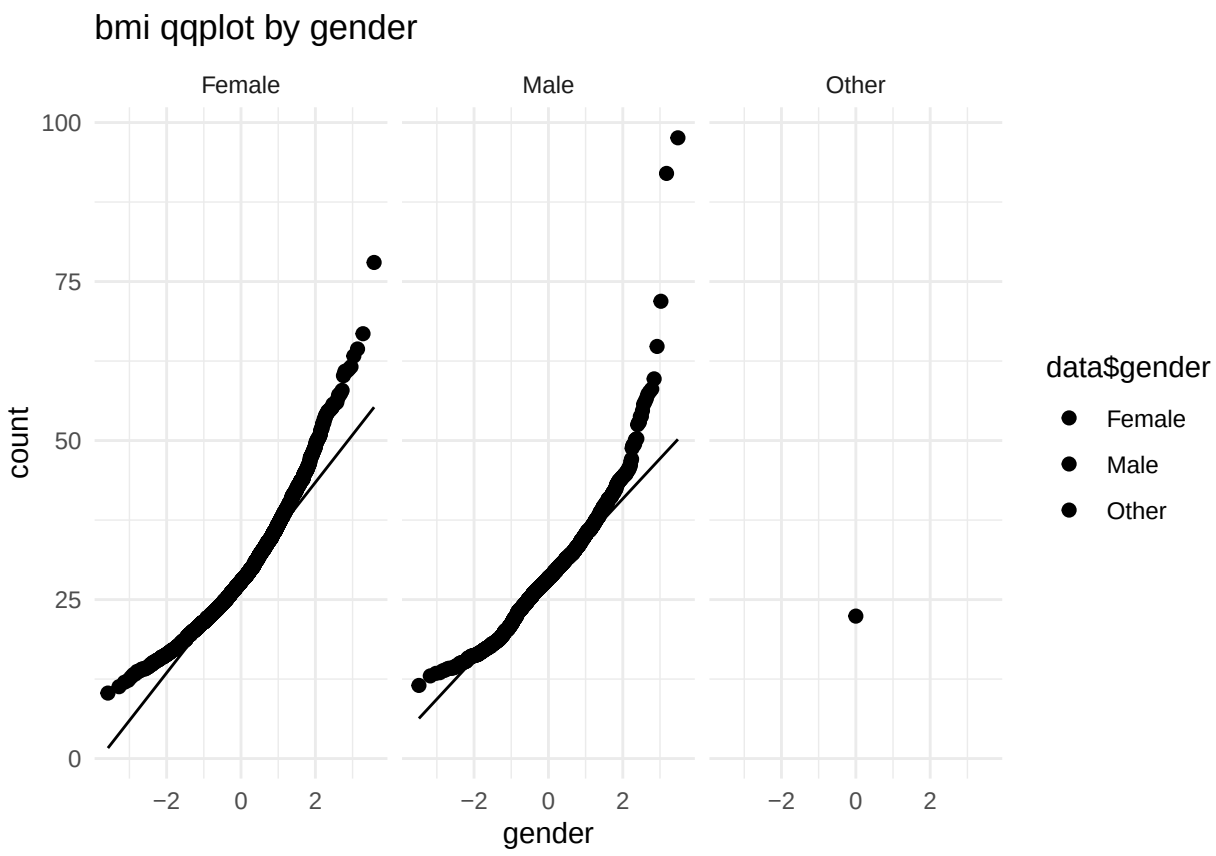
BMI with gender

```
## # A tibble: 5 x 3
##   gender stroke  mean
##   <fct>  <fct>  <dbl>
## 1 Female 0       29.0
## 2 Female 1       30.2
## 3 Male   0       28.5
## 4 Male   1       30.8
## 5 Other  0       22.4
```

```
ggplot(data, aes(x = data$bmi, fill = data$gender)) +
  geom_histogram(binwidth = 5.5)+
  facet_wrap(~gender)+theme_minimal()+labs(title = "bmi histogram by gender",x="bmi",y="count")
```




```
ggplot(data, aes(sample = data$bmi, fill = data$gender))+
  stat_qq(size=2)+ stat_qq_line() +
  facet_wrap(~gender)+theme_minimal()+labs(title = "bmi qqplot by gender",x="gender",y="count")
```




```
data_sub_bmi_hyper= data %>% group_by(hypertension,stroke) %>% summarise(mean = mean(bmi))
```

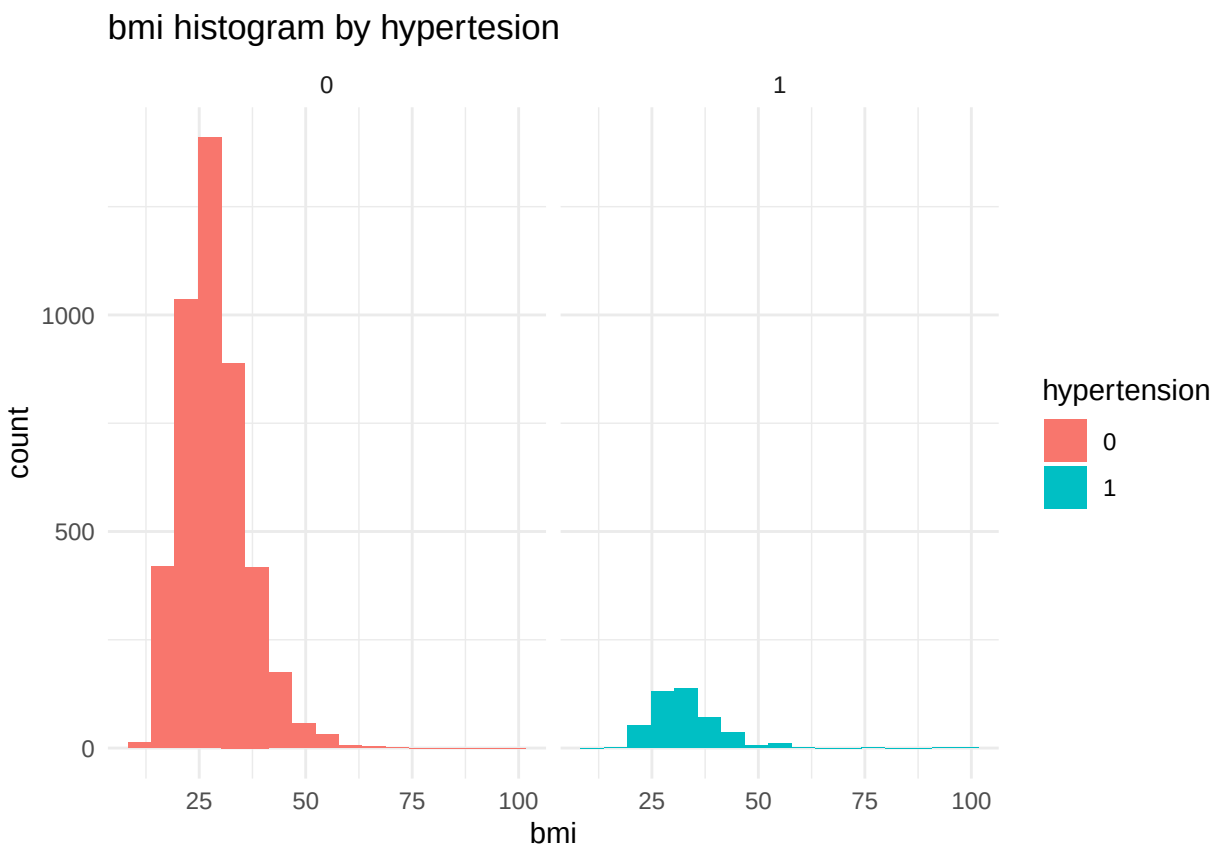
BMI with hypertension

```
## `summarise()` has grouped output by 'hypertension'. You can override using the
## `.groups` argument.
```

```
print(data_sub_bmi_hyper)
```

```
## # A tibble: 4 x 3
## # Groups:   hypertension [2]
##   hypertension stroke  mean
##   <fct>        <fct>  <dbl>
## 1 0            0       28.4
## 2 0            1       30.3
## 3 1            0       33.4
## 4 1            1       30.9
```

```
ggplot(data, aes(x = bmi, fill = hypertension)) +
  geom_histogram(binwidth = 5.5)+
  facet_wrap(~hypertension)+theme_minimal()+labs(title = "bmi histogram by hypertesion",x="bmi",y="coun
```




```
data_sub_bmi_catw= data %>% group_by(cat_weight,stroke) %>% summarise(mean = mean(bmi))
```

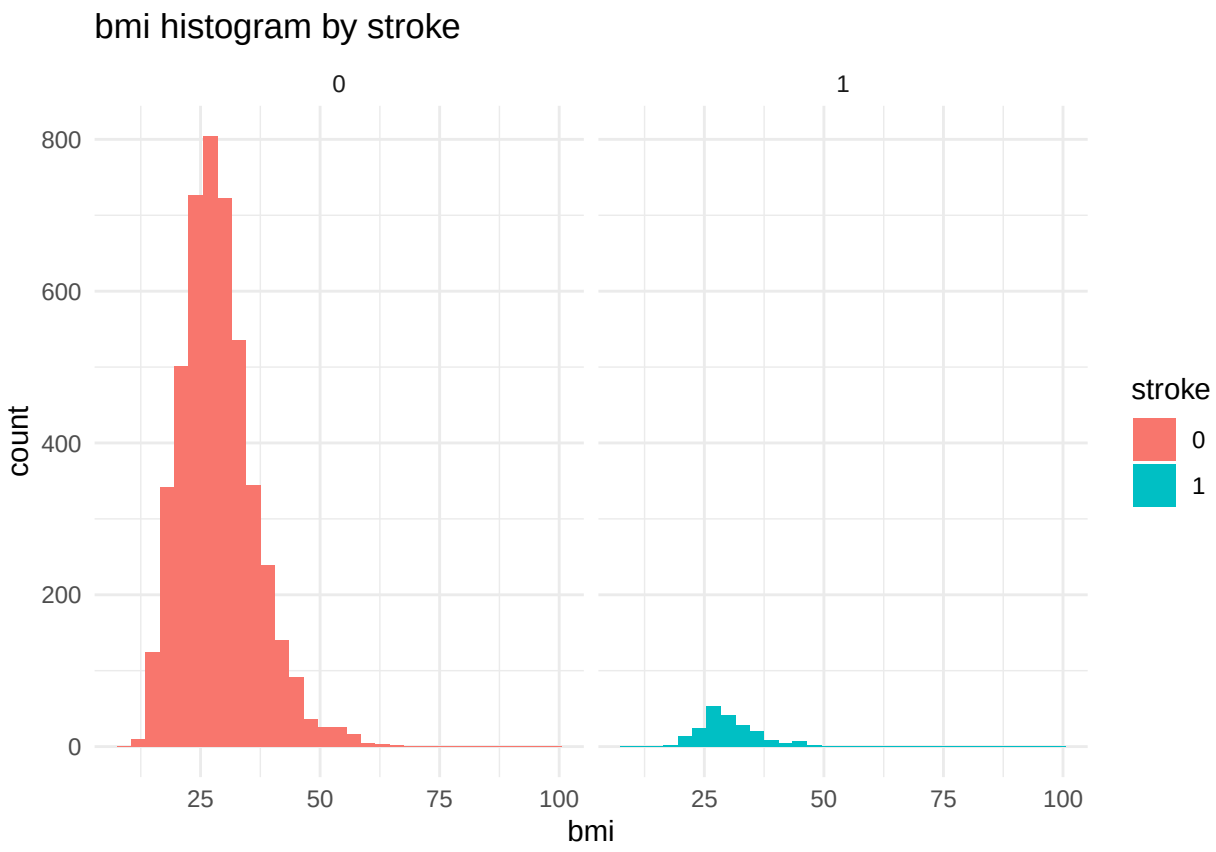
BMI with stroke

```
## `summarise()` has grouped output by 'cat_weight'. You can override using the
## `.groups` argument.
```

```
print(data_sub_bmi_catw)
```

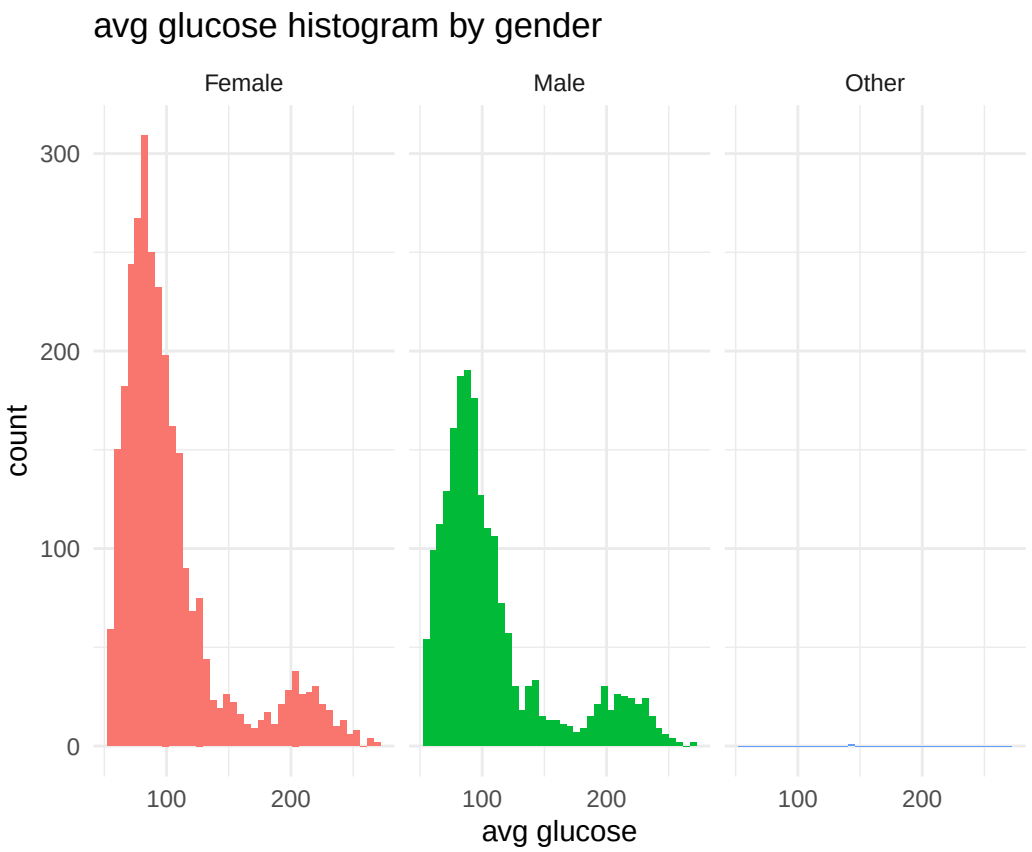
```
## # A tibble: 10 x 3
## # Groups:   cat_weight [5]
##    cat_weight      stroke  mean
##    <fct>           <fct>  <dbl>
##  1 Underweight     0       16.7
##  2 Underweight     1       16.9
##  3 Normal          0       22.2
##  4 Normal          1       22.6
##  5 Overweight      0       27.5
##  6 Overweight      1       27.6
##  7 Obese           0       32.2
##  8 Obese           1       32.1
##  9 Extremely Obese 0       41.1
## 10 Extremely Obese 1       40.3
```

```
ggplot(data, aes(x = data$bmi, fill = stroke)) +
  geom_histogram(binwidth = 3)+
  facet_wrap(~stroke)+theme_minimal()+labs(title = "bmi histogram by stroke",x="bmi",y="count")
```



Glucose levels

```
ggplot(data, aes(x = avg_glucose_level, fill = gender)) +
  geom_histogram(binwidth = 5.5)+
  facet_wrap(~gender)+theme_minimal()+labs(title = "avg glucose histogram by gender",x="avg glucose",y=
```



Glucose levels with gender

```
data_sub_glu_hyp= data %>% group_by(hypertension,stroke) %>% summarise(mean = mean(avg_glucose_level))
```

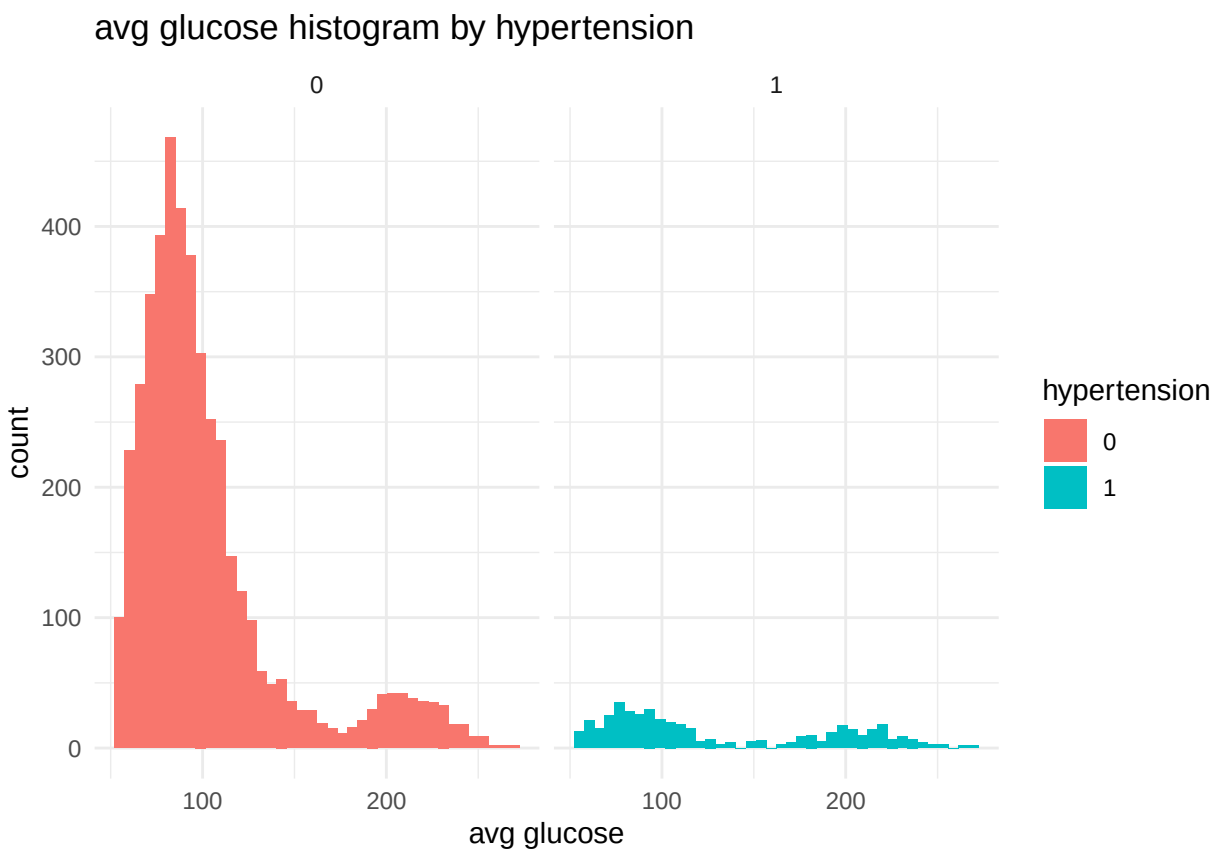
Glucose levels with hypertension

```
## `summarise()` has grouped output by 'hypertension'. You can override using the
## `.groups` argument.
```

```
print(data_sub_glu_hyp)
```

```
## # A tibble: 4 x 3
## # Groups:   hypertension [2]
##   hypertension stroke  mean
##   <fct>        <fct>  <dbl>
## 1 0            0       102.
## 2 0            1       130.
## 3 1            0       128.
## 4 1            1       146.
```

```
ggplot(data, aes(x = avg_glucose_level, fill = hypertension)) +
  geom_histogram(binwidth = 5.5)+
  facet_wrap(~hypertension)+theme_minimal()+labs(title = "avg glucose histogram by hypertension",x="avg
```

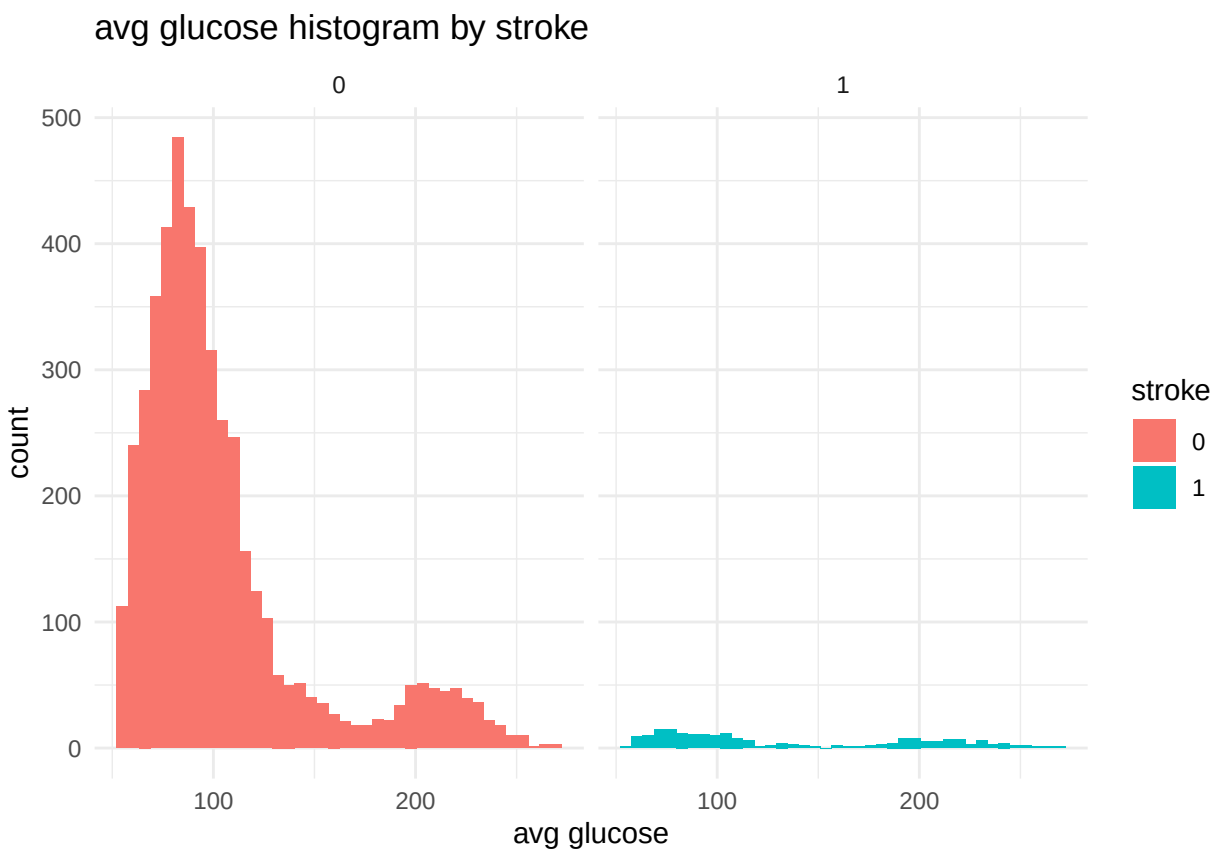



```
data_sub_glu= data %>% group_by(stroke) %>% summarise(mean = mean(avg_glucose_level))
print(data_sub_glu)
```

Glucose levels with stroke

```
## # A tibble: 2 x 2
##   stroke  mean
##   <fct>  <dbl>
## 1 0       104.
## 2 1       135.
```

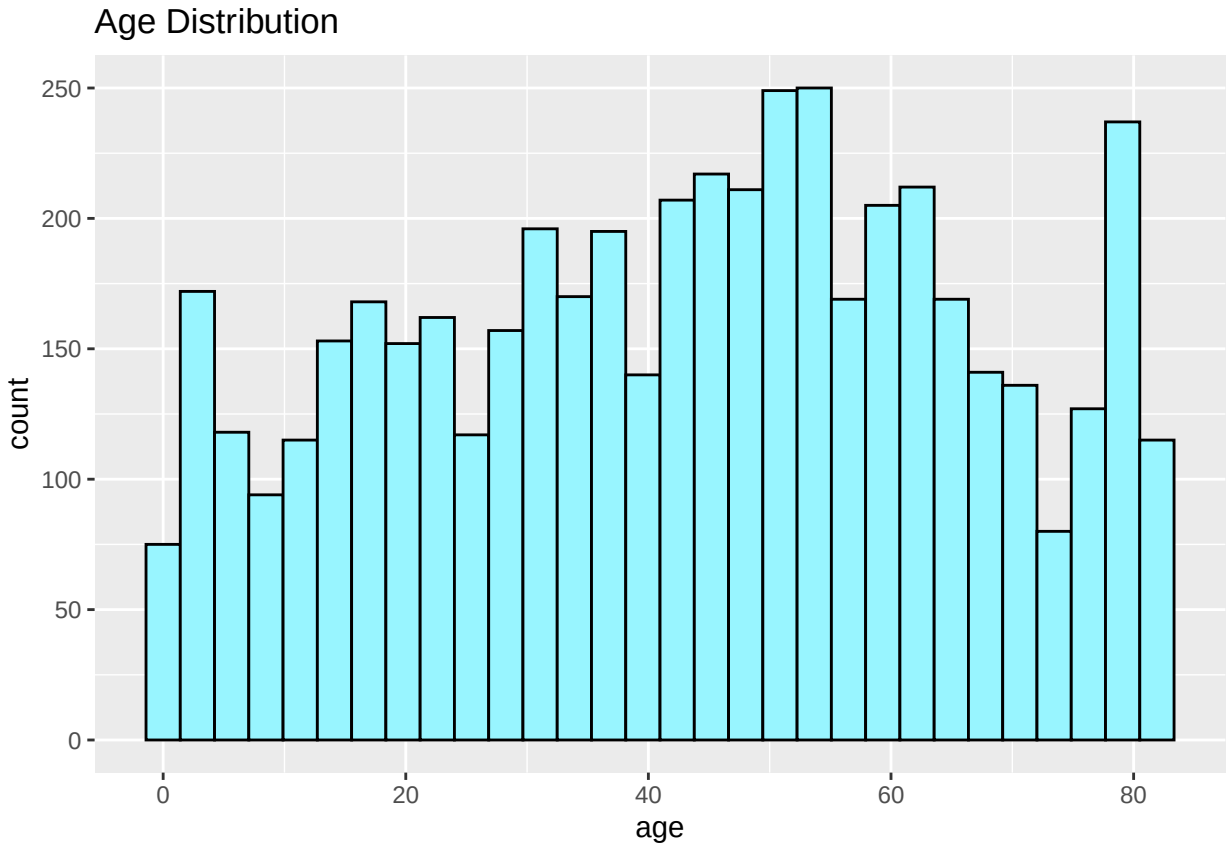
```
ggplot(data, aes(x = avg_glucose_level, fill = stroke)) +
  geom_histogram(binwidth = 5.5)+
  facet_wrap(~stroke)+theme_minimal()+labs(title = "avg glucose histogram by stroke",x="avg glucose",y=
```



Age

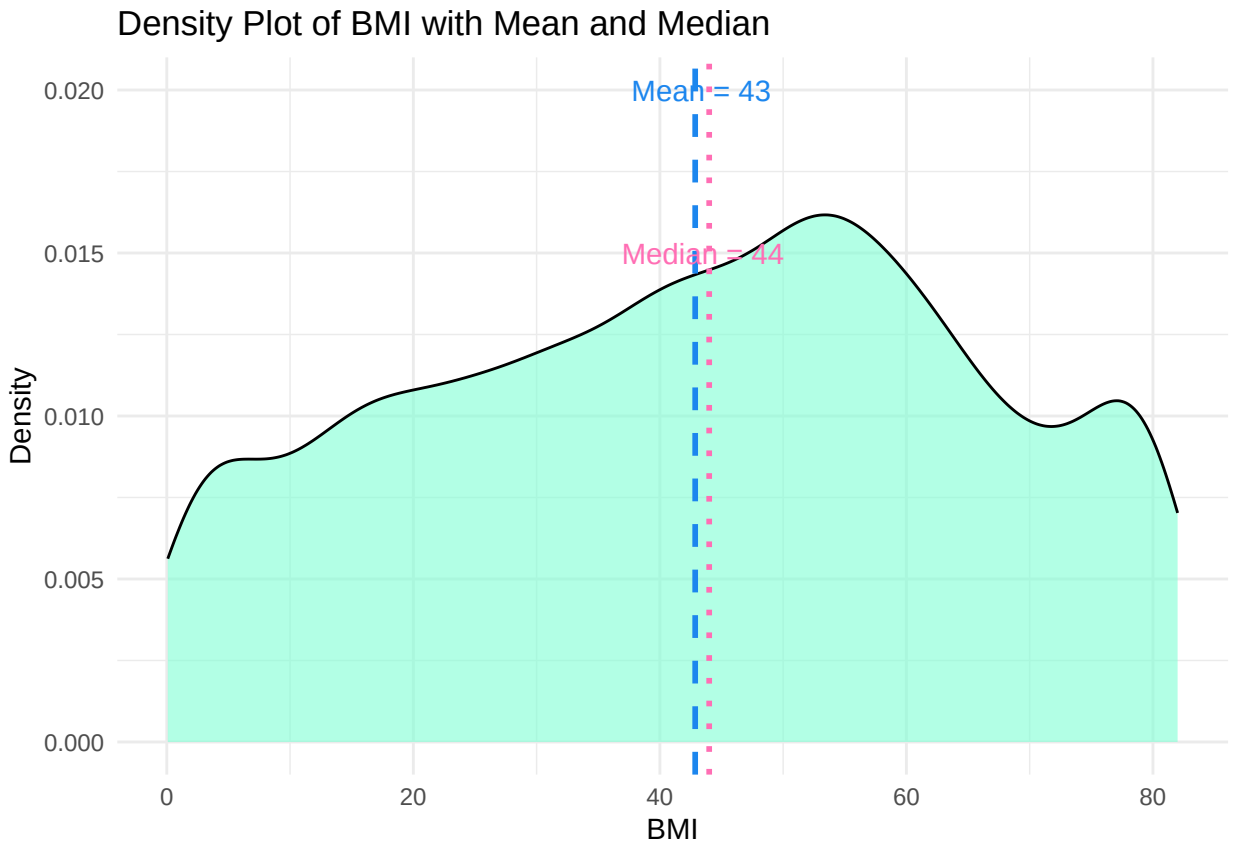
```
ggplot(data, aes(x=age)) +
  geom_histogram(color="black", fill="cadetblue1")+
  labs(title = "Age Distribution")
```

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




```r
age_mean <- mean(data$age)
age_median <- median(data$age)

# Density plot with a vertical line at the mean
ggplot(data, aes(x = data$age)) +
  geom_density(fill = "aquamarine1", alpha = 0.6) +
  geom_vline(aes(xintercept = age_mean), color = "dodgerblue2", linetype = "dashed", size = 1) +
  geom_vline(aes(xintercept = age_median), color = "hotpink1", linetype = "dotted", size = 1) +
  labs(title = "Density Plot of BMI with Mean and Median", x = "BMI", y = "Density") +
  annotate("text", x = age_mean + 0.5, y = 0.02, label = paste("Mean =", round(age_mean, 0)), color = "
  annotate("text", x = age_median - 0.5, y = 0.015, label = paste("Median =", round(age_median, 0)), col
  theme_minimal()
```




```
data_sub_age_gender= data %>% group_by(gender,stroke) %>% summarise(mean = mean(age))
```

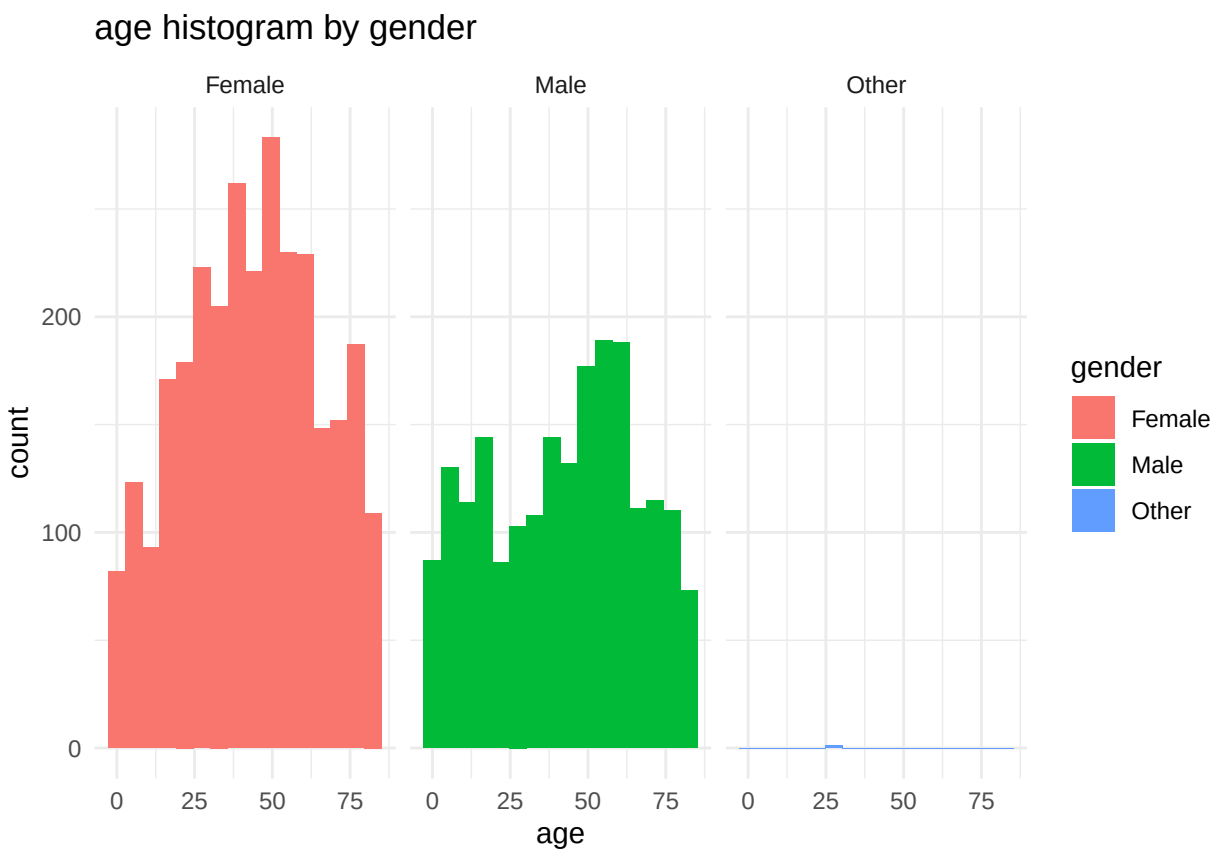
Age levels with gender

```
## `summarise()` has grouped output by 'gender'. You can override using the
## `.groups` argument.
```

```
print(data_sub_age_gender)
```

```
## # A tibble: 5 x 3
## # Groups:   gender [3]
##   gender stroke  mean
##   <fct>  <fct>  <dbl>
## 1 Female 0       42.4
## 2 Female 1       67.2
## 3 Male   0       40.8
## 4 Male   1       68.3
## 5 Other  0       26
```

```
ggplot(data, aes(x = age, fill = gender)) +
  geom_histogram(binwidth = 5.5)+
  facet_wrap(~gender)+theme_minimal()+labs(title = "age histogram by gender",x="age",y="count")
```




```
data_sub_age_hyp= data %>% group_by(hypertension,stroke) %>% summarise(mean = mean(age))
```

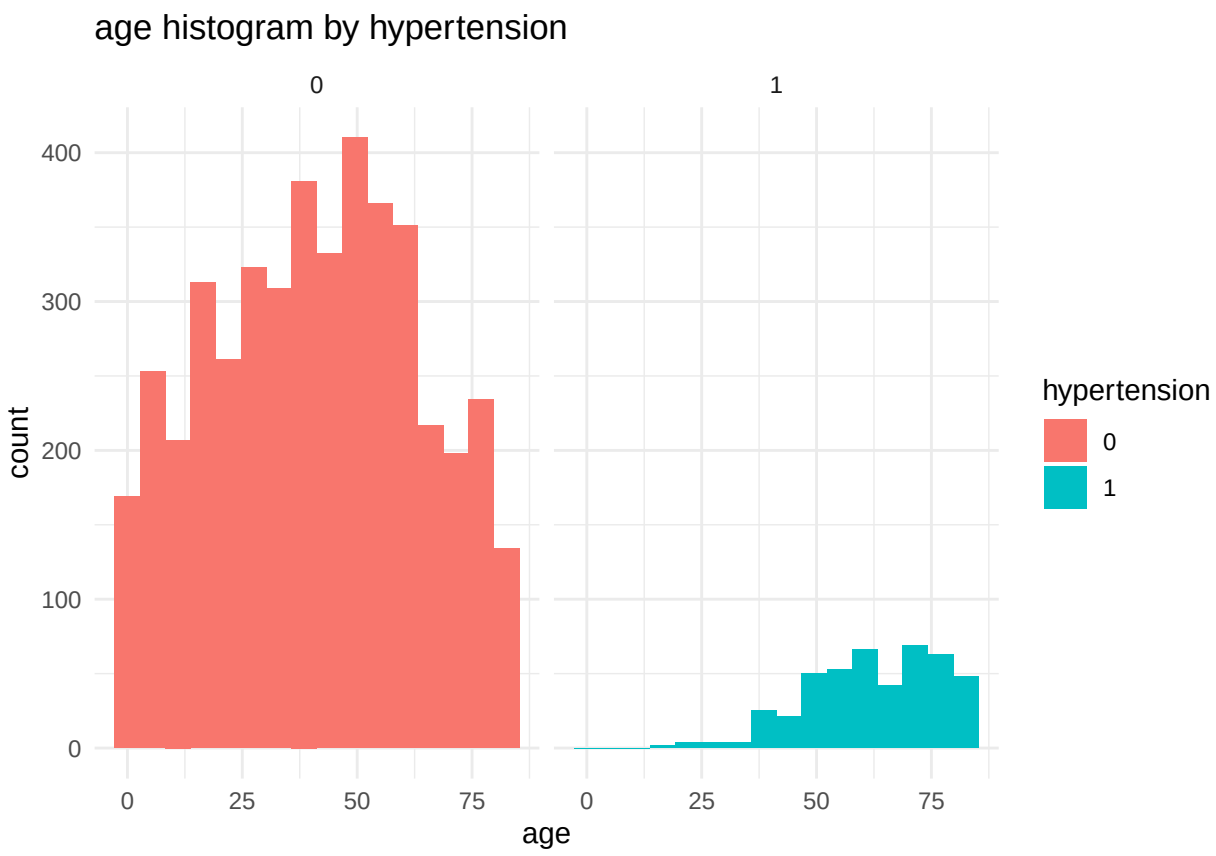
Age levels with hypertension

```
## `summarise()` has grouped output by 'hypertension'. You can override using the
## `.groups` argument.
```

```
print(data_sub_age_hyp)
```

```
## # A tibble: 4 x 3
## # Groups:   hypertension [2]
##   hypertension stroke  mean
##   <fct>        <fct>  <dbl>
## 1 0            0       40.0
## 2 0            1       67.0
## 3 1            0       61.2
## 4 1            1       69.6
```

```
ggplot(data, aes(x = age, fill = hypertension)) +
  geom_histogram(binwidth = 5.5)+
  facet_wrap(~hypertension)+theme_minimal()+labs(title = "age histogram by hypertension",x="age",y="cou
```

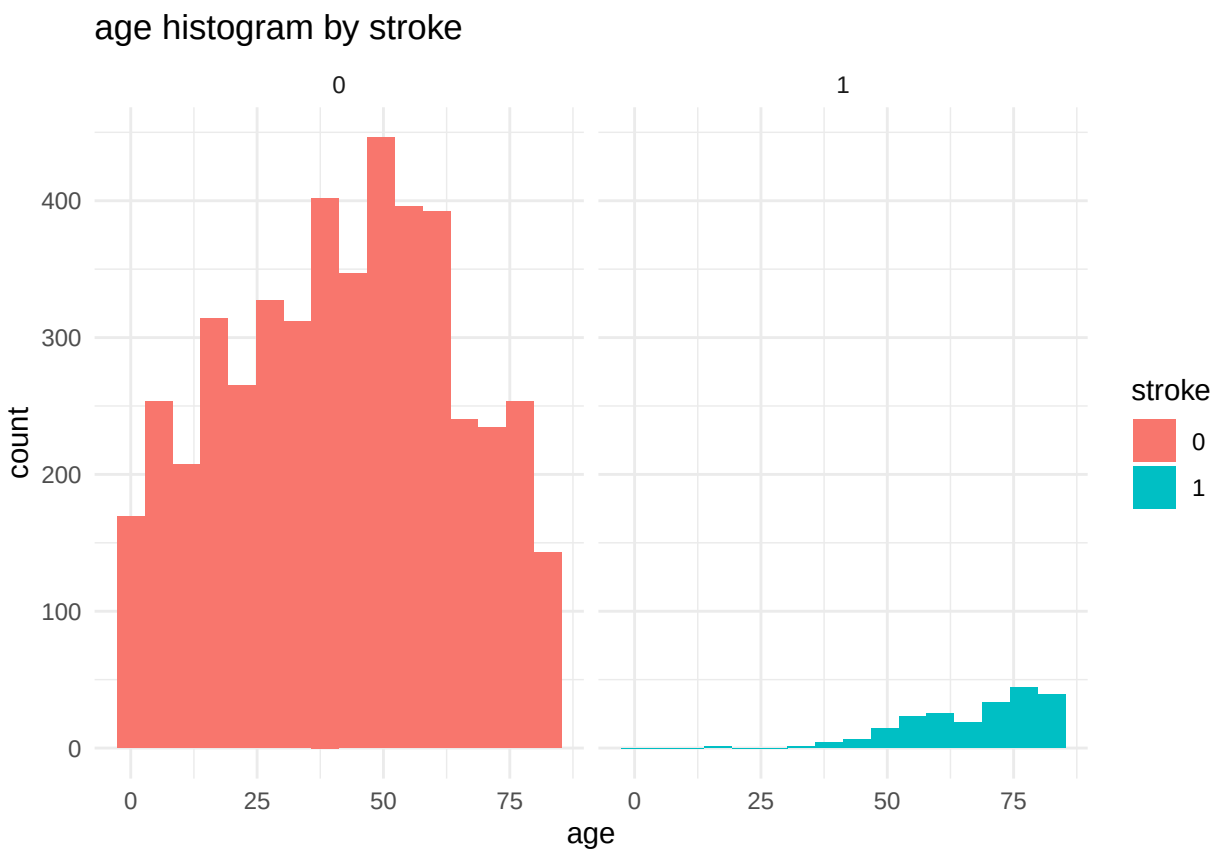



```
data_sub_age= data %>% group_by(stroke) %>% summarise(mean = mean(age))
print(data_sub_age)
```

Age levels with stroke

```
## # A tibble: 2 x 2
##   stroke  mean
##   <fct>  <dbl>
## 1 0       41.8
## 2 1       67.7
```

```
ggplot(data, aes(x = age, fill = stroke)) +
  geom_histogram(binwidth = 5.5)+
  facet_wrap(~stroke)+theme_minimal()+labs(title = "age histogram by stroke",x="age",y="count")
```


age histogram by stroke
0
1
count
400
300
200
100
0
0
25
50
75
0
25
50
75
age
stroke
0
1