



GURU TEGH BAHADUR 4TH CENTENARY ENGINEERING COLLEGE

G-8 AREA, RAJOURI GARDEN, NEW DELHI-110064

DATA SCIENCE PRACTICAL FILE

Course Code: CIE-405P

Semester: 7th

Submitted to :

Geeta Yadav

Submitted by :

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CSE 1



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CSE - 01

S.NO.	AIM OF EXPERIMENT	DATE OF EXPERIMENT	SIGNATURE
1.	Installation of R and Basic Syntax	29-08-2025	
2.	Describing Data, Viewing, and Manipulating Data Using R	29-08-2025	
3.	Plotting Probability Distribution Curve in R	12-09-2025	
4.	Implementing Linear Regression in R	19-09-2025	
5.	Logistic Regression	19-09-2025	
6.	Principal Component Analysis (PCA) on dataset using R	26-09-2025	
7.	Chi-Square Test in R	26-09-2025	
8.	Edit and Execute a Program Involving Functions in R	17-10-2025	
9.	Edit and Execute a Program Involving Flow Chart	17-10-2025	
10.	Data Aggregation and Group Operations in R	24-10-2025	

Experiment 1: Installation of R and Basic Syntax.

AIM: To install R and learn the basic syntax of R programming.

Theory

R is a statistical programming language widely used for data analysis and visualization. The installation of R and RStudio provides an environment to write, edit, and execute R programs.

Basic syntax includes variables, arithmetic operations, vectors, sequences, and printing results.

Program (R code):

```
# Basic syntax demonstration in R
```

```
# Assigning values
```

```
x <- 25
```

```
y <- 15
```

```
# Arithmetic operations
```

```
sum_result<- x + y
```

```
diff_result<- x - y
```

```
prod_result<- x * y
```

```
div_result<- x / y
```

```
# Creating a vector
```

```
numbers<- c(2, 4, 6, 8, 10)
```

```
# Generating a sequence
```

```
sequence<- seq(1, 20, by = 2)
```

```
# Mean and Sum of vector
```

```
mean_val<- mean(numbers)
```

```
sum_val<- sum(numbers)
```

Displaying results

```
print(paste("Sum of x and y is:", sum_result))

print(paste("Difference of x and y is:", diff_result))

print(paste("Product of x and y is:", prod_result))

print(paste("Division of x and y is:", div_result))

print("Vector values:")

print(numbers)

print("Sequence from 1 to 20 with step 2:")

print(sequence)

print(paste("Mean of vector:", mean_val))

print(paste("Sum of vector:", sum_val))
```

Expected Output:

```
[1] "Sum of x and y is: 40"

[1] "Difference of x and y is: 10"

[1] "Product of x and y is: 375"

[1] "Division of x and y is: 1.6667"

[1] "Vector values:"

[1] 2 4 6 8 10

[1] "Sequence from 1 to 20 with step 2:"

[1] 1 3 5 7 9 11 13 15 17 19

[1] "Mean of vector: 6"

[1] "Sum of vector: 30"
```

Conclusion:

The installation of R was successfully verified. Basic syntax like variables, arithmetic operations, vectors, and sequences were executed correctly.

Experiment 2: Describing Data, Viewing, and Manipulating Data Using R

AIM: To learn how to describe, view, and manipulate datasets in R.

Theory

R provides various data structures such as vectors, lists, and data frames. Data can be viewed using head(), tail(), and described using functions like summary() and str(). Manipulations include column selection, row filtering, and transformations.

Program (R code):

Creating a sample data frame

```
students<- data.frame(  
  RollNo = 1:5,  
  Name = c("Aman", "Riya", "Kunal", "Simran", "Arjun"),  
  Marks = c(85, 92, 76, 89, 95),  
  Age = c(20, 21, 20, 22, 21)  
)
```

Viewing data

```
print("Complete Data Frame:")
```

```
print(students)
```

```
print("First 3 rows:")
```

```
print(head(students, 3))
```

```
print("Last 2 rows:")
```

```
print(tail(students, 2))
```

Descriptive statistics

```
print("Summary of dataset:")
```

```
print(summary(students))

# Manipulation - selecting a column

print("Marks Column:")

print(students$Marks)

# Filtering data

print("Students with Marks > 85:")

print(subset(students, Marks > 85))
```

Output (Sample):

```
[1] "Complete Data Frame:"
```

```
RollNo Name Marks Age
```

```
1 1 Aman 85 20
```

```
2 2 Riya 92 21
```

```
3 3 Kunal 76 20
```

```
4 4 Simran 89 22
```

```
5 5 Arjun 95 21
```

```
[1] "First 3 rows:"
```

```
RollNo Name Marks Age
```

```
1 1 Aman 85 20
```

```
2 2 Riya 92 21
```

```
3 3 Kunal 76 20
```

```
[1] "Last 2 rows:"
```

```
RollNo Name Marks Age
```

```
4 4 Simran 89 22
```

```
5 5 Arjun 95 21
```

```
[1] "Summary of dataset:"
```

RollNo	Name	Marks	Age
Min.:1	Length:5	Min. :76.0	Min. :20.0
1st Qu.:2	Class :character	1st Qu.:85.0	1st Qu.:20.0
Median :3	Mode :character	Median :89.0	Median :21.0
Mean :3		Mean :87.4	Mean :20.8
3rd Qu.:4		3rd Qu.:92.0	3rd Qu.:21.0
Max. :5		Max. :95.0	Max. :22.0

```
[1] "Marks Column:"
```

```
[1] 85 92 76 89 95
```

```
[1] "Students with Marks > 85:"
```

RollNo	Name	Marks	Age
2	2	Riya	92 21
4	4	Simran	89 22
5	5	Arjun	95 21

Conclusion:

The dataset was successfully created, viewed, and manipulated in R using data frames, column selection, and filtering.

Experiment 3: Plotting Probability Distribution Curve in R

AIM: To plot and visualize probability distribution curves (Normal distribution) using R software.

Theory

A probability distribution describes how values of a random variable are spread across possible outcomes.

Normal Distribution (Gaussian Distribution): Symmetrical, bell-shaped curve.

Defined by two parameters:

Mean (μ): Determines the center/shift of the curve.

Standard Deviation (σ): Determines the spread/width of the curve.

Properties of Normal Distribution:

The total area under the curve = 1.

R Functions for Probability Distribution:

`dnorm(x, mean, sd)` → Probability density at value x.

`pnorm(x)` → Cumulative probability up to x.

`rnorm(n, mean, sd)` → Generates n random values.

`hist()` and `plot()` → Visualize data.

`ggplot2` package → Advanced plotting with better visuals.

Program (Rcode):

```
# Install package if not already installed
```

```
# install.packages("ggplot2")
```

```

library(ggplot2)

# Create a sequence of values
x<- seq(-5, 5, by = 0.1)

# Create a data frame for multiple distributions
df<- data.frame(
  x = rep(x, 3),
  density = c(dnorm(x, mean = 0, sd = 1),
              dnorm(x, mean = 0, sd = 2),
              dnorm(x, mean = 2, sd = 1)),
  dist = factor(rep(c("mean=0, sd=1", "mean=0, sd=2", "mean=2, sd=1"),
                    each = length(x))),
  )

# Plot distribution curves
ggplot(df, aes(x = x, y = density, color = dist)) +
  geom_line(size = 1.2) +
  labs(title = "Normal Distribution Curves using ggplot2",
       x = "X values", y = "Probability Density") +
  theme_minimal()

# --- Histogram Example with ggplot2 ---

# Generate 1000 random normal values
random_data<- data.frame(values = rnorm(1000, mean = 0, sd = 1))

```

```
# Plothistogramwithdensityoverlay  
ggplot(random_data, aes(x = values)) +  
  geom_histogram(aes(y = ..density..), bins = 30, fill = "skyblue", color = "black") +  
  geom_density(color = "red", size = 1.2) +  
  labs(title = "HistogramwithNormalCurve (ggplot2)",  
       x = "RandomValues", y = "Density") +  
  theme_minimal()
```

ExpectedOutput:

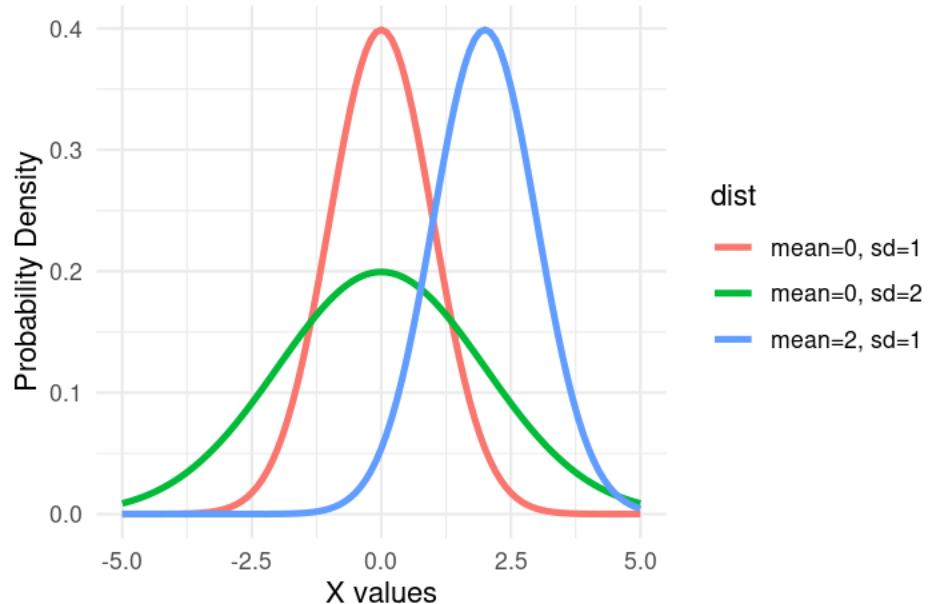
LineGraph → 3 curves (blue, red, green) showing different means & standard deviations.

Histogram → Bars in light blue with a smooth red density curve overlaid.

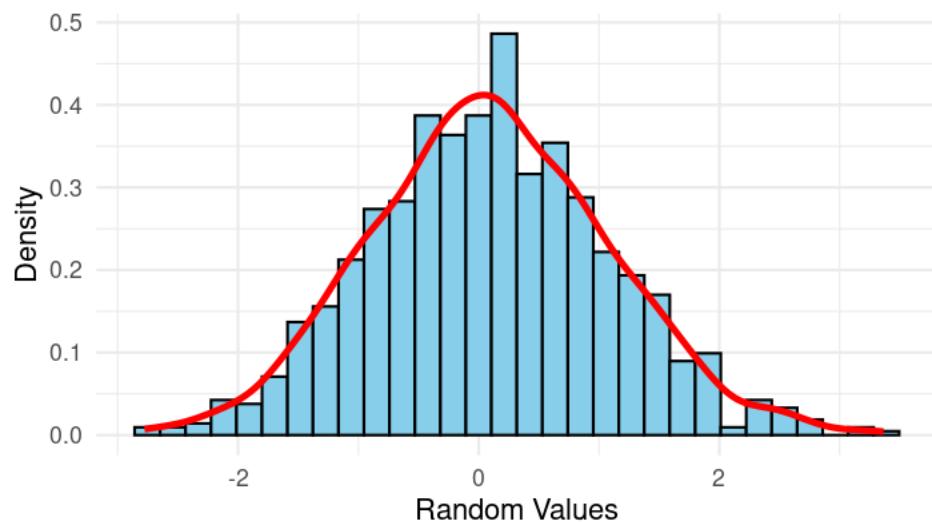
Conclusion :

Using ggplot2, the probability distribution curves and histograms look more professional and clear compared to base R. This demonstrates both traditional and modern plotting methods in R.

Normal Distribution Curves using ggplot2



Histogram with Normal Curve (ggplot2)



Experiment 4: Implementing Linear Regression in R

AIM:

To implement simple linear regression in R and understand how to model the relationship between two variables.

Theory

Regression Analysis is a statistical method for modeling relationships between variables.

In R:

`lm(Y ~ X, data)` → fits a linear model.

`summary(model)` → displays coefficients and accuracy.

`plot()` and `abline()` → visualize regression line.

Program (R code):

```
# Simple Linear Regression in R
```

```
# Create sample dataset
```

```
study_hours<- c(2, 3, 4, 5, 6, 7, 8)
```

```
marks<- c(50, 55, 60, 65, 70, 75, 80)
```

```
data<- data.frame(study_hours, marks)
```

```
# Fit linear regression model
```

```
model<- lm(marks ~ study_hours, data = data)
```

```
# Display summary
```

```
print(summary(model))
```

```

# Plot scatter plot with regression line

plot(data$study_hours, data$marks,
      col = "blue", pch = 16,
      main = "Linear Regression in R",
      xlab = "Study Hours",
      ylab = "Marks")

abline(model, col = "red", lwd = 2)

# Predict marks for new data

new_hours<- data.frame(study_hours = c(9, 10))
predicted_marks<- predict(model, new_hours)
print("Predicted Marks for 9 and 10 hours of study:")
print(predicted_marks)

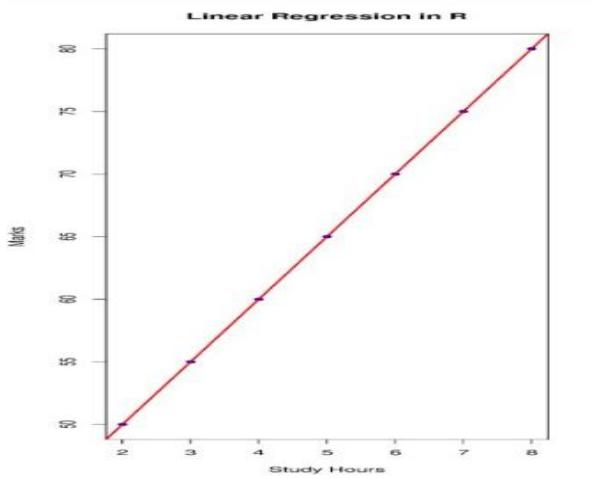
```

Expected Output:

Summary → Regression coefficients (Intercept ≈ 45 , Slope ≈ 5).

Plot → Blue points (data), red regression line.

Predictions → Marks ≈ 85 (for 9 hrs), 90 (for 10 hrs).



Conclusion:

Linear regression successfully modeled the relationship between study hours and marks. The model predicts that every additional study hour increases marks by about 5.

Experiment 5: Logistic Regression

Aim: To implement logistic regression in R and analyze the relationship between study hours and exam result (pass/fail).

Theory

Logistic Regression is a statistical method used for classification problems where the dependent variable is categorical (e.g., 0 = Fail, 1 = Pass).

It models the probability of an event occurring using the sigmoid (logistic) function:

Unlike linear regression, the output of logistic regression is always between 0 and 1, making it suitable for probability prediction.

It is widely used in fields like medicine, machine learning, and social sciences for binary classification problems.

Program (R Code)

```
# Logistic Regression Example

# Dataset: study hours vs pass (0=Fail, 1=Pass)
study_hours<- c(1, 2, 2, 3, 3, 4, 4, 5, 5, 6, 6, 7, 8, 9, 10)
pass<-    c(0, 0, 0, 0, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1)

data<- data.frame(study_hours, pass)

# Fit logistic regression model
model<- glm(pass ~ study_hours, data = data, family = binomial)

# Show summary
print(summary(model))
```

```
# Predict probabilities  
data$predicted_prob<- predict(model, type = "response")  
print(data)  
  
# Plot logistic regression curve  
plot(data$study_hours, data$pass,  
col = "blue", pch = 16,  
xlab = "Study Hours", ylab = "Pass (0/1)",  
main = "Logistic Regression")  
curve(predict(model, data.frame(study_hours = x), type = "response"),  
add = TRUE, col = "red", lwd = 2)
```

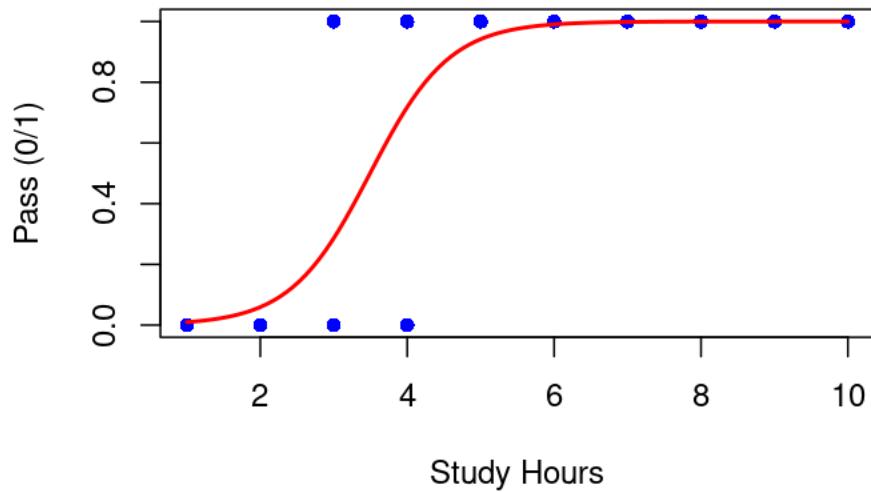
Expected Output

Summary of Model – Coefficients for intercept and slope showing how study hours affect passing probability.

Predicted Probabilities – Each student's probability of passing.

Graph – Blue points (actual data) and a red S-shaped curve showing logistic regression fit.

Logistic Regression



Conclusion

Logistic regression successfully models the relationship between study hours and exam results. As the number of study hours increases, the probability of passing the exam also increases. The S-shaped logistic curve clearly shows the transition from low pass probability (for fewer hours) to high pass probability (for more hours).

Experiment 6: Principal Component Analysis (PCA) on dataset using R.

Aim: To perform Principal Component Analysis (PCA) on a dataset in R and visualize the results.

Theory

Principal Component Analysis (PCA) is a dimensionality reduction technique.

It transforms correlated variables into a set of uncorrelated variables called principal components.

Properties: The first principal component captures the maximum variance in the data.

Each subsequent component captures the remaining variance while being orthogonal to the previous ones.

Applications:

Reducing dataset dimensions.

Removing redundancy.

Data visualization and preprocessing for machine learning.

Program (RCode)

```
# PCA in R

# Load dataset (built-in iris dataset)
data(iris)

# Remove the categorical column (Species) for PCA
iris_data <- iris[, 1:4]

# Perform PCA (scale=TRUE standardizes data)
pca_result <- prcomp(iris_data, scale.=TRUE)
```

```

# PrintPCAsummary
summary(pca_result)

# Print loadings (rotationmatrix)
print(pca_result$rotation)

# BiplotofPCA
biplot(pca_result, col = c("red", "blue"), main = "PCABiplotofIrisData")

# Screeplot (varianceexplainedbyeachcomponent)
plot(pca_result, type = "l", main = "ScreePlotofPCA")

```

ExpectedOutput

Summary of PCA – Shows standard deviation, proportion of variance explained by each component, and cumulative variance.

Loadings (rotation matrix) – Shows contribution of each original variable to principal components.

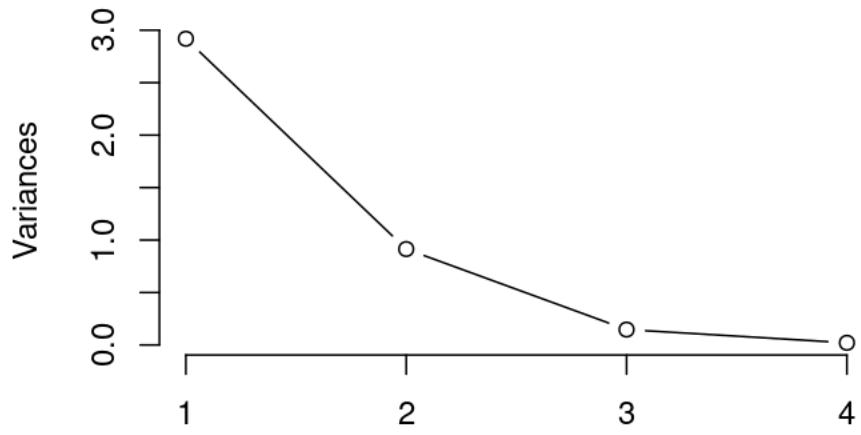
Biplot – Graph with data points and variable vectors showing direction of variance.

Scree Plot – Line graph showing how much variance is explained by each principal component.

Conclusion

PCA reduces the dimensionality of the dataset while retaining most of the information. In the iris dataset, the first two principal components capture most of the variance, making it possible to visualize a 4-dimensional dataset in just 2 dimensions without losing much information.

Scree Plot of PCA



Experiment 7: Chi-Square Test in R

Aim: To perform the Chi-Square test on different datasets in R to check the association between categorical variables.

Theory

The Chi-Square Test is a non-parametric statistical test used to check if there is a significant association between two categorical variables.

Types of Chi-Square tests:

Goodness of Fit Test – Checks if sample data matches expected distribution.

Test of Independence – Checks if two categorical variables are related.

Applications:

Market research.

Genetics.

Survey data analysis.

Program (R Code)

1. Chi-Square Goodness of Fit Test

```
# Observed frequencies (e.g., dice roll results)
```

```
observed<- c(18, 22, 20, 16, 24, 20)
```

```
# Expected frequencies (fair dice → equal probability)
```

```
expected<- rep(sum(observed) / 6, 6)
```

```
# Perform Chi-Square test  
chisq_test1 <- chisq.test(x = observed, p = rep(1/6, 6))  
  
print(chisq_test1)
```

2. Chi-Square Test of Independence

```
# Example dataset: Gender vs Preference  
data<- matrix(c(30, 10, # Male: Like, Dislike  
                20, 20), # Female: Like, Dislike  
                nrow = 2, byrow = TRUE)
```

```
colnames(data) <- c("Like", "Dislike")  
rownames(data) <- c("Male", "Female")
```

```
print(data)
```

```
# Perform Chi-Square test  
chisq_test2 <- chisq.test(data)
```

```
print(chisq_test2)
```

Expected Output

Goodness of Fit Test – p-value shows whether dice is fair.

Test of Independence – p-value indicates whether gender and preference are related.

Conclusion

The Chi-Square test helps determine if differences between observed and expected frequencies are due to chance or a real relationship. In practical applications, it is used for survey data analysis and testing associations between categorical variables.

Experiment 8: Edit and Execute a Program Involving Functions in R

Aim: To create, edit, and execute a program in R using functions for modular programming.

Theory

A function in R is a block of code that performs a specific task.

Functions improve modularity, reusability, and readability of code.

Structure of a function in R:

```
function_name<- function(arguments) {  
  # body of the function  
  return(result)  
}
```

R has two types of functions:

Built-in functions (e.g., mean(), sum())

User-defined functions (written by the programmer)

In this experiment, we define a user-defined function to calculate the factorial of a number.

Program (RCode)

```
# Define factorial function  
  
factorial_fun<- function(n) {  
  if (n == 0) {  
    return(1)  
  } else {  
    result<- 1
```

```

for (i in 1:n) {
  result <- result * i
}
return(result)
}

# Test the function
num <- 5
cat("Factorial of", num, "is", factorial_fun(num), "\n")

num <- 0
cat("Factorial of", num, "is", factorial_fun(num), "\n")

```

Expected Output

Factorial of 5 is 120

Factorial of 0 is 1

Conclusion

The factorial program was successfully implemented in R using a user-defined function. This demonstrates the use of modular programming, where functions make code easier to edit, reuse, and execute for different inputs.

Experiment 9: Edit and Execute a Program Involving Flow Chart

Aim: To design a flow chart and implement its equivalent program in R for decision making.

Theory

A flow chart is a step-by-step diagram that shows the flow of control in a program.

Symbols used:

Oval → Start / End

Rectangle → Process / Task

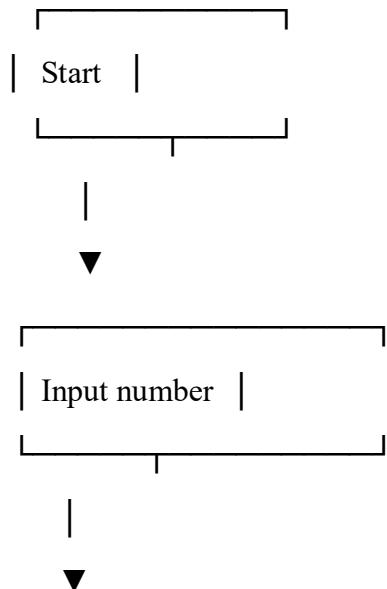
Diamond → Decision (Yes/No)

Arrow → Flow direction

Flow charts make program logic easier to understand before writing code.

In this practical, we check whether a number is positive, negative, or zero.

Flow Chart (Logic)



```
| num> 0 ? |
```

Yes | No



```
| Print |  
| Positive |
```



```
| num< 0 ? |
```

Yes | No



```
| Print |  
| Negative |
```



```
| Print Zero |
```



```
| End |
```

Program (R Code)

↳ Corrected for Posit Cloud (no input issues):

```
# Assign number directly (change value for testing)
```

```
num<- -3 # try 0 or 5 also
```

```
# Decision making using if-else
```

```
if (num > 0) {
```

```
  print("The number is Positive")
```

```
} else if (num < 0) {
```

```
  print("The number is Negative")
```

```
} else {
```

```
  print("The number is Zero")
```

```
}
```

Expected Output

Case 1:

```
num<- 5
```

```
[1] "The number is Positive"
```

Case 2:

```
num<- -3
```

```
[1] "The number is Negative"
```

Case 3:

```
num<- 0
```

```
[1] "The number is Zero"
```

Conclusion

The flow chart was successfully implemented in R.

By using if–else conditions, we checked whether a number is positive, negative, or zero.

This practical shows how algorithm design using flow charts can be directly translated into executable R programs.

Experiment 10: Data Aggregation and Group Operations in R

Aim: To perform data aggregation and group operations on datasets using R software.

Theory

Data aggregation is the process of summarizing data, such as calculating sums, means, or counts over groups of observations.

Group operations allow us to divide the dataset into groups based on one or more variables and then apply summary functions.

Common R functions/packages used:

aggregate() – base R function for group-wise operations

tapply() – applies a function to subsets of a vector

dplyr package (group_by(), summarise()) – modern, faster way for aggregation

Program (R Code)

```
install.packages("dplyr")
library(dplyr)
# Sample dataset: Employee salary data
data<- data.frame(
  Department = c("HR", "HR", "IT", "IT", "Finance", "Finance", "Finance"),
  Employee = c("A", "B", "C", "D", "E", "F", "G"),
  Salary = c(40000, 45000, 60000, 62000, 50000, 52000, 48000)
)

print("Original Dataset:")
print(data)

# 1. Using aggregate() - average salary by department
```

```
avg_salary<- aggregate(Salary ~ Department, data = data, FUN = mean)
print("Average Salary by Department:")
print(avg_salary)
```

```
# 2. Using tapply() - total salary by department
total_salary<- tapply(data$Salary, data$Department, sum)
print("Total Salary by Department:")
print(total_salary)
```

```
# 3. Using dplyr for group operations
```

```
library(dplyr)
```

```
summary_data<- data %>%
  group_by(Department) %>%
  summarise(
    Avg_Salary = mean(Salary),
    Max_Salary = max(Salary),
    Min_Salary = min(Salary),
    Total_Salary = sum(Salary)
  )
```

```
print("Department-wise Summary using dplyr:")
print(summary_data)
```

Expected Output

Original Dataset

Department Employee Salary

1	HR	A	40000
2	HR	B	45000
3	IT	C	60000
4	IT	D	62000
5	Finance	E	50000
6	Finance	F	52000
7	Finance	G	48000

Average Salary by Department

Department Salary

1	Finance	50000
2	HR	42500
3	IT	61000

Total Salary by Department

Finance	HR	IT
150000	85000	122000

Department-wise Summary using dplyr

```
# Atibble: 3 × 5
  Department Avg_Salary Max_Salary Min_Salary Total_Salary
  <chr> <dbl> <dbl> <dbl> <dbl>
1 Finance 50000 52000 48000 150000
2 HR      42500 45000 40000 85000
3 IT      61000 62000 60000 122000
```

Conclusion

Data aggregation and group operations were successfully performed using `aggregate()`, `tapply()`, and `dplyr`.

This practical demonstrates how datasets can be summarized efficiently to extract meaningful insights.