Stroke dataset

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```
##
## 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
```

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.

Categorical Variables

Gender

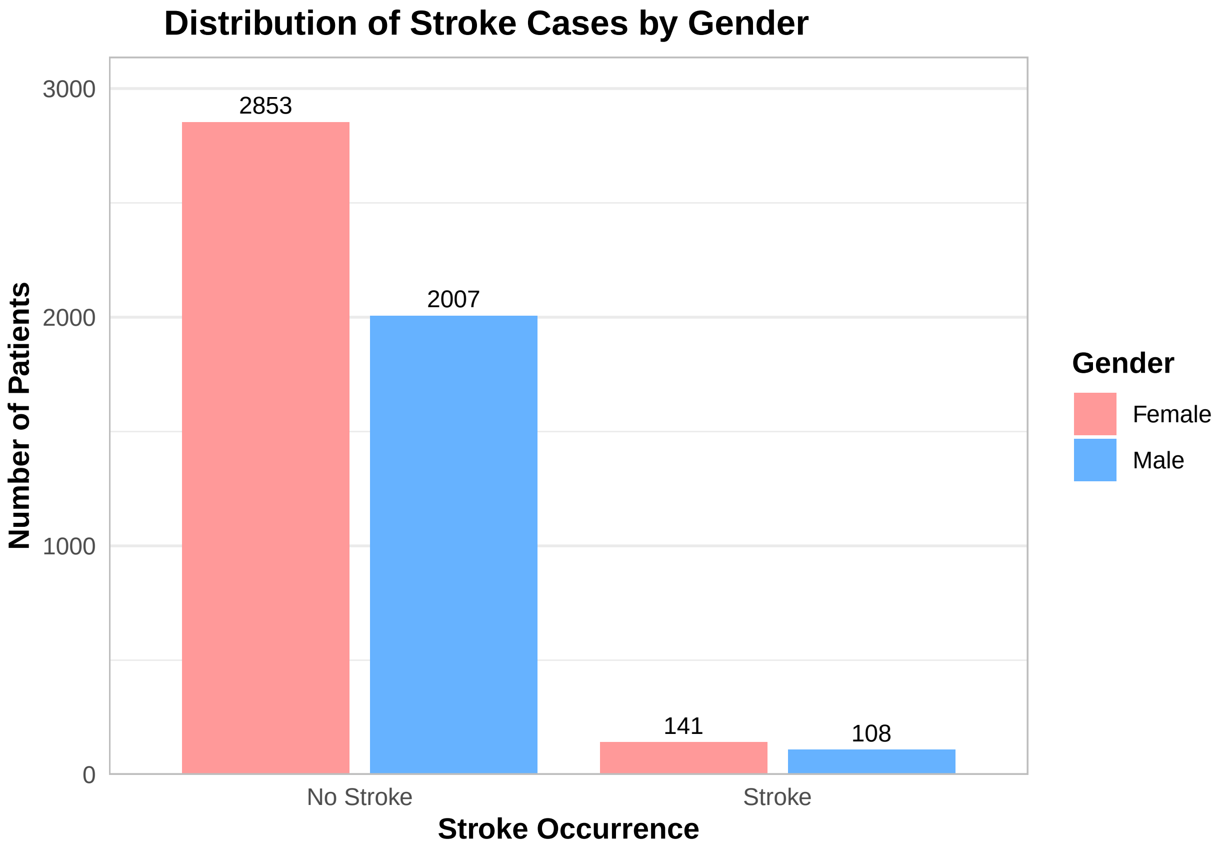
This variable has 2 categories Male and Female (there's one person who is Other but it's only one so we can't make any assumptions about this data).

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

```r
stroke_gender = stroke_data %>% group_by(stroke,gender) %>% summarise(n = n(),.groups = "drop") %>% grou
pander(stroke_gender)
```

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

```r
ggplot(stroke_data, aes(x = stroke, fill = gender)) +
  geom_bar(position = position_dodge(width = 0.9), width = 0.8) +
  geom_text(stat = 'count', aes(label = after_stat(count)),
            position = position_dodge(width = 0.9), vjust = -0.5, size = 3) +
  scale_x_discrete(labels = c("No Stroke", "Stroke")) +
  scale_fill_manual(values = c("Female" = "#FF9999", "Male" = "#66B2FF")) +
  labs(title = "Distribution of Stroke Cases by Gender",
       x = "Stroke Occurrence",
       y = "Number of Patients",
       fill = "Gender") +
  theme_minimal() +
  theme(
    plot.title = element_text(hjust = 0.2, face = "bold"),
    axis.title = element_text(face = "bold"),
    legend.title = element_text(face = "bold"),
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(color = "grey", fill = NA, linewidth = 0.5)  # Changed 'size' to 'linew
  ) +
  scale_y_continuous(expand = expansion(mult = c(0, 0.1)))
```



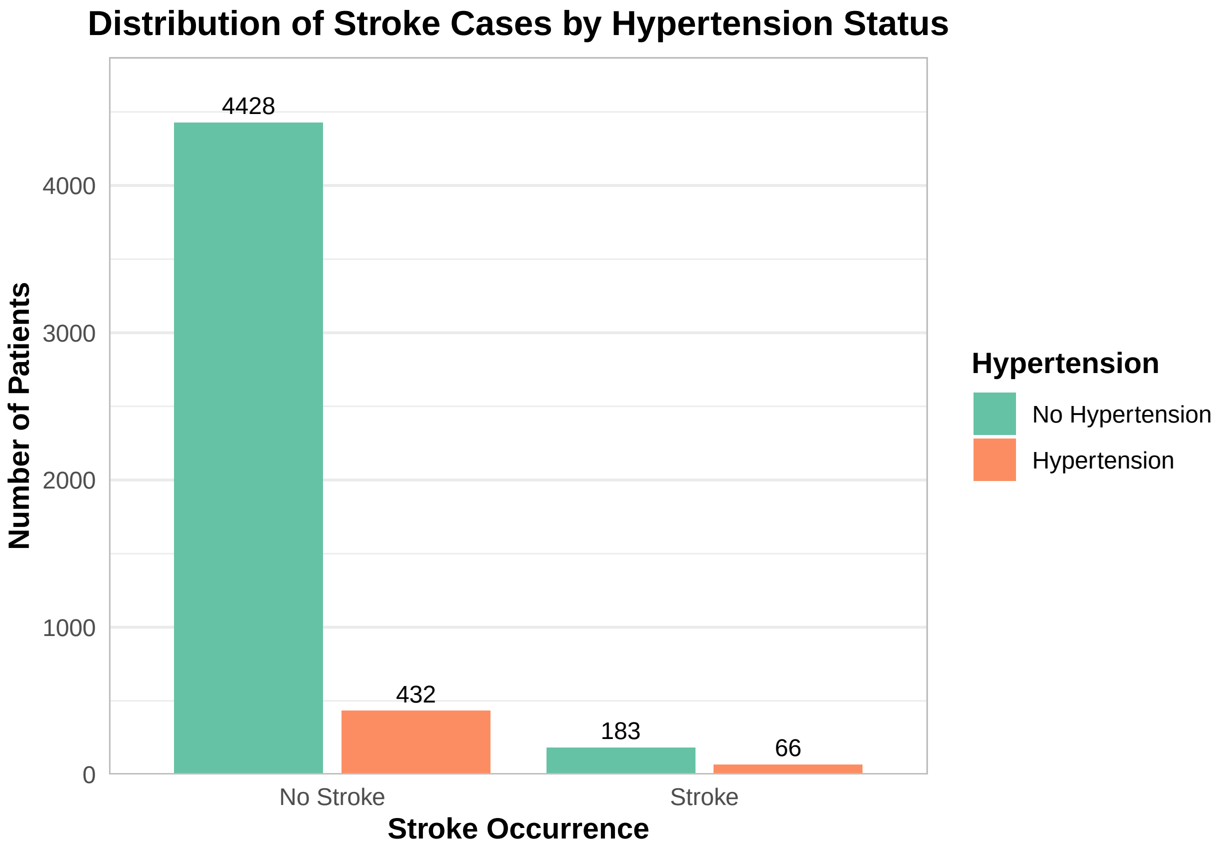
The majority of both female and male patients did not have a stroke, with 95.29% of females and 94.89% of males in the "no stroke" category. However, 4.71% of females and 5.11% of males did experience a stroke. As we can see there is a higher percentage of males that have had a stroke in the data. This number is slightly higher than the stroke rate for population.

Hypertension

```
pander(stroke_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	4428	96.03
0	1	432	86.75
1	0	183	3.969
1	1	66	13.25

```
ggplot(stroke_data, aes(x = stroke, fill = hypertension)) +
  geom_bar(position = position_dodge(width = 0.9), width = 0.8) +
  geom_text(stat = 'count', aes(label = after_stat(count)),
            position = position_dodge(width = 0.9), vjust = -0.5, size = 3) +
  scale_x_discrete(labels = c("No Stroke", "Stroke")) +
  scale_fill_manual(values = c("0" = "#66C2A5", "1" = "#FC8D62"),
                    labels = c("No Hypertension", "Hypertension")) +
  labs(title = "Distribution of Stroke Cases by Hypertension Status",
       x = "Stroke Occurrence",
       y = "Number of Patients",
       fill = "Hypertension") +
  theme_minimal() +
  theme(
    plot.title = element_text(hjust = 0.5, face = "bold"),
    axis.title = element_text(face = "bold"),
    legend.title = element_text(face = "bold"),
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(color = "grey", fill = NA, linewidth = 0.5)
  ) +
  scale_y_continuous(expand = expansion(mult = c(0, 0.1)))
```



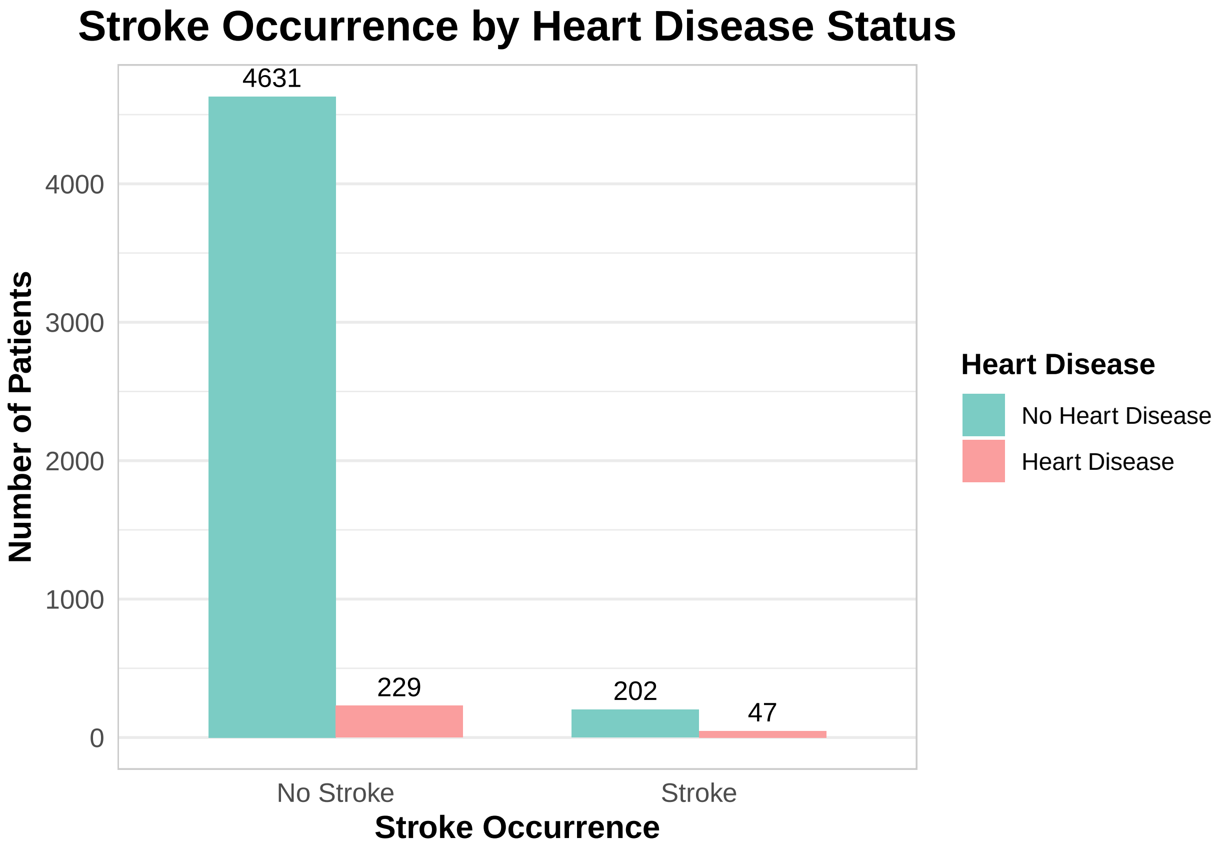
The stroke rate among hypertensive individuals (13.25%) is more than three times higher than among non-hypertensive individuals (3.969%). This difference suggests a strong correlation between hypertension and increased stroke risk. In addition, The hypertensive group's stroke rate (13.25%) is above the overall population rate (4.8%). The non-hypertensive group's rate (3.969%) is slightly below the overall rate. This suggests that Having hypertension is associated with an increase in stroke risk compared to not having hypertension.

Heart disease

```
pander(stroke_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	4631	95.82
0	1	229	82.97
1	0	202	4.18
1	1	47	17.03

```r
ggplot(stroke_data, aes(x = stroke, y = ..count.., fill = heart_disease)) +
  geom_bar(position = "dodge", width = 0.7) +
  scale_fill_manual(values = c("0" = "#7BCCC4", "1" = "#FA9E9E"), labels = c("No Heart Disease", "Heart
  labs(
    title = "Stroke Occurrence by Heart Disease Status",
    x = "Stroke Occurrence",
    y = "Number of Patients",
    fill = "Heart Disease"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  ) +
  geom_text(stat = "count",
            aes(label = ..count..),
            position = position_dodge(width = 0.7),
            vjust = -0.5,
            size = 3.5)
```



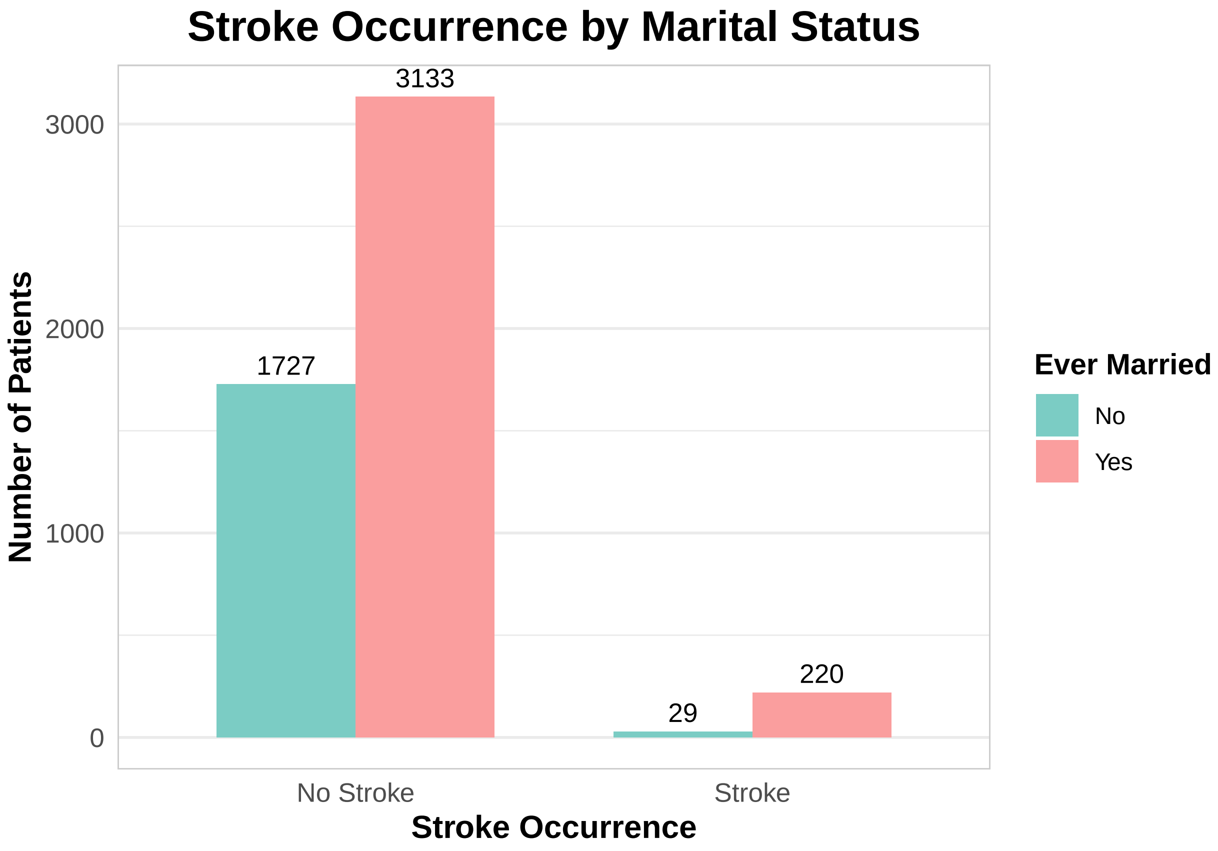
The data of the people who have a heart disease look even more likely to get a stroke than the ones who have hypertension. There can be a correlation between hypertension and having a heart disease. The majority of patients without heart disease (95.82%) did not experience a stroke, whereas those with heart disease have a lower percentage (82.97%) of avoiding a stroke. Among the patients who had a stroke, those with heart disease were more likely to experience one (17.03%) compared to those without heart disease (4.18%).

Ever Married

```
pander(stroke_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	1727	98.35
0	Yes	3133	93.44
1	No	29	1.651
1	Yes	220	6.561

```
ggplot(stroke_data, aes(x = stroke, y = ..count.., fill = ever_married)) +
  geom_bar(position = "dodge", width = 0.7) +
  scale_fill_manual(values = c("No" = "#7BCCC4", "Yes" = "#FA9E9E")) +
  scale_x_discrete(labels = c("0" = "No Stroke", "1" = "Stroke")) +
  labs(
    title = "Stroke Occurrence by Marital Status",
    x = "Stroke Occurrence",
    y = "Number of Patients",
    fill = "Ever Married"
  ) +
  theme_minimal() +
    theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )+
  geom_text(stat = "count",
            aes(label = ..count..),
            position = position_dodge(width = 0.7),
            vjust = -0.5,
            size = 3.5)
```



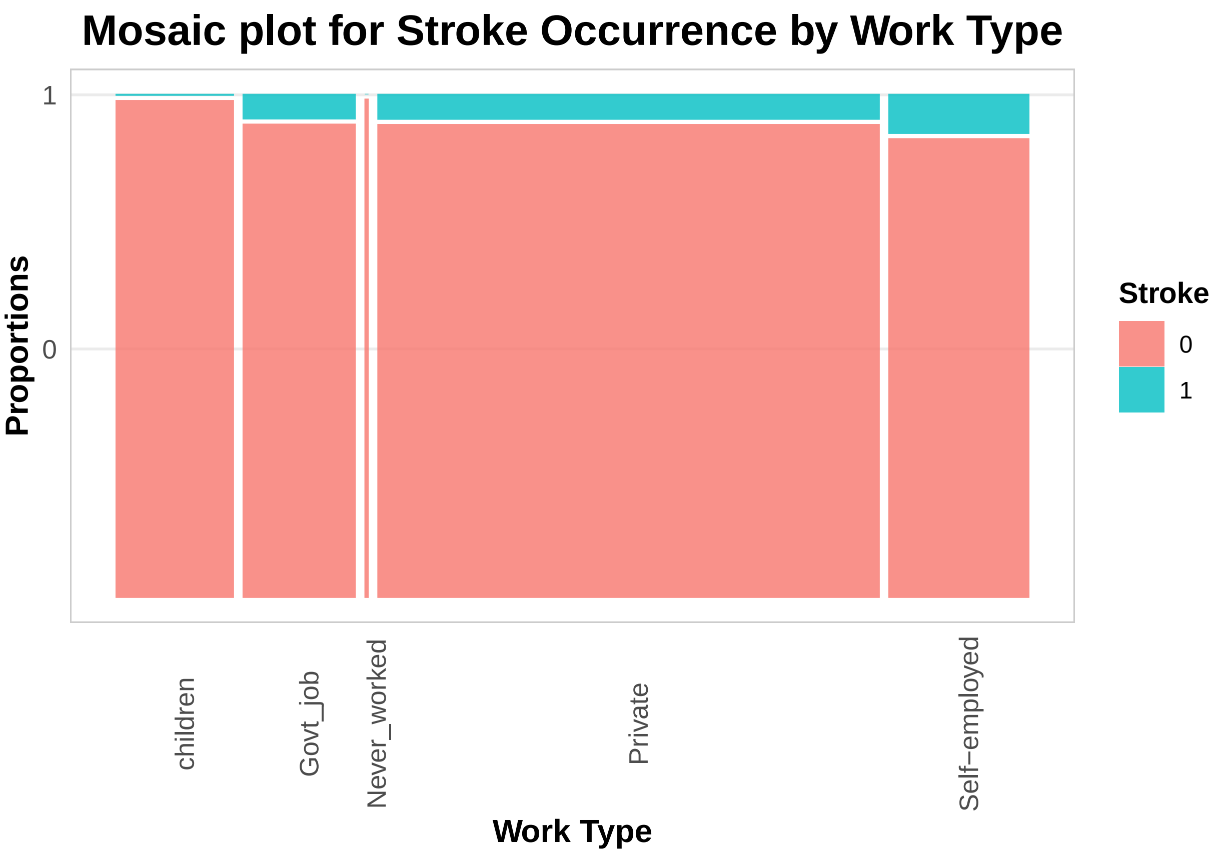
There are more people who are ever married and had a stroke than not ever married. Among individuals who have never been married, 98.35% did not experience a stroke, while 1.65% did. In contrast, among those who have been married, 93.44% did not have a stroke, and 6.56% did. This suggests that those who have ever been married are more likely to experience a stroke compared to those who have never been married.

Work Type

```r
pander(stroke_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	2775	94.9
0	Self-employed	754	92.06
1	children	2	0.2911
1	Govt_job	33	5.023
1	Private	149	5.096
1	Self-employed	65	7.937

```r
ggplot(data = stroke_data) +
  geom_mosaic(aes(x = product(stroke,work_type), fill = stroke), na.rm = TRUE)+
  theme_minimal()+
    theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    axis.text.x = element_text(angle = 90),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )+
  labs(
    title = "Mosaic plot for Stroke Occurrence by Work Type",
    x = "Work Type",
    y = "Proportions",
    fill = "Stroke"
  )
```



Clearly the self employed have the highest % of people who have had 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.

Numeric Variables

BMI

The first continuous 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(stroke_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 frequency 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.

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

```r
stroke_data$cat_weight = frec_table

# Create frequency table
bmi_freq_table <- table(frec_table)
bmi_rel_freq <- prop.table(bmi_freq_table)*100
pander(bmi_rel_freq)
```

Underweight	Normal	Overweight	Obese	Extremely Obese
7.111	25.06	28.71	20.37	18.74

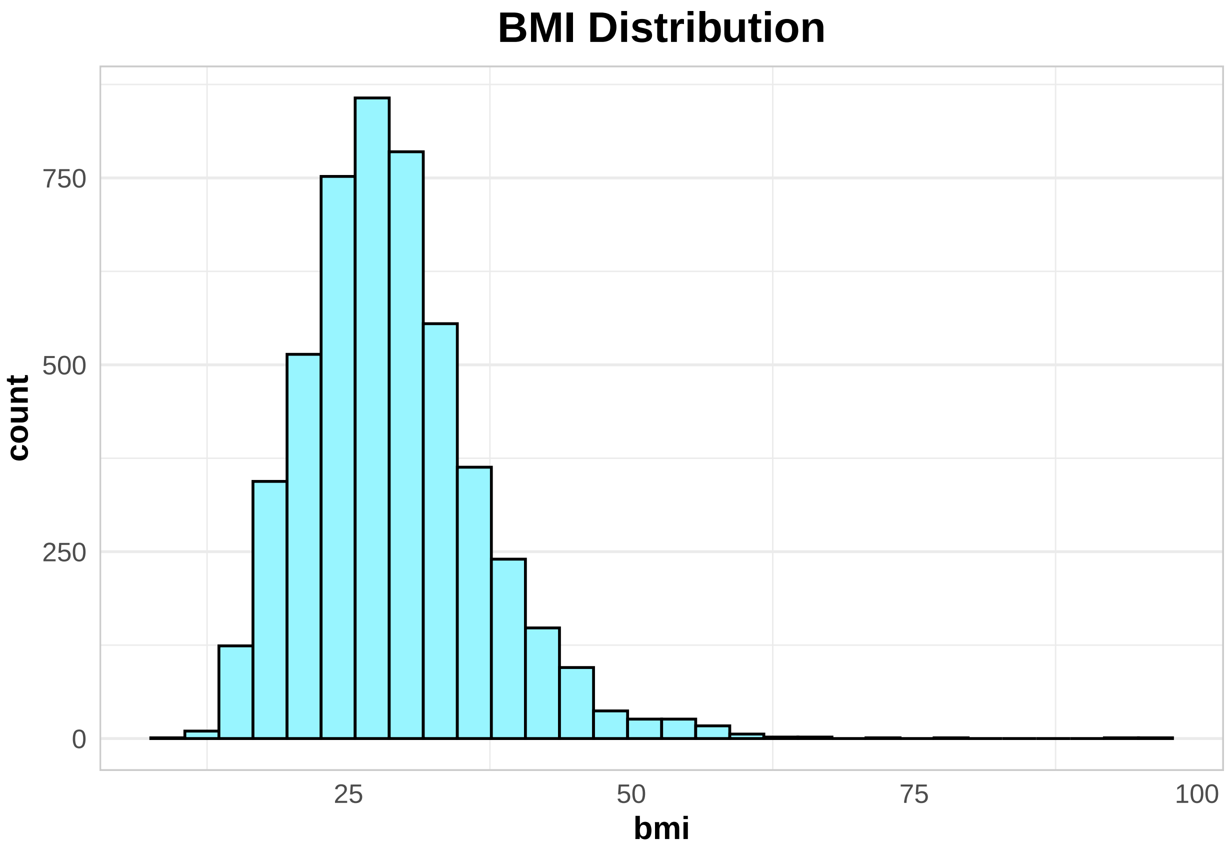
If we check this with a graph we can see that the graph looks a bit symmetrical with an inclination to the right. This could it mean that the distribution is not a normal like could it seem. We are going to check the kurtosis and skewness shape to check if there´s a problem.

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

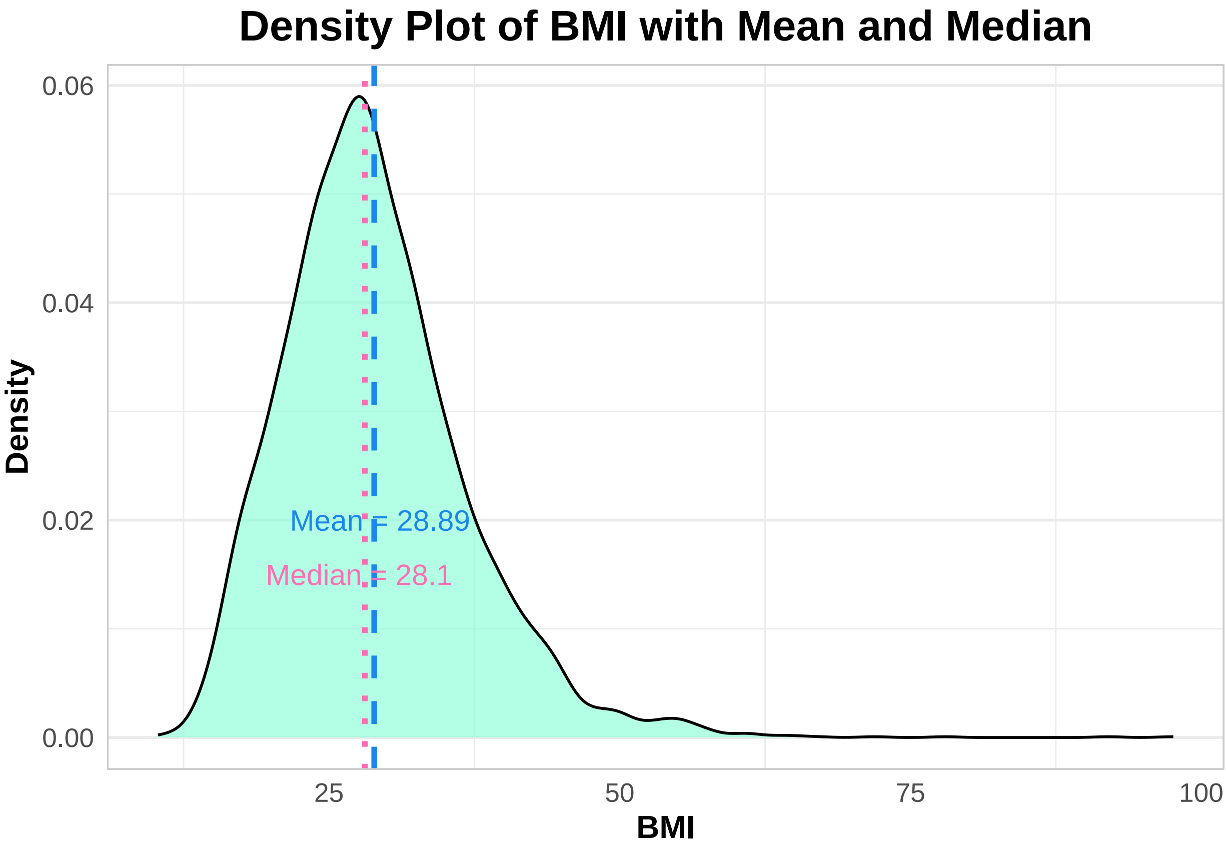
```
## $variance
## [1] 63.33528
##
## $mean
## [1] 28.84576
##
## $median
## [1] 28.00923
##
## $mode
##      [- -]     mode
## [1,] 25 30 27.22513
```

```r
ggplot(stroke_data, aes(x=bmi)) +
  geom_histogram(color="black", fill="cadetblue1")+
  labs(title = "BMI Distribution")+
  theme_minimal()+
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```

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



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

# Density plot with a vertical line at the mean
ggplot(stroke_data, aes(x = 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()+
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



```
skewness(stroke_data$bmi)
```

```
## [1] 1.055063
```

```
kurtosis(stroke_data$bmi)
```

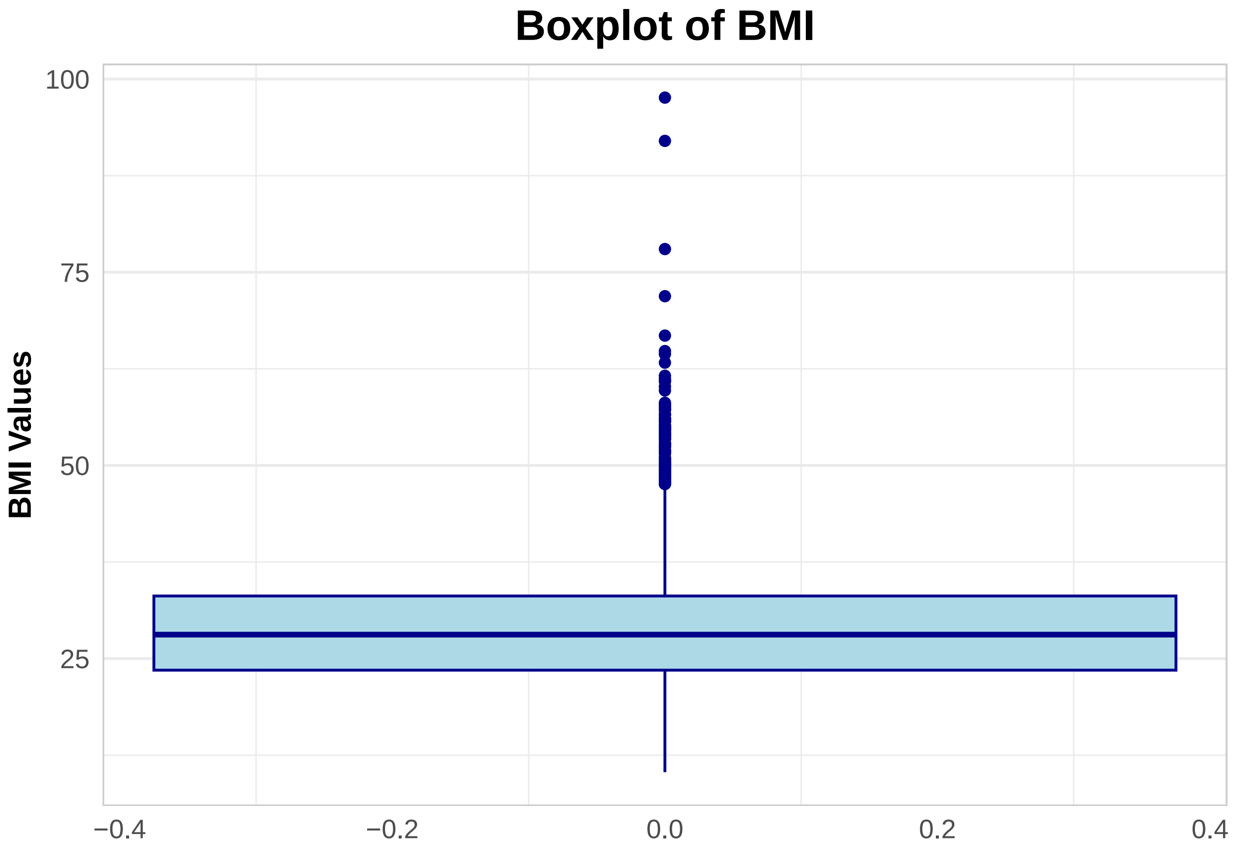
```
## [1] 3.36233
```

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.

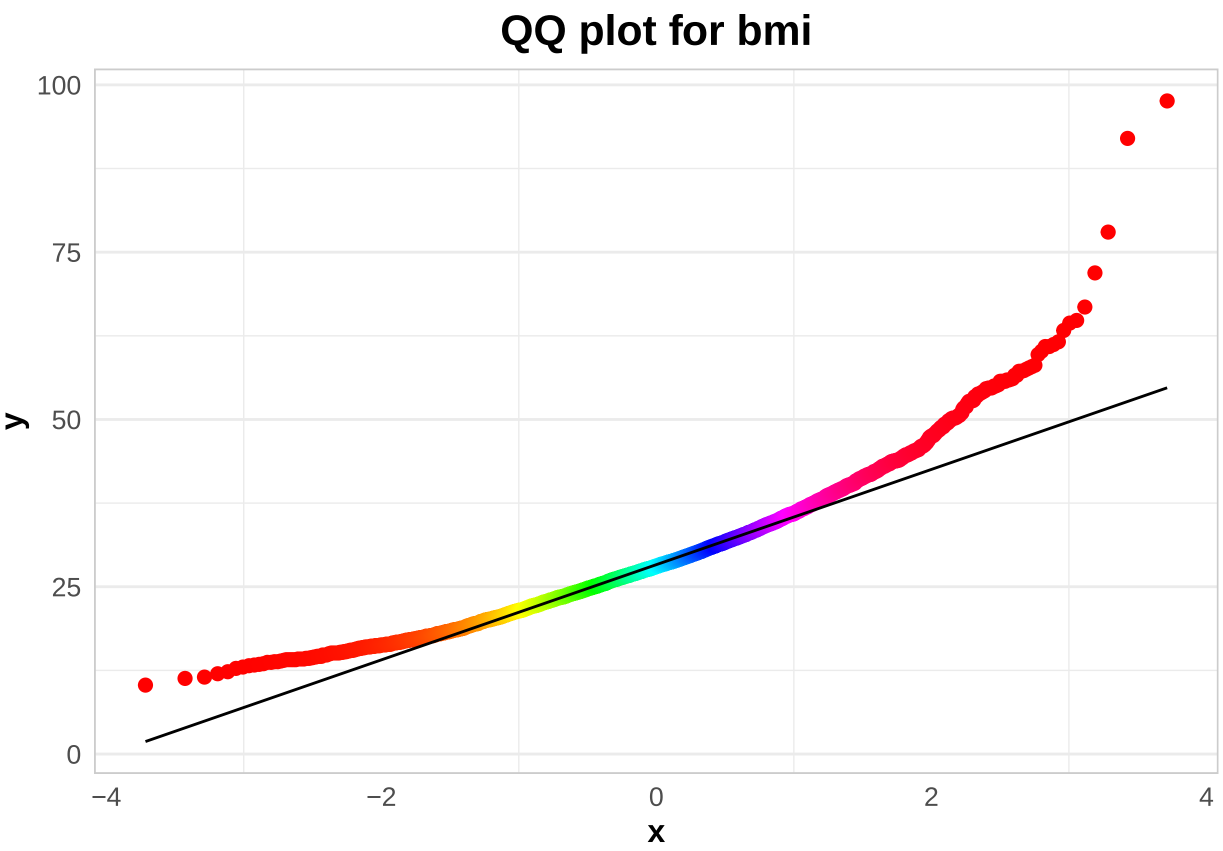
To see if the outliers are correctly in the heavier side we can check the boxplot of the *bmi*

```
ggplot(stroke_data, aes(y = stroke_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()+
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



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(stroke_data, aes(sample=bmi)) + stat_qq(size=2,color=rainbow(4908))+stat_qq_line()+theme_minimal
  labs(title = "QQ plot for bmi")+
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```

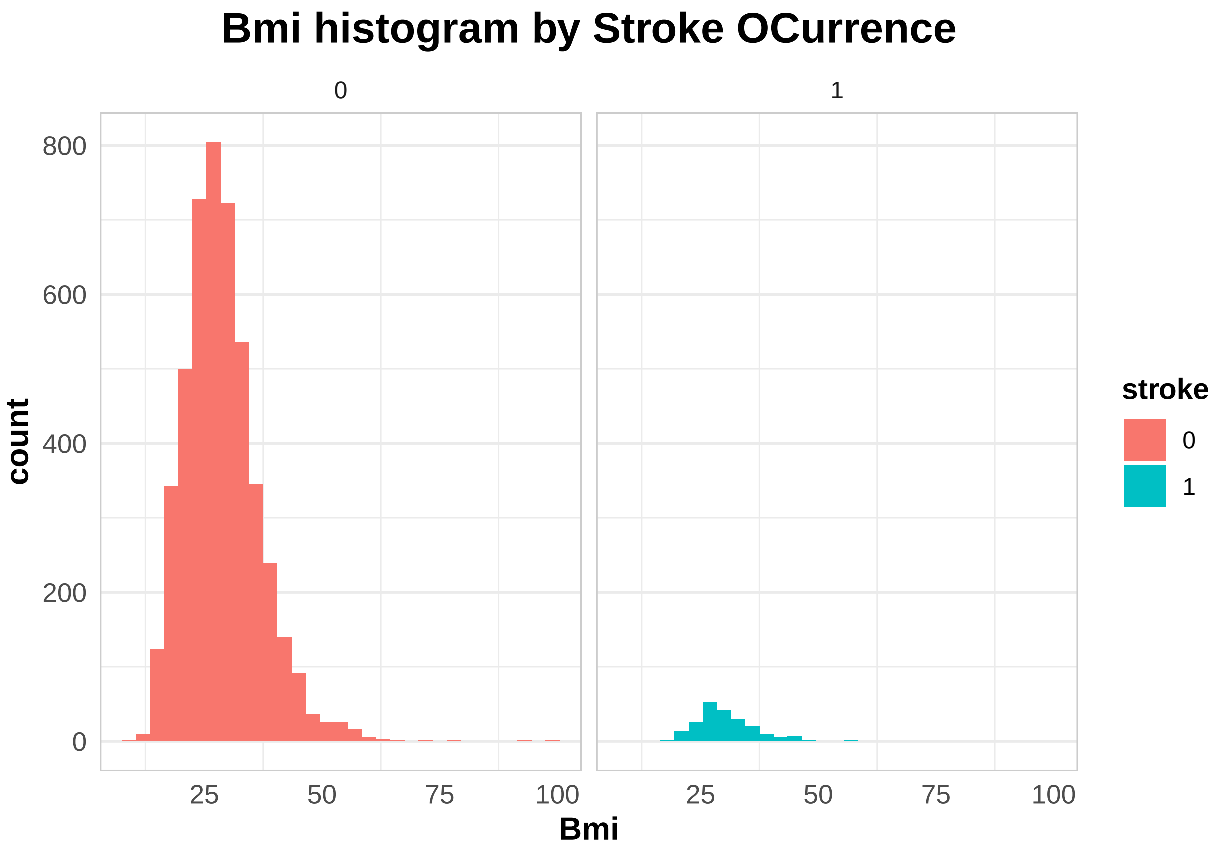


```
data_sub_bmi_catw= stroke_data %>% group_by(cat_weight,stroke) %>% summarise(mean = mean(bmi),.groups =
pander(data_sub_bmi_catw)
```

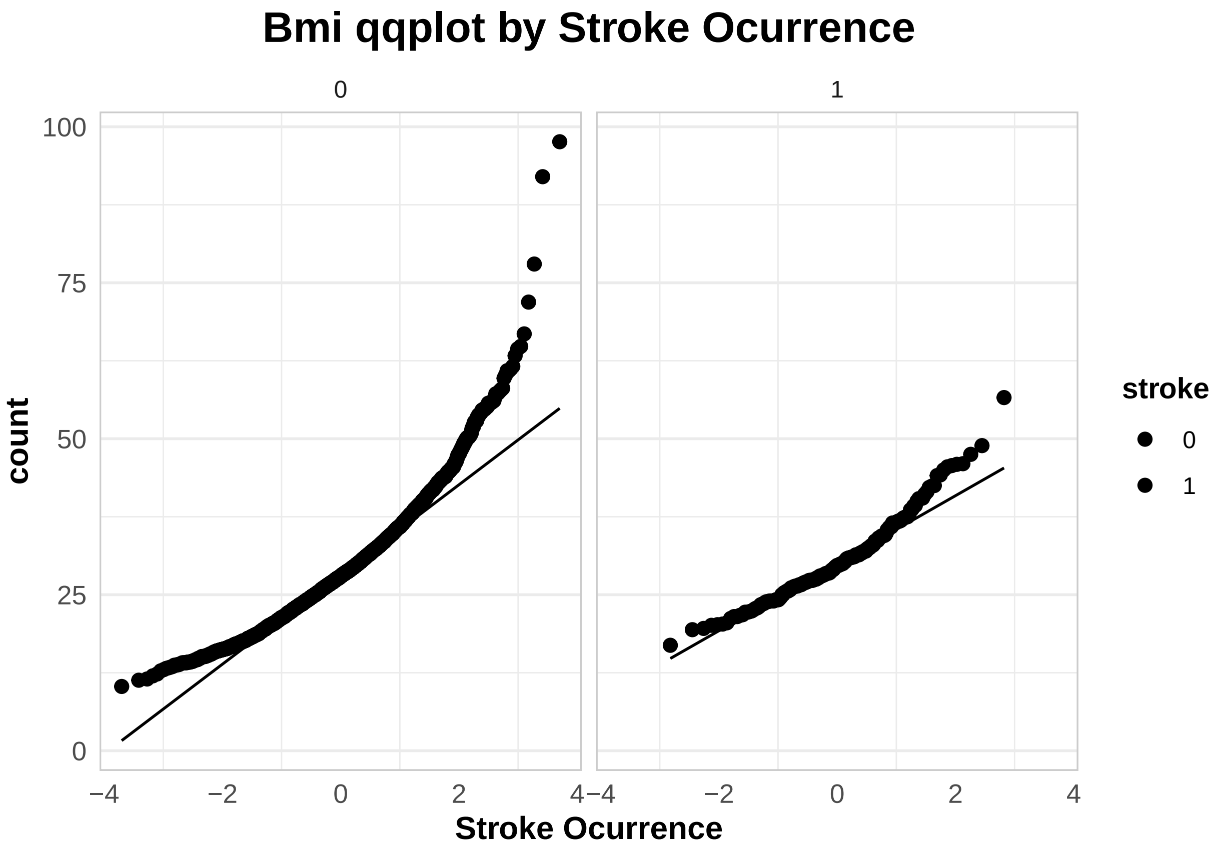
BMI with stroke

cat_weight	stroke	mean
Underweight	0	16.69
Underweight	1	16.9
Normal	0	22.17
Normal	1	22.63
Overweight	0	27.46
Overweight	1	27.58
Obese	0	32.24
Obese	1	32.12
Extremely Obese	0	41.09
Extremely Obese	1	40.3

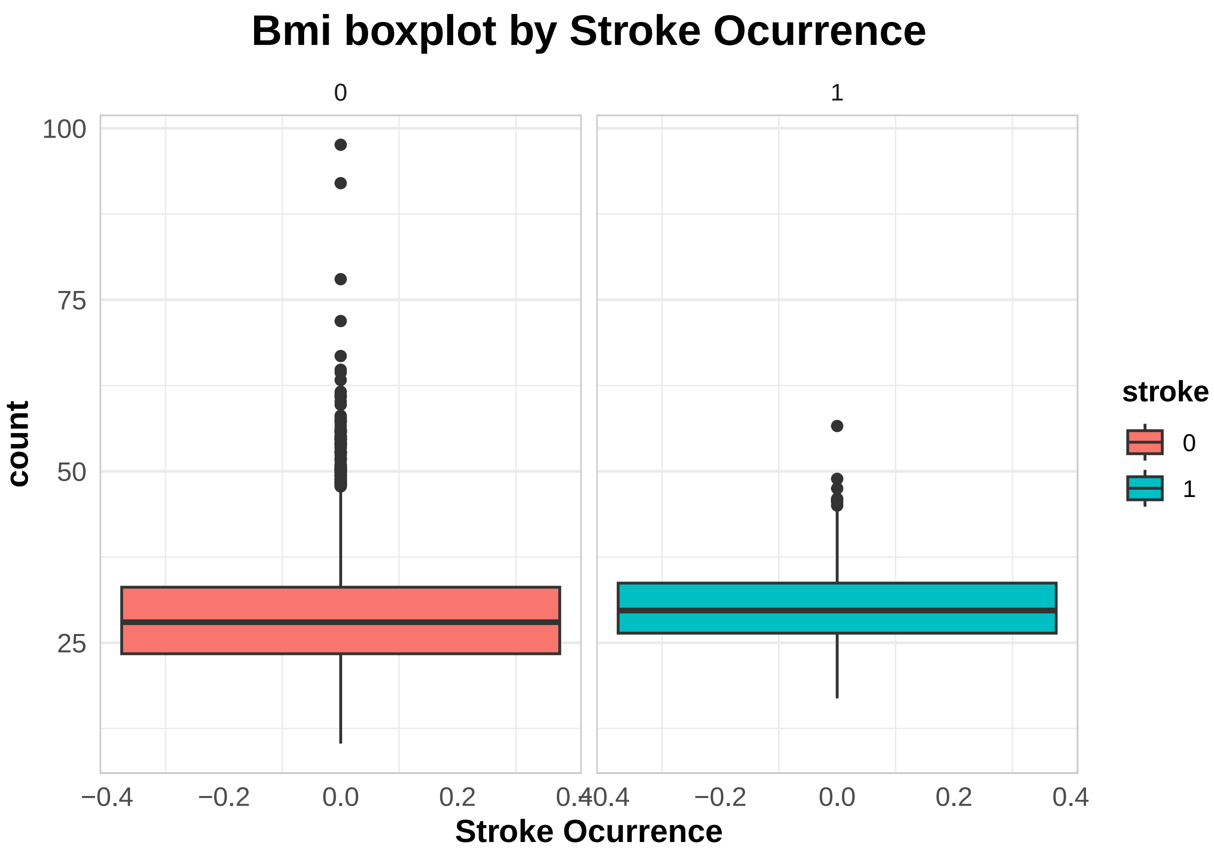
```
ggplot(stroke_data, aes(x = bmi, fill = stroke)) +
  geom_histogram(binwidth = 3)+
  facet_wrap(~stroke)+theme_minimal()+labs(title = "Bmi histogram by Stroke OCurrence",x="Bmi",y="count
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



```
ggplot(stroke_data, aes(sample = bmi, fill = stroke))+
  stat_qq(size=2)+ stat_qq_line() +
  facet_wrap(~stroke)+theme_minimal()+labs(title = "Bmi qqplot by Stroke Ocurrence",x="Stroke Ocurrence
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



```r
ggplot(stroke_data, aes(y = bmi, fill =stroke))+
  geom_boxplot()+
  facet_wrap(~stroke)+theme_minimal()+labs(title = "Bmi boxplot by Stroke Ocurrence",x="Stroke Ocurrenc
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```

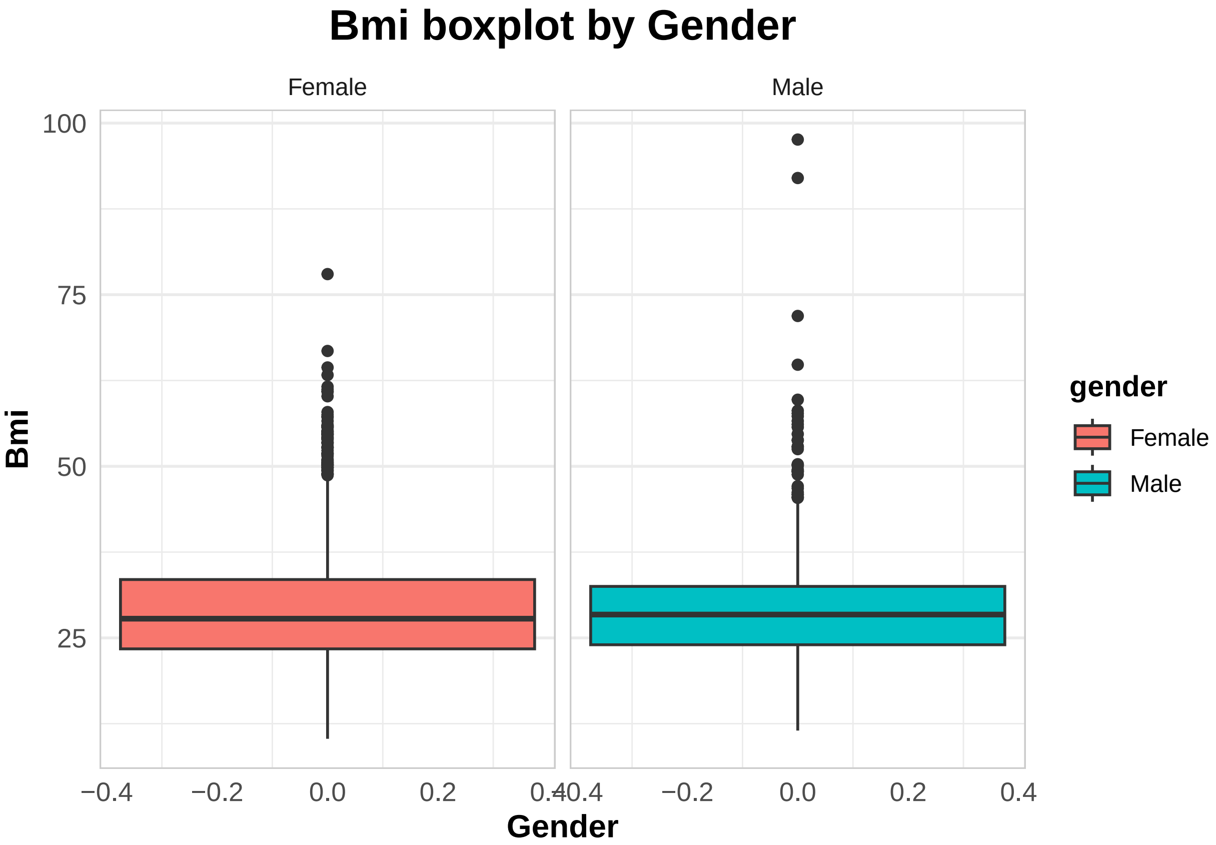


When you compare the distribution of *bmi* by stroke you can see that for the individuals who did not have a stroke you have more outliers in the right tail and for those who had one the distribution is a bit closer to a normal one. The bmi is a little bit higher over all with a stroke and the values are more concentrate. This doesn't show us any indication that the *bmi* could have a impact on getting a stroke. #### BMI with gender

```
#gender

data_sub_bmi_gender= stroke_data %>% group_by(gender,stroke) %>% summarise(mean = mean(bmi),.groups = "
pander(data_sub_bmi_gender)
```

gender	stroke	mean
Female	0	29.02
Female	1	30.22
Male	0	28.55
Male	1	30.81

```
ggplot(stroke_data, aes(y = bmi, fill = gender))+
  geom_boxplot()+
  facet_wrap(~gender)+theme_minimal()+labs(title = "Bmi boxplot by Gender",x="Gender",y="Bmi")+
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```

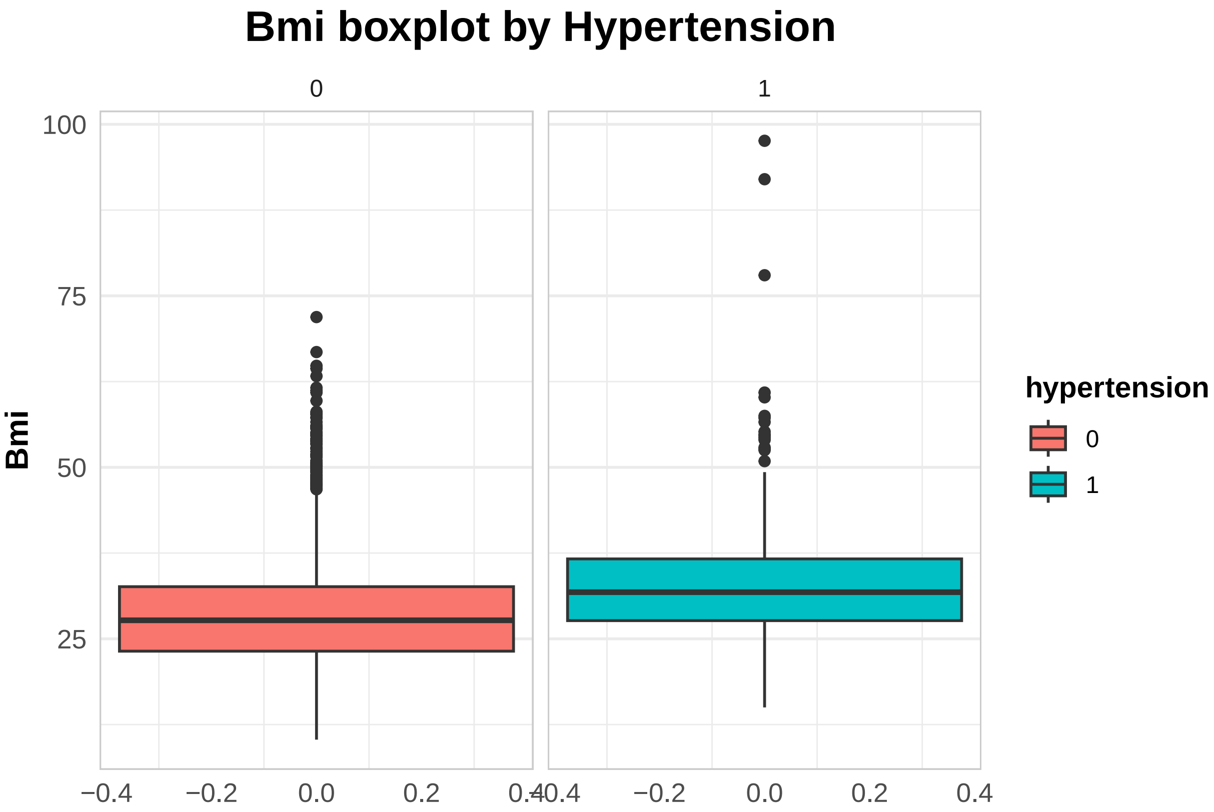


The *bmi* of females and males is very similar in distribution. The males have more outliers. The mean is higher for those who had a stroke in both genders. Those males who had an stroke have a bigger *bmi* almost a 2 increase in the mean. #### BMI with hypertension

```
#hypertension

data_sub_bmi_hyper= stroke_data %>% group_by(hypertension,stroke) %>% summarise(mean = mean(bmi),.group
pander(data_sub_bmi_hyper)
```

hypertension	stroke	mean
0	0	28.41
0	1	30.3
1	0	33.37
1	1	30.89

```
ggplot(stroke_data, aes(y = bmi, fill =hypertension))+
  geom_boxplot()+
  facet_wrap(~hypertension)+theme_minimal()+labs(title = "Bmi boxplot by Hypertension",x="",y="Bmi")+
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```

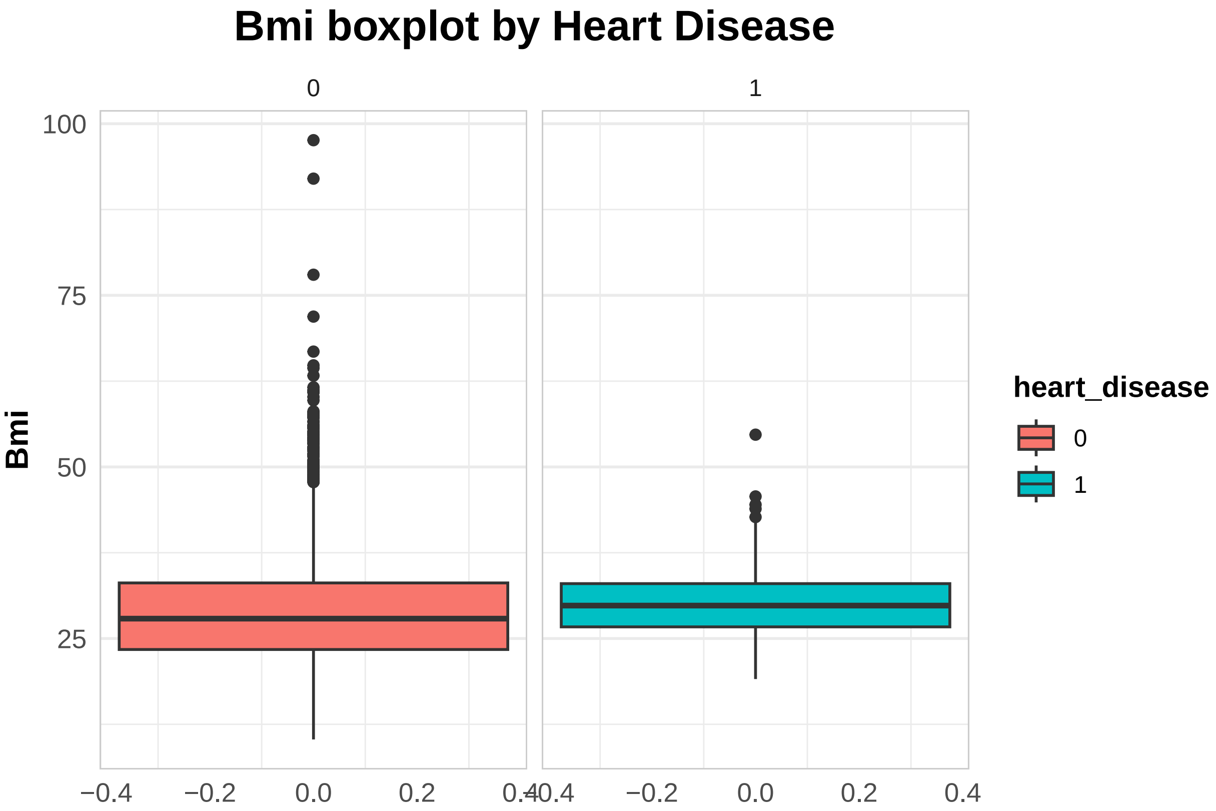


The *bmi* for people who have hypertension is over all bigger.The distributions look very similar. The mean for those you had have a stroke is bigger with or without hypertension. This could indicate that with hypertension your changes could increase. #### BMI by heart diseased

```
data_sub_bmi_hd= stroke_data %>% group_by(heart_disease,stroke) %>% summarise(mean = mean(bmi),.groups
pander(data_sub_bmi_hd)
```

heart_disease	stroke	mean
0	0	28.76
0	1	30.41
1	0	30.23
1	1	30.75

```
ggplot(stroke_data, aes(y = bmi, fill =heart_disease))+
  geom_boxplot()+
  facet_wrap(~heart_disease)+theme_minimal()+labs(title = "Bmi boxplot by Heart Disease",x="",y="Bmi")+
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



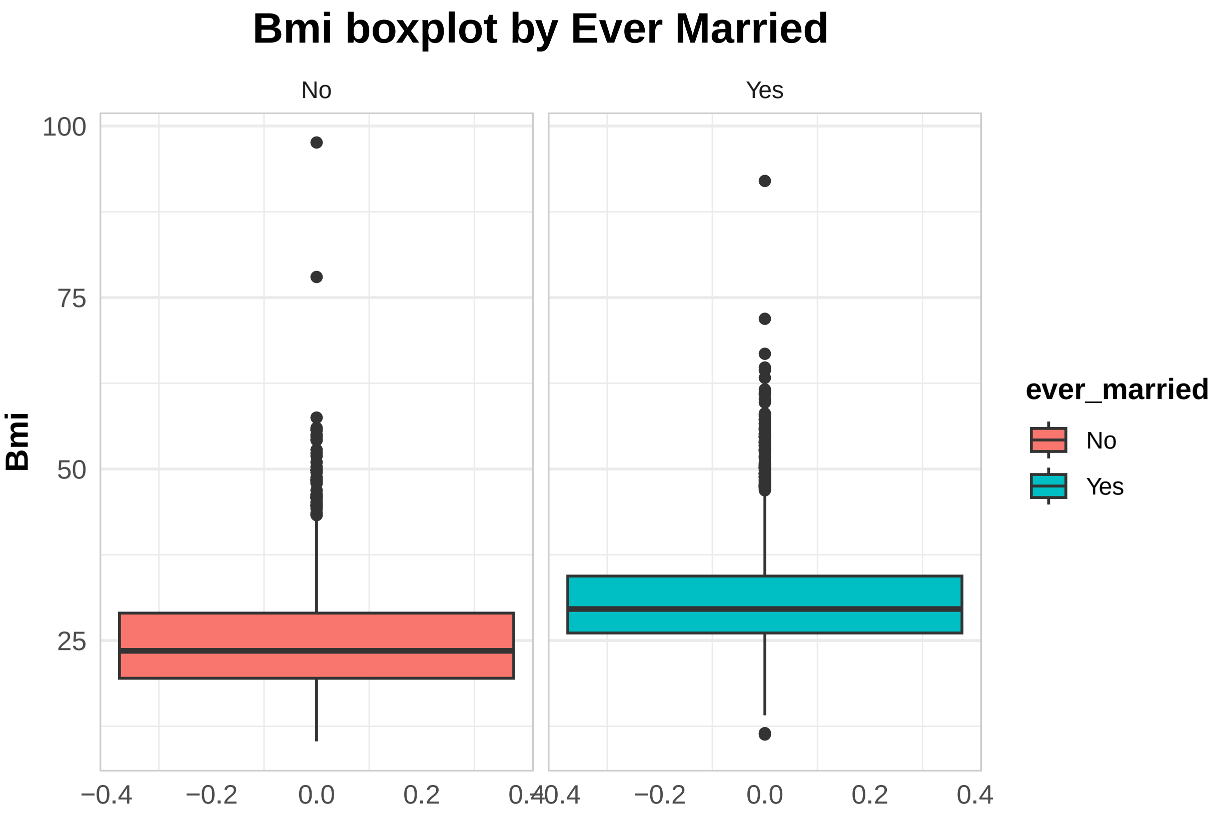
The distribution os those who don't have a heart disease is more dispersed. You can see a concentration of the *bmi* for the ones that have a heart disease. The mean over all for those you have a heart disease is bigger and you can see the gap between those who had a stroke and those who didn't.

```
data_sub_bmi_em= stroke_data %>% group_by(ever_married,stroke) %>% summarise(mean = mean(bmi),.groups =
pander(data_sub_bmi_em)
```

BMI by ever married

ever_married	stroke	mean
No	0	25.15
No	1	29.92
Yes	0	30.87
Yes	1	30.54

```
ggplot(stroke_data, aes(y = bmi, fill =ever_married))+
  geom_boxplot()+
  facet_wrap(~ever_married)+theme_minimal()+labs(title = "Bmi boxplot by Ever Married",x="",y="Bmi")+
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



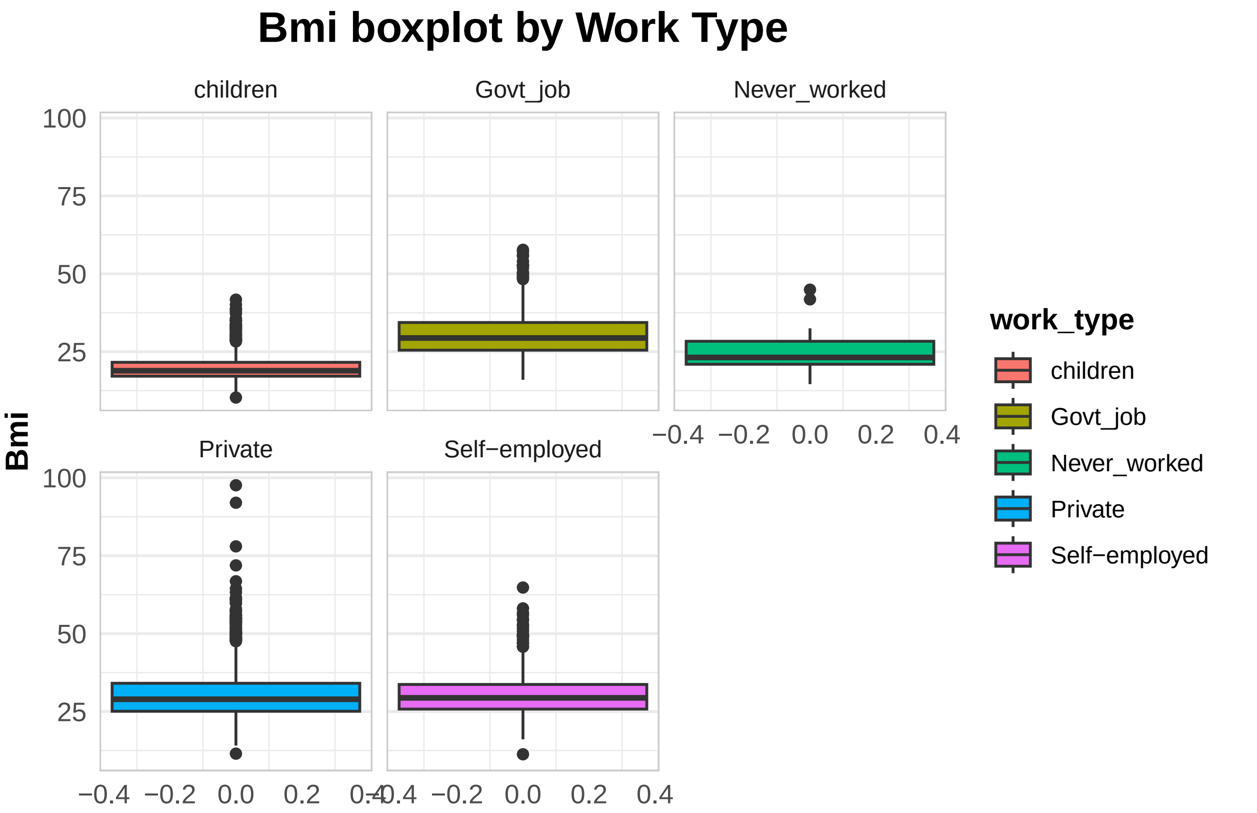
With this data we can say that have been ever been married make the *bmi* higher over all. You can see that in both cases there's outliers and they have very similar distributions. For the mean you can see a bigger difference with it the one that haven't been married and had have a stroke with a difference of 4. #### BMI by work type

```
data_sub_bmi_wt= stroke_data %>% group_by(work_type,stroke) %>% summarise(mean = mean(bmi),.groups = "d
pander(data_sub_bmi_wt)
```

work_type	stroke	mean
children	0	20.02
children	1	30.9
Govt_job	0	30.58
Govt_job	1	29.36
Never_worked	0	25.55

work_type	stroke	mean
Private	0	30.27
Private	1	31.06
Self-employed	0	30.25
Self-employed	1	29.64

```
ggplot(stroke_data, aes(y = bmi, fill =work_type))+
  geom_boxplot()+
  facet_wrap(~work_type)+theme_minimal()+labs(title = "Bmi boxplot by Work Type",x="",y="Bmi")+
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



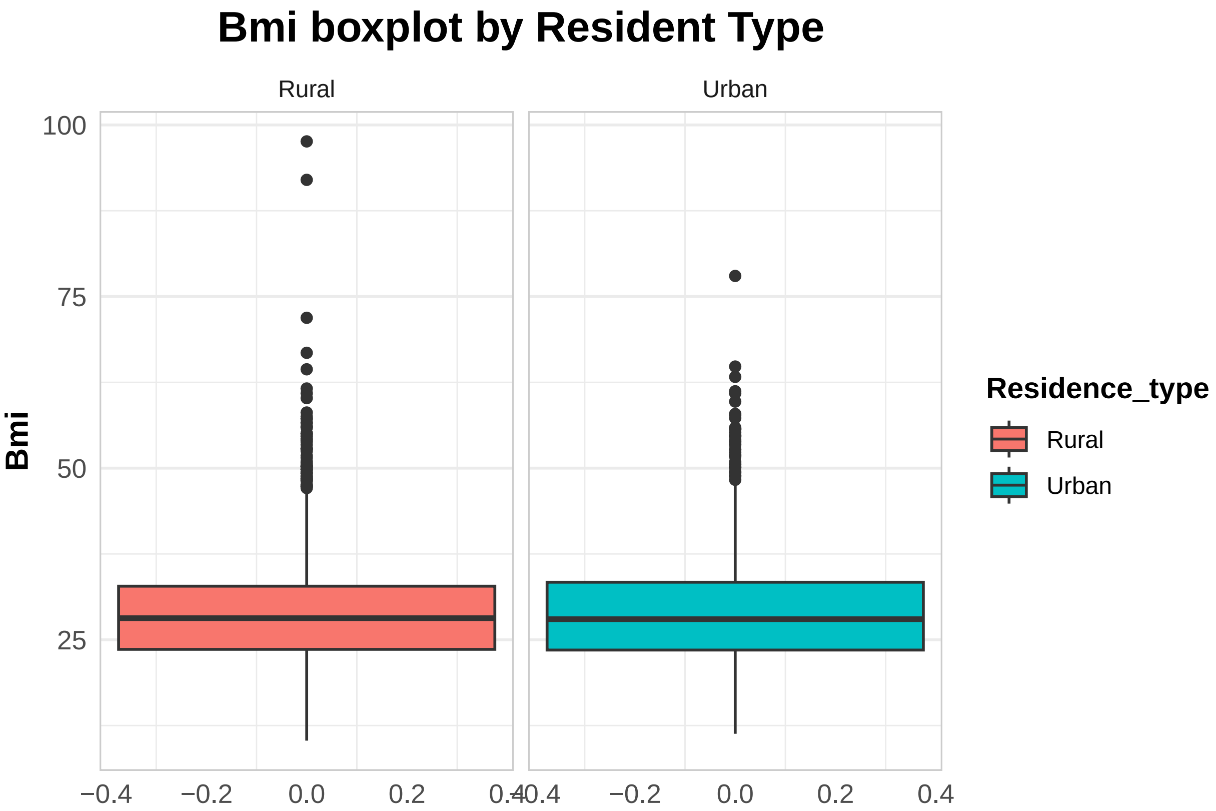
The work type looks like if you never work or you work with children your over all *bmi* will be lower and if you work in any other type of work your *bmi* will be higher. If we add the stroke we can see that if you work with children and you had have a stroke the mean of the *bmi* is the higher. If you self-employed or work with the government those who had a stroke had lower *bmi* than those you didn't. This could be a stroke by stress.

```
data_sub_bmi_tr= stroke_data %>% group_by(Residence_type,stroke) %>% summarise(mean = mean(bmi),.groups
pander(data_sub_bmi_tr)
```

BMI by resident type

Residence_type	stroke	mean
Rural	0	28.85
Rural	1	30.07
Urban	0	28.8
Urban	1	30.84

```
ggplot(stroke_data, aes(y = bmi, fill =Residence_type))+
  geom_boxplot()+
  facet_wrap(~Residence_type)+theme_minimal()+labs(title = "Bmi boxplot by Resident Type",x="",y="Bmi")
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



The type of resident is almost identical as the over all *bmi* population. The mean didn't have any difference with the population. This could mean that the type of resident doesn't have any effect on the *bmi*.

Glucose levels

The second continuous variable that we examine is average glucose levels. This variable measures on average, the amount of glucose found in blood.

```
summary(stroke_data$avg_glucose_level)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   55.12   77.07   91.68  105.30  113.50  271.74
```

Next, we examined the frequency distribution of average glucose levels using categories based on common medical standards. We used the cut function to create the following categories:

1. Normal: (0-99.9] mg/dL
2. Prediabetes: (99.9-125.9] mg/dL
3. Diabetes: (125.9-Inf] mg/dL

These categories correspond to the standard clinical definitions for fasting glucose levels:

- Normal: Less than 100 mg/dL
- Prediabetes: 100 to 125 mg/dL
- Diabetes: 126 mg/dL or higher

```
glc_mean <- mean(stroke_data$avg_glucose_level)
glc_median <- median(stroke_data$avg_glucose_level)

glucose_categories <- cut(stroke_data$avg_glucose_level,
                          breaks = c(0, 99.9, 125.9, Inf),
                          labels = c("Normal", "Prediabetes", "Diabetes"))

# Reorder the levels to put Normal in the middle
glucose_categories <- factor(glucose_categories, levels = c("Prediabetes", "Normal", "Diabetes"))

# Add the categories to the data frame
stroke_data$glucose_category = glucose_categories

# Create frequency table
glucose_freq_table <- table(glucose_categories)
# Calculate relative frequencies
glucose_rel_freq <- prop.table(glucose_freq_table) * 100
pander(glucose_rel_freq)
```

Prediabetes	Normal	Diabetes
19.74	61.61	18.64

```
stats_glu = stat.freq(hist_glu)


# If you want a more formatted output:
cat("Variance:", stats_glu$variance, "\n")
```

```
## Variance: 2012.656
```

```
cat("Mean:", stats_glu$mean, "\n")
```

```
## Mean: 105.2852
```

```
cat("Median:", stats_glu$median, "\n")
```

```
## Median: 92.54851
```

```
cat("Mode:", stats_glu$mode, "\n")
```

```
## Mode: 80 100 85.58559
```

As we can see:

- The mean glucose level (105.30 mg/dL) falls within the prediabetes range, suggesting that on average, the population has slightly elevated glucose levels.
- However, the median (92.5 mg/dL) is in the normal range, indicating that more than half of the population has normal glucose levels.
- The mode is (85.5 mg/dL) being well within the normal range suggests that normal glucose levels are the most common in the dataset.

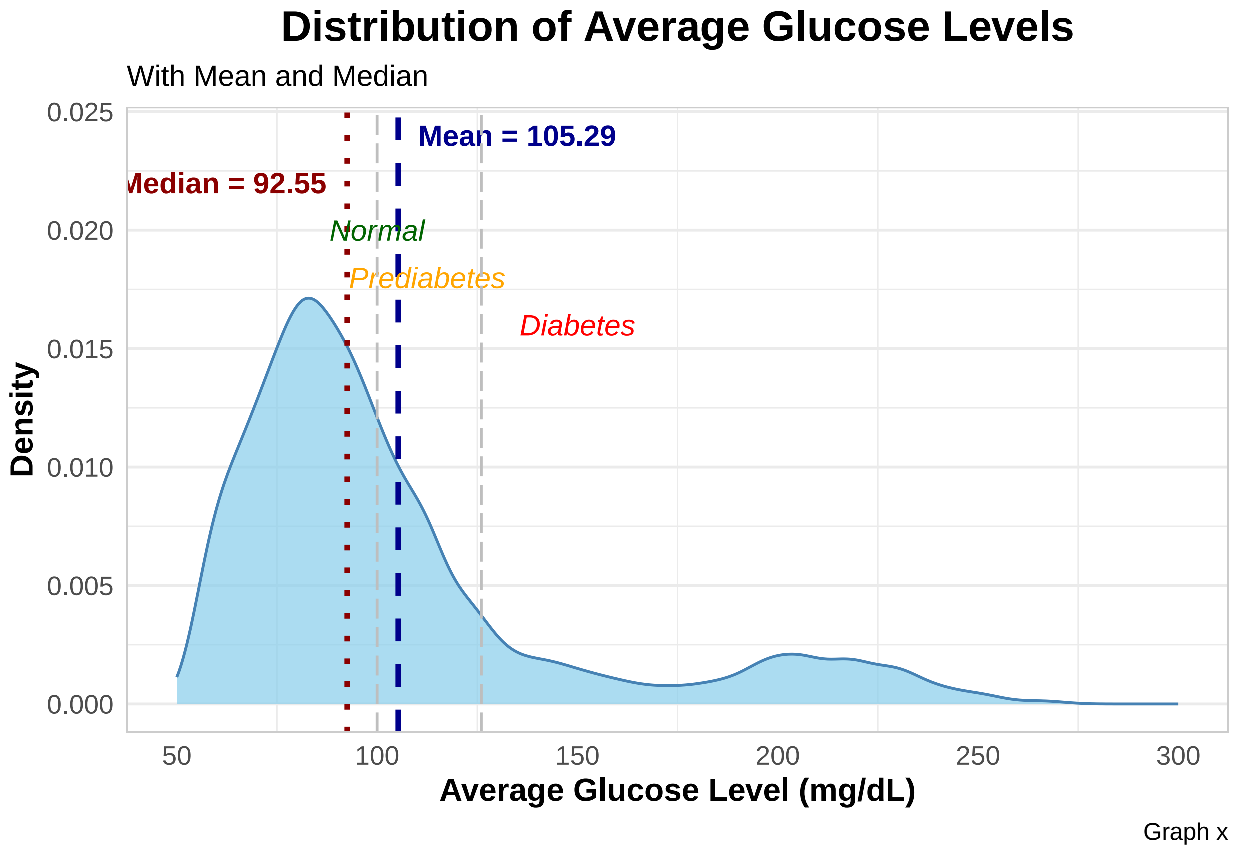
In addition, the high variance (2012.65) indicates considerable spread in the glucose levels, which is consistent with the presence of both normal and elevated (prediabetic and diabetic) levels in the population.

The mean being higher than the median suggests a right-skewed distribution. This is consistent with having a majority in the normal range but a significant number of higher values pulling the mean up. While the majority (61.61%) have normal glucose levels, the combined 38.38% with prediabetes or diabetes represents a significant portion of the population at increased risk for various health issues, including potentially higher stroke risk.

The mean (105.30 mg/dL) being in the prediabetic range while the median (92.5 mg/dL) is in the normal range highlights the impact of the higher values on the overall distribution.

```
# Create the plot
ggplot(stroke_data, aes(x = avg_glucose_level)) +
  geom_density(fill = "skyblue", color = "steelblue", alpha = 0.7) +
  geom_vline(aes(xintercept = stats_glu$mean), color = "darkblue", linetype = "dashed", size = 1) +
  geom_vline(aes(xintercept = stats_glu$median), color = "darkred", linetype = "dotted", size = 1) +
  labs(
    title = "Distribution of Average Glucose Levels",
    subtitle = "With Mean and Median",
```

```r
    x = "Average Glucose Level (mg/dL)",
    y = "Density",
    caption = "Graph x"
  ) +
  annotate("text", x = stats_glu$mean, y = 0.024,
           label = paste("Mean =", round(stats_glu$mean, 2)),
           color = "darkblue", hjust = -0.1, size = 4, fontface = "bold") +
  annotate("text", x = stats_glu$median, y = 0.022,
           label = paste("Median =", round(stats_glu$median, 2)),
           color = "darkred", hjust = 1.1, size = 4, fontface = "bold") +
  annotate("text", x = 100, y = 0.02, label = "Normal", color = "darkgreen", size = 4, fontface = 3) +
  annotate("text", x = 112.5, y = 0.018, label = "Prediabetes", color = "orange", size = 4, fontface = 3
  annotate("text", x = 150, y = 0.016, label = "Diabetes", color = "red", size = 4, fontface = 3) +
  geom_vline(xintercept = c(100, 126), color = "gray", linetype = "longdash", size = 0.5) +
  scale_x_continuous(breaks = seq(50, 300, by = 50), limits = c(50, 300)) +
  theme_minimal()+
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



As we can see, the graph confirms our findings from the frequency tables we had above. The distribution is not normal and heavily skewed to the right due to extreme values of Glucose level.

```
skewness(stroke_data$avg_glucose_level)
```

```
## [1] 1.614619
```

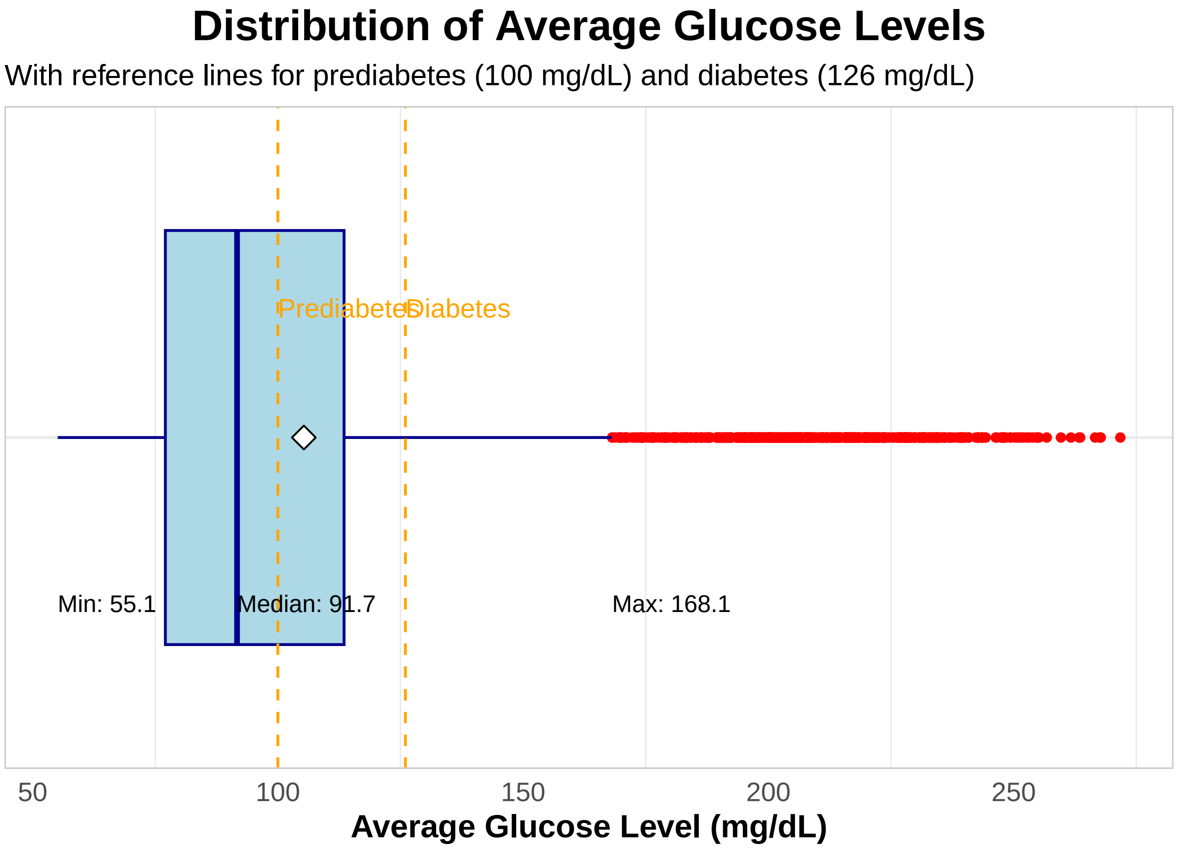
```
kurtosis(stroke_data$avg_glucose_level)
```

```
## [1] 1.907085
```

The value of Skewness also confirms this substantial right skew. This suggests a long tail on the right side of the distribution, indicating the presence of some very high glucose values that are pulling the mean higher than the median.

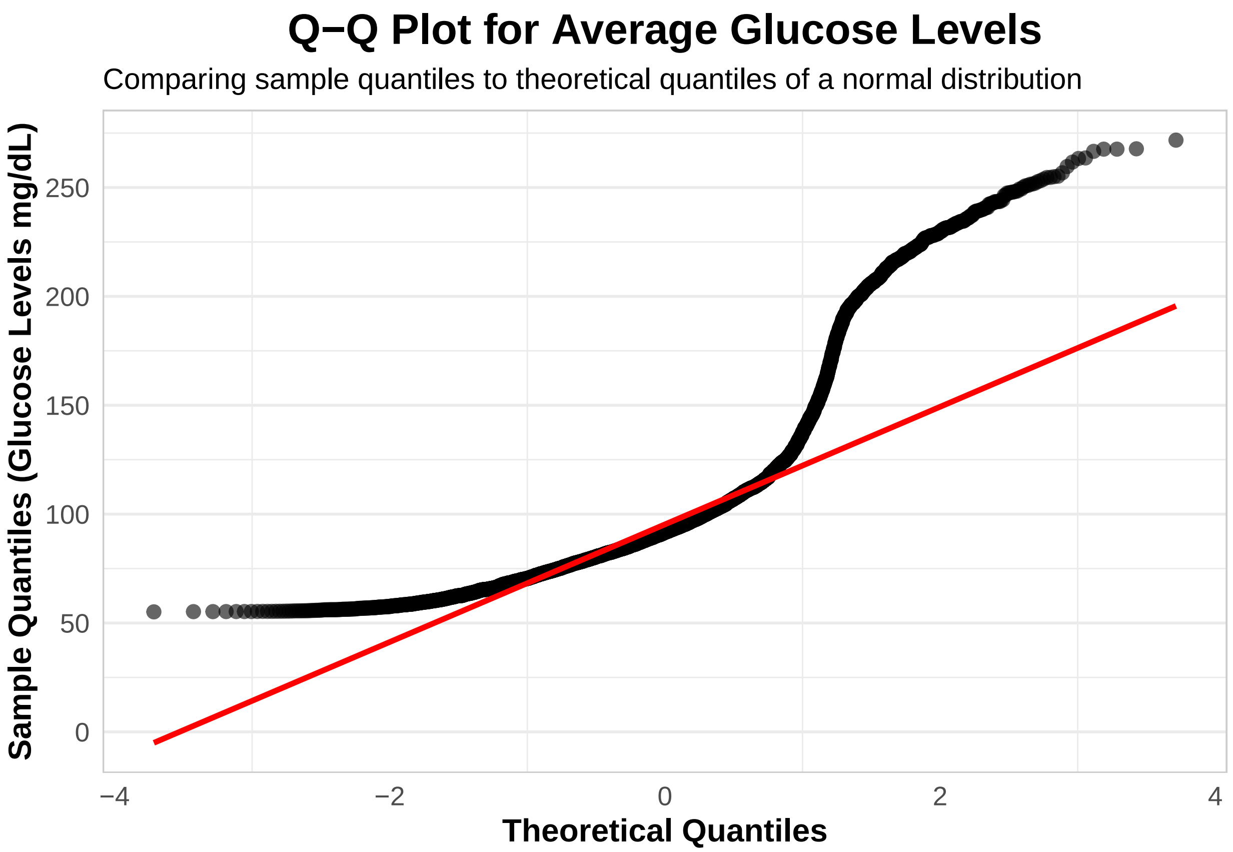
The positive value of Kurtosis also confirms that the distribution has more extreme values (in the tails) than a normal distribution would. Our value of 1.907085 suggests the distribution has heavier tails and a higher, sharper peak compared to a normal distribution.

```
# Calculate summary statistics
q1 <- quantile(stroke_data$avg_glucose_level, 0.25)
q3 <- quantile(stroke_data$avg_glucose_level, 0.75)
iqr <- q3 - q1
lower_whisker <- max(min(stroke_data$avg_glucose_level), q1 - 1.5 * iqr)
upper_whisker <- min(max(stroke_data$avg_glucose_level), q3 + 1.5 * iqr)

ggplot(stroke_data, aes(y = avg_glucose_level, x = "")) +
  geom_boxplot(fill = "lightblue", color = "darkblue", outlier.colour = "red", outlier.shape = 16) +
  stat_summary(fun = mean, geom = "point", shape = 23, size = 3, fill = "white") +  # Add mean point
  geom_hline(yintercept = c(100, 126), linetype = "dashed", color = "orange", size = 0.5) +  # Add refe
  scale_y_continuous(breaks = seq(0, 300, by = 50)) +
  coord_flip() +  # Flip coordinates for horizontal boxplot
  labs(
    title = "Distribution of Average Glucose Levels",
    subtitle = "With reference lines for prediabetes (100 mg/dL) and diabetes (126 mg/dL)",
    x = "",
    y = "Average Glucose Level (mg/dL)"
  ) +
  annotate("text", x = 1.2, y = c(100, 126), label = c("Prediabetes", "Diabetes"),
           hjust = 0, vjust = -0.5, color = "orange", size = 3.5) +
  annotate("text", x = 0.7, y = lower_whisker, label = paste("Min:", round(lower_whisker, 1)),
           hjust = 0, size = 3) +
  annotate("text", x = 0.7, y = upper_whisker, label = paste("Max:", round(upper_whisker, 1)),
           hjust = 0, size = 3) +
  annotate("text", x = 0.7, y = median(stroke_data$avg_glucose_level),
           label = paste("Median:", round(median(stroke_data$avg_glucose_level), 1)),
           hjust = 0, size = 3) +
  theme_minimal()+
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



The box plot also confirms our findings that there is a concentration of values around the peak (likely in the normal glucose range) with a notable number of extreme values (likely in the diabetic range).

```
ggplot(stroke_data, aes(sample = avg_glucose_level)) +
  stat_qq(size = 2, alpha = 0.6) +
  stat_qq_line(color = "red", size = 1) +
  labs(
    title = "Q-Q Plot for Average Glucose Levels",
    subtitle = "Comparing sample quantiles to theoretical quantiles of a normal distribution",
    x = "Theoretical Quantiles",
    y = "Sample Quantiles (Glucose Levels mg/dL)"
  ) +
  scale_y_continuous(breaks = seq(0, 300, by = 50)) +
  theme_minimal() +
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



This Q-Q plot also confirms that the average Glucose levels do not follow a normal distribution and are heavily skewed to the right.

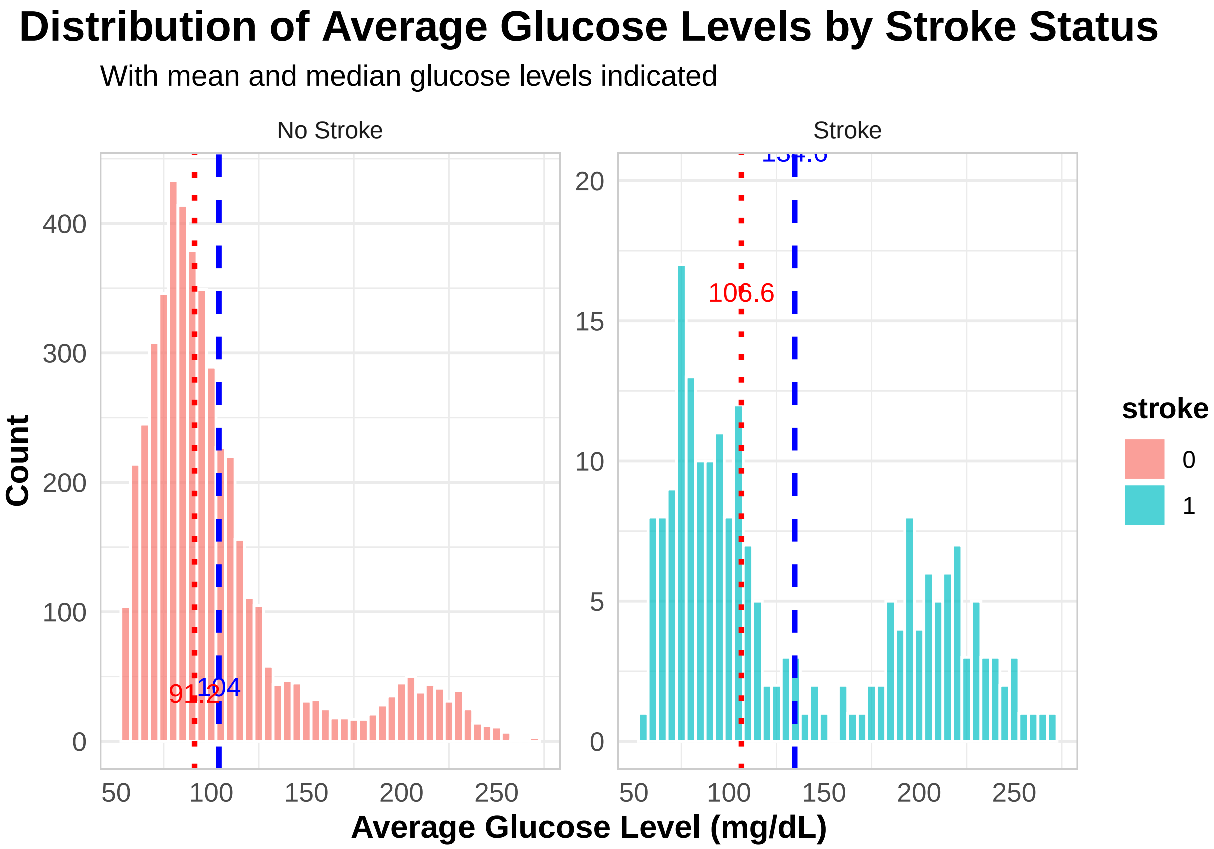
```
# categorize glucose levels
dataG <- stroke_data %>%
  mutate(glucose_category = case_when(
    avg_glucose_level < 100 ~ "Normal",
    avg_glucose_level >= 100 & avg_glucose_level < 126 ~ "Prediabetes",
    avg_glucose_level >= 126 ~ "Diabetes"
  ))

# Now summarize mean glucose levels by category and stroke
data_sub_glucose_cat <- dataG %>%
  group_by(glucose_category, stroke) %>%
  summarise(mean = mean(avg_glucose_level), .groups = "drop")

# Print the summary
pander(data_sub_glucose_cat)
```

Avg. Glucose levels with stroke

glucose_category	stroke	mean
Diabetes	0	183.5
Diabetes	1	202
Normal	0	79.49
Normal	1	79.21
Prediabetes	0	110.6
Prediabetes	1	109.7

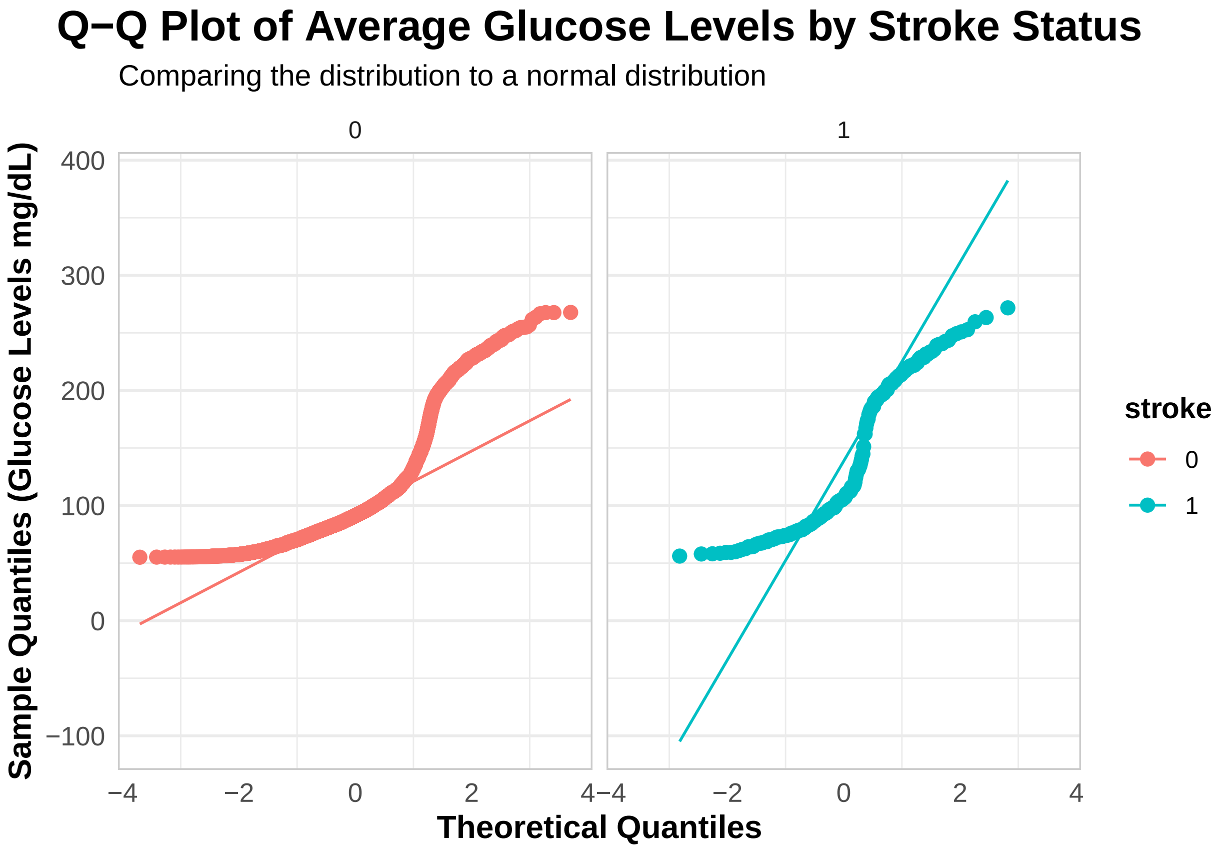
From the table, we can see that the most significant difference is in the Diabetes category, where those with stroke had substantially higher mean glucose levels. In the Normal and Prediabetes categories, there is minimal difference between stroke and no-stroke groups. The data suggests that very high glucose levels (Diabetes range) may be associated with increased stroke risk.

```
stats_glucose <- stroke_data %>%
  group_by(stroke) %>%
  summarise(mean_glucose = mean(avg_glucose_level, na.rm = TRUE),
            median_glucose = median(avg_glucose_level, na.rm = TRUE))

ggplot(stroke_data, aes(x = avg_glucose_level, fill = stroke)) +
  geom_histogram(binwidth = 5, color = "white", alpha = 0.7) +
geom_vline(data = stats_glucose, aes(xintercept = mean_glucose),
             linetype = "dashed", color = "blue", size = 1) +
    geom_vline(data = stats_glucose, aes(xintercept = median_glucose),
             linetype = "dotted", color = "red", size = 1) +
  facet_wrap(~stroke, scales = "free_y",
             labeller = labeller(stroke = c("0" = "No Stroke", "1" = "Stroke")))  +
  labs(
    title = "Distribution of Average Glucose Levels by Stroke Status",
    subtitle = "With mean and median glucose levels indicated",
    x = "Average Glucose Level (mg/dL)",
    y = "Count"
  ) +
  geom_text(data = stats_glucose, aes(x = mean_glucose, y = 20, label = round(mean_glucose, 1)),
            vjust = -1, color = "blue", size = 3.5) +
  geom_text(data = stats_glucose, aes(x = median_glucose, y = 15, label = round(median_glucose, 1)),
            vjust = -1, color = "red", size = 3.5) +
  theme_minimal()+
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



As we can see, On average, those who had a stroke have significantly higher glucose levels (mean: 134.68 mg/dL) compared to those without a stroke (mean: 104 mg/dL). A higher proportion of stroke patients fall into the prediabetes and diabetes ranges, as indicated by the clinical thresholds. This suggests a potential association between elevated glucose levels and stroke occurrence.

```r
ggplot(stroke_data, aes(sample = avg_glucose_level, color = stroke)) +
  stat_qq(size = 2) +
  stat_qq_line() +
  facet_wrap(~stroke) +
  labs(
    title = "Q-Q Plot of Average Glucose Levels by Stroke Status",
    subtitle = "Comparing the distribution to a normal distribution",
    x = "Theoretical Quantiles",
    y = "Sample Quantiles (Glucose Levels mg/dL)"
  ) +
  theme_minimal()+
        theme(
    plot.title = element_text(hjust = 0.5, face = "bold", size = 16),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



From these two Q-Q plots, we can observe that for both groups, the points deviate from the diagonal line, indicating that the glucose levels do not follow a normal distribution. In addition, the deviation is more pronounced in the stroke group, where higher glucose levels show a greater departure from normality, particularly in the upper quantiles.This suggests that the stroke group has a higher concentration of extreme glucose values compared to the no-stroke group, further supporting the observed association between elevated glucose levels and stroke.

```
data_sub_glu_gd= stroke_data %>% group_by(gender,stroke) %>% summarise(mean_avg_glucose_level = mean(av
pander(data_sub_glu_gd)
```

Avg. Glucose levels with gender/Stroke

gender	stroke	mean_avg_glucose_level
Female	0	102.3
Female	1	126.2
Male	0	106.4
Male	1	145.8

From above, we can see the mean average glucose levels for males and females with and without a history of stroke. For both genders, individuals who have had a stroke exhibit significantly higher average glucose levels compared to those who have not. In particular, males with a stroke have the highest mean glucose level (145.85 mg/dL), followed by females with a stroke (126.21 mg/dL). Males without a stroke have a slightly higher mean glucose level (106.39 mg/dL) compared to females without a stroke (102.34 mg/dL).

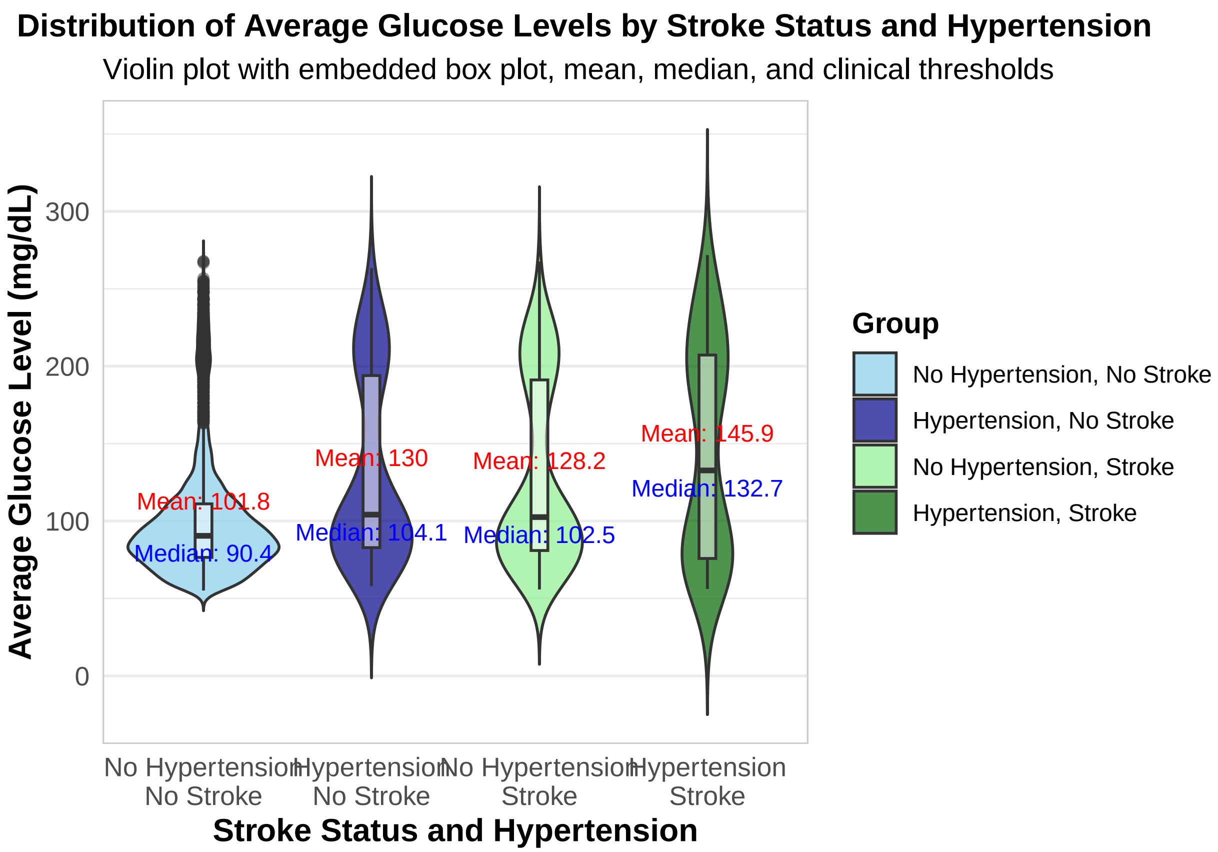
```
data_sub_glu_hyp= stroke_data %>% group_by(hypertension,stroke) %>% summarise(mean = mean(avg_glucose_l
pander(data_sub_glu_hyp)
```

Avg. Glucose levels with hypertension/Stroke

hypertension	stroke	mean
0	0	101.8
0	1	130
1	0	128.2
1	1	145.9

The data indicates that individuals with both hypertension and a history of stroke have the highest mean glucose level (145.90 mg/dL), followed by those with hypertension but no stroke (128.16 mg/dL). Individuals without hypertension who have had a stroke have a mean glucose level of 130.01 mg/dL, while those without hypertension or stroke have the lowest mean glucose level (101.80 mg/dL). These findings suggest that both hypertension and stroke are associated with elevated glucose levels.

```
# Calculate mean and median glucose levels for each group
summary_stats <- stroke_data %>%
  group_by(hypertension, stroke) %>%
  summarise(
    mean_glucose = mean(avg_glucose_level, na.rm = TRUE),
    median_glucose = median(avg_glucose_level, na.rm = TRUE),
    .groups = "drop"
  )

# Create the plot
ggplot(stroke_data, aes(x = interaction(stroke, hypertension), y = avg_glucose_level, fill = interactio
  geom_violin(trim = FALSE, alpha = 0.7) +
  geom_boxplot(width = 0.1, fill = "white", alpha = 0.5) +
  scale_fill_manual(values = c("0.0" = "skyblue", "0.1" = "lightgreen",
                               "1.0" = "darkblue", "1.1" = "darkgreen"),
                    labels = c("No Hypertension, No Stroke", "Hypertension, No Stroke",
                               "No Hypertension, Stroke", "Hypertension, Stroke")) +
  scale_x_discrete(labels = c("No Hypertension\nNo Stroke", "Hypertension\nNo Stroke",
                              "No Hypertension\nStroke", "Hypertension\nStroke")) +
  geom_text(data = summary_stats, aes(x = interaction(stroke, hypertension), y = mean_glucose,
                                      label = paste("Mean:", round(mean_glucose, 1))),
            position = position_dodge(width = 0.75), vjust = -0.5, color = "red", size = 3) +
  geom_text(data = summary_stats, aes(x = interaction(stroke, hypertension), y = median_glucose,
                                      label = paste("Median:", round(median_glucose, 1))),
            position = position_dodge(width = 0.75), vjust = 1.5, color = "blue", size = 3) +
  labs(
    title = "Distribution of Average Glucose Levels by Stroke Status and Hypertension",
    subtitle = "Violin plot with embedded box plot, mean, median, and clinical thresholds",
    x = "Stroke Status and Hypertension",
    y = "Average Glucose Level (mg/dL)",
    fill = "Group"
  ) +
  theme_minimal()+
        theme(
    plot.title = element_text(hjust = 0.2, face = "bold", size = 12),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.title = element_text(face = "bold"),
    legend.position = "right",
    panel.grid.major.x = element_blank(),
    panel.border = element_rect(fill = NA, color = "gray80")
  )
```



This violin plot shows the distribution of average glucose levels across four groups categorized by stroke status and hypertension. The group with neither hypertension nor stroke has the lowest median (90.4 mg/dL) and mean (101.8 mg/dL) glucose levels, both below the prediabetes threshold of 100 mg/dL. In contrast, the groups with hypertension (with or without stroke) exhibit significantly higher glucose levels. The group with both hypertension and stroke has the highest mean (145.9 mg/dL) and median (132.7 mg/dL), surpassing the diabetes threshold of 126 mg/dL. The data suggests that hypertension and stroke are associated with elevated glucose levels, with a clear increase in glucose levels as health conditions worsen.

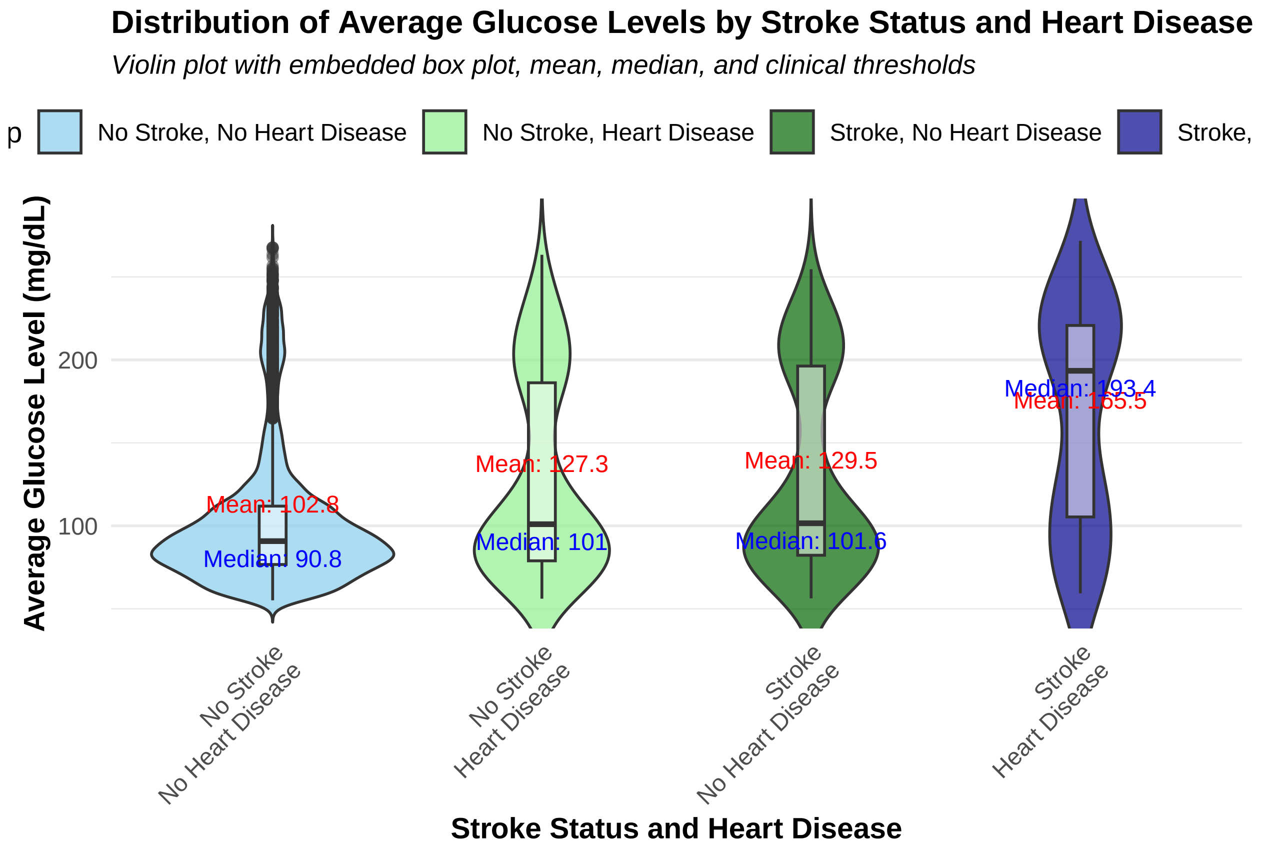
```
data_sub_glu_hd= stroke_data %>% group_by(heart_disease,stroke) %>% summarise(mean_glucose_level = mean
pander(data_sub_glu_hd)
```

Avg. Glucose levels with heart disease/Stroke

heart_disease	stroke	mean_glucose_level
0	0	102.8
0	1	127.3
1	0	129.5
1	1	165.5

We can observe that individuals with neither heart disease nor stroke have a mean glucose level of 102.85 mg/dL, which is below the prediabetes threshold. Those without heart disease but with a stroke have a higher mean glucose level of 127.26 mg/dL, approaching the diabetes threshold. For individuals with heart disease but no stroke, the mean glucose level is 129.46 mg/dL, exceeding the diabetes threshold. The highest glucose level, 165.46 mg/dL, is observed in individuals with both heart disease and stroke, indicating a strong association between these conditions and elevated glucose levels.

```r
summary_stats <- stroke_data %>%
  group_by(stroke, heart_disease) %>%
  summarise(
    mean_glucose = mean(avg_glucose_level, na.rm = TRUE),
    median_glucose = median(avg_glucose_level, na.rm = TRUE),
    .groups = "drop"
  )

# Create the plot with corrected label order
ggplot(stroke_data, aes(x = interaction(stroke, heart_disease), y = avg_glucose_level, fill = interacti
  geom_violin(trim = FALSE, alpha = 0.7) +
  geom_boxplot(width = 0.1, fill = "white", alpha = 0.5) +
  scale_fill_manual(values = c("0.0" = "skyblue",    # No Stroke, No Heart Disease
                               "0.1" = "darkgreen",  # No Stroke, Heart Disease
                               "1.0" = "lightgreen", # Stroke, No Heart Disease
                               "1.1" = "darkblue"),  # Stroke, Heart Disease
                    labels = c("No Stroke, No Heart Disease",
                               "No Stroke, Heart Disease",
                               "Stroke, No Heart Disease",
                               "Stroke, Heart Disease")) +

  # Correct x-axis label order: "No Stroke" comes first
  scale_x_discrete(labels = c("No Stroke\nNo Heart Disease",
                              "No Stroke\nHeart Disease",
                              "Stroke\nNo Heart Disease",
                              "Stroke\nHeart Disease")) +

  geom_text(data = summary_stats, aes(x = interaction(stroke, heart_disease), y = mean_glucose,
                                      label = paste("Mean:", round(mean_glucose, 1))),
            position = position_dodge(width = 0.75), vjust = -0.5, color = "red", size = 3) +
  geom_text(data = summary_stats, aes(x = interaction(stroke, heart_disease), y = median_glucose,
                                      label = paste("Median:", round(median_glucose, 1))),
            position = position_dodge(width = 0.75), vjust = 1.5, color = "blue", size = 3) +
  labs(
    title = "Distribution of Average Glucose Levels by Stroke Status and Heart Disease",
    subtitle = "Violin plot with embedded box plot, mean, median, and clinical thresholds",
    x = "Stroke Status and Heart Disease",
    y = "Average Glucose Level (mg/dL)",
    fill = "Group"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 12),
    plot.subtitle = element_text(face = "italic", size = 10),
    axis.title = element_text(face = "bold"),
    legend.position = "top",
    axis.text.x = element_text(angle = 45, hjust = 1),
    panel.grid.major.x = element_blank()
  ) +
  coord_cartesian(ylim = c(50, max(stroke_data$avg_glucose_level, na.rm = TRUE) * 1.05))
```



From this violin plot we can see that, individuals without heart disease or stroke have the lowest mean glucose level at 102.8 mg/dL, which is just above the prediabetes threshold, and a median of 90.8 mg/dL, below the prediabetes threshold. The group with heart disease but no stroke has a higher mean glucose level of 127.3 mg/dL, approaching the diabetes threshold, and a median of 101 mg/dL. Individuals without heart disease but with a stroke have a mean glucose level of 129.5 mg/dL, exceeding the diabetes threshold, with a median of 101.6 mg/dL. Finally, the group with both heart disease and stroke shows the highest mean glucose level at 165.5 mg/dL and a median of 193.4 mg/dL, far exceeding the diabetes threshold.

```
data_sub_glu_em= stroke_data %>% group_by(ever_married,stroke) %>% summarise(mean = mean(avg_glucose_le
pander(data_sub_glu_em)
```

Avg. Glucose levels with ever married/Stroke

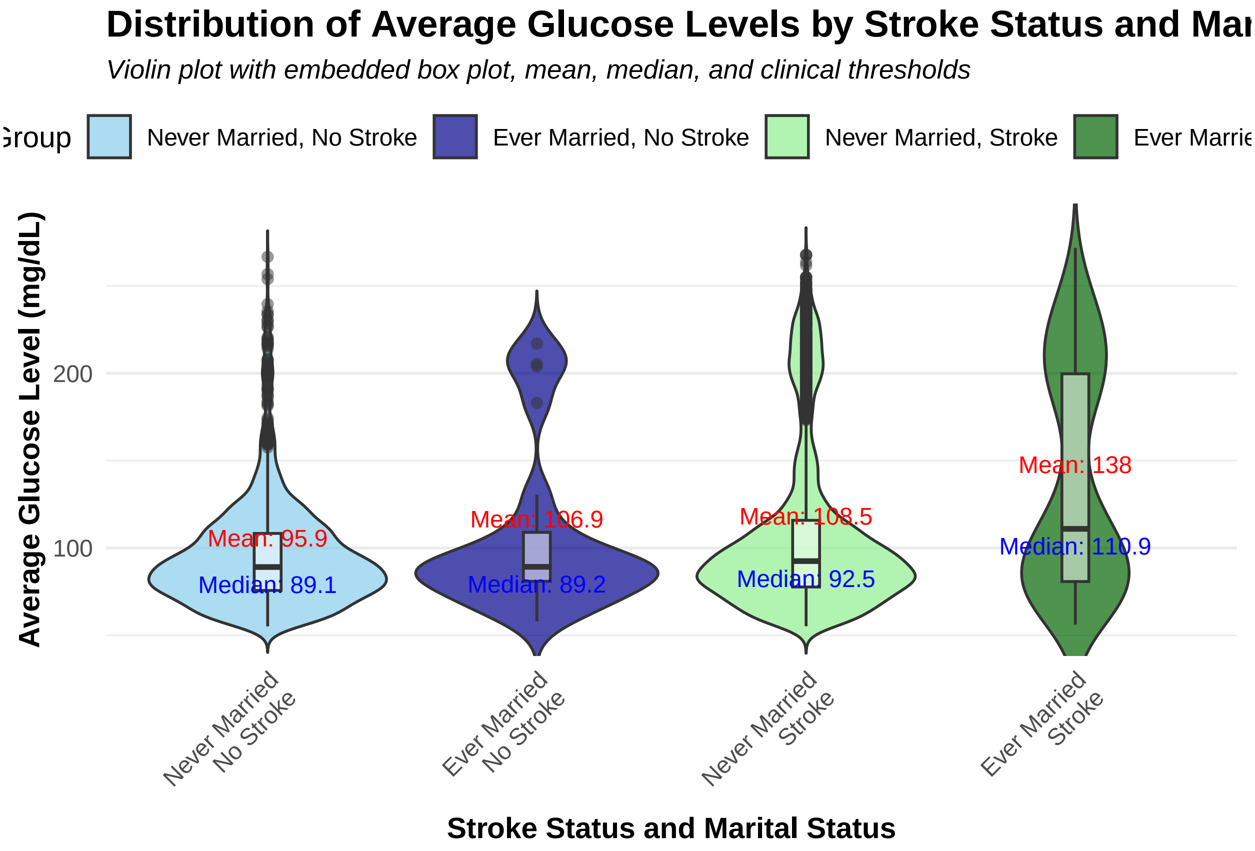
ever_married	stroke	mean
No	0	95.91
No	1	106.9
Yes	0	108.5
Yes	1	138

Based on the table:

1. Not married, no stroke individuals have an average glucose level of 95.91 mg/dL, which is below the prediabetes threshold.
2. Not married, stroke individuals show a higher mean glucose level of 106.86 mg/dL, which exceeds the prediabetes threshold.
3. Married, no stroke individuals have a mean glucose level of 108.50 mg/dL, also above the prediabetes threshold.
4. Married, stroke individuals exhibit the highest mean glucose level of 138 mg/dL, which is above the diabetes threshold.

This suggests that both marital status and stroke occurrence are associated with elevated glucose levels, with married individuals, especially those who have had a stroke, showing the highest average glucose levels.

```r
# Calculate mean and median glucose levels for each group
summary_stats <- stroke_data %>%
  group_by(ever_married, stroke) %>%
  summarise(
    mean_glucose = mean(avg_glucose_level, na.rm = TRUE),
    median_glucose = median(avg_glucose_level, na.rm = TRUE),
    .groups = "drop"
  )

ggplot(stroke_data, aes(x = interaction(stroke, ever_married), y = avg_glucose_level, fill = interactio
  geom_violin(trim = FALSE, alpha = 0.7) +
  geom_boxplot(width = 0.1, fill = "white", alpha = 0.5) +
  scale_fill_manual(values = c("0.No" = "skyblue",
                               "0.Yes" = "lightgreen",
                               "1.No" = "darkblue",
                               "1.Yes" = "darkgreen"),
                    labels = c("Never Married, No Stroke",
                               "Ever Married, No Stroke",
                               "Never Married, Stroke",
                               "Ever Married, Stroke")) +

  scale_x_discrete(labels = c("Never Married\nNo Stroke",
                              "Ever Married\nNo Stroke",
                              "Never Married\nStroke",
                              "Ever Married\nStroke")) +
  geom_text(data = summary_stats, aes(x = interaction(stroke, ever_married), y = mean_glucose,
                                      label = paste("Mean:", round(mean_glucose, 1))),
            position = position_dodge(width = 0.75), vjust = -0.5, color = "red", size = 3) +
  geom_text(data = summary_stats, aes(x = interaction(stroke, ever_married), y = median_glucose,
                                      label = paste("Median:", round(median_glucose, 1))),
            position = position_dodge(width = 0.75), vjust = 1.5, color = "blue", size = 3) +

  labs(
    title = "Distribution of Average Glucose Levels by Stroke Status and Marital Status",
    subtitle = "Violin plot with embedded box plot, mean, median, and clinical thresholds",
    x = "Stroke Status and Marital Status",
    y = "Average Glucose Level (mg/dL)",
    fill = "Group"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 10),
    axis.title = element_text(face = "bold"),
    legend.position = "top",
    axis.text.x = element_text(angle = 45, hjust = 1),
    panel.grid.major.x = element_blank()
  ) +

  coord_cartesian(ylim = c(50, max(stroke_data$avg_glucose_level, na.rm = TRUE) * 1.05))
```



1. Never married, no stroke individuals have a mean glucose level of 95.9 mg/dL, just below the prediabetes threshold, and a median of 89.10 mg/dL, suggesting relatively normal glucose levels.

2. Ever married, no stroke individuals have a higher mean glucose level of 106.9 mg/dL, slightly above the prediabetes threshold, and a median of 89.2 mg/dL.

3. Never married, stroke individuals show an elevated mean glucose level of 108.5 mg/dL, also above the prediabetes threshold, and a median of 92.5 mg/dL.
4. Ever married, stroke individuals have the highest mean glucose level of 138 mg/dL, above the diabetes threshold, and a median of 110.9 mg/dL.

Those who have experienced a stroke, regardless of marital status, tend to have higher glucose levels, with the "ever married, stroke" group showing the highest risk, as their glucose levels exceed the diabetes threshold.

```

data_sub_glu_wt= stroke_data %>% group_by(work_type,stroke) %>% summarise(mean = mean(avg_glucose_level
pander(data_sub_glu_wt)
```

Avg. Glucose levels with work type/Stroke

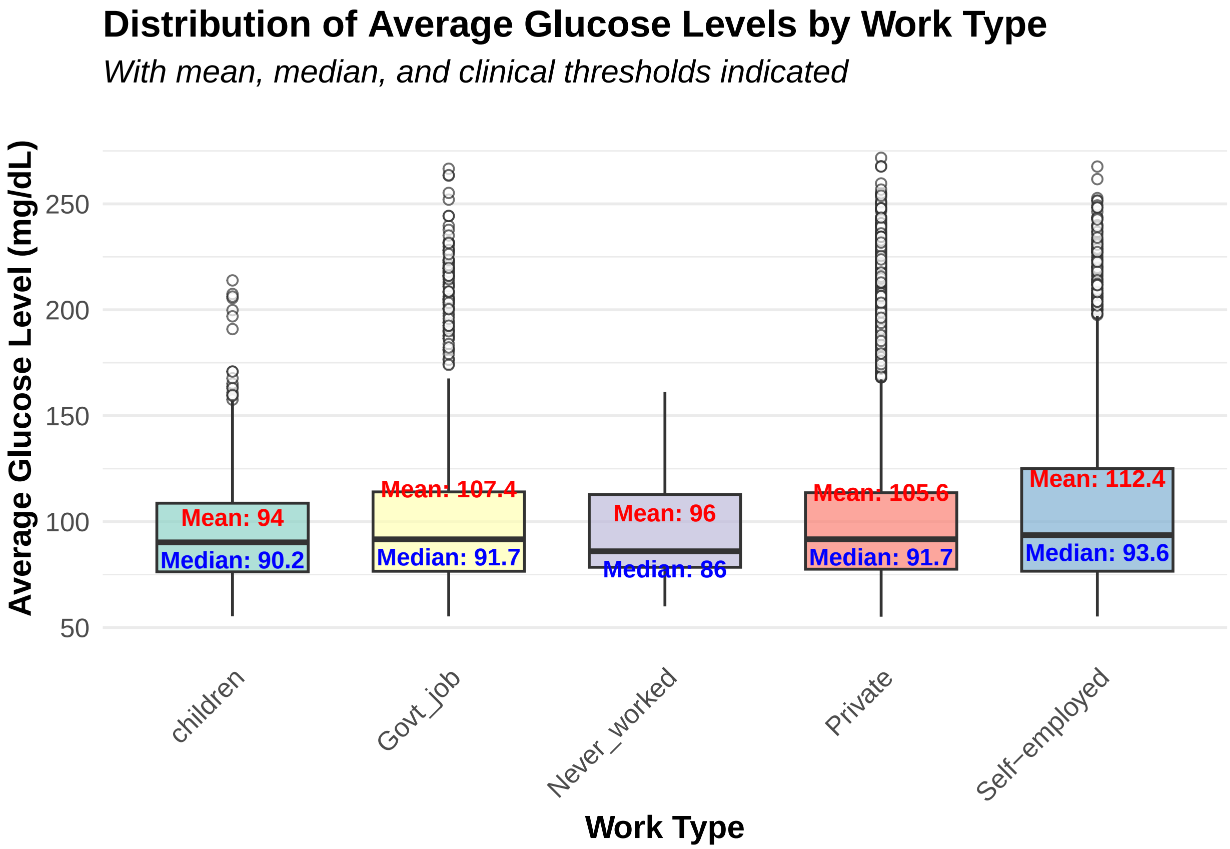
work_type	stroke	mean
children	0	94.06
children	1	57.93
Govt_job	0	106
Govt_job	1	137.3
Never_worked	0	96.04
Private	0	104.1
Private	1	139.3
Self-employed	0	111.6
Self-employed	1	123.2

1. Children type without a stroke have a mean glucose level of 94.01 mg/dL, while those with a stroke have significantly lower levels, at 57.93.2 mg/dL, likely due to the small sample size in this group.
2. Government job workers without a stroke have a mean glucose level of 105.96 mg/dL, which rises to 137.3 mg/dL for those with a stroke.
3. Individuals who never worked show similar glucose levels to government job workers, with a mean of 96.04 mg/dL for those without a stroke.
4. Private sector workers without a stroke have a mean glucose level of 104.05 mg/dL, while those with a stroke have a much higher mean at 139.32 mg/dL.
5. Self-employed individuals have a mean glucose level of 111.59 mg/dL without a stroke, which increases to 123.20 mg/dL in those who have had a stroke.

This data suggests that individuals in government jobs, the private sector, and self-employed groups with a stroke tend to have the highest glucose levels.

```
# Calculate summary statistics
summary_stats <- stroke_data %>%
  group_by(work_type) %>%
  summarise(
    mean_glucose = mean(avg_glucose_level, na.rm = TRUE),
    median_glucose = median(avg_glucose_level, na.rm = TRUE),
    .groups = "drop"
```

```r
  )

ggplot(stroke_data, aes(x = work_type, y = avg_glucose_level, fill = work_type)) +
  geom_boxplot(width = 0.7, alpha = 0.7, outlier.shape = 21, outlier.fill = "white") +
  scale_fill_brewer(palette = "Set3") +
  scale_y_continuous(breaks = seq(0, 300, by = 50)) +
  labs(
    title = "Distribution of Average Glucose Levels by Work Type",
    subtitle = "With mean, median, and clinical thresholds indicated",
    x = "Work Type",
    y = "Average Glucose Level (mg/dL)",
    fill = "Work Type"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 12),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    axis.text.x = element_text(angle = 45, hjust = 1),
    legend.position = "none",
    panel.grid.major.x = element_blank()
  ) +
  geom_text(data = summary_stats, aes(x = work_type, y = mean_glucose,
                                     label = paste("Mean:", round(mean_glucose, 1))),
            color = "red", vjust = -0.5, size = 3, fontface = "bold") +
  geom_text(data = summary_stats, aes(x = work_type, y = median_glucose,
                                     label = paste("Median:", round(median_glucose, 1))),
            color = "blue", vjust = 1.5, size = 3, fontface = "bold") +
  coord_cartesian(ylim = c(50, max(stroke_data$avg_glucose_level, na.rm = TRUE) * 1.05))
```



From this plot, we can observe that:

```
- Poeple whose work involve children have the lowest glucose levels, with a mean of 94 mg/dL and a media
- Government job workers have a mean glucose level of 107.4 mg/dL, slightly above the prediabetes thres
-Those who never worked show a mean glucose level of 96 mg/dL, just below the prediabetes threshold, wi
- Private sector workers have a mean glucose level of 105.6 mg/dL, slightly above the prediabetes thres
- Self-employed individuals show the highest glucose levels, with a mean of 112.4 mg/dL, well above the
```

The self-employed and government job workers show elevated glucose levels compared to the other groups, suggesting a higher risk of prediabetes or diabetes.

```
data_sub_glu_rt= stroke_data %>% group_by(Residence_type,stroke) %>% summarise(mean = mean(avg_glucose_
pander(data_sub_glu_rt)
```

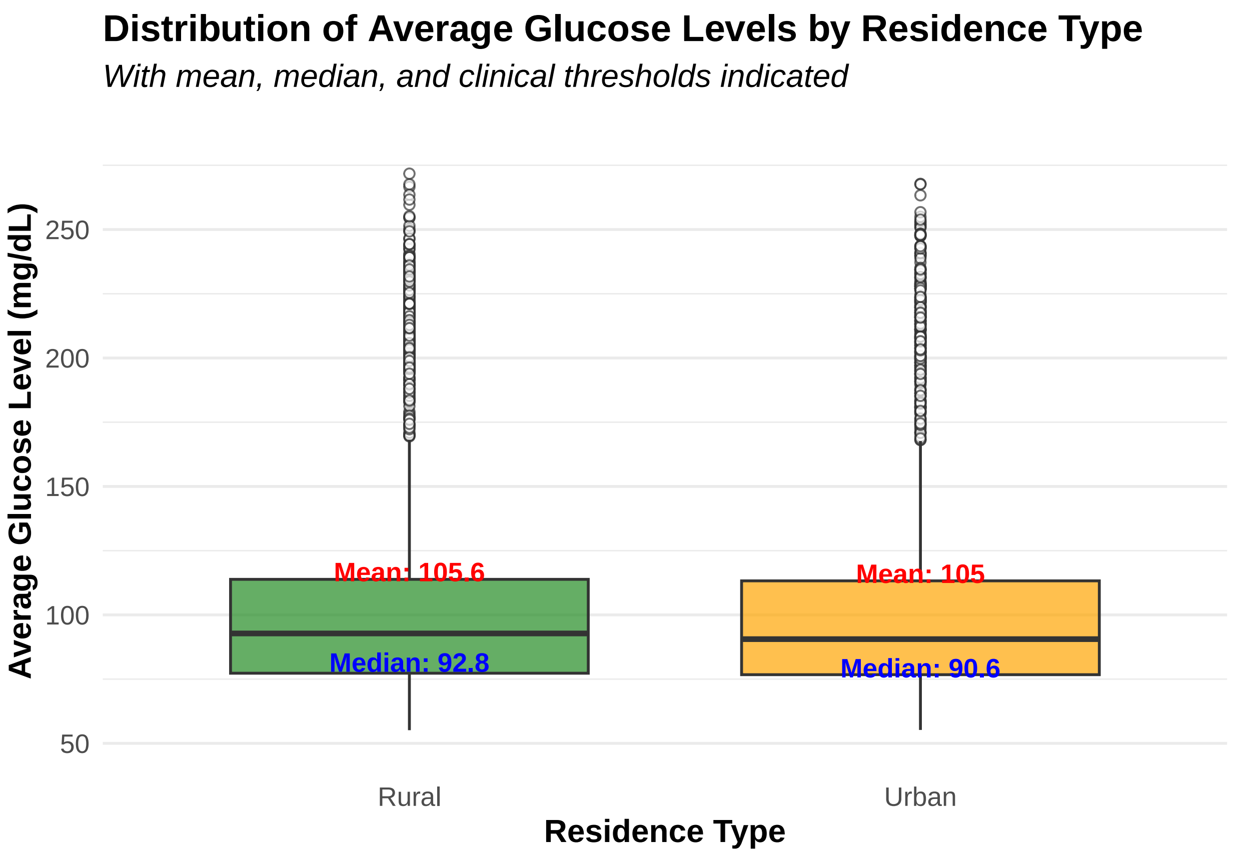
Avg. Glucose levels with resident type/Stroke

Residence_type	stroke	mean
Rural	0	104.5
Rural	1	132.5
Urban	0	103.5
Urban	1	136.5

This tells us that in rural areas, individuals without a stroke have a mean glucose level of 104.47 mg/dL, while those with a stroke show significantly higher glucose levels at 132.51 mg/dL.

For urban residents, those without a stroke have a mean glucose level of 103.53 mg/dL, similar to rural residents without a stroke. However, urban individuals with a stroke exhibit the highest mean glucose levels at 136.46 mg/dL.

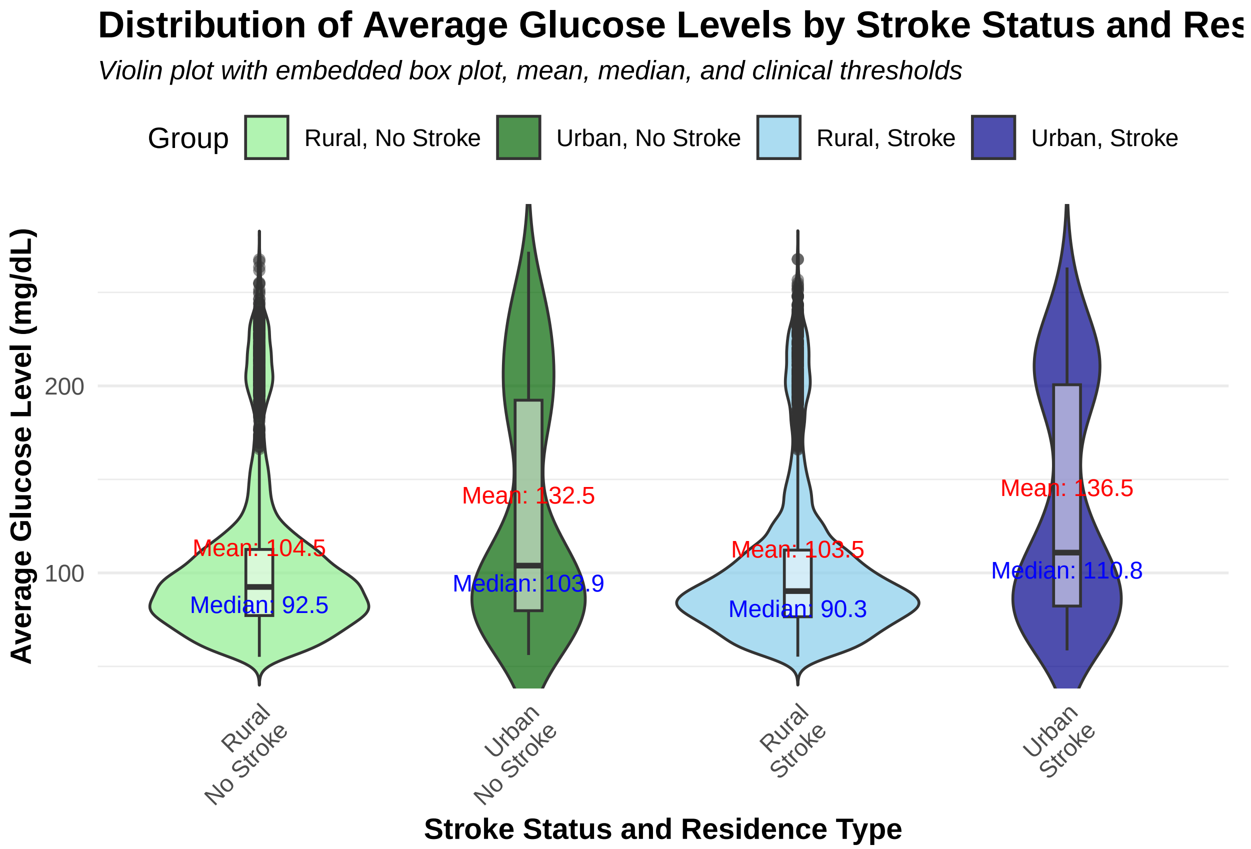
```r
# Calculate summary statistics
summary_stats <- stroke_data %>%
  group_by(Residence_type) %>%
  summarise(
    mean_glucose = mean(avg_glucose_level, na.rm = TRUE),
    median_glucose = median(avg_glucose_level, na.rm = TRUE),
    .groups = "drop"
  )

ggplot(stroke_data, aes(x = Residence_type, y = avg_glucose_level, fill = Residence_type)) +
  geom_boxplot(width = 0.7, alpha = 0.7, outlier.shape = 21, outlier.fill = "white") +
  scale_fill_manual(values = c("Rural" = "forestgreen", "Urban" = "orange")) +
  scale_y_continuous(breaks = seq(0, 300, by = 50)) +
  labs(
    title = "Distribution of Average Glucose Levels by Residence Type",
    subtitle = "With mean, median, and clinical thresholds indicated",
    x = "Residence Type",
    y = "Average Glucose Level (mg/dL)",
    fill = "Residence Type"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 12),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.position = "none",
    panel.grid.major.x = element_blank()
  ) +
  geom_text(data = summary_stats, aes(x = Residence_type, y = mean_glucose,
                                     label = paste("Mean:", round(mean_glucose, 1))),
            color = "red", vjust = -1, size = 3.5, fontface = "bold") +
  geom_text(data = summary_stats, aes(x = Residence_type, y = median_glucose,
                                     label = paste("Median:", round(median_glucose, 1))),
            color = "blue", vjust = 2, size = 3.5, fontface = "bold") +
  coord_cartesian(ylim = c(50, max(stroke_data$avg_glucose_level, na.rm = TRUE) * 1.05))
```



For rural residents, the mean glucose level is 105.6 mg/dL, slightly above the prediabetes threshold, while the median is 92.8 mg/dL, suggesting that the majority of individuals in this group have normal glucose levels, but some outliers raise the mean.

For urban residents, the mean glucose level is 105 mg/dL, very similar to the rural group, and also above the prediabetes threshold. The median glucose level is 90.6 mg/dL, which is slightly lower than the rural group's median.

```
summary_stats <- stroke_data %>%
  group_by(Residence_type, stroke) %>%
  summarise(
    mean_glucose = mean(avg_glucose_level, na.rm = TRUE),
    median_glucose = median(avg_glucose_level, na.rm = TRUE),
    .groups = "drop"
  )

ggplot(stroke_data, aes(x = interaction(stroke, Residence_type), y = avg_glucose_level, fill = interacti
  geom_violin(trim = FALSE, alpha = 0.7) +
  geom_boxplot(width = 0.1, fill = "white", alpha = 0.5) +
  scale_fill_manual(values = c("0.Rural" = "lightgreen",
                               "0.Urban" = "skyblue",
                               "1.Rural" = "darkgreen",
                               "1.Urban" = "darkblue"),
                    labels = c("Rural, No Stroke", "Urban, No Stroke",
                               "Rural, Stroke", "Urban, Stroke")) +
  scale_x_discrete(labels = c("Rural\nNo Stroke", "Urban\nNo Stroke",
                              "Rural\nStroke", "Urban\nStroke")) +
  geom_text(data = summary_stats, aes(x = interaction(stroke, Residence_type), y = mean_glucose,
                                      label = paste("Mean:", round(mean_glucose, 1))),
            position = position_dodge(width = 0.75), vjust = -0.5, color = "red", size = 3) +
  geom_text(data = summary_stats, aes(x = interaction(stroke, Residence_type), y = median_glucose,
                                      label = paste("Median:", round(median_glucose, 1))),
            position = position_dodge(width = 0.75), vjust = 1.5, color = "blue", size = 3) +
  labs(
    title = "Distribution of Average Glucose Levels by Stroke Status and Residence Type",
    subtitle = "Violin plot with embedded box plot, mean, median, and clinical thresholds",
    x = "Stroke Status and Residence Type",
    y = "Average Glucose Level (mg/dL)",
    fill = "Group"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 10),
    axis.title = element_text(face = "bold"),
    legend.position = "top",
    axis.text.x = element_text(angle = 45, hjust = 1),
    panel.grid.major.x = element_blank()
  ) +
  coord_cartesian(ylim = c(50, max(stroke_data$avg_glucose_level, na.rm = TRUE) * 1.05))
```



This plot shows us that individuals living in rural areas without a stroke have a mean glucose level of 104.5 mg/dL, just above the prediabetes threshold, while their median glucose level is lower at 92.5 mg/dL. Urban residents without a stroke show higher glucose levels, with a mean of 132.5 mg/dL, which is well above the diabetes threshold, and a median of 103.9 mg/dL.

Among those with a stroke, rural residents have a mean glucose level of 103.5 mg/dL and a median of 90.3 mg/dL, suggesting slightly lower glucose levels compared to those without a stroke. In contrast, urban residents with a stroke exhibit the highest glucose levels, with a mean of 136.5 mg/dL and a median of 110.8 mg/dL, both above the diabetes threshold.

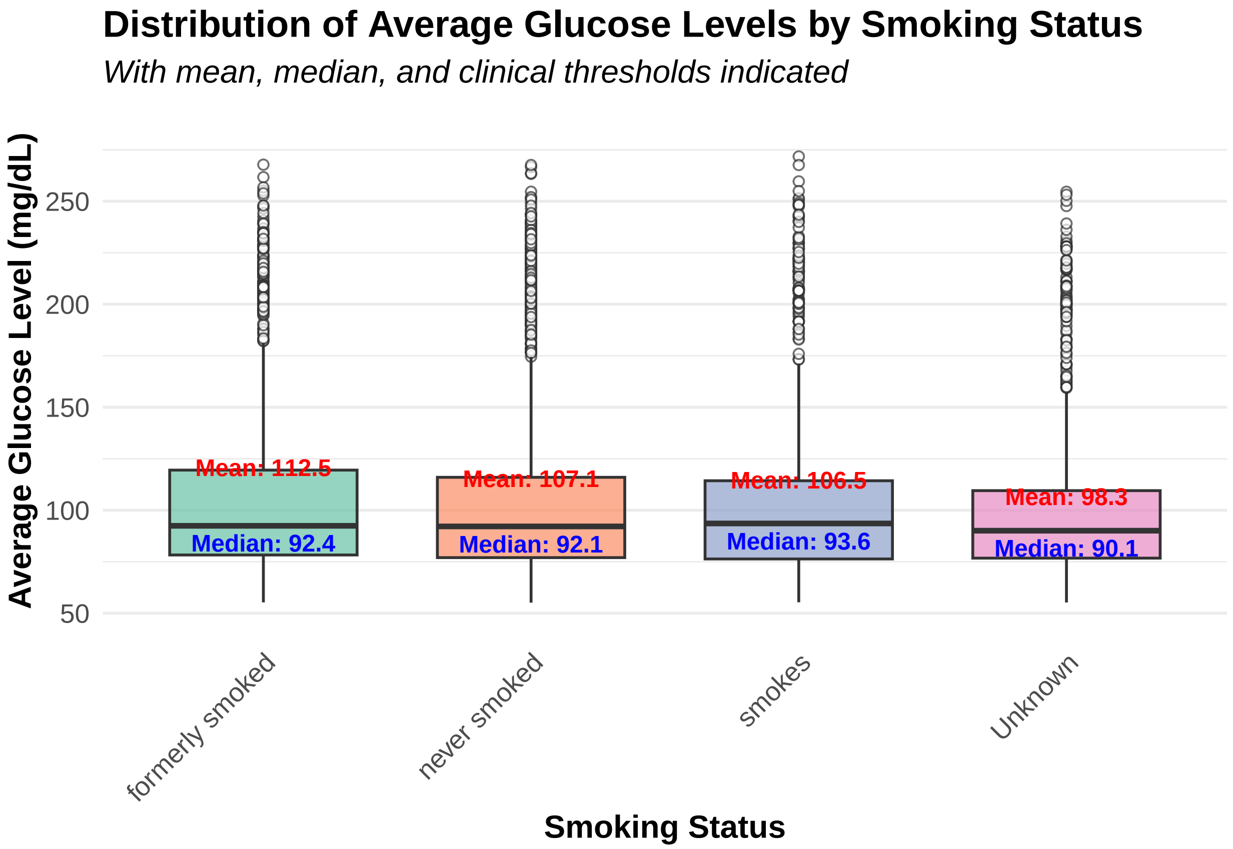
```
data_sub_glu_st= stroke_data %>% group_by(smoking_status,stroke) %>% summarise(mean = mean(avg_glucose_l
pander(data_sub_glu_st)
```

Avg. Glucose levels with smoking status/Stroke

smoking_status	stroke	mean
formerly smoked	0	110.6
formerly smoked	1	138.7
never smoked	0	105.9
never smoked	1	133.3
smokes	0	104.5
smokes	1	141.4
Unknown	0	97.89
Unknown	1	120.9

We can see that across all groups, individuals who have had a stroke tend to have higher glucose levels than those without a stroke. For example, former smokers with a stroke have higher glucose levels than those without a stroke, and a similar pattern is observed for those who never smoked or currently smoke. The highest glucose levels are seen in smokers who had a stroke, while those with an "unknown" smoking status and no stroke have the lowest glucose levels.

```
# Calculate summary statistics
summary_stats <- stroke_data %>%
  group_by(smoking_status) %>%
  summarise(
    mean_glucose = mean(avg_glucose_level, na.rm = TRUE),
    median_glucose = median(avg_glucose_level, na.rm = TRUE),
    .groups = "drop"
  )

ggplot(stroke_data, aes(x = smoking_status, y = avg_glucose_level, fill = smoking_status)) +
  geom_boxplot(width = 0.7, alpha = 0.7, outlier.shape = 21, outlier.fill = "white") +
  scale_fill_brewer(palette = "Set2") +
  scale_y_continuous(breaks = seq(0, 300, by = 50)) +
  labs(
    title = "Distribution of Average Glucose Levels by Smoking Status",
    subtitle = "With mean, median, and clinical thresholds indicated",
    x = "Smoking Status",
    y = "Average Glucose Level (mg/dL)",
    fill = "Smoking Status"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 12),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    axis.text.x = element_text(angle = 45, hjust = 1),
    legend.position = "none",
    panel.grid.major.x = element_blank()
  ) +
  geom_text(data = summary_stats, aes(x = smoking_status, y = mean_glucose,
                                      label = paste("Mean:", round(mean_glucose, 1))),
            color = "red", vjust = -0.5, size = 3, fontface = "bold") +
  geom_text(data = summary_stats, aes(x = smoking_status, y = median_glucose,
                                      label = paste("Median:", round(median_glucose, 1))),
            color = "blue", vjust = 1.5, size = 3, fontface = "bold") +
  coord_cartesian(ylim = c(50, max(stroke_data$avg_glucose_level, na.rm = TRUE) * 1.05))
```



For individuals who formerly smoked, the mean glucose level is 112.5 mg/dL, which is above the prediabetes threshold but below the diabetes threshold. The median is 92.4 mg/dL, indicating that many individuals in this group have glucose levels within a normal range, but some outliers raise the mean.

In the "never smoked" group, the mean glucose level is 107.1 mg/dL, still above the prediabetes threshold, with a median of 92.1 mg/dL. Similar to the "formerly smoked" group, most people have normal glucose levels, but the mean is influenced by higher values.

For current smokers, the mean glucose level is 106.5 mg/dL, with a median of 93.6 mg/dL. This group has slightly higher glucose levels compared to those who never smoked, again with outliers pushing the mean into the prediabetes range.

Individuals with an "unknown" smoking status have a mean glucose level of 98.3 mg/dL, below the prediabetes threshold, and a median of 90.1 mg/dL. This group appears to have lower glucose levels compared to the other categories, with both the mean and median closer to normal levels.

Age

The last variable that we consider is age.

```
summary(stroke_data$age)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.08   25.00   44.00   42.87   60.00   82.00
```

We can see that 1.The youngest individual is 0.08 years old (approximately 1 month). 2. 25% of the individuals are younger than 25 years. 3. The median age is 44 years, meaning that half of the individuals are younger than 45 and half are older. 4. The average age is 42.87 years, slightly lower than the median, indicating a small skew towards younger individuals. 5. 75% of the individuals are younger than 60 years. 6. The oldest individual is 82 years old.

This distribution suggests that the age variable is fairly spread out, with a slight skew towards younger ages. The majority of individuals are between 25 and 61 years old.

```
# Calculate frequency statistics for age
cat("More Statistics for Age:\n")
```

```
## More Statistics for Age:
```

```
age_stats = agricolae::stat.freq(a)
age_stats
```

```
## $variance
## [1] 508.1025
##
## $mean
## [1] 42.40831
##
## $median
## [1] 43.73278
##
## $mode
##      [- -]     mode
## [1,] 50 55 52.98165
```

```
cat("Skewness:", skewness(stroke_data$age), "\n")
```

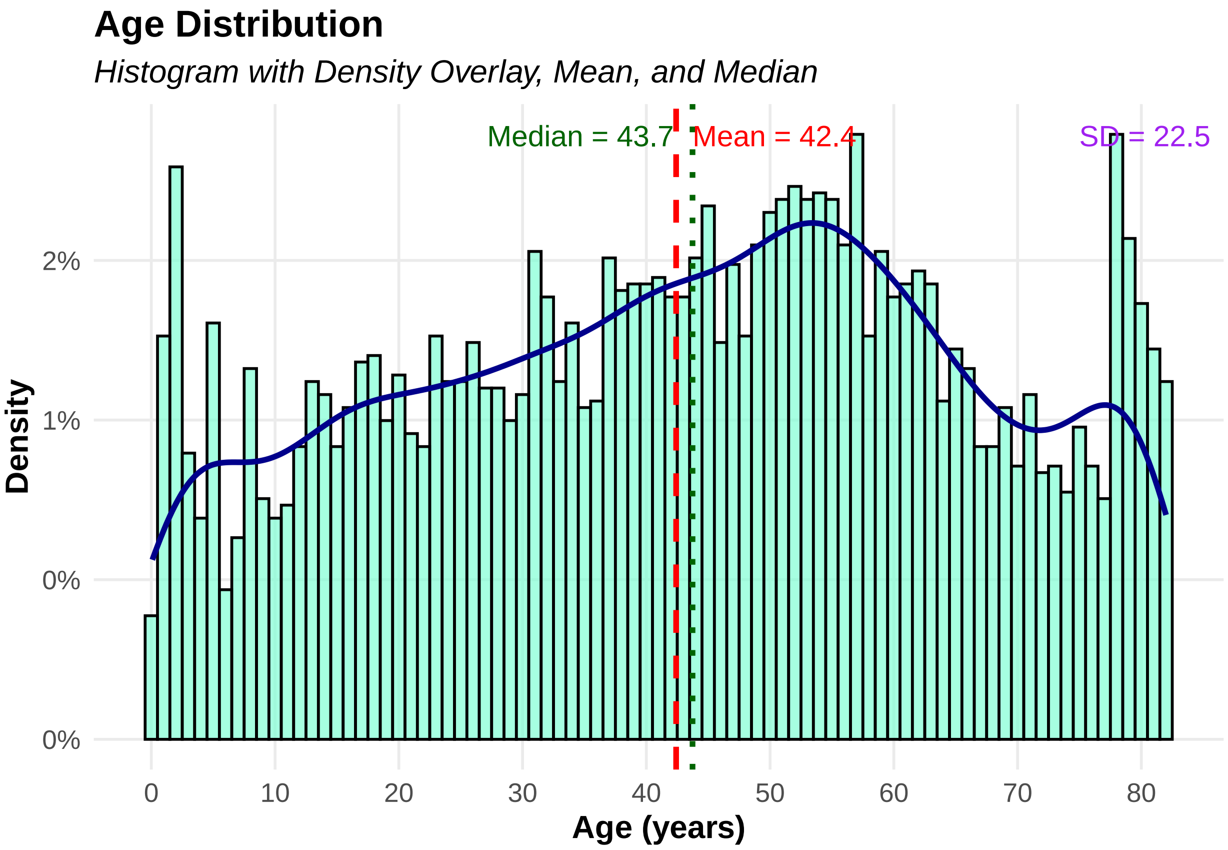
```
## Skewness: -0.1194497
```

```
cat("Kurtosis:", kurtosis(stroke_data$age), "\n")
```

```
## Kurtosis: -0.9880331
```

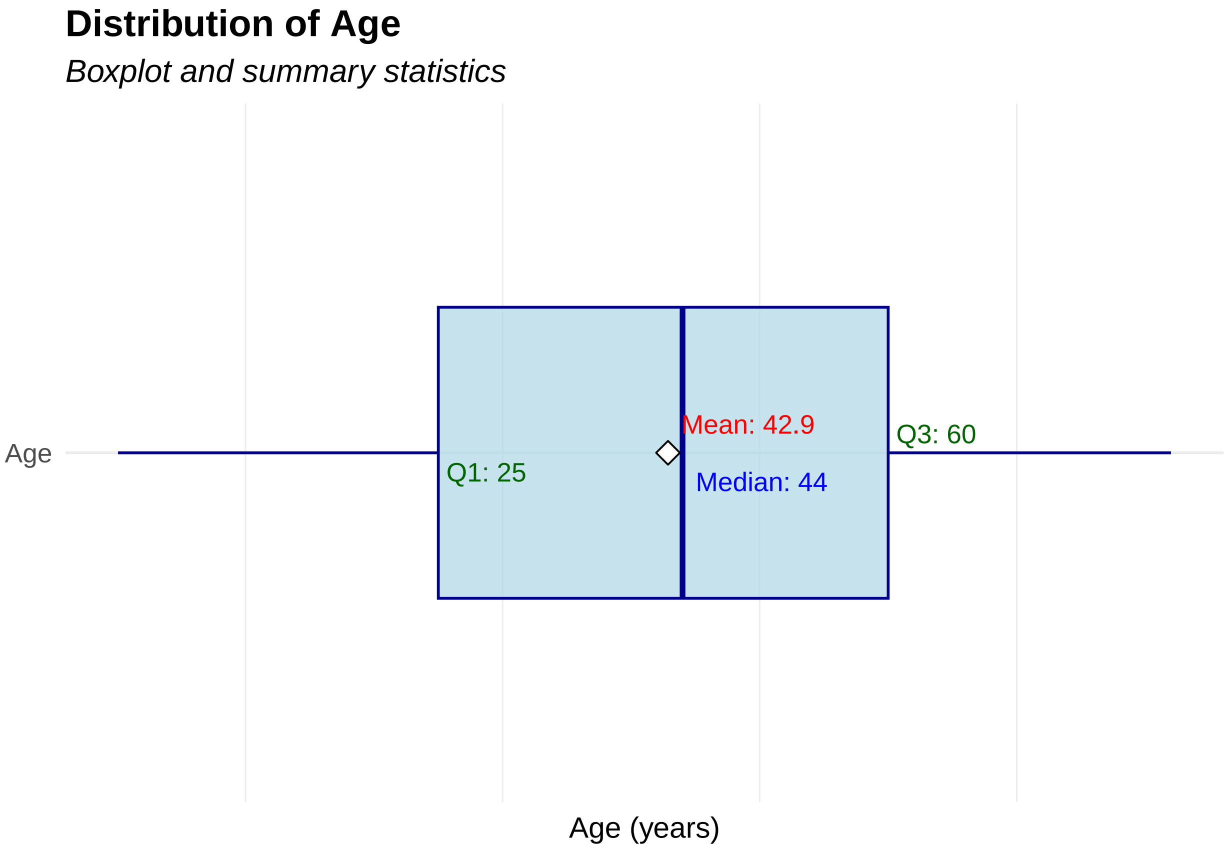
The most frequently occurring age is around 53 years. The skewness is -0.120, which is slightly negative. This suggests that the age distribution is slightly skewed to the left, indicating that there are slightly more older individuals pulling the distribution in that direction. The kurtosis is -0.99, his means the age distribution has lighter tails and a flatter peak compared to a normal distribution, suggesting fewer extreme values.

```r
# Calculate summary statistics
age_stats <- stroke_data %>%
  summarise(
    mean_age = mean(age, na.rm = TRUE),
    median_age = median(age, na.rm = TRUE),
    sd_age = sd(age, na.rm = TRUE)
  )

age_stats = agricolae::stat.freq(a)


ggplot(stroke_data, aes(x = age)) +
  # Histogram
  geom_histogram(aes(y = ..density..), binwidth = 1, fill = "aquamarine", color = "black", alpha = 0.7)
  # Density plot
  geom_density(color = "darkblue", size = 1) +
  # Mean line
  geom_vline(aes(xintercept = age_stats$mean), color = "red", linetype = "dashed", size = 1) +
  # Median line
  geom_vline(aes(xintercept = age_stats$median), color = "darkgreen", linetype = "dotted", size = 1) +
  # Annotations
  annotate("text", x = age_stats$mean, y = Inf, label = paste("Mean =", round(age_stats$mean, 1)),
           color = "red", vjust = 2, hjust = -0.1, size = 4) +
  annotate("text", x = age_stats$median, y = Inf, label = paste("Median =", round(age_stats$median, 1))
           color = "darkgreen", vjust = 2, hjust = 1.1, size = 4) +
  annotate("text", x = Inf, y = Inf,
           label = paste("SD =", round(sqrt(age_stats$variance), 1)),
           color = "purple", vjust = 2, hjust = 1.1, size = 4) +
  # Labels and title
  labs(
    title = "Age Distribution",
    subtitle = "Histogram with Density Overlay, Mean, and Median",
    x = "Age (years)",
    y = "Density"
  ) +
  # Theme customization
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 12),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    panel.grid.minor = element_blank()
  ) +
  # Scale customization
  scale_x_continuous(breaks = seq(0, max(stroke_data$age, na.rm = TRUE), by = 10)) +
  scale_y_continuous(labels = scales::percent_format(accuracy = 1))
```



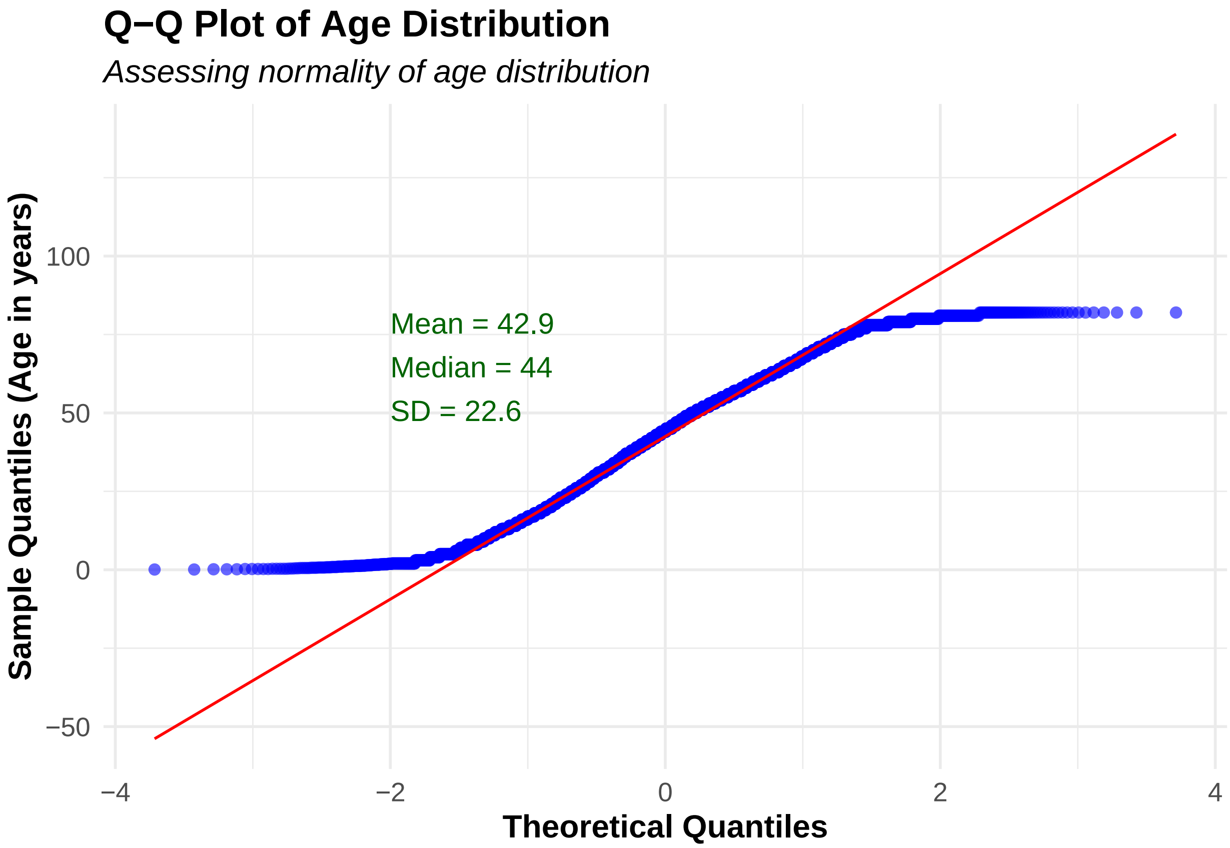
This density plot confirms our findings from earlier tables.This plot shows multiple peaks, with significant frequencies at various points such as early childhood (around 0-5 years) and older age groups (around 70-80 years). This multimodal characteristic is not typical of a normal distribution, which should be unimodal and bell-shaped. In addition, it has asymmetry, particularly with a longer tail on the right and The dispersion appears broader than what we would expect in a normal distribution, with a wide range of ages and a higher frequency in the older age groups.

```
# Calculate summary statistics
age_stats <- stroke_data %>%
  summarise(
    mean_age = mean(age, na.rm = TRUE),
    median_age = median(age, na.rm = TRUE),
    q1_age = quantile(age, 0.25, na.rm = TRUE),
    q3_age = quantile(age, 0.75, na.rm = TRUE)
  )

# Create the boxplot
ggplot(stroke_data, aes(x = "Age", y = age)) +
  geom_boxplot(fill = "lightblue", color = "darkblue", alpha = 0.7, width = 0.5) +
  stat_summary(fun = mean, geom = "point", shape = 23, size = 3, fill = "white") +
  geom_text(data = age_stats, aes(x = "Age", y = mean_age, label = paste("Mean:", round(mean_age, 1))),
            color = "red", vjust = -1, hjust = -0.1, size = 3.5) +
  geom_text(data = age_stats, aes(x = "Age", y = median_age, label = paste("Median:", median_age)),
            color = "blue", vjust = 2, hjust = -0.1, size = 3.5) +
  geom_text(data = age_stats, aes(x = "Age", y = q1_age, label = paste("Q1:", q1_age)),
            color = "darkgreen", vjust = 1.5, hjust = -0.1, size = 3.5) +
  geom_text(data = age_stats, aes(x = "Age", y = q3_age, label = paste("Q3:", q3_age)),
            color = "darkgreen", vjust = -0.5, hjust = -0.1, size = 3.5) +
  labs(
    title = "Distribution of Age",
    subtitle = "Boxplot and summary statistics",
    y = "Age (years)",
    x = NULL
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 12),
    axis.title.y = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    panel.grid.major.x = element_blank(),
    axis.text.x = element_blank(),
    axis.ticks.x = element_blank()
  ) +
  coord_flip()
```



As expected, The boxplot shows moderate spread in the data, with a few potential outliers on both sides of the whiskers. This confirms a wide age distribution, with a slight skew to the left.

```
# Calculate summary statistics
age_stats <- stroke_data %>%
  summarise(
    mean_age = mean(age, na.rm = TRUE),
    median_age = median(age, na.rm = TRUE),
    sd_age = sd(age, na.rm = TRUE)
  )

# Create the Q-Q plot
ggplot(stroke_data, aes(sample = age)) +
  stat_qq(color = "blue", alpha = 0.6) +
  stat_qq_line(color = "red") +
  labs(
    title = "Q-Q Plot of Age Distribution",
    subtitle = "Assessing normality of age distribution",
    x = "Theoretical Quantiles",
    y = "Sample Quantiles (Age in years)"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 12),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10)
  ) +
  annotate("text", x = -2, y = max(stroke_data$age, na.rm = TRUE),
           label = paste("Mean =", round(age_stats$mean_age, 1),
                         "\nMedian =", round(age_stats$median_age, 1),
                         "\nSD =", round(age_stats$sd_age, 1)),
           hjust = 0, vjust = 1, size = 4, color = "darkgreen")
```



From the Q-Q plot we can see that there are deviations at the tails with standard deviation of 22.6 years.

Which suggests a spread with some outliers, particularly in the higher age range.

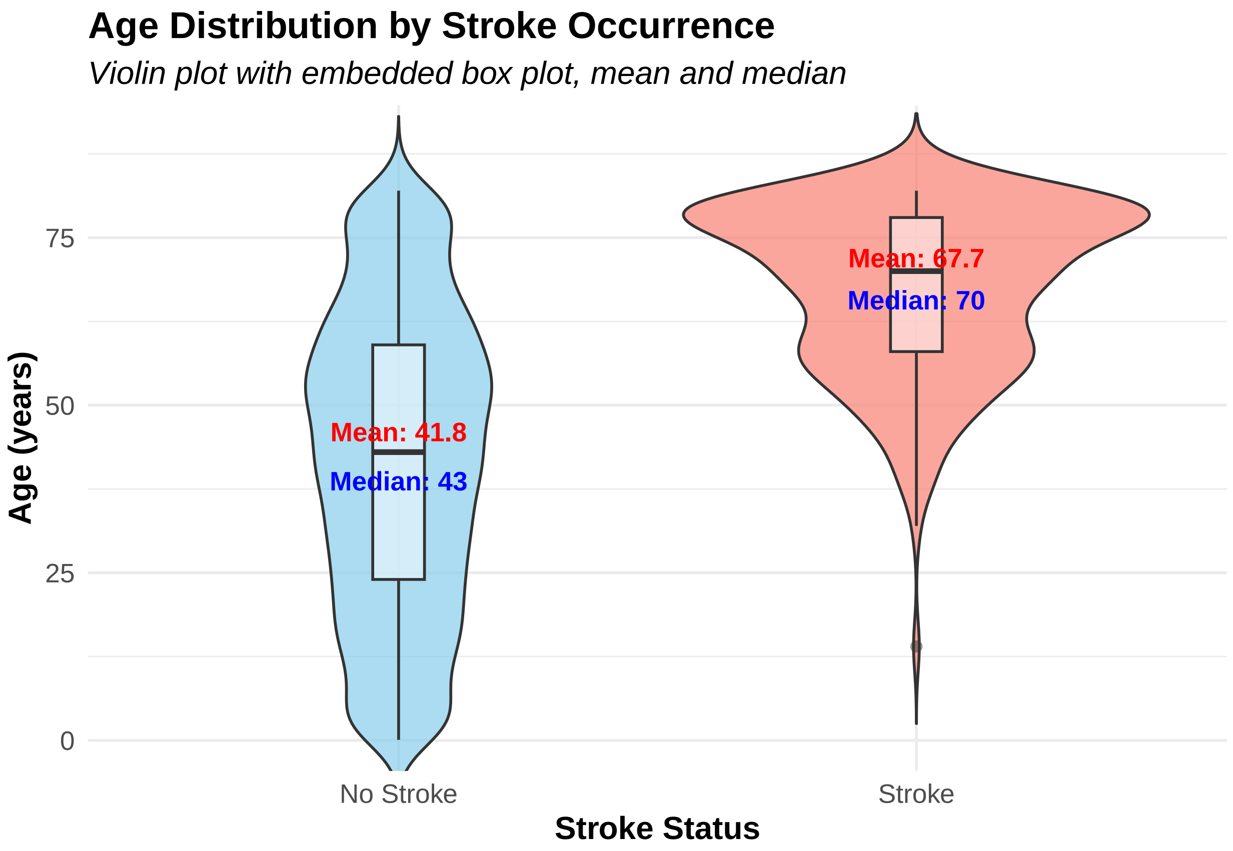
```r
data_sub_age= stroke_data %>% group_by(stroke) %>% summarise(Age_mean = mean(age),.groups = "drop")
pander(data_sub_age)
```

Age levels with Stroke

stroke	Age_mean
0	41.76
1	67.71

For those who have not had a stroke, the mean age is 41.8 years, indicating that the population without stroke tends to be younger. In contrast, individuals who have experienced a stroke are significantly older, with a mean age of 67.7 years. This data suggests that stroke occurrence is more common among older individuals, while younger people are less likely to have had a stroke.

```r
# Calculate summary statistics
summary_stats <- stroke_data %>%
  group_by(stroke) %>%
  summarise(
    mean_age = mean(age, na.rm = TRUE),
    median_age = median(age, na.rm = TRUE),
    .groups = "drop"
  )

# Create the violin plot
ggplot(stroke_data, aes(x = as.factor(stroke), y = age, fill = as.factor(stroke))) +
  geom_violin(trim = FALSE, alpha = 0.7) +
  geom_boxplot(width = 0.1, fill = "white", alpha = 0.5) +
  scale_fill_manual(values = c("0" = "skyblue", "1" = "salmon")) +
  labs(
    title = "Age Distribution by Stroke Occurrence",
    subtitle = "Violin plot with embedded box plot, mean and median",
    x = "Stroke Status",
    y = "Age (years)",
    fill = "Stroke Status"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 12),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.position = "none"
  ) +
  geom_text(data = summary_stats,
            aes(x = as.factor(stroke), y = mean_age,
                label = paste("Mean:", round(mean_age, 1))),
            color = "red", vjust = -1, size = 3.5, fontface = "bold") +
  geom_text(data = summary_stats,
            aes(x = as.factor(stroke), y = median_age,
                label = paste("Median:", round(median_age, 1))),
            color = "blue", vjust = 2, size = 3.5, fontface = "bold") +
  coord_cartesian(ylim = c(0, max(stroke_data$age, na.rm = TRUE) * 1.1)) +
  scale_x_discrete(labels = c("0" = "No Stroke", "1" = "Stroke"))
```



The violin plot confirms that for individuals who have not had a stroke, the mean age is 41.8 years and the median is 43 years, with a relatively wide distribution, suggesting that people of various ages may not experience strokes. In contrast, the group that has experienced a stroke is significantly older, with a mean age of 67.7 years and a median of 70 years. The distribution is more concentrated in the older age range, indicating that strokes are much more common among older individuals.

```
data_sub_age= stroke_data %>% group_by(heart_disease, stroke) %>% summarise(Age_mean = mean(age),.group
pander(data_sub_age)
```

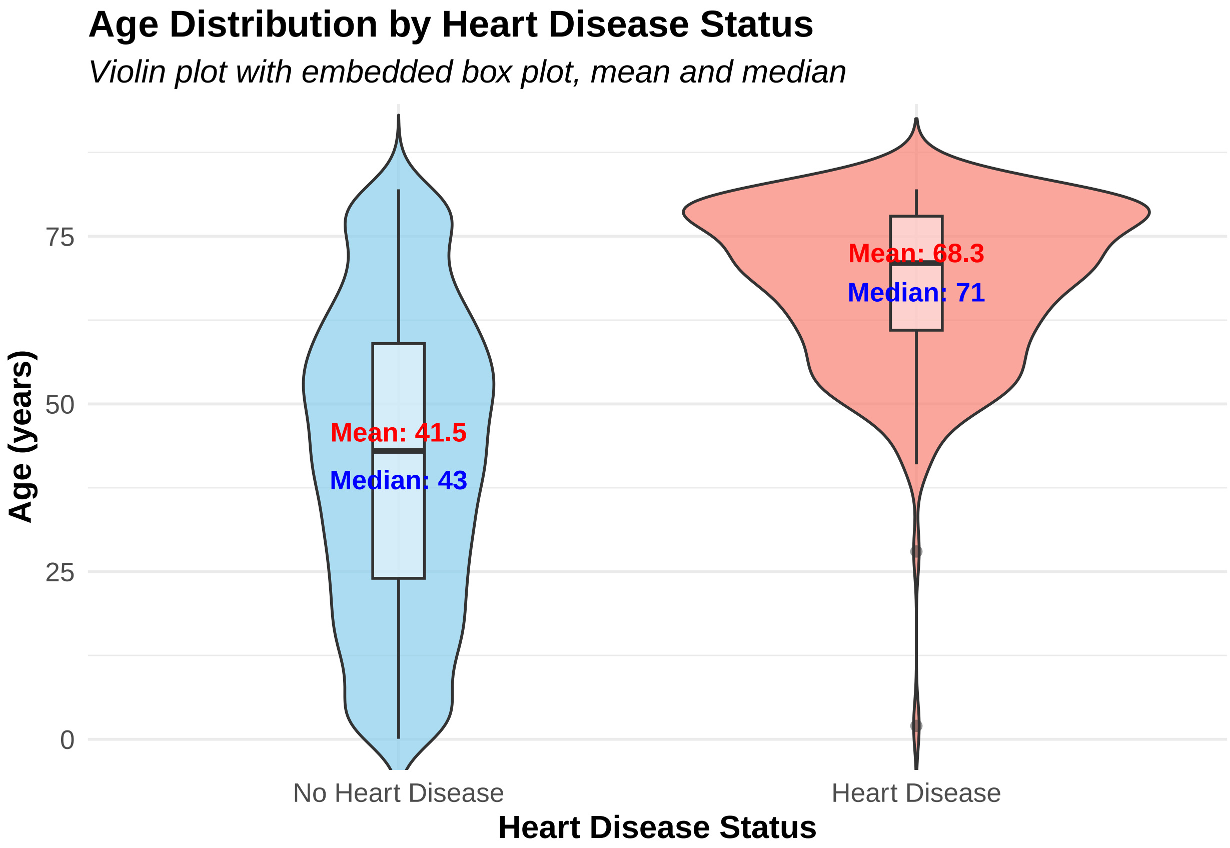
Age levels with Heart Disease/Stroke

heart_disease	stroke	Age_mean
0	0	40.6
0	1	66.71
1	0	67.55
1	1	71.95

heart_disease	stroke	Age_mean

For those without heart disease and no stroke, the mean age is 40.6 years, whereas for those with no heart disease but with a stroke, the mean age is significantly higher at 66.7 years. Among individuals with heart disease, those without a stroke have a mean age of 67.6 years, while those with both heart disease and stroke have the highest mean age of 72 years. This suggests that both heart disease and stroke are more prevalent among older individuals.

```r
# Define labels for heart disease
heart_disease_labels <- c("0" = "No Heart Disease", "1" = "Heart Disease")

# Calculate summary statistics
summary_stats <- stroke_data %>%
  group_by(heart_disease) %>%
  summarise(
    mean_age = mean(age, na.rm = TRUE),
    median_age = median(age, na.rm = TRUE),
    .groups = "drop"
  )

# Create the violin plot
ggplot(stroke_data, aes(x = heart_disease, y = age, fill = heart_disease)) +
  geom_violin(trim = FALSE, alpha = 0.7) +
  geom_boxplot(width = 0.1, fill = "white", alpha = 0.5) +
  scale_fill_manual(values = c("0" = "skyblue", "1" = "salmon"),
                    labels = heart_disease_labels) +
  scale_x_discrete(labels = heart_disease_labels) +
  labs(
    title = "Age Distribution by Heart Disease Status",
    subtitle = "Violin plot with embedded box plot, mean and median",
    x = "Heart Disease Status",
    y = "Age (years)",
    fill = "Heart Disease Status"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 12),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.position = "none"
  ) +
  geom_text(data = summary_stats,
            aes(x = heart_disease, y = mean_age,
                label = paste("Mean:", round(mean_age, 1))),
            color = "red", vjust = -1, size = 3.5, fontface = "bold") +
  geom_text(data = summary_stats,
            aes(x = heart_disease, y = median_age,
                label = paste("Median:", round(median_age, 1))),
            color = "blue", vjust = 2, size = 3.5, fontface = "bold") +
  coord_cartesian(ylim = c(0, max(stroke_data$age, na.rm = TRUE) * 1.1))
```



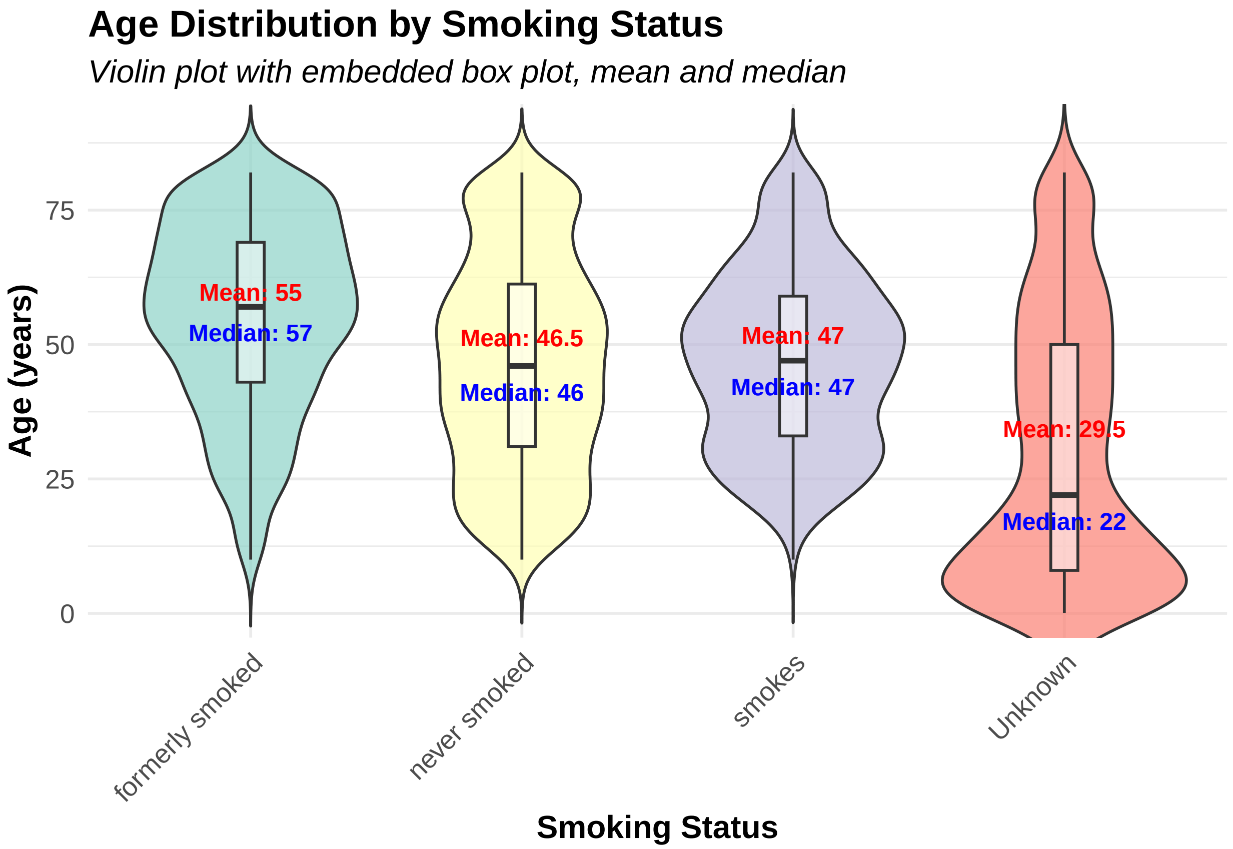
For those without heart disease, the mean age is 41.5 years, and the median is 43 years, with a broader spread of ages. In contrast, individuals with heart disease have a much higher mean age of 68.3 years and a median of 71 years, with a tighter distribution around the higher age range. The plot highlights that heart disease is more prevalent among older individuals, with a visible difference in the central tendency between the two groups.

```
#### Age levels with Smoking Status/Stroke


‘‘‘ r
data_sub_age_gender= stroke_data %>% group_by(smoking_status, stroke) %>% summarise(Age_mean = mean(age
pander(data_sub_age_gender)
```

smoking_status	stroke	Age_mean
formerly smoked	0	53.98
formerly smoked	1	68.35
never smoked	0	45.33
never smoked	1	70.49
smokes	0	46.13
smokes	1	62.38
Unknown	0	28.79
Unknown	1	65.59

We can see that former smokers tend to be older on average, with those who experienced a stroke being significantly older (68.4 years) than those without a stroke (54 years). Similarly, individuals who never smoked but had a stroke are much older (mean age of 70.5 years) compared to those who never smoked and did not experience a stroke (45.3 years). Smokers, on the other hand, are generally younger compared to former smokers and non-smokers. However, smokers who had a stroke (62.3 years) are older than those who did not (46.1 years). Interestingly, individuals with an unknown smoking status show a stark difference based on stroke status: those with a stroke are much older (65.6 years) than those without (28.8 years).

```r
# Calculate summary statistics
summary_stats <- stroke_data %>%
  group_by(smoking_status) %>%
  summarise(
    mean_age = mean(age, na.rm = TRUE),
    median_age = median(age, na.rm = TRUE),
    .groups = "drop"
  )

# Create the violin plot
ggplot(stroke_data, aes(x = smoking_status, y = age, fill = smoking_status)) +
  geom_violin(trim = FALSE, alpha = 0.7) +
  geom_boxplot(width = 0.1, fill = "white", alpha = 0.5) +
  scale_fill_brewer(palette = "Set3") +
  labs(
    title = "Age Distribution by Smoking Status",
    subtitle = "Violin plot with embedded box plot, mean and median",
    x = "Smoking Status",
    y = "Age (years)",
    fill = "Smoking Status"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 12),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    axis.text.x = element_text(angle = 45, hjust = 1),
    legend.position = "none"
  ) +
  geom_text(data = summary_stats,
            aes(x = smoking_status, y = mean_age,
                label = paste("Mean:", round(mean_age, 1))),
            color = "red", vjust = -1, size = 3, fontface = "bold") +
  geom_text(data = summary_stats,
            aes(x = smoking_status, y = median_age,
                label = paste("Median:", round(median_age, 1))),
            color = "blue", vjust = 2, size = 3, fontface = "bold") +
  coord_cartesian(ylim = c(0, max(stroke_data$age, na.rm = TRUE) * 1.1))
```



Above indicates that former smokers tend to be the oldest group, with a mean age of 55 years and a median of 57 years, showing that people who have quit smoking are generally older. Those who never smoked or currently smoke have similar age profiles, with mean and median ages around 46 years, indicating that these groups are somewhat younger than former smokers. The "unknown" smoking status group stands out with a significantly lower mean age of 29.5 years and a median of 22 years, suggesting that this group consists of much younger individuals compared to the others.

```
#stroke_data <- load_stroke_data()
data_sub_age_hyp= stroke_data %>% group_by(hypertension,stroke) %>% summarise(Age_mean = mean(age),.grou
pander(data_sub_age_hyp)
```

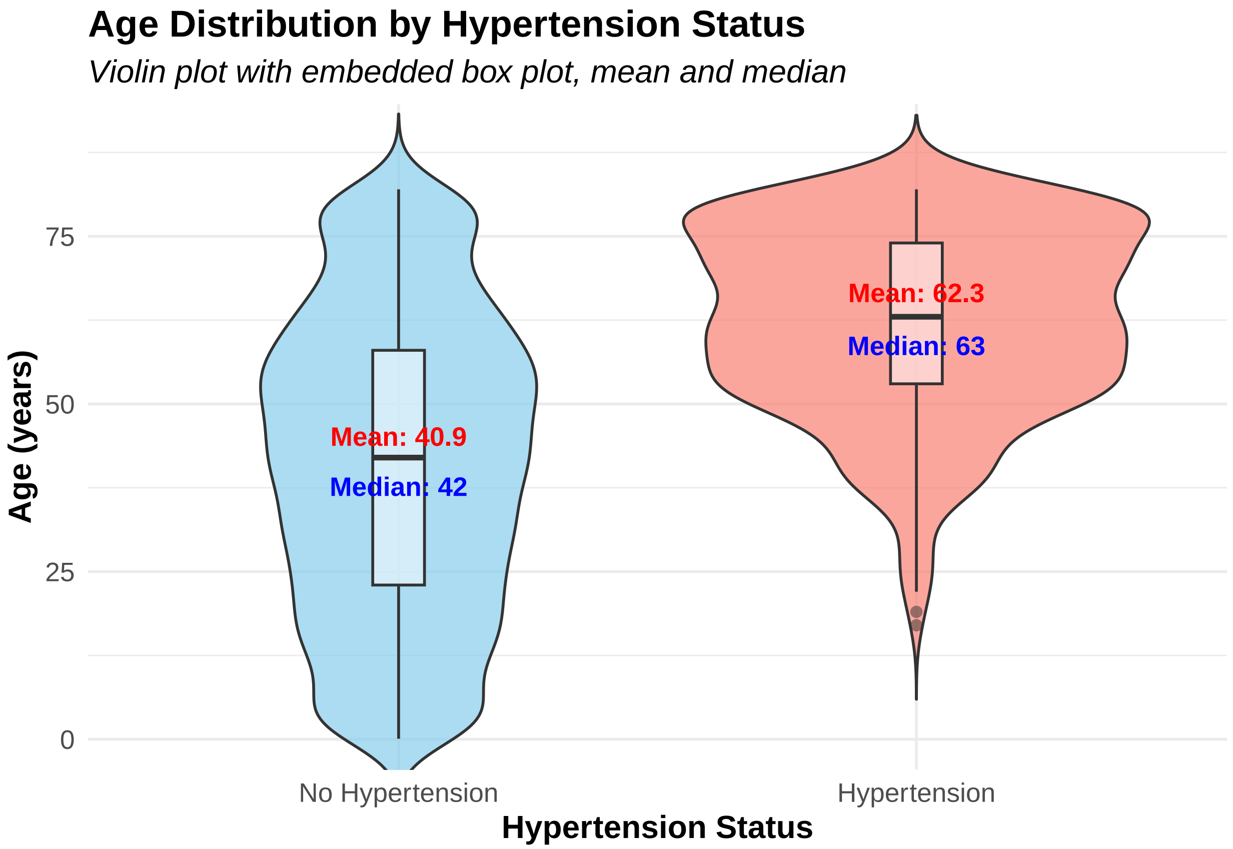
Age levels with hypertension/Stroke

hypertension	stroke	Age_mean
0	0	40
0	1	66.97
1	0	61.21
1	1	69.55

Among individuals without hypertension, those who have not had a stroke are younger, with a mean age of 40 years, while those who have experienced a stroke are significantly older, with a mean age of 67 years. For individuals with hypertension, the pattern is similar: those without a stroke have a mean age of 61.2 years, and those with a stroke are older still, with a mean age of 69.6 years.

The data suggests that both stroke and hypertension are associated with older age, with those having both conditions (hypertension and stroke) being the oldest group. Conversely, individuals without either condition tend to be much younger.

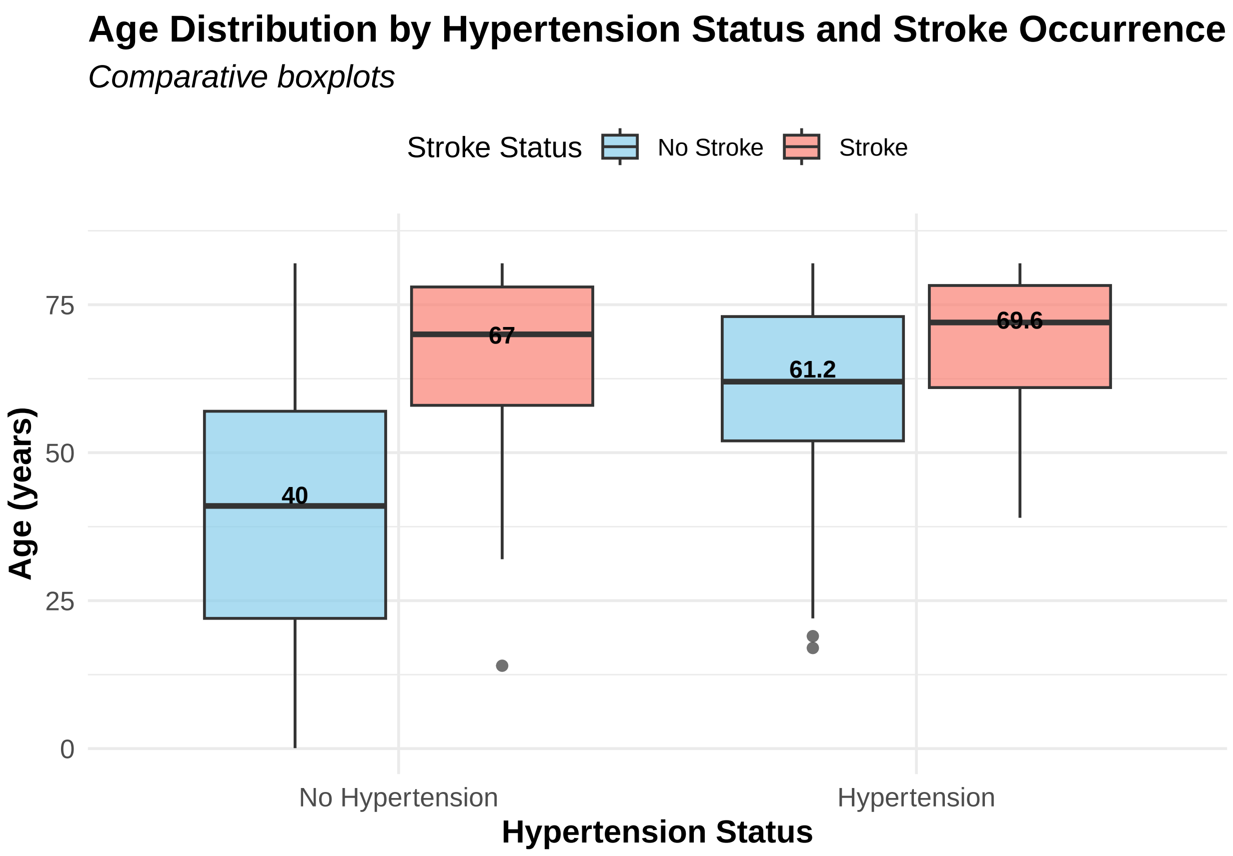
```r
# Define labels for hypertension
hypertension_labels <- c("0" = "No Hypertension", "1" = "Hypertension")

# Calculate summary statistics
summary_stats <- stroke_data %>%
  group_by(hypertension) %>%
  summarise(
    mean_age = mean(age, na.rm = TRUE),
    median_age = median(age, na.rm = TRUE),
    .groups = "drop"
  )

# Create the violin plot
ggplot(stroke_data, aes(x = hypertension, y = age, fill = hypertension)) +
  geom_violin(trim = FALSE, alpha = 0.7) +
  geom_boxplot(width = 0.1, fill = "white", alpha = 0.5) +
  scale_fill_manual(values = c("0" = "skyblue", "1" = "salmon"),
                    labels = hypertension_labels) +
  scale_x_discrete(labels = hypertension_labels) +
  labs(
    title = "Age Distribution by Hypertension Status",
    subtitle = "Violin plot with embedded box plot, mean and median",
    x = "Hypertension Status",
    y = "Age (years)",
    fill = "Hypertension Status"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 12),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.position = "none"
  ) +
  geom_text(data = summary_stats,
            aes(x = hypertension, y = mean_age,
                label = paste("Mean:", round(mean_age, 1))),
            color = "red", vjust = -1, size = 3.5, fontface = "bold") +
  geom_text(data = summary_stats,
            aes(x = hypertension, y = median_age,
                label = paste("Median:", round(median_age, 1))),
            color = "blue", vjust = 2, size = 3.5, fontface = "bold") +
  coord_cartesian(ylim = c(0, max(stroke_data$age, na.rm = TRUE) * 1.1))
```



The plots indicate that individuals without hypertension tend to be younger, with a mean age of 40.9 years and a median of 42 years. The distribution for this group shows a wide spread with a relatively high concentration of younger individuals.

In contrast, individuals with hypertension are significantly older, with a mean age of 62.3 years and a median of 63 years. The distribution for this group is more tightly concentrated around the older age range. The stark difference between the two groups suggests that hypertension is more prevalent among older individuals, while younger individuals tend to have no hypertension.

```r
# Define labels for hypertension and stroke
hypertension_labels <- c("0" = "No Hypertension", "1" = "Hypertension")
stroke_labels <- c("0" = "No Stroke", "1" = "Stroke")

# Calculate summary statistics
summary_stats <- stroke_data %>%
  group_by(hypertension, stroke) %>%
  summarise(
    mean_age = mean(age, na.rm = TRUE),
    median_age = median(age, na.rm = TRUE),
    .groups = "drop"
  )

# Create the comparative boxplot
ggplot(stroke_data, aes(x = hypertension, y = age, fill = stroke)) +
  geom_boxplot(position = position_dodge(width = 0.8), width = 0.7, alpha = 0.7) +
  scale_fill_manual(values = c("0" = "skyblue", "1" = "salmon"),
                    labels = stroke_labels) +
  scale_x_discrete(labels = hypertension_labels) +
  labs(
    title = "Age Distribution by Hypertension Status and Stroke Occurrence",
    subtitle = "Comparative boxplots",
    x = "Hypertension Status",
    y = "Age (years)",
    fill = "Stroke Status"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 12),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.position = "top"
  ) +
  geom_text(data = summary_stats,
            aes(x = hypertension, y = mean_age, label = round(mean_age, 1), group = stroke),
            position = position_dodge(width = 0.8),
            vjust = -0.5, size = 3, fontface = "bold") +
  coord_cartesian(ylim = c(0, max(stroke_data$age, na.rm = TRUE) * 1.05))
```



Among individuals without hypertension, those who have experienced a stroke are significantly older, with a mean age of 67 years, compared to those without a stroke who have a mean age of 40 years. This shows that stroke is much more common in older individuals within the no-hypertension group.

For those with hypertension, the trend persists: individuals with a stroke are older, with a mean age of 69.6 years, compared to those without a stroke, who have a mean age of 61.2 years.

```r
data_sub_age_hyp= stroke_data %>% group_by(ever_married,stroke) %>% summarise(Age_mean = mean(age),.grou
pander(data_sub_age_hyp)
```

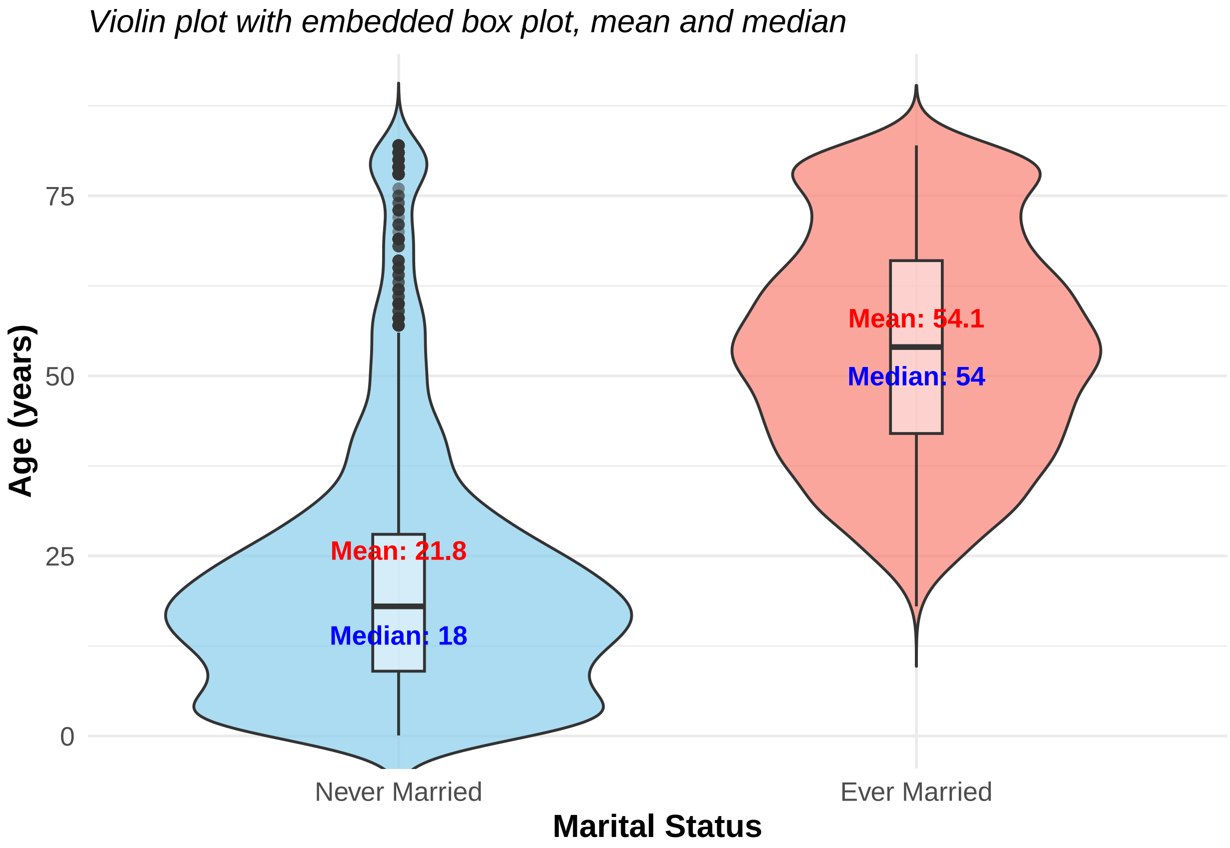
Age levels with Marital Status/Stroke

ever_married	stroke	Age_mean
No	0	21.2
No	1	66.52
Yes	0	53.22
Yes	1	67.86

For individuals who have never been married, those without a stroke are much younger, with a mean age of 21.2 years, while those who have had a stroke are considerably older, with a mean age of 66.5 years. This suggests that stroke is rare among younger, unmarried individuals but more prevalent in older unmarried individuals.

Among those who have been married, the mean age without a stroke is 53.2 years, and it increases to 67.9 years for those who have experienced a stroke. This indicates that married individuals tend to be older on average, and those who suffer from strokes are generally older as well.

```r
# Calculate summary statistics
summary_stats <- stroke_data %>%
  group_by(ever_married) %>%
  summarise(
    mean_age = mean(age, na.rm = TRUE),
    median_age = median(age, na.rm = TRUE),
    .groups = "drop"
  )

# Create the violin plot
ggplot(stroke_data, aes(x = ever_married, y = age, fill = ever_married)) +
  geom_violin(trim = FALSE, alpha = 0.7) +
  geom_boxplot(width = 0.1, fill = "white", alpha = 0.5) +
  scale_fill_manual(values = c("No" = "skyblue", "Yes" = "salmon"),
                    labels = c("No" = "Never Married", "Yes" = "Ever Married")) +
  scale_x_discrete(labels = c("No" = "Never Married", "Yes" = "Ever Married")) +
  labs(
    subtitle = "Violin plot with embedded box plot, mean and median",
    x = "Marital Status",
    y = "Age (years)",
    fill = "Marital Status"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 12),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.position = "none"
  ) +
  geom_text(data = summary_stats,
            aes(x = ever_married, y = mean_age,
                label = paste("Mean:", round(mean_age, 1))),
            color = "red", vjust = -1, size = 3.5, fontface = "bold") +
  geom_text(data = summary_stats,
            aes(x = ever_married, y = median_age,
                label = paste("Median:", round(median_age, 1))),
            color = "blue", vjust = 2, size = 3.5, fontface = "bold") +
  coord_cartesian(ylim = c(0, max(stroke_data$age, na.rm = TRUE) * 1.1))
```



The “never married” group is notably younger, with a mean age of 21.8 years and a median age of 18 years, indicating a concentration of young individuals in this group. The distribution is narrow and primarily concentrated in the lower age range, suggesting that most of the individuals who have never married are quite young.

On the other hand, the “ever married” group is significantly older, with a mean age of 54.1 years and a median age of 54 years. The distribution for this group is much wider and more evenly spread across the higher age ranges, indicating a broader age spectrum among those who have been married.

```
data_sub_age_hyp= stroke_data %>% group_by(gender,stroke) %>% summarise(Age_mean = mean(age),.groups =
pander(data_sub_age_hyp)
```

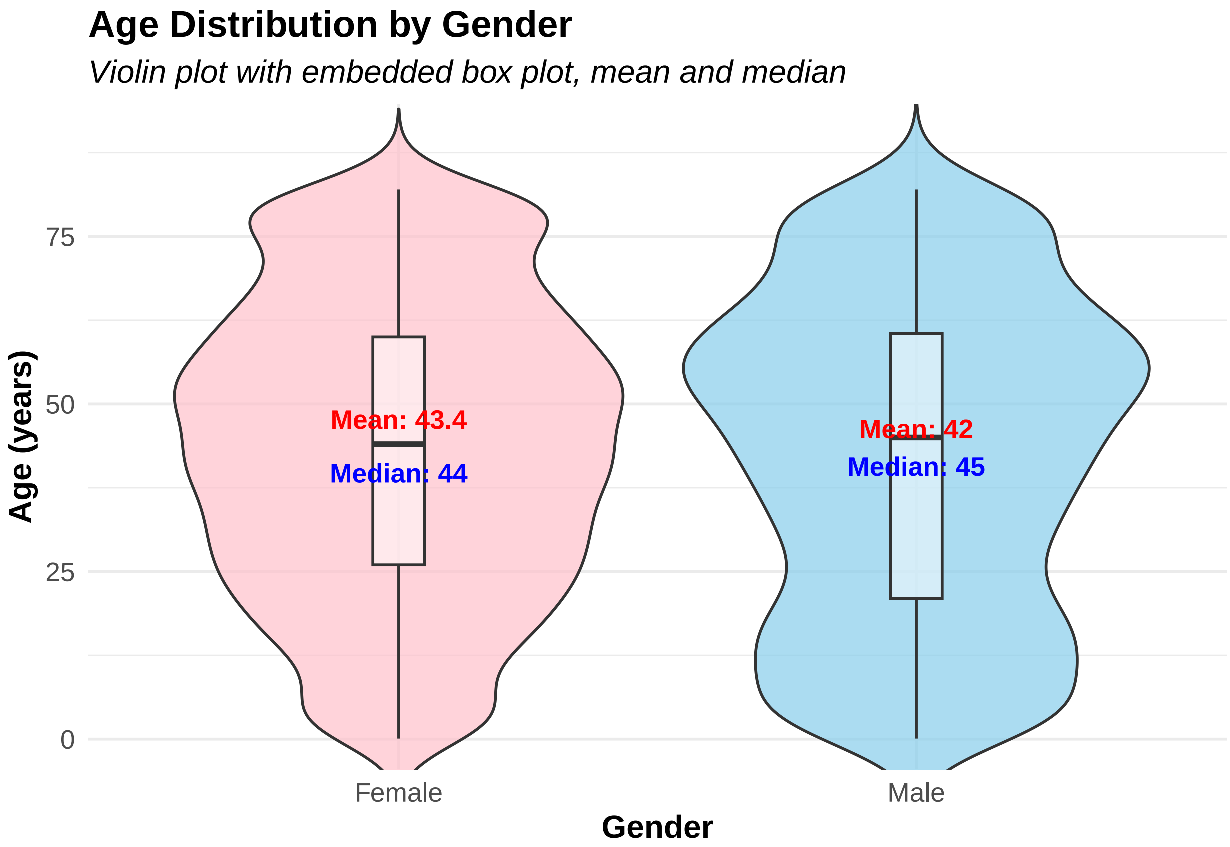
Age levels with Gender/Stroke

gender	stroke	Age_mean
Female	0	42.41
Female	1	67.24
Male	0	40.83
Male	1	68.35

For females, the mean age of those who have not experienced a stroke is 42.4 years, while females who have had a stroke are significantly older, with a mean age of 67.2 years.

For males, a similar pattern is observed. Males without a stroke have a mean age of 40.8 years, whereas males who have experienced a stroke are older, with a mean age of 68.3 years.

```r
# Calculate summary statistics
summary_stats <- stroke_data %>%
  group_by(gender) %>%
  summarise(
    mean_age = mean(age, na.rm = TRUE),
    median_age = median(age, na.rm = TRUE),
    .groups = "drop"
  )

# Create the violin plot
ggplot(stroke_data, aes(x = gender, y = age, fill = gender)) +
  geom_violin(trim = FALSE, alpha = 0.7) +
  geom_boxplot(width = 0.1, fill = "white", alpha = 0.5) +
  scale_fill_manual(values = c("Male" = "skyblue", "Female" = "pink", "Other" = "purple")) +
  labs(
    title = "Age Distribution by Gender",
    subtitle = "Violin plot with embedded box plot, mean and median",
    x = "Gender",
    y = "Age (years)",
    fill = "Gender"
  ) +
  theme_minimal() +
  theme(
    plot.title = element_text(face = "bold", size = 14),
    plot.subtitle = element_text(face = "italic", size = 12),
    axis.title = element_text(face = "bold", size = 12),
    axis.text = element_text(size = 10),
    legend.position = "none"
  ) +
  geom_text(data = summary_stats,
            aes(x = gender, y = mean_age,
                label = paste("Mean:", round(mean_age, 1))),
            color = "red", vjust = -1, size = 3.5, fontface = "bold") +
  geom_text(data = summary_stats,
            aes(x = gender, y = median_age,
                label = paste("Median:", round(median_age, 1))),
            color = "blue", vjust = 2, size = 3.5, fontface = "bold") +
  coord_cartesian(ylim = c(0, max(stroke_data$age, na.rm = TRUE) * 1.1))
```



For females, the mean age is 43.4 years, and the median is 42 years. The distribution for females shows a relatively even spread across ages, though it is slightly more concentrated around the central values.

For males, the mean age is 42 years, and the median is 45 years, showing a similar spread to females but with a slightly different central tendency. The distribution for males also shows a broad spread, with a similar concentration around middle ages.