

# Integration of AI and R Programming

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**Demonstration of implementing OpenAI in R programming for generating neat document in PDF, Presentation, and Word.**

```
rm(list = ls())  
library(tidyverse)  
library(ggplot2)  
library(readxl)  
library(writexl)  
library(httr)  
library(jsonlite)
```

Attaching package: 'jsonlite'

The following object is masked from 'package:purrr':

flatten

```
library(flextable)
```

Attaching package: 'flextable'

The following object is masked from 'package:purrr':

compose

```
library(table1)
```

Attaching package: 'table1'

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

```
units, units<-
```

```
set.seed(123)
options(width = 70)
source("src/func.R")
```

**Ask AI to generate a dummy patient characteristic, demographic, baseline, treatment, and binary clinical response data set**

```
question <- "Can you give R code to generate a dummy data frame for 100
  ↪ patients with their characteristics such as gender, age, bmi, height,
  ↪ race, baseline, treatment, and binary clinical response data set?"
result1 <- chatgpt_query_with_history(question)
cat("Assistant's answer:\n", result1$answer, "\n")
```

Assistant's answer:

Sure! Here is R code to generate a dummy data frame for 100 patients with the characteristics

```
```R
# Set seed for reproducibility
set.seed(123)

# Generate dummy data for 100 patients
gender <- sample(c("Male", "Female"), 100, replace = TRUE)
age <- round(rnorm(100, mean = 50, sd = 10))
bmi <- round(rnorm(100, mean = 25, sd = 5), 1)
height <- round(rnorm(100, mean = 170, sd = 10), 1)
race <- sample(c("White", "Black", "Asian", "Hispanic"), 100, replace = TRUE)
baseline <- round(runif(100, min = 100, max = 200), 1)
treatment <- sample(c("Placebo", "Drug A", "Drug B"), 100, replace = TRUE)
```

```

clinical_response <- sample(c(0, 1), 100, replace = TRUE)

# Create a data frame
patients <- data.frame(Gender = gender, Age = age, BMI = bmi, Height = height, Race = race,
                      Baseline = baseline, Treatment = treatment, Clinical_Response = clinical_response)

# Display the first few rows of the data frame
head(patients)
```

```

This code will create a data frame `patients` with 100 rows and the following columns: Gender, Age, BMI, Height, Race, Baseline, Treatment, Clinical\_Response.

```

# Optionally, extract R code:
eval(parse(text = extract_r_code(result1)))

```

|   | Gender | Age | BMI  | Height | Race     | Baseline | Treatment |
|---|--------|-----|------|--------|----------|----------|-----------|
| 1 | Male   | 53  | 28.9 | 166.2  | Black    | 147.1    | Placebo   |
| 2 | Male   | 50  | 28.8 | 164.4  | White    | 136.6    | Placebo   |
| 3 | Male   | 50  | 26.7 | 166.6  | White    | 112.1    | Drug A    |
| 4 | Female | 64  | 20.0 | 170.9  | Asian    | 104.7    | Drug B    |
| 5 | Male   | 48  | 24.4 | 186.0  | Hispanic | 126.3    | Drug B    |
| 6 | Female | 65  | 23.6 | 169.1  | White    | 196.9    | Drug A    |

|   | Clinical_Response |
|---|-------------------|
| 1 | 1                 |
| 2 | 0                 |
| 3 | 0                 |
| 4 | 0                 |
| 5 | 0                 |
| 6 | 0                 |

**Continue asking AI to make a characteristics table for the patients between treatment**

```

question2 <- "Can you give me the R code to generate the patient
↪ characteristics
table using R package table1 between treatment? I already installed the
↪ package."
result2 <- chatgpt_query_with_history(question2, history = result1$history)
cat("Assistant's answer:\n", result2$answer, "\n")

```

Assistant's answer:

Sure! To generate a patient characteristics table using the `table1` package in R between treatment groups:

```
```R
# Load the required library
library(table1)

# Generate the patient characteristics table between treatment groups
table1(~ Gender + Age + BMI + Height + Race + Baseline + Clinical_Response | Treatment, data = patients)
```
```

In this code:

- `~ Gender + Age + BMI + Height + Race + Baseline + Clinical\_Response | Treatment` specifies the variables to be included in the table.
- `data = patients` specifies that the data for the analysis is stored in the `patients` dataset.

When you run this code, you will get a table summarizing the patient characteristics by treatment group.

```
eval(parse(text = extract_r_code(result2)))
```

|                          | Drug A            | Drug B            | Placebo           | Overall           |
|--------------------------|-------------------|-------------------|-------------------|-------------------|
|                          | (N=35)            | (N=38)            | (N=27)            | (N=100)           |
| <b>Gender</b>            |                   |                   |                   |                   |
| Female                   | 14 (40.0%)        | 18 (47.4%)        | 11 (40.7%)        | 43 (43.0%)        |
| Male                     | 21 (60.0%)        | 20 (52.6%)        | 16 (59.3%)        | 57 (57.0%)        |
| <b>Age</b>               |                   |                   |                   |                   |
| Mean (SD)                | 48.5 (10.3)       | 50.0 (9.17)       | 49.8 (9.65)       | 49.5 (9.62)       |
| Median [Min, Max]        | 48.0 [27.0, 72.0] | 49.5 [35.0, 71.0] | 51.0 [29.0, 69.0] | 49.5 [27.0, 72.0] |
| <b>BMI</b>               |                   |                   |                   |                   |
| Mean (SD)                | 25.4 (3.86)       | 24.5 (5.40)       | 25.4 (4.64)       | 25.1 (4.68)       |
| Median [Min, Max]        | 25.3 [18.2, 33.4] | 23.2 [18.4, 41.2] | 25.5 [18.4, 34.8] | 24.1 [18.2, 41.2] |
| <b>Height</b>            |                   |                   |                   |                   |
| Mean (SD)                | 173 (9.98)        | 170 (10.1)        | 170 (9.53)        | 171 (9.92)        |
| Median [Min, Max]        | 174 [153, 190]    | 171 [150, 193]    | 170 [153, 190]    | 171 [150, 193]    |
| <b>Race</b>              |                   |                   |                   |                   |
| Asian                    | 5 (14.3%)         | 10 (26.3%)        | 6 (22.2%)         | 21 (21.0%)        |
| Black                    | 5 (14.3%)         | 9 (23.7%)         | 8 (29.6%)         | 22 (22.0%)        |
| Hispanic                 | 11 (31.4%)        | 9 (23.7%)         | 7 (25.9%)         | 27 (27.0%)        |
| White                    | 14 (40.0%)        | 10 (26.3%)        | 6 (22.2%)         | 30 (30.0%)        |
| <b>Baseline</b>          |                   |                   |                   |                   |
| Mean (SD)                | 152 (30.6)        | 147 (30.1)        | 147 (26.3)        | 149 (29.1)        |
| Median [Min, Max]        | 157 [100, 199]    | 149 [101, 199]    | 149 [101, 181]    | 152 [100, 199]    |
| <b>Clinical_Response</b> |                   |                   |                   |                   |
| Mean (SD)                | 0.457 (0.505)     | 0.500 (0.507)     | 0.444 (0.506)     | 0.470 (0.502)     |
| Median [Min, Max]        | 0 [0, 1.00]       | 0.500 [0, 1.00]   | 0 [0, 1.00]       | 0 [0, 1.00]       |

**Continue asking AI to make a bar plot for the response rate between the treatment groups**

```
question3 <- "Can you give me the R code to make a barplot for the response
rates between treatment groups?"
result3 <- chatgpt_query_with_history(question3, history = result1$history)
cat("Assistant's answer:\n", result3$answer, "\n")
```

Assistant's answer:

Sure! Here is the R code to create a barplot showing the response rates between different treatment groups:

```

```R
# Load the necessary library
library(ggplot2)

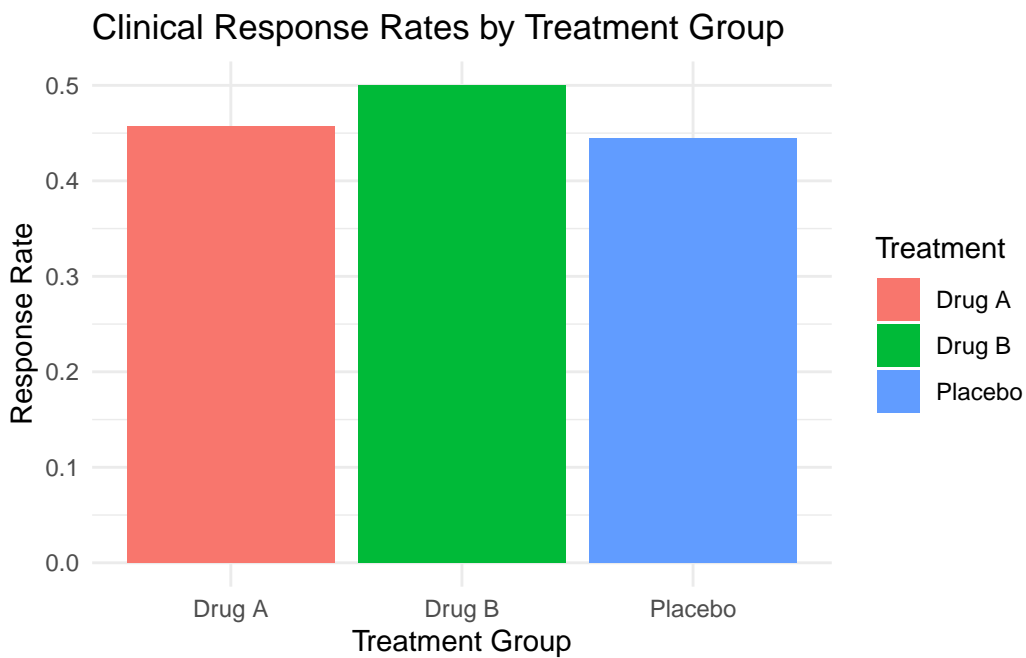
# Create a summary table of response rates by treatment group
response_summary <- aggregate(Clinical_Response ~ Treatment, data = patients, FUN = mean)

# Create a bar plot showing response rates by treatment group
ggplot(response_summary, aes(x = Treatment, y = Clinical_Response, fill = Treatment)) +
  geom_bar(stat = "identity") +
  labs(title = "Clinical Response Rates by Treatment Group",
        x = "Treatment Group",
        y = "Response Rate") +
  theme_minimal()
```

```

This code will generate a barplot displaying the clinical response rates for each treatment group.

```
eval(parse(text = extract_r_code(result3)))
```



## Continue asking AI to statistical test for the response rate between the treatment groups

```
question4 <- "Can you give me the R code to evaluate statistical differences  
  ↪ for  
the response rates between treatment groups?"  
result4 <- chatgpt_query_with_history(question4, history = result1$history)  
cat("Assistant's answer:\n", result4$answer, "\n")
```

Assistant's answer:

Sure! To evaluate statistical differences in response rates between treatment groups, you can

```
```R  
# Create a contingency table of Treatment and Clinical_Response  
cont_table <- table(patients$Treatment, patients$Clinical_Response)  
  
# Perform a chi-squared test  
chi_test <- chisq.test(cont_table)  
  
# Display the results  
print(chi_test)  
```
```

This code will create a contingency table of Treatment and Clinical\_Response in the `patients`

```
eval(parse(text = extract_r_code(result4)))
```

Pearson's Chi-squared test

```
data:  cont_table  
X-squared = 0.23131, df = 2, p-value = 0.8908
```