Hypothesis testing

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This is an R Markdown Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Ctrl+Shift+Enter*.

```
library(pacman)
p_load(dplyr, GGally, ggplot2, ggthemes, ggvis, httr, lubridate, plotly, rio, rmarkdown, shiny, stringr
```

Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.

```
stroke_data<-import("./../data/healthcare-dataset-stroke-data.csv")
stroke_data<-na.omit(stroke_data)
clean_stroke_data<-stroke_data[!apply(stroke_data=="N/A",1,any),]
clean_g_stroke_data<-clean_stroke_data %>%
  filter(gender!="Other")
clean_g_stroke_data$bmi<-as.numeric(clean_g_stroke_data$bmi)
str(clean_g_stroke_data)
```

```
## 'data.frame':    4908 obs. of  12 variables:
##  $ id               : int  9046 31112 60182 1665 56669 53882 10434 60491 12109 12095 ...
##  $ gender           : chr  "Male" "Male" "Female" "Female" ...
##  $ age              : num  67 80 49 79 81 74 69 78 81 61 ...
##  $ hypertension     : int  0 0 0 1 0 1 0 0 1 0 ...
##  $ heart_disease    : int  1 1 0 0 0 1 0 0 0 1 ...
##  $ ever_married     : chr  "Yes" "Yes" "Yes" "Yes" ...
##  $ work_type        : chr  "Private" "Private" "Private" "Self-employed" ...
##  $ Residence_type   : chr  "Urban" "Rural" "Urban" "Rural" ...
##  $ avg_glucose_level: num  229 106 171 174 186 ...
##  $ bmi              : num  36.6 32.5 34.4 24 29 27.4 22.8 24.2 29.7 36.8 ...
##  $ smoking_status   : chr  "formerly smoked" "never smoked" "smokes" "never smoked" ...
##  $ stroke           : int  1 1 1 1 1 1 1 1 1 1 ...
```

```
clean_g_stroke_data$hypertension<-as.factor(clean_g_stroke_data$hypertension)
clean_g_stroke_data$heart_disease<-as.factor(clean_g_stroke_data$heart_disease)
clean_g_stroke_data$stroke<-as.factor(clean_g_stroke_data$stroke)
data<-clean_g_stroke_data
sample_n(data,5)
```

```
##      id gender age hypertension heart_disease ever_married work_type
## 1 24058 Female  50            0             0          Yes  Govt_job
## 2 46767 Female   8            0             0           No  children
## 3 22969 Female  26            0             0          Yes   Private
## 4 38771 Female  41            0             0           No  Govt_job
## 5  4449   Male  48            0             0          Yes  Govt_job
##   Residence_type avg_glucose_level  bmi  smoking_status stroke
## 1          Rural             77.67 25.6    never smoked      0
## 2          Rural             67.84 24.0         Unknown      0
## 3          Rural             91.88 24.9 formerly smoked      0
## 4          Urban            129.01 42.4         Unknown      0
## 5          Rural            124.64 26.4          smokes      0
```

Let's check wether the mean of average glucose level differs between men and women. null hypothesis H0:mu_1-mu_2 = 0 alternative hypothesis HA:mu_1-mu_2 != 0 (two-sided test) alpha=0.05

```
avg_glu_m<-data$avg_glucose_level[data$gender=="Male"]
print(paste("male avg glucose level:", mean(avg_glu_m)))
```

```
## [1] "male avg glucose level: 108.131720537046"
```

```
avg_glu_f<-data$avg_glucose_level[data$gender=="Female"]
print(paste("female avg glucose level:", mean(avg_glu_f)))
```

```
## [1] "female avg glucose level: 103.329913703832"
```

```
glu_m_mean<-mean(avg_glu_m)
glu_m_len<-length(avg_glu_m)
glu_m_var<-var(avg_glu_m)
glu_f_mean<-mean(avg_glu_f)
glu_f_len<-length(avg_glu_f)
glu_f_var<-var(avg_glu_m)

mu0=0
mean_diff<- glu_m_mean-glu_f_mean
se<-sqrt(glu_m_var/glu_m_len + glu_f_var/glu_f_len)

t<-(mean_diff - mu0)/se
print(paste("calculate Z-score:", t))
```

```
## [1] "calculate Z-score: 3.55782983108098"
```

```
print(paste("For 95% CI Z-score:", round(qnorm(0.975),3)))
```

```
## [1] "For 95% CI Z-score: 1.96"
```

Here, we are seeing that our calculated Z-score is way outside of 95% CI. So, we reject the null hypothesis.

```
# Confidence Interval
round(mean_diff+c(-1,1)*qnorm(0.975)*se,3)
```

```
## [1] 2.157 7.447
```

here 95% interval doesn't contain 0. so we reject the null hypothesis.

```
#using R library
t.test(data$avg_glucose_level~data$gender, var.equal=FALSE)
```

```
##
##  Welch Two Sample t-test
##
## data:  data$avg_glucose_level by data$gender
## t = -3.6739, df = 4089.7, p-value = 0.0002419
## alternative hypothesis: true difference in means between group Female and group Male is not equal to
## 95 percent confidence interval:
##  -7.364237 -2.239377
## sample estimates:
## mean in group Female   mean in group Male
##             103.3299             108.1317
```

We believe that average BMI for the population is larger than 30 (regardless of the gender). Let's check our beliefs:

null hypothesis H0:mu_0=30 alternative hypothesis HA:mu_0>30 (one-sided test) alpha=0.05

```
bmi= data %>% select(bmi) %>% summarise(mean=mean(bmi), sd=sd(bmi))
bmi
```

```
##       mean      sd
## 1 28.89456 7.85432
```

```
length(data$bmi)
```

```
## [1] 4908
```

```
mu_o<- 30
alpha<-0.05
z<- (bmi$mean-mu_o)/(bmi$sd/sqrt(length(data$bmi)))

print(paste("calculate Z-score:", z))
```

```
## [1] "calculate Z-score: -9.86004516573277"
```

```
print(paste("For 95% CI Z-score:", round(qnorm(0.95),3)))
```

```
## [1] "For 95% CI Z-score: 1.645"
```

calculate z-score is less than .95 quantile.so, we accept the Null hypothesis.

```
#using R library
t.test(data$bmi, mu=mu_o,alternative="greater")
```

```
##
##  One Sample t-test
##
## data:  data$bmi
## t = -9.86, df = 4907, p-value = 1
## alternative hypothesis: true mean is greater than 30
## 95 percent confidence interval:
##  28.71012      Inf
## sample estimates:
## mean of x
##  28.89456
```

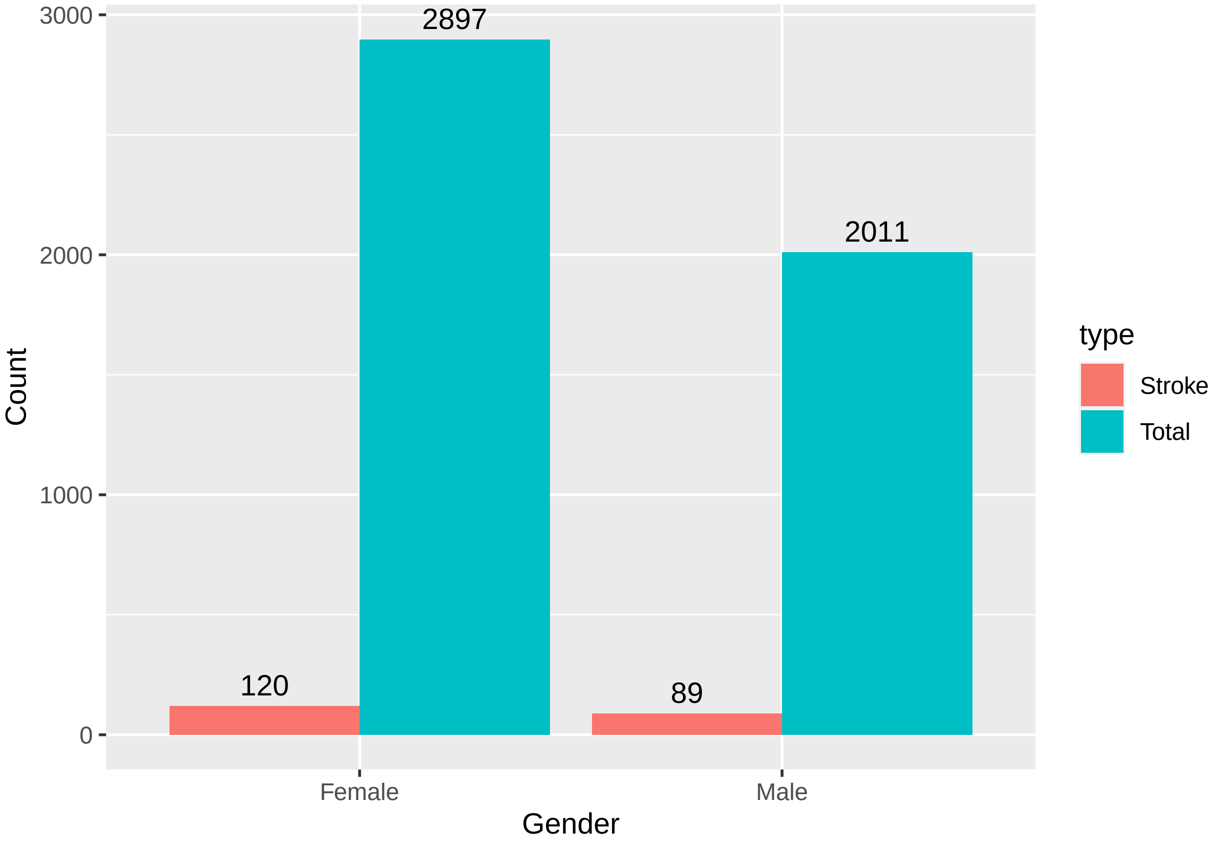
If the claim is: H0: ratio of strokes among men and women is the same: p_m-p_f =0 HA: ratio of strokes among men and women is different: p_m-p_f !=0 alpha= 0.05

```
# Number of males and females with stroke
stroke_m <- nrow(data %>% filter(gender == "Male", stroke == 1))
stroke_f <- nrow(data %>% filter(gender == "Female", stroke == 1))

# Total number of males and females
```

```r
total_m <- nrow(data %>% filter(gender == "Male"))
total_f <- nrow(data %>% filter(gender == "Female"))

# Proportion test
result <- prop.test(x = c(stroke_m, stroke_f), n = c(total_m, total_f), alternative="two.sided")

# Print result
print(result)
```

```
##
##  2-sample test for equality of proportions with continuity correction
##
## data:  c(stroke_m, stroke_f) out of c(total_m, total_f)
## X-squared = 0.16955, df = 1, p-value = 0.6805
## alternative hypothesis: two.sided
## 95 percent confidence interval:
##  -0.009138838  0.014807694
## sample estimates:
##     prop 1     prop 2
## 0.04425659 0.04142216
```

```r
# Create a data frame
bar_data <- data.frame(
  gender = rep(c("Male", "Female"), 2),
  count = c(stroke_m, stroke_f, total_m, total_f),
  type = rep(c("Stroke", "Total"), each = 2)
)

# Create the bar plot
ggplot(bar_data, aes(x = gender, y = count, fill = type)) +
  geom_bar(stat = "identity", position = "dodge") +
  geom_text(aes(label = count), vjust = -0.5, position = position_dodge(0.9)) +
  labs(y = "Count", x = "Gender")
```



```r
print(paste0("Calculated p-value is: ", round(result$p.value, 3)))
```

```
## [1] "Calculated p-value is: 0.681"
```

```r
print(paste0("Significance level alpha is: 0.05"))
```

```
## [1] "Significance level alpha is: 0.05"
```

As, p-value>alpha : accept H_o That means, proportion of both Males and females havinf stroke is quite similar.