

SHETH L.U.J AND SIR M.V COLLEGE

Subject: Data Analysis with SAS / SPSS /R

Practical no. 12

Aim:Combining datasets vertically
(concatenation) using rbind() (R).

Outputs→

The screenshot shows the RStudio interface. The top menu bar includes File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, and Help. The source editor on the left contains R code for loading datasets, performing cleaning steps, and concatenating them. The environment browser on the right lists various objects like combined_data, flower_clean, and Iris. The file browser at the bottom shows the local directory structure.

```
R - R 4.5.2 · ~/ ~
> data(iris)
> # Load custom flower dataset
> flower_df <- read.csv("flower_dataset - flower_dataset.csv")
> # Preview column names
> print("--- Data Structure Before Transformation ---")
[1] "--- Data Structure Before Transformation ---"
> print("Iris columns:")
[1] "Iris columns:"
> print(names(iris))      # Sepal.Length, Sepal.Width, Petal.Length, Petal.Width, Species
[1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "Species"
> print("Flower dataset columns:")
[1] "Flower dataset columns:"
> print(names(flower_df)) # species, height_cm, etc.
[1] "species" "size" "fragrance" "height_cm"
> iris_clean <- iris[, c("Species", "Sepal.Length")]
> names(iris_clean) <- c("Species", "Height")
> iris_clean$height <- as.numeric(iris_clean$height) # Ensure numeric
> flower_clean <- flower_df[, c("species", "height_cm")]
> names(flower_clean) <- c("species", "Height")
> flower_clean$height <- as.numeric(flower_clean$height)
> combined_data <- rbind(iris_clean, flower_clean)
> #RESULTS
> print("--- Combined Data Summary ---")
[1] "--- Combined Data Summary ---"
> print(paste("Iris rows:", nrow(iris_clean)))
[1] "Iris rows: 150"
> print(paste("Flower rows:", nrow(flower_clean)))
[1] "Flower rows: 10000"
> print(paste("Total rows (Expected):", nrow(iris_clean) + nrow(flower_clean)))
[1] "Total rows (Expected): 10150"
> print(paste("Total rows (Actual):", nrow(combined_data)))
[1] "Total rows (Actual): 10150"
> print("--- Preview of Combined Data (Top and Bottom) ---")
[1] "--- Preview of Combined Data (Top and Bottom) ---"
> print(head(combined_data))
  Species Height
1  setosa    5.1
2  setosa    4.9
3  setosa    4.7
```

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The screenshot shows the RStudio interface. The Source pane contains R code for data cleaning and combining datasets. The Environment pane shows a file browser with various R data files and other files like .RData and desktop.ini. The taskbar at the bottom includes icons for search, file explorer, and various applications.

```
R - R 4.5.2 · ~/ ~/  
print(names(flower_df))      # species, height_cm, etc.  
[1] "species"    "size"       "fragrance" "height_cm"  
> iris_clean <- iris[, c("Species", "Sepal.Length")]  
> names(iris_clean) <- c("Species", "Height")  
> iris_clean$height <- as.numeric(iris_clean$Height) # Ensure numeric  
> flower_clean <- flower_df[, c("species", "height_cm")]  
> names(flower_clean) <- c("Species", "Height")  
> flower_clean$height <- as.numeric(flower_clean$height)  
> combined_data <- rbind(iris_clean, flower_clean)  
> #RESULTS  
> print("--- Combined Data Summary ---")  
[1] "--- Combined Data Summary ---"  
> print(paste("Iris rows:", nrow(iris_clean)))  
[1] "Iris rows: 150"  
> print(paste("Flower rows:", nrow(flower_clean)))  
[1] "Flower rows: 10000"  
> print(paste("Total rows (Expected):", nrow(iris_clean) + nrow(flower_clean)))  
[1] "Total rows (Expected): 10150"  
> print(paste("Total rows (Actual):", nrow(combined_data)))  
[1] "Total rows (Actual): 10150"  
> print("--- Preview of Combined Data (Top and Bottom) ---")  
[1] "--- Preview of Combined Data (Top and Bottom) ---"  
> print(head(combined_data))  
Species Height  
1 setosa 5.1  
2 setosa 4.9  
3 setosa 4.7  
4 setosa 4.6  
5 setosa 5.0  
6 setosa 5.4  
> print(tail(combined_data))  
Species Height  
10145 rose 87.69  
10146 hibiscus 109.52  
10147 shoeblack plant 145.23  
10148 hibiscus 126.69  
10149 shoeblack plant 77.62  
10150 rose 88.11
```