Thang_Activity 2

2025-10-24

```
## Set global CRAN mirror
options(repos = c(CRAN = "https://cran.rstudio.com/"))

## Install the tableone package
install.packages("tableone")
```

```
## Installing package into 'C:/Users/Thang/AppData/Local/R/win-library/4.3'
## (as 'lib' is unspecified)
```

```
## package 'tableone' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
##  C:\Users\Thang\AppData\Local\Temp\RtmpyY9ShT\downloaded_packages
```

```
## Load the package
library(tableone)
library(readxl)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

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

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

```
library(janitor)
```

```
##
## Attaching package: 'janitor'
```

```
## The following objects are masked from 'package:stats':
##
##     chisq.test, fisher.test
```

```r
setwd("C:/Users/Thang/OneDrive/Desktop/Activity2")
Data <- read_excel("CPAPAdherence_Data_Clean.xlsx")
str(Data)
```

```
## tibble [174 x 15] (S3: tbl_df/tbl/data.frame)
##  $ subject_id    : chr [1:174] "11-01102" "11-01153" "11-01442" "11-01634" ...
##  $ ethnicity     : chr [1:174] "Not Hispanic or Latino" "Not Hispanic or Latino" "Not Hispanic or La
##  $ education     : chr [1:174] "> high school" "> high school" "> high school" "> high school" ...
##  $ race          : chr [1:174] "Black" "White" "White" "White" ...
##  $ age           : num [1:174] 62 71 75 62 55 70 67 75 75 63 ...
##  $ sex           : chr [1:174] "Female" "Male" "Female" "Male" ...
##  $ bmi           : num [1:174] 51 42.8 53.5 35.8 41.4 ...
##  $ ahi           : num [1:174] 22.4 24.4 19.9 21.5 18.2 33.4 15.3 22 79.7 37 ...
##  $ ess           : num [1:174] 17 6 4 9 7 8 1 5 6 22 ...
##  $ mmse          : num [1:174] 27 30 30 29 29 26 29 29 30 26 ...
##  $ avg_daily_cpap: num [1:174] 6.45 9.05 4.57 7.62 6.3 ...
##  $ adherence     : chr [1:174] "Adherent" "Adherent" "Adherent" "Adherent" ...
##  $ odsi_bl       : num [1:174] 5 0 2 16 10 2 0 0 4 19 ...
##  $ odsi_6m       : num [1:174] 4 0 2 0 8 2 0 1 3 18 ...
##  $ adcs_12m      : num [1:174] 4 2 4 1 1 2 4 1 1 6 ...
```

```r
head(Data)
```

```
## # A tibble: 6 x 15
##   subject_id ethnicity       education race    age sex     bmi   ahi   ess  mmse
##   <chr>      <chr>           <chr>     <chr> <dbl> <chr> <dbl> <dbl> <dbl> <dbl>
## 1 11-01102   Not Hispanic o~ > high s~ Black    62 Fema~  51.0  22.4    17    27
## 2 11-01153   Not Hispanic o~ > high s~ White    71 Male   42.8  24.4     6    30
## 3 11-01442   Not Hispanic o~ > high s~ White    75 Fema~  53.5  19.9     4    30
## 4 11-01634   Not Hispanic o~ > high s~ White    62 Male   35.8  21.5     9    29
## 5 11-01769   Not Hispanic o~ > high s~ Black    55 Fema~  41.4  18.2     7    29
## 6 11-01777   Not Hispanic o~ > high s~ White    70 Fema~  37.5  33.4     8    26
## # i 5 more variables: avg_daily_cpap <dbl>, adherence <chr>, odsi_bl <dbl>,
## #   odsi_6m <dbl>, adcs_12m <dbl>
```

```r
dim(Data)
```

```
## [1] 174  15
```

```r
Data <- clean_names(Data)

Data <- Data %>%
  mutate(
    ethnicity = factor(ethnicity),
    education = factor(education, levels = c("<= high school", "> high school")),
    race = factor(race, levels = c("White", "Black", "Other")),
    adherence = factor(adherence, levels = c("Non-adherent", "Adherent"))
  )

Data <- Data %>%
  mutate(
```

```
    age = as.numeric(age),
    ahi = as.numeric(ahi),
    ess = as.numeric(ess),
    mmse = as.numeric(mmse),
    avg_daily_cpap = as.numeric(avg_daily_cpap)
  )
## --- Check for missing values ---
colSums(is.na(Data))
```

```
##     subject_id      ethnicity      education           race            age
##              0              0              0              1              0
##            sex            bmi            ahi           ess           mmse
##              0              0              0              0              0
## avg_daily_cpap      adherence        odsi_bl       odsi_6m       adcs_12m
##              0              0              0             21             45
```

```
## --- Summary of all variables ---
summary(Data)
```

```
##   subject_id                         ethnicity            education
##  Length:174         Hispanic or Latino    : 13   <= high school: 36
##  Class :character   Not Hispanic or Latino:161   > high school :138
##  Mode  :character
##
##
##
##
##     race          age            sex                bmi
##  White:124   Min.   :55.00   Length:174         Min.   :20.00
##  Black: 37   1st Qu.:61.00   Class :character   1st Qu.:37.50
##  Other: 12   Median :66.50   Mode  :character   Median :42.32
##  NA's :  1   Mean   :66.86                      Mean   :42.18
##              3rd Qu.:72.00                      3rd Qu.:46.88
##              Max.   :85.00                      Max.   :65.11
##
##       ahi              ess              mmse       avg_daily_cpap
##  Min.   : 15.00   Min.   : 0.000   Min.   :21.00   Min.   :0.000
##  1st Qu.: 19.50   1st Qu.: 6.000   1st Qu.:26.25   1st Qu.:3.800
##  Median : 28.45   Median : 8.000   Median :28.00   Median :5.667
##  Mean   : 34.78   Mean   : 8.885   Mean   :27.60   Mean   :5.151
##  3rd Qu.: 44.62   3rd Qu.:12.000   3rd Qu.:29.00   3rd Qu.:7.046
##  Max.   :119.40   Max.   :22.000   Max.   :30.00   Max.   :9.300
##
##         adherence      odsi_bl          odsi_6m          adcs_12m
##  Non-adherent: 46   Min.   : 0.000   Min.   : 0.000   Min.   :1.000
##  Adherent    :128   1st Qu.: 2.000   1st Qu.: 2.000   1st Qu.:2.000
##                     Median : 6.000   Median : 3.000   Median :3.000
##                     Mean   : 7.983   Mean   : 5.268   Mean   :3.194
##                     3rd Qu.:13.000   3rd Qu.: 8.000   3rd Qu.:4.000
##                     Max.   :22.000   Max.   :18.000   Max.   :6.000
##                                      NA's   :21       NA's   :45
```

```r
## Save cleaned dataset
write.csv(Data, "CPAPAdherence_Data_Clean_Ready.csv", row.names = FALSE)

library(gtsummary)
library(dplyr)
library(broom)

names(Data)
```

```
##  [1] "subject_id"     "ethnicity"      "education"      "race"
##  [5] "age"            "sex"            "bmi"            "ahi"
##  [9] "ess"            "mmse"           "avg_daily_cpap" "adherence"
## [13] "odsi_bl"        "odsi_6m"        "adcs_12m"
```

```r
Data <- Data %>%
  rename(
    Ethnicity = ethnicity,
    Education = education,
    Race = race,
    Age = age,
    Sex = sex,
    BMI = bmi,
    AHI = ahi,
    ESS = ess,
    MMSE = mmse,
    ODSI_baseline = odsi_bl,
    ADCS_MCI_12m = adcs_12m,
    ODSI_6m = odsi_6m,
    `Average daily CPAP (hr/night)` = avg_daily_cpap
  )


Data$adherence <- factor(Data$adherence,
                         levels = c("Non-adherent", "Adherent"))
library(dplyr)
table1 <- Data %>%
  select(Ethnicity, Education, Race, Age, Sex, BMI, AHI, ESS, MMSE,
         `Average daily CPAP (hr/night)`, adherence, ODSI_baseline, ODSI_6m,
         ADCS_MCI_12m) %>%
  tbl_summary(
    by = adherence,
    statistic = list(
      all_continuous() ~ "{mean} ± {sd}",
      all_categorical() ~ "{n} ({p}%)"
    ),
    digits = all_continuous() ~ 2
  ) %>%
  add_p(test = list(
    all_continuous() ~ "t.test",
    all_categorical() ~ "chisq.test"
  )) %>%
  add_n() %>%
  modify_header(label ~ "**Characteristic**") %>%
```

```
  modify_caption("Demographic and Clinical Characteristics (n = 174)")
```

```
## The following warnings were returned during `modify_caption()`:

## ! For variable `ADCS_MCI_12m` (`adherence`) and "statistic", "p.value", and
##   "parameter" statistics: Chi-squared approximation may be incorrect
## ! For variable `Ethnicity` (`adherence`) and "statistic", "p.value", and
##   "parameter" statistics: Chi-squared approximation may be incorrect
## ! For variable `MMSE` (`adherence`) and "statistic", "p.value", and "parameter"
##   statistics: Chi-squared approximation may be incorrect
## ! For variable `Race` (`adherence`) and "statistic", "p.value", and "parameter"
##   statistics: Chi-squared approximation may be incorrect
```

```
vars <- c("ethnicity", "education", "race", "age", "sex", "BMI", "AHI",
          "ESS", "MMSE","Average daily CPAP (hr/night)", "ODSI_baseline",
          "ODSI_6m", "ADCS_MCI_12m")
library(tableone)
tab1 <- CreateTableOne(vars = vars, strata = "adherence", data = Data)
```

```
## Warning in ModuleReturnVarsExist(vars, data): The data frame does not have:
## ethnicity education race age sex Dropped
```

```
print(tab1, showAllLevels = TRUE, smd = TRUE)
```

```
##                                                Stratified by adherence
##                                                 level Non-adherent  Adherent
##   n                                                        46           128
##   BMI (mean (SD))                                    42.15 (7.37)  42.20 (7.18)
##   AHI (mean (SD))                                    35.59 (19.91) 34.49 (21.20)
##   ESS (mean (SD))                                     9.02 (4.79)   8.84 (5.04)
##   MMSE (mean (SD))                                   27.39 (1.81)  27.67 (1.77)
##   Average daily CPAP (hr/night) (mean (SD))           1.61 (1.35)   6.42 (1.32)
##   ODSI_baseline (mean (SD))                           8.30 (5.77)   7.87 (6.21)
##   ODSI_6m (mean (SD))                                 6.18 (5.35)   5.01 (4.80)
##   ADCS_MCI_12m (mean (SD))                            3.69 (1.41)   3.07 (1.47)
##                                                Stratified by adherence
##                                                 p      test SMD
##   n
##   BMI (mean (SD))                               0.966       0.007
##   AHI (mean (SD))                               0.758       0.054
##   ESS (mean (SD))                               0.828       0.038
##   MMSE (mean (SD))                              0.361       0.157
##   Average daily CPAP (hr/night) (mean (SD)) <0.001       3.613
##   ODSI_baseline (mean (SD))                     0.677       0.073
##   ODSI_6m (mean (SD))                           0.224       0.230
##   ADCS_MCI_12m (mean (SD))                      0.053       0.434
```

```
write.csv(print(tab1, showAllLevels = TRUE, smd = TRUE),
          "Table1_Summary.csv", row.names = FALSE)
```

```
##                                                Stratified by adherence
##                                                 level Non-adherent  Adherent
##   n                                                        46           128
##   BMI (mean (SD))                                     42.15 (7.37)  42.20 (7.18)
##   AHI (mean (SD))                                     35.59 (19.91) 34.49 (21.20)
##   ESS (mean (SD))                                      9.02 (4.79)   8.84 (5.04)
##   MMSE (mean (SD))                                    27.39 (1.81)  27.67 (1.77)
##   Average daily CPAP (hr/night) (mean (SD))            1.61 (1.35)   6.42 (1.32)
##   ODSI_baseline (mean (SD))                            8.30 (5.77)   7.87 (6.21)
##   ODSI_6m (mean (SD))                                  6.18 (5.35)   5.01 (4.80)
##   ADCS_MCI_12m (mean (SD))                             3.69 (1.41)   3.07 (1.47)
##                                                Stratified by adherence
##                                                 p      test SMD
##   n
##   BMI (mean (SD))                               0.966       0.007
##   AHI (mean (SD))                               0.758       0.054
##   ESS (mean (SD))                               0.828       0.038
##   MMSE (mean (SD))                              0.361       0.157
##   Average daily CPAP (hr/night) (mean (SD)) <0.001       3.613
##   ODSI_baseline (mean (SD))                     0.677       0.073
##   ODSI_6m (mean (SD))                           0.224       0.230
##   ADCS_MCI_12m (mean (SD))                      0.053       0.434
```

```
table1     #
```

1B.Choose a single characteristic with a significant p-value when comparing between adherence and non-adherent groups, and describe in 2-3 sentences what this means in plain English.

The adherent group's average daily CPAP usage was considerably higher (approximately 6.4 hours per night) than that of the non-adherent group (approximately 1.6 hours per night, $p < 0.001$).

In plain English, adherent participants utilized their CPAP machines for significantly extended periods of time each night. This affirms that the adherence status is indicative of the actual treatment behavior and emphasizes that device utilization is the primary determining factor between the 2 groups.

1C.Choose a single characteristic with a non-significant p-value when comparing between adherence and non-adherent groups, and describe in 2-3 sentences what this means in plain English.

There was no significant difference in age between adherent and non-adherent participants (p 0.90).

This implies that the adherence to CPAP was not influenced by the age of the participants; younger and older individuals were equally likely to be adherent or non-adherent. In layman's terms, the frequency with which an individual employs their CPAP device does not seem to be influenced by their age.

2.Test the null hypothesis that there is no difference in change from baseline to 6 months for ODSI for adherent versus non-adherent participants. Write out each step of the hypothesis test and clearly interpret your results in plain English in 2-3 sentences.

Null Hypothesis (H): There is no difference in the change of ODSI from baseline to 6 months between adherent and non-adherent participants.

$$H_0 : \mu_{\text{adherent}} = \mu_{\text{non-adherent}}$$

Alternative Hypothesis: # Alternative Hypothesis (H): There is a difference in the change of ODSI between adherent and non-adherent participants.

$$H_1 : \mu_{\text{adherent}} \neq \mu_{\text{non-adherent}}$$

```
## Remove rows with missing values in 'odsi_6m'
clean_data <- Data %>%
  filter(!is.na(ODSI_6m))

## Check the structure of the cleaned data
str(clean_data)
```

```
## tibble [153 x 15] (S3: tbl_df/tbl/data.frame)
##  $ subject_id                   : chr [1:153] "11-01102" "11-01153" "11-01442" "11-01634" ...
##  $ Ethnicity                    : Factor w/ 2 levels "Hispanic or Latino",..: 2 2 2 2 2 2 2 2 2 2 ..
##  $ Education                    : Factor w/ 2 levels "<= high school",..: 2 2 2 2 2 2 1 2 2 2 ...
##  $ Race                         : Factor w/ 3 levels "White","Black",..: 2 1 1 1 2 1 2 1 1 2 ...
##  $ Age                          : num [1:153] 62 71 75 62 55 70 67 75 75 63 ...
##  $ Sex                          : chr [1:153] "Female" "Male" "Female" "Male" ...
##  $ BMI                          : num [1:153] 51 42.8 53.5 35.8 41.4 ...
##  $ AHI                          : num [1:153] 22.4 24.4 19.9 21.5 18.2 33.4 15.3 22 79.7 37 ...
##  $ ESS                          : num [1:153] 17 6 4 9 7 8 1 5 6 22 ...
##  $ MMSE                         : num [1:153] 27 30 30 29 29 26 29 29 30 26 ...
##  $ Average daily CPAP (hr/night): num [1:153] 6.45 9.05 4.57 7.62 6.3 ...
##  $ adherence                    : Factor w/ 2 levels "Non-adherent",..: 2 2 2 2 2 2 1 2 2 2 ...
##  $ ODSI_baseline                : num [1:153] 5 0 2 16 10 2 0 0 4 19 ...
##  $ ODSI_6m                      : num [1:153] 4 0 2 0 8 2 0 1 3 18 ...
##  $ ADCS_MCI_12m                 : num [1:153] 4 2 4 1 1 2 4 1 1 6 ...
```

```
## Calculate the change in ODSI score from baseline to 6 months
clean_data$odsi_change <- clean_data$ODSI_6m - clean_data$ODSI_baseline

## Impute missing values with the median of 'odsi_6m'
Data$ODSI_6m[is.na(Data$ODSI_6m)] <- median(Data$ODSI_6m, na.rm = TRUE)
summary(Data$ODSI_6m)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.000   2.000   3.000   4.994   8.000  18.000
```

```r
## Calculate ODSI change again
clean_data <- clean_data %>%
  mutate(odsi_change = ODSI_6m - ODSI_baseline)

## Test normality
shapiro.test(clean_data$odsi_change)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  clean_data$odsi_change
## W = 0.95872, p-value = 0.0001592
```

```r
wilcox.test(odsi_change ~ adherence, data = clean_data,
            alternative = "two.sided")
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  odsi_change by adherence
## W = 2282.5, p-value = 0.254
## alternative hypothesis: true location shift is not equal to 0
```

Since the p-value is less than 0.05, we reject the null hypothesis of normality. This indicates that the odsi_change data are not normally distributed.

Wilcoxon Rank-Sum Test (Mann-Whitney U test): The p-value from the Mann-Whitney U test is greater than 0.05, so we fail to reject the null hypothesis. This means there is no significant difference in the change of ODSI scores from baseline to 6 months between adherent and non-adherent participants.

3. Hypothesis Test: Probability of Excessive Daytime Sleepiness at Baseline vs. 6 Months

The objective is to ascertain if the likelihood of excessive daytime drowsiness, as determined by a cutoff score of 6 or above on the ODSI (Observation and Interview Based Diurnal drowsiness Inventory), is consistent from baseline to 6 months.

State the Hypotheses Null Hypothesis (H): The likelihood of excessive daytime drowsiness remains constant from baseline to the 6-month mark.

$$H_0 : P(\text{ODSI} \geq 6 \text{ at baseline}) = P(\text{ODSI} \geq 6 \text{ at 6 months})$$

Alternative Hypothesis (H): The probability of excessive daytime sleepiness is different at baseline compared to at 6 months.

$$H_1 : P(\text{ODSI} \geq 6 \text{ at baseline}) \neq P(\text{ODSI} \geq 6 \text{ at 6 months})$$

Pick the Right TesTest: This is a comparison of the probabilities (proportions) of two groups: baseline and 6 months. Because we are working with categorical data (whether or not someone is excessively sleepy), a McNemar's test or a Chi-squared test would work. However, we will utilize the McNemar's test for paired categorical data (baseline vs. 6 months for the same people).

Get the Data Ready: We need to make a variable that shows if someone has excessive daytime sleepiness (ODSI $>$ 6) at the start and again at 6 months.

Make a variable with two values: 1 for too much sleepiness during the day (ODSI 6) 0 for not being too sleepy during the day (ODSI $<$ 6)

```
# Create a binary variable for ODSI  6 at baseline and 6 months
Data$baseline_sleepy <- ifelse(Data$ODSI_baseline >= 6, 1, 0)
Data$month6_sleepy <- ifelse(Data$ODSI_6m >= 6, 1, 0)

## Create a contingency table for McNemar's test
table_sleepiness <- table(Data$baseline_sleepy, Data$month6_sleepy)

## Perform McNemar's test
mcnemar_test <- mcnemar.test(table_sleepiness)
mcnemar_test
```

```
##
##  McNemar's Chi-squared test with continuity correction
##
## data:  table_sleepiness
## McNemar's chi-squared = 14.561, df = 1, p-value = 0.0001357
```

Conclusion: Reject the null hypothesis because the p-value (0.0001357) is less than 0.05. There is a statistically significant difference in the likelihood of excessive daytime sleepiness (ODSI $>$ 6) between the baseline and 6 months. To put it another way, the chances of experiencing too much daytime sleepiness at the start are not the same as the chances at 6 months. This indicates that the variation in tiredness across time is substantial in the sample.

4A.Test the Null Hypothesis with Known Population Standard Deviation 1.

Null Hypothesis (H): The average MMSE score for all study participants is over 23, which means they are not having any cognitive problems.

Alternative Hypothesis (H): The mean MMSE score for all study participants is less than or equal to 23, signifying cognitive impairment.

$$H_0 : \mu_{\text{study participants}} \geq 23$$
$$H_1 : \mu_{\text{study participants}} \leq 23$$

```
## Sample data check

sample_mean <- mean(Data$MMSE, na.rm = TRUE)  # Calculate the sample mean
population_mean <- 23  # The threshold for cognitive impairment
population_sd <- 2.0  # Known population standard deviation
n <- length(Data$MMSE)  # Sample size

## Calculate the Z statistic

Z <- (sample_mean - population_mean) / (population_sd / sqrt(n))

## Calculate p-value for the one-tailed test (lower-tailed)
```

```r
p_value <- pnorm(Z)

## Print results

Z
```

```
## [1] 30.32392
```

```r
p_value
```

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

Understand the Z Statistic: very high number, 30.32, is the Z statistic. This means that the sample mean MMSE is far higher than the criteria for cognitive impairment, which is 23.

p-value: The p-value of 1 means that it is very unlikely that the sample mean MMSE is less than 23. The p-value being more than 0.05 means that there isn't enough evidence to reject the null hypothesis. To put it another way: This indicates that there is no substantial difference between the sample mean and the threshold value of 23, hence supporting the null hypothesis.

Conclusion for non-statistical people: We do not reject the null hypothesis because the p-value is quite high (1). This indicates that the study participants possess a mean MMSE score exceeding 23, with no substantial evidence of cognitive impairment among the sample.

4B.Test the Null Hypothesis with an Unknown Population Standard Deviation

Null Hypothesis (H): The average MMSE score of the study participants is 23 or higher, which means there is no cognitive impairment.

Alternative Hypothesis (H): The average MMSE score of the people in the study is 23 or lower, which means they have cognitive problems.

$$H_0 : \mu_{\text{study participants}} \geq 23$$

$$H_1 : \mu_{\text{study participants}} \leq 23$$

```r
## Sample data check:

sample_mean <- mean(Data$MMSE, na.rm = TRUE)  # Calculate the sample mean
population_mean <- 23  # The threshold for cognitive impairment
sample_sd <- sd(Data$MMSE, na.rm = TRUE)  # Sample standard deviation
n <- length(Data$MMSE)  # Sample size

## Calculate the t-statistic

t_stat <- (sample_mean - population_mean) / (sample_sd / sqrt(n))

## Degrees of freedom for the t-distribution

df <- n - 1  # Degrees of freedom
```

```r
## Calculate p-value for the one-tailed test

p_value_t <- pt(t_stat, df)  # For one-tailed lower test

## Print results
t_stat
```

```
## [1] 34.08097
```

```r
p_value_t
```

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

Understanding the t-statistic: The t-statistic of 34.08 is exceptionally high, which means that the sample mean MMSE is far higher than the criterion for cognitive impairment, which is 23. This shows that the sample mean and the hypothesized population mean are very different from each other.

Understanding the p-value: The p-value of 1 is exceptionally high. This means that the sample mean MMSE is very unlikely to be less than 23. This means that there is no proof to reject the null hypothesis.

We can't reject the null hypothesis because the p-value is higher than 0.05.

Conclusion for an Audience Without a Statistics Background: The p-value is 1, which suggests that the participants' average MMSE score is much higher than 23. This means that there is no proof that the individuals are cognitively impaired based on the MMSE score. In other words, we can't say for sure that the people in this study have cognitive problems solely based on the MMSE results.

5.Compute and Report the Mean and Standard Deviation for the Variable Representing Average Daily CPAP Use

```r
## 5A Calculate the mean and standard deviation for 'avg_daily_cpap'
mean_cpap <- mean(Data$`Average daily CPAP (hr/night)`, na.rm = TRUE)
sd_cpap <- sd(Data$`Average daily CPAP (hr/night)`, na.rm = TRUE)

## Report the results
mean_cpap
```

```
## [1] 5.150766
```

```r
sd_cpap
```

```
## [1] 2.504029
```

#Interpretation: The average daily CPAP use in this sample is approximately 5.15 hours per night. The standard deviation is 2.50 hours, indicating that there is a fairly wide variation in CPAP usage among participants. This suggests that while some individuals use CPAP consistently for long durations, others use it much less, reflecting differences in adherence or treatment habits.

```r
##5B Proportion of Participants with Average Daily CPAP Use Less Than 3 Hours

# Calculate the proportion of participants with average daily CPAP use < 3 hours
proportion_less_than_3 <- mean(Data$`Average daily CPAP (hr/night)` < 3,
                               na.rm = TRUE)

# Report the proportion
proportion_less_than_3
```

```
## [1] 0.2068966
```

Interpretation: About 20.7% of the participants in the study use their CPAP machine for less than three hours per night. This suggests that a significant portion of participants may not be adhering to the recommended CPAP usage, which could potentially reduce the effectiveness of the therapy in managing sleep apnea.

In simpler terms, roughly one in five people in this study are not using their CPAP machine long enough each night, which may make the treatment less effective in improving their sleep and breathing.

6A.Compute and Report the Mean and Standard Deviation for BMI

```r
# Calculate the mean and standard deviation for BMI
mean_bmi <- mean(Data$BMI, na.rm = TRUE)
sd_bmi <- sd(Data$BMI, na.rm = TRUE)

# Report the results
mean_bmi
```

```
## [1] 42.18415
```

```r
sd_bmi
```

```
## [1] 7.206295
```

6B. Estimate and Report the Proportion of Participants Who Are Considered Obese (BMI 30)

```r
# Calculate the proportion of participants who are considered obese (BMI >= 30)
proportion_obese <- mean(Data$BMI >= 30, na.rm = TRUE)

# Report the proportion
proportion_obese
```

```
## [1] 0.9597701
```

Interpretation: The individuals in this study have an average BMI of 42.18, which is far higher than the normal healthy range of 18.5 to 24.9. The standard deviation of 7.21 indicates considerable variability in BMI among participants.

Furthermore, about 96% of participants had a BMI of 30 or higher, classifying them as obese. This finding suggests that the majority of individuals in this study are overweight or obese, an important factor to consider when evaluating potential health outcomes and risks associated with obesity.

7A.Among those who are adherent to CPAP, describe the distribution of the variable AHI with appropriate statistics and data visualizations. Then, summarize your findings in 2-3 sentences in plain language suitable for a non-statistical audience.

```
##7A

# Filter for adherent participants
adherent_data <- Data %>%
  filter(adherence == "Adherent")

# Summary statistics for AHI
summary(adherent_data$AHI)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   15.00   19.50   26.75   34.49   43.65  112.70
```

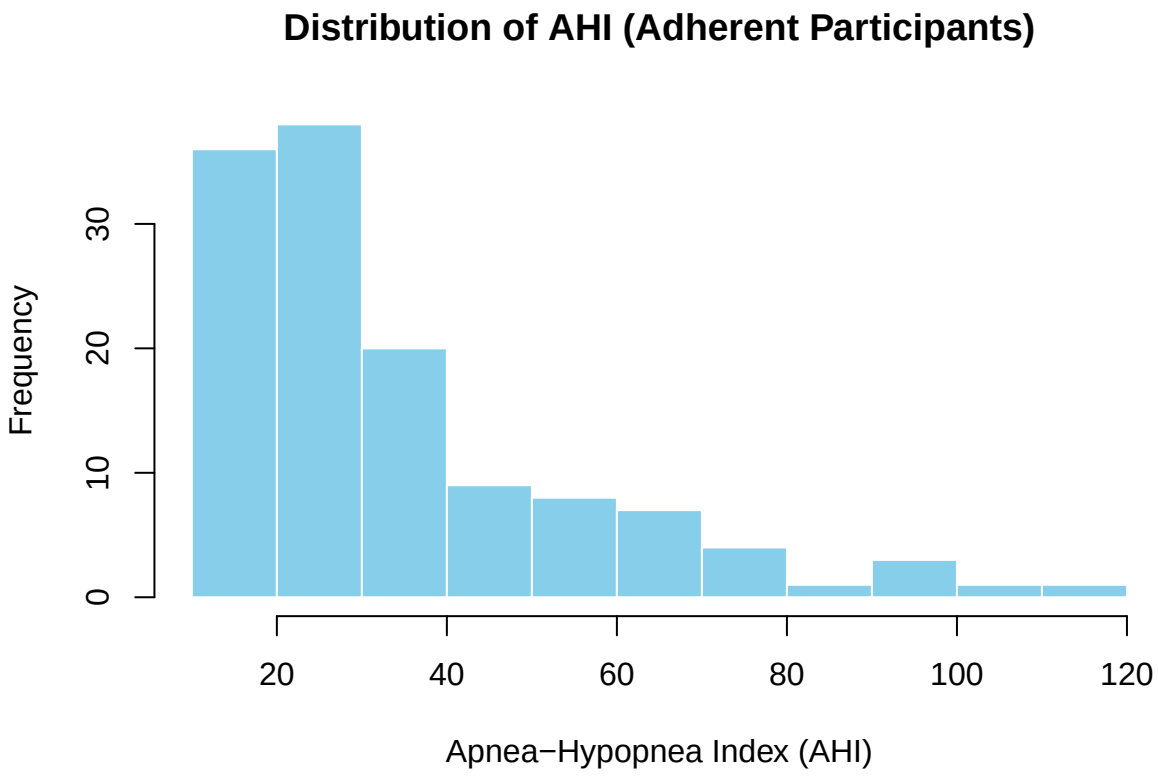
```
mean_ahi <- mean(adherent_data$AHI, na.rm = TRUE)
sd_ahi <- sd(adherent_data$AHI, na.rm = TRUE)

cat("Mean AHI:", mean_ahi, "\n")
```

```
## Mean AHI: 34.48664
```

```
cat("SD AHI:", sd_ahi, "\n")
```

```
## SD AHI: 21.20208
```

```
# Histogram
hist(adherent_data$AHI,
     main = "Distribution of AHI (Adherent Participants)",
     xlab = "Apnea-Hypopnea Index (AHI)",
     col = "skyblue", border = "white")
```



Interpretation: For the adherent CPAP participants, the Apnea–Hypopnea Index (AHI) has an average value of approximately 34.5, with a standard deviation of 21.2. The AHI values range from 15 to 112.7, indicating a wide spread. The histogram shows a right-skewed distribution, suggesting that a few participants with very high AHI values substantially influence the overall data pattern.

In plain English: Among people who regularly use CPAP, the AHI usually averages around 34.5, but it can vary widely—from 15 to over 110. This means that while many participants have moderate AHI scores, some experience much more severe sleep apnea. Because a small group has very high AHI values, the data are unevenly distributed, making the average appear higher.

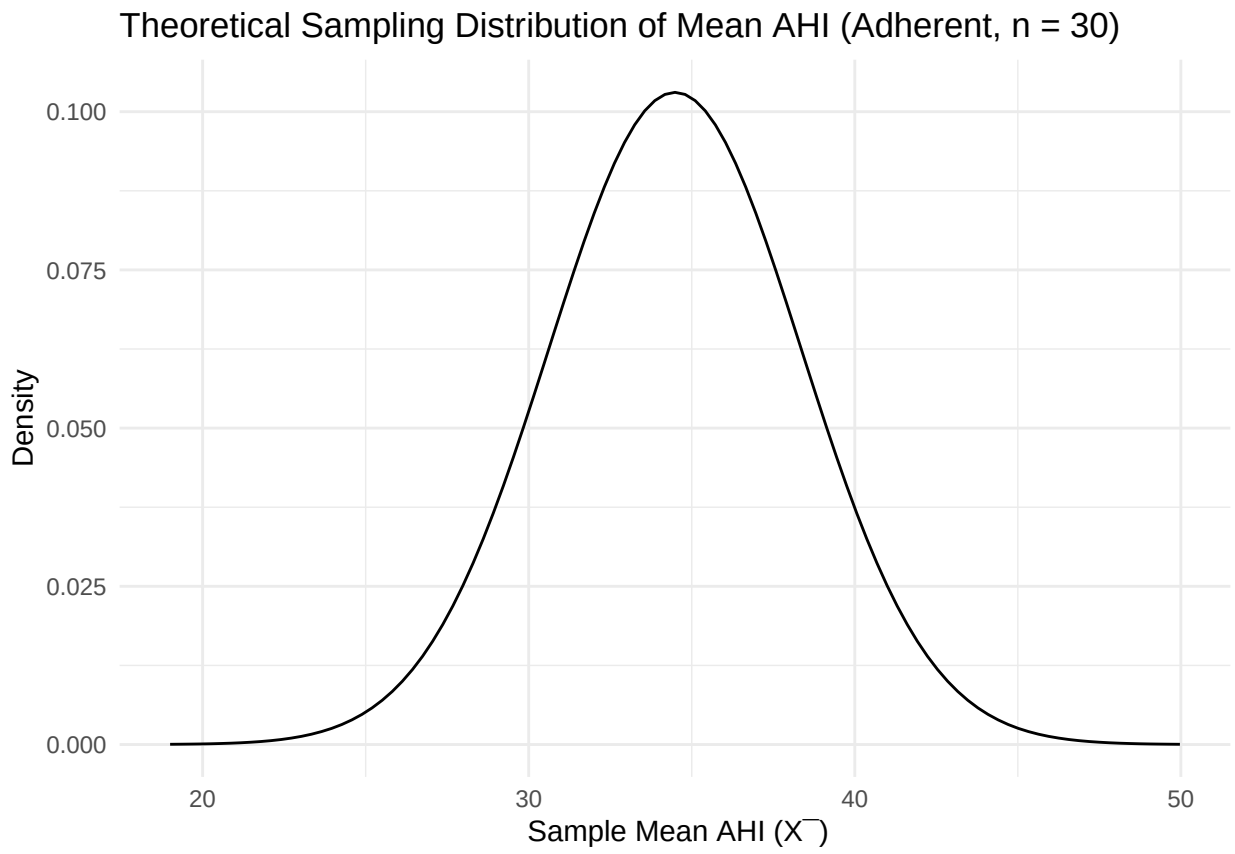
7B. Among those who are adherent to CPAP, describe the sampling distribution based on samples of size 30 from the variable AHI based on theory with appropriate statistics and data visualizations. Then, summarize findings in 2-3 sentences in plain language suitable for a non-statistical audience.

```
##7B

library(dplyr)
library(ggplot2)
# 1) Subset + ensure numeric
adherent_data <- Data %>%
  filter(adherence == "Adherent") %>%
  mutate(AHI = as.numeric(AHI))
```

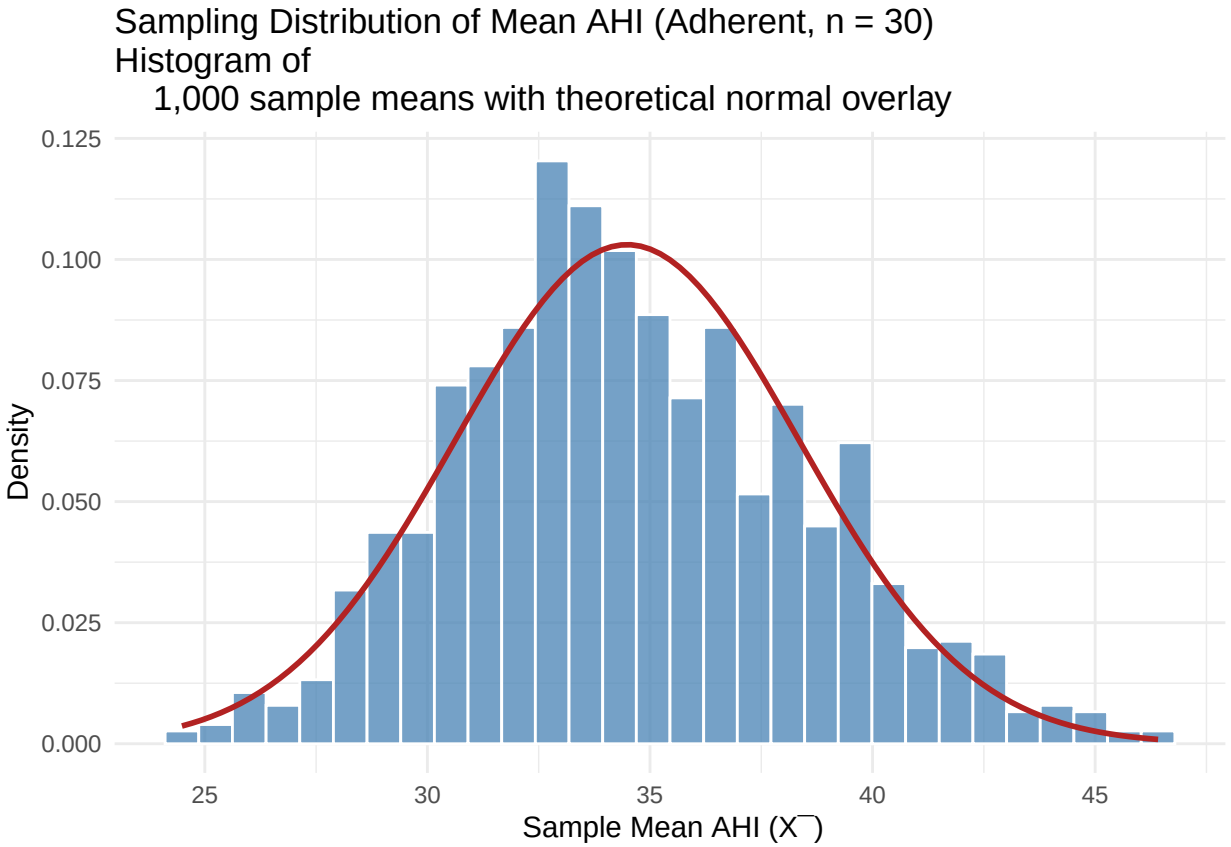
```r
# 2) Population (group) parameters for AHI among adherent participants
mu_hat  <- mean(adherent_data$AHI, na.rm = TRUE)
sd_hat  <- sd(adherent_data$AHI,   na.rm = TRUE)
n_theory <- 30
SE_theory <- sd_hat / sqrt(n_theory)

cat(
  "Adherent AHI (theory, n = 30)\n",
  "Mean (^):", round(mu_hat, 2), "\n",
  "SD (^):", round(sd_hat, 2), "\n",
  "Standard Error (SE = ^/sqrt(30)):", round(SE_theory, 3), "\n"
)
```

```
## Adherent AHI (theory, n = 30)
##  Mean (^): 34.49
##  SD (^): 21.2
##  Standard Error (SE = ^/sqrt(30)): 3.871
```

```r
# 3) Visual 1 (theoretical normal curve for X, no data histogram)
xgrid <- data.frame(
  x = seq(mu_hat - 4*SE_theory, mu_hat + 4*SE_theory, length.out = 400)
)
ggplot(xgrid, aes(x)) +
  stat_function(fun = dnorm, args = list(mean = mu_hat, sd = SE_theory)) +
  labs(
    title = "Theoretical Sampling Distribution of Mean AHI (Adherent, n = 30)",
    x = "Sample Mean AHI (X)",
    y = "Density"
  ) +
  theme_minimal()
```




```r
#Visual 2: simulate to illustrate CLT and overlay theory
set.seed(2025)
B <- 1000
samp_means <- replicate(
  B,
  mean(sample(adherent_data$AHI, size = n_theory, replace = TRUE), na.rm = TRUE)
)

ggplot(data.frame(samp_means), aes(x = samp_means)) +
  geom_histogram(aes(y = after_stat(density)), bins = 30, fill = "steelblue",
                 color = "white", alpha = 0.75) +
  stat_function(fun = dnorm, args = list(mean = mu_hat, sd = SE_theory),
                linewidth = 1, color = "firebrick") +
  labs(
    title = "Sampling Distribution of Mean AHI (Adherent, n = 30)\nHistogram of
    1,000 sample means with theoretical normal overlay",
    x = "Sample Mean AHI (X)",
    y = "Density"
  ) +
  theme_minimal()
```



Interpretation: If we repeatedly take random groups of 30 adherent CPAP users and calculate their average AHI, those averages would tend to cluster around 34.5. The standard error of 3.9 indicates that the sample means would typically vary by about 3.9 AHI points from one sample to another. In other words, most of the group averages would lie close to the true mean, forming a bell-shaped (normal) distribution.

In short, when drawing samples of 30 adherent users, the average AHI for each group would generally be close to 34.5, with only moderate variation between samples.

7C. Randomly draw 1,000 samples of size 30 (with replacement) from the 128 AHI scores of adherent participants. For each sample, compute the sample mean AHI. Use these 1,000 sample means to:

```
#7C
# Ensure the AHI column is numeric
adherent_data$AHI <- as.numeric(adherent_data$AHI)

# Define the parameters
MY_DATA_1 <- adherent_data
VARIABLE <- "AHI"          # The variable to sample
SAMPLES <- 1000            # Number of samples
SIZE <- 30                 # Sample size

# Initialize an empty vector to store the means
meanValues <- numeric(SAMPLES)
```

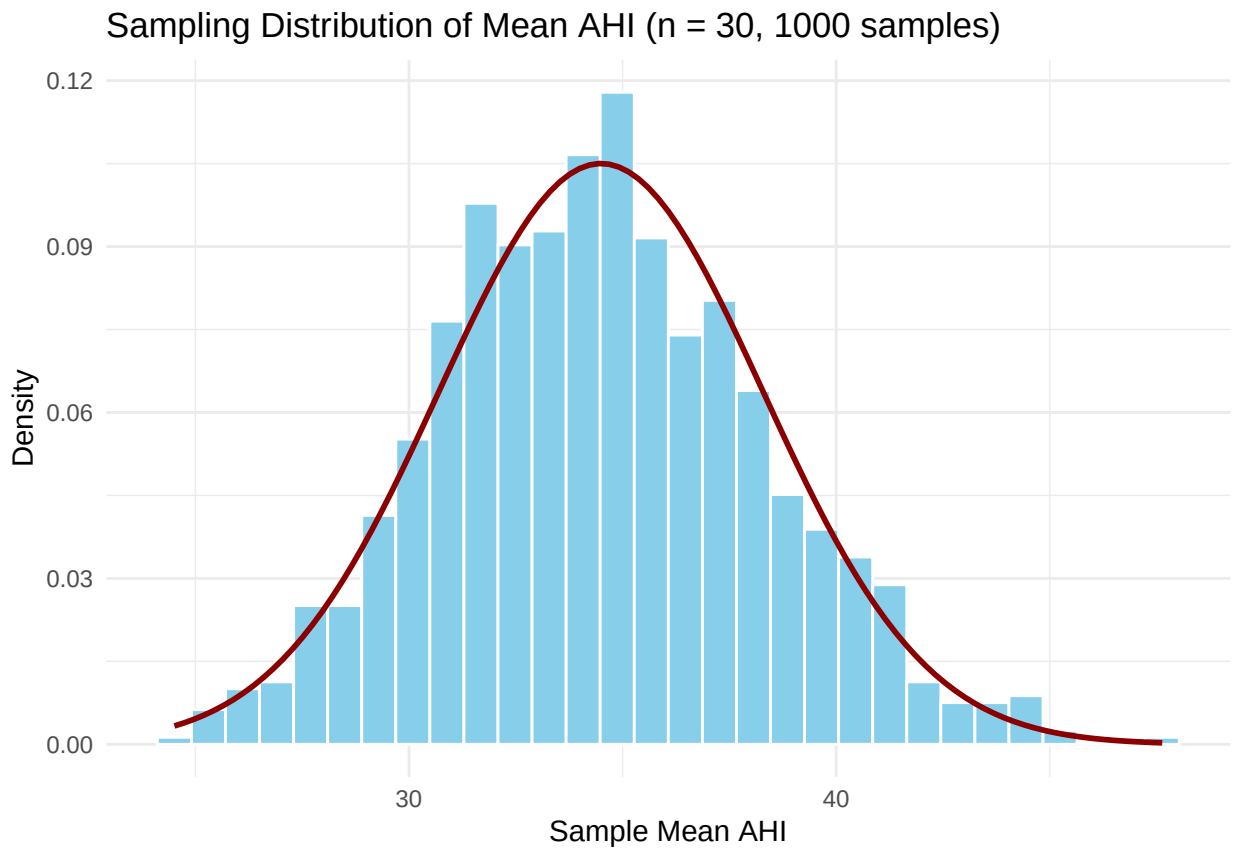
```r
# Sampling loop (1000 samples, sample size 30)
for (i in 1:SAMPLES) {
  sampSpots <- sample(1:nrow(MY_DATA_1), size = SIZE, replace = TRUE)
  thisSamp <- MY_DATA_1[sampSpots, VARIABLE]

  # Ensure the sample is numeric and handle any NA values
  thisSamp <- thisSamp[!is.na(thisSamp)]

  if(length(thisSamp) == SIZE) {  # Check if the sample is the correct size
    meanValues[i] <- mean(thisSamp)
  } else {
    meanValues[i] <- NA  # If the sample is not valid, mark as NA
  }
}

# Check if valid sample means are calculated
if(sum(!is.na(meanValues)) == 0) {
  stop("No valid means were calculated. Check the sampling process.")
}

# Calculate and report mean and SD of the sampling distribution
mean_sampling_1 <- mean(meanValues, na.rm = TRUE)
sd_sampling_1 <- sd(meanValues, na.rm = TRUE)

cat("Mean of sample means:", mean_sampling_1, "\n")
```

```
## Mean of sample means: 34.49511
```

```r
cat("Standard deviation of sample means (Standard Error):", sd_sampling_1, "\n")
```

```
## Standard deviation of sample means (Standard Error): 3.798762
```

```r
# Plot the histogram and overlay normal curve
library(ggplot2)
ggplot(data.frame(meanValues), aes(x = meanValues)) +
  geom_histogram(aes(y = after_stat(density)), bins = 30, fill = "skyblue",
                 color = "white") +
  stat_function(fun = dnorm, args = list(mean = mean_sampling_1,
                                         sd = sd_sampling_1),
                color = "darkred", linewidth = 1) +
  labs(title = "Sampling Distribution of Mean AHI (n = 30, 1000 samples)",
       x = "Sample Mean AHI", y = "Density") +
  theme_minimal()
```



Interpretation: The histogram of the 1,000 sample means forms a smooth, symmetric, bell-shaped curve centered around 34.5, with the red normal curve closely overlapping it. This shows that the sample means follow an approximately normal distribution with only moderate variability, meaning that averages from groups of 30 adherent participants are highly consistent.

The observed sampling distribution matches the theoretical distribution predicted earlier, with nearly the same mean (34.5) and standard error (3.9). This agreement provides strong evidence of the Central Limit Theorem in action—even though individual AHI scores vary widely, the averages from groups of 30 adherent users remain stable and normally distributed around the true mean.

7D. Among those who are non-adherent to CPAP, describe the sampling distribution based on samples of size 100 from the variable AHI based on theory with appropriate statistics and data visualizations. Then summarize your findings in 2-3 sentences in plain language suitable for a non-statistical audience.

```
## 7D
# Load necessary libraries
library(dplyr)
library(ggplot2)

# Filter for non-adherent participants
non_adherent_data <- Data %>%
  filter(adherence == "Non-adherent")
```

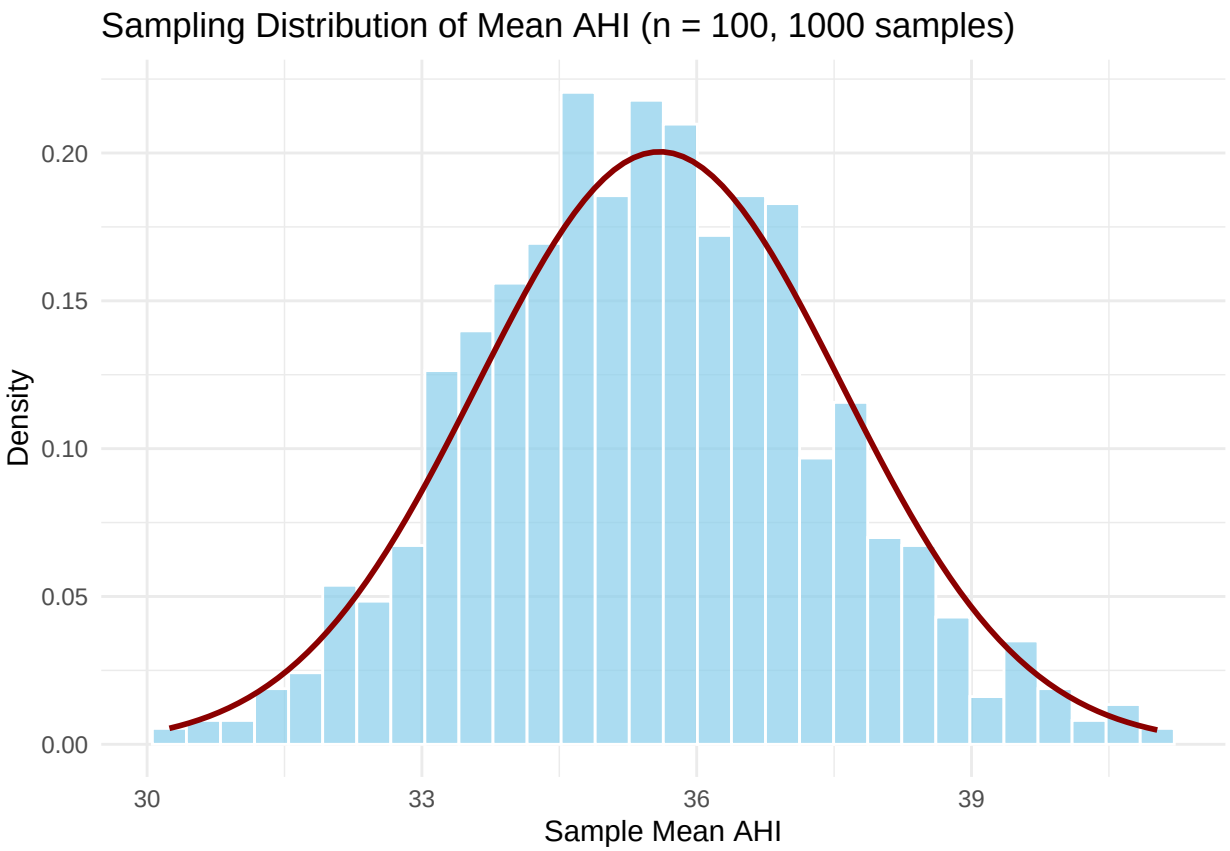
```r
# Ensure the AHI column is numeric
non_adherent_data$AHI <- as.numeric(non_adherent_data$AHI)

# Calculate population parameters (mean and standard deviation of AHI)
population_mean <- mean(non_adherent_data$AHI, na.rm = TRUE)
population_sd <- sd(non_adherent_data$AHI, na.rm = TRUE)

# Parameters for sampling
sample_size <- 100  # Sample size
n_samples <- 1000   # Number of samples

# Calculate the standard error
standard_error <- population_sd / sqrt(sample_size)

# Simulate the sampling distribution of the mean
set.seed(123)  # Set a seed for reproducibility
sample_means <- numeric(n_samples)

for (i in 1:n_samples) {
  # Randomly sample 100 values from the population with replacement
  sample_data <- sample(non_adherent_data$AHI, size = sample_size, replace = TRUE)
  sample_means[i] <- mean(sample_data, na.rm = TRUE)
}

# Calculate mean and standard deviation of the sampling distribution
mean_sampling <- mean(sample_means, na.rm = TRUE)
sd_sampling <- sd(sample_means, na.rm = TRUE)

cat("Theoretical Mean of the Sampling Distribution:", mean_sampling, "\n")
```

```
## Theoretical Mean of the Sampling Distribution: 35.49504
```

```r
cat("Theoretical Standard Deviation of the Sampling Distribution
    (Standard Error):", sd_sampling, "\n")
```

```
## Theoretical Standard Deviation of the Sampling Distribution
##     (Standard Error): 1.881024
```

```r
# Plot the histogram of the sample means and overlay a normal distribution curve
ggplot(data.frame(sample_means), aes(x = sample_means)) +
  geom_histogram(aes(y = after_stat(density)), bins = 30, fill = "skyblue",
                 color = "white", alpha = 0.7) +
  stat_function(fun = dnorm,
                args = list(mean = population_mean, sd = standard_error),
                color = "darkred", linewidth = 1) +  # Overlay normal curve
  labs(title = "Sampling Distribution of Mean AHI (n = 100, 1000 samples)",
       x = "Sample Mean AHI", y = "Density") +
  theme_minimal()
```



Interpretation: If we repeatedly take random groups of 100 non-adherent CPAP users and calculate their average AHI, those averages would cluster around 35.6. The standard error of about 2 AHI points indicates that the sample means would vary only slightly from one sample to another. This means most group averages would fall close to the true mean, forming a bell-shaped (normal) distribution.

In short, when taking samples of 100 non-adherent users, the average AHI is estimated very precisely around 35–36, showing that larger sample sizes produce more stable and reliable estimates of the true mean.

7E. Randomly draw 1,000 samples of size 100 (with replacement) from the 46 AHI scores of non-adherent participants. For each sample, compute the sample mean AHI.

```
##7E
# Replace the following with actual values:
MY_DATA_2 <- non_adherent_data
VARIABLE <- "AHI"
SAMPLES <- 1000
SIZE <- 100

# Ensure the AHI column is numeric
non_adherent_data$AHI <- as.numeric(non_adherent_data$AHI)
# Ensure the variable is numeric
MY_DATA_2[[VARIABLE]] <- as.numeric(MY_DATA_2[[VARIABLE]])
# Initialize an empty vector to store sample means
meanValues <- NULL
```

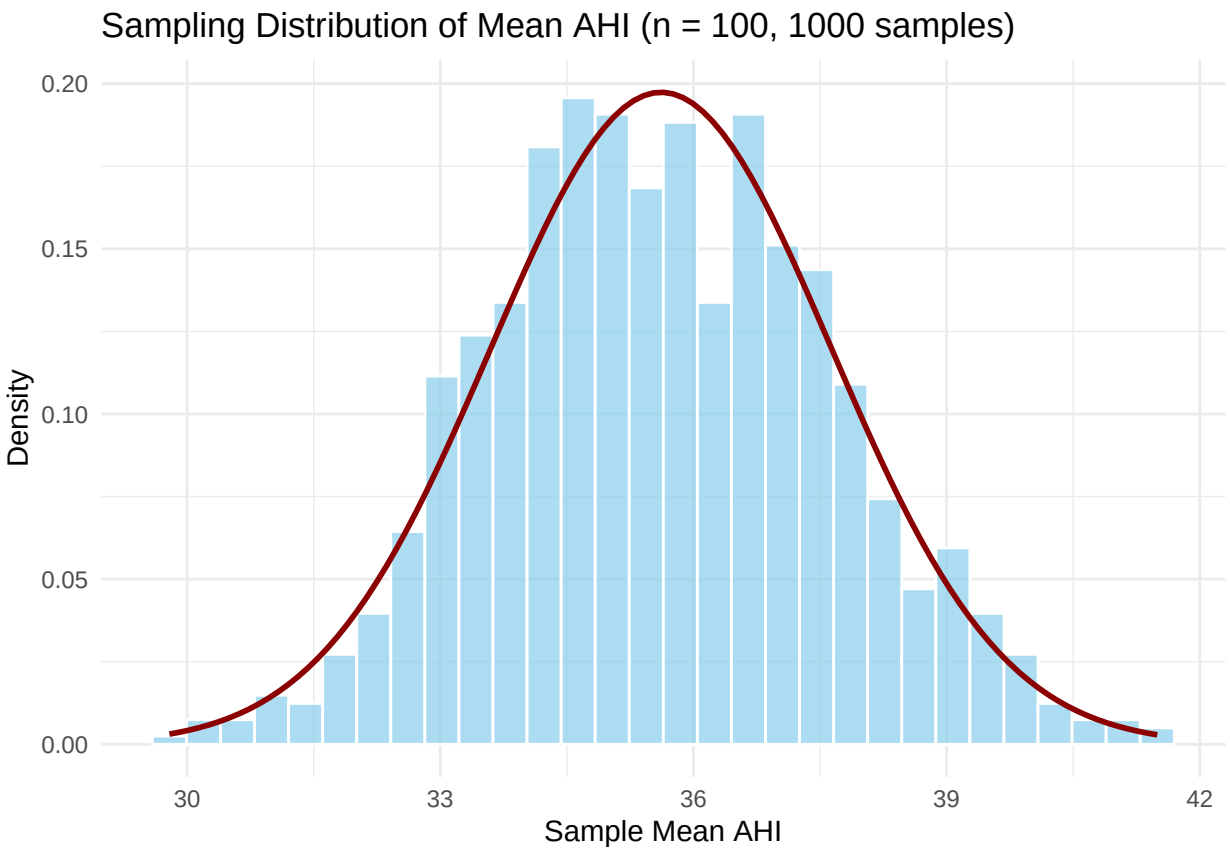
```r
# Loop to draw SAMPLES number of samples and calculate mean AHI for each sample
for (i in 1:SAMPLES) {
  # Sample with replacement
  sampSpots <- sample(x = 1:nrow(MY_DATA_2), size = SIZE, replace = TRUE)

  # Extract the sample data for the variable specified
  thisSamp <- MY_DATA_2[sampSpots, ][[VARIABLE]]



# Calculate and store the mean of the sample
  meanValues <- c(meanValues, mean(thisSamp, na.rm = TRUE))
}


# Calculate and print the mean and sd of the sampling distribution
mean_sampling_2 <- mean(meanValues, na.rm = TRUE)
sd_sampling_2 <- sd(meanValues, na.rm = TRUE)

cat("Mean of the sampling distribution:", mean_sampling_2, "\n")
```

```
## Mean of the sampling distribution: 35.61692
```

```r
cat("Standard deviation of the sampling distribution (Standard Error):", sd_sampling_2, "\n")
```

```
## Standard deviation of the sampling distribution (Standard Error): 2.021068
```

```r
# Plot the histogram of sample means and overlay a normal distribution curve
library(ggplot2)

ggplot(data.frame(meanValues), aes(x = meanValues)) +
  geom_histogram(aes(y = after_stat(density)), bins = 30, fill = "skyblue", color = "white", alpha = 0.
  stat_function(fun = dnorm,
                args = list(mean = mean_sampling_2, sd = sd_sampling_2),
                color = "darkred", linewidth = 1) +  # Overlay normal curve
  labs(title = "Sampling Distribution of Mean AHI (n = 100, 1000 samples)",
       x = "Sample Mean AHI", y = "Density") +
  theme_minimal()
```



Interpretation: The histogram of 1,000 sample averages for the non-adherent group forms a smooth, bell-shaped curve centered around 35.6, with the red normal curve fitting closely on top. This indicates that the sample means follow an approximately normal distribution. The spread is small—about 2 AHI points—showing that the averages from groups of 100 non-adherent participants vary very little between samples.

Comparison with Part (D): This empirical sampling distribution, generated from multiple simulations, closely matches the theoretical distribution described in Part (D). Both have nearly identical means (35.6) and standard errors (2), confirming that theoretical expectations and simulated results agree.

In plain terms: Whether calculated mathematically or obtained through resampling, the results show that the average AHI among non-adherent users is stable, predictable, and normally distributed when the sample size is large.

7F. Compare the sampling distributions among adherent versus non-adherent participants. How do the means and spreads of the two sampling distributions compare? Why do you think they are the same or different? Summarize your findings in 3-5 sentences in plain language suitable for a non-statistical audience.

```
##7F
#Filter for adherent and non-adherent participants
adherent_data <- Data %>% filter(adherence == "Adherent")
non_adherent_data <- Data %>% filter(adherence == "Non-adherent")

# Ensure AHI is numeric
adherent_data$AHI <- as.numeric(adherent_data$AHI)
```

```r
non_adherent_data$AHI <- as.numeric(non_adherent_data$AHI)

# Set parameters
SAMPLES <- 1000
SIZE_ADHERENT <- 30
SIZE_NONADHERENT <- 100

# Initialize vectors
sample_means_adherent <- numeric(SAMPLES)
sample_means_non_adherent <- numeric(SAMPLES)

set.seed(123)

# Loop to calculate sample means
for (i in 1:SAMPLES) {
  sample_adherent <- sample(adherent_data$AHI, size = SIZE_ADHERENT,
                            replace = TRUE)
  sample_non_adherent <- sample(non_adherent_data$AHI, size = SIZE_NONADHERENT,
                                replace = TRUE)

  sample_means_adherent[i] <- mean(sample_adherent, na.rm = TRUE)
  sample_means_non_adherent[i] <- mean(sample_non_adherent, na.rm = TRUE)
}

# Calculate summary stats
mean_adherent <- mean(sample_means_adherent)
std_adherent <- sd(sample_means_adherent)

mean_non_adherent <- mean(sample_means_non_adherent)
std_non_adherent <- sd(sample_means_non_adherent)

cat("Adherent Mean:", mean_adherent, "\n")
```

```
## Adherent Mean: 34.51462
```

```r
cat("Non-Adherent Mean:", mean_non_adherent, "\n")
```

```
## Non-Adherent Mean: 35.55352
```

```r
cat("Adherent SD:", std_adherent, "\n")
```

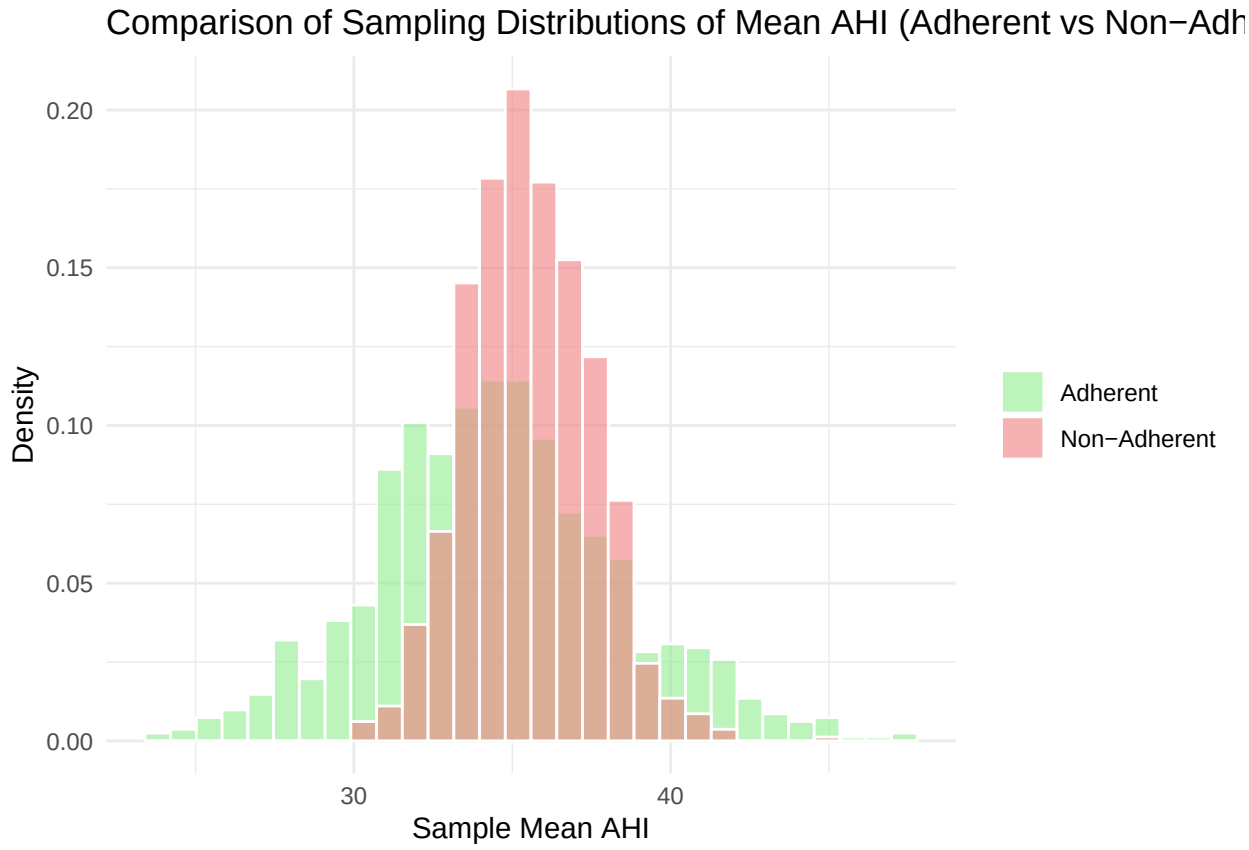
```
## Adherent SD: 3.876826
```

```r
cat("Non-Adherent SD:", std_non_adherent, "\n")
```

```
## Non-Adherent SD: 1.954662
```

```r
# Combine data for plotting
data_for_plot <- data.frame(
  mean_values = c(sample_means_adherent, sample_means_non_adherent),
```

```
  group = rep(c("Adherent", "Non-Adherent"), each = SAMPLES)
)

# Plot the overlapping histograms
ggplot(data_for_plot, aes(x = mean_values, fill = group)) +
  geom_histogram(aes(y = after_stat(density)), bins = 30, alpha = 0.6,
                 position = "identity", color = "white") +
  labs(title = "Comparison of Sampling Distributions of Mean AHI (Adherent vs Non-Adherent)",
       x = "Sample Mean AHI", y = "Density") +
  scale_fill_manual(values = c("lightgreen", "lightcoral")) +
  theme_minimal() +
  theme(legend.title = element_blank())
```



Interpretation: The average Apnea–Hypopnea Index (AHI) levels for both groups are quite similar, ranging from 34 to 36. However, their sampling distributions differ in spread. The non-adherent group shows a tighter, more consistent distribution because it is based on a larger sample size (n = 100), which reduces random variation.

In contrast, the adherent group's distribution is wider, as smaller samples (n = 30) naturally produce more fluctuation in their averages.

In simple terms: Both groups have roughly the same average severity of sleep apnea, but the results for non-adherent users are more stable and predictable, while those for adherent users vary more from sample to sample.

‘‘‘

Table 1: Demographic and Clinical Characteristics (n = 174)

Characteristic	**N**	**Non-adherent** N = 46[1]	**Adherent** N = 128[1]	**p-value**[2]
Ethnicity	174			>0.9
Hispanic or Latino		3 (6.5%)	10 (7.8%)	
Not Hispanic or Latino		43 (93%)	118 (92%)	
Education	174			0.4
<= high school		12 (26%)	24 (19%)	
> high school		34 (74%)	104 (81%)	
Race	173			<0.001
White		23 (51%)	101 (79%)	
Black		19 (42%)	18 (14%)	
Other		3 (6.7%)	9 (7.0%)	
Unknown		1	0	
Age	174	66.98 ± 7.57	66.81 ± 7.53	0.9
Sex	174			>0.9
Female		22 (48%)	58 (45%)	
Male		24 (52%)	70 (55%)	
BMI	174	42.15 ± 7.37	42.20 ± 7.18	>0.9
AHI	174	35.59 ± 19.91	34.49 ± 21.20	0.8
ESS	174	9.02 ± 4.79	8.84 ± 5.04	0.8
MMSE	174			0.6
21		1 (2.2%)	0 (0%)	
23		0 (0%)	3 (2.3%)	
24		2 (4.3%)	4 (3.1%)	
25		3 (6.5%)	10 (7.8%)	
26		6 (13%)	15 (12%)	
27		9 (20%)	20 (16%)	
28		11 (24%)	24 (19%)	
29		11 (24%)	35 (27%)	
30		3 (6.5%)	17 (13%)	
Average daily CPAP (hr/night)	174	1.61 ± 1.35	6.42 ± 1.32	<0.001
ODSI_baseline	174	8.30 ± 5.77	7.87 ± 6.21	0.7
ODSI_6m	153	6.18 ± 5.35	5.01 ± 4.80	0.3
Unknown		12	9	
ADCS_MCI_12m	129			0.5
1		2 (7.7%)	17 (17%)	
2		3 (12%)	25 (24%)	
3		6 (23%)	19 (18%)	
4		8 (31%)	25 (24%)	
5		4 (15%)	10 (9.7%)	
6		3 (12%)	7 (6.8%)	
Unknown		20	25	

[1]n (%); Mean ± SD

[2]Pearson's Chi-squared test; Welch Two Sample t-test