

SETH L.U.J and SIR M.V COLLEGE

PRAC 12

Aim:- Combining datasets vertically (concatenation) using rbind() (R).Write code toCombining datasets vertically (concatenation) using rbind() in R studio.

INPUT:-

```
bats_df <- read.csv("C:/Users/mvlui/Downloads/bats_information.csv")
student_df <- read.csv("C:/Users/mvlui/Downloads/Student_Marks.csv")
```

```
lifespan_numeric <- as.numeric(sub(".*", "", bats_df$Average.Lifespan))
```

```
bats_clean <- data.frame(
  Name = bats_df$Species,
  Value = lifespan_numeric
)
```

```
student_clean <- data.frame(
  Name = student_df$number_courses,
  Value = as.numeric(student_df$Marks)
)
```

```
combined_data <- rbind(bats_clean, student_clean)
```

```
cat("--- Combined Data Summary ---\n")
cat("Bats rows:", nrow(bats_clean), "\n")
cat("Students rows:", nrow(student_clean), "\n")
cat("Total rows:", nrow(combined_data), "\n")
```

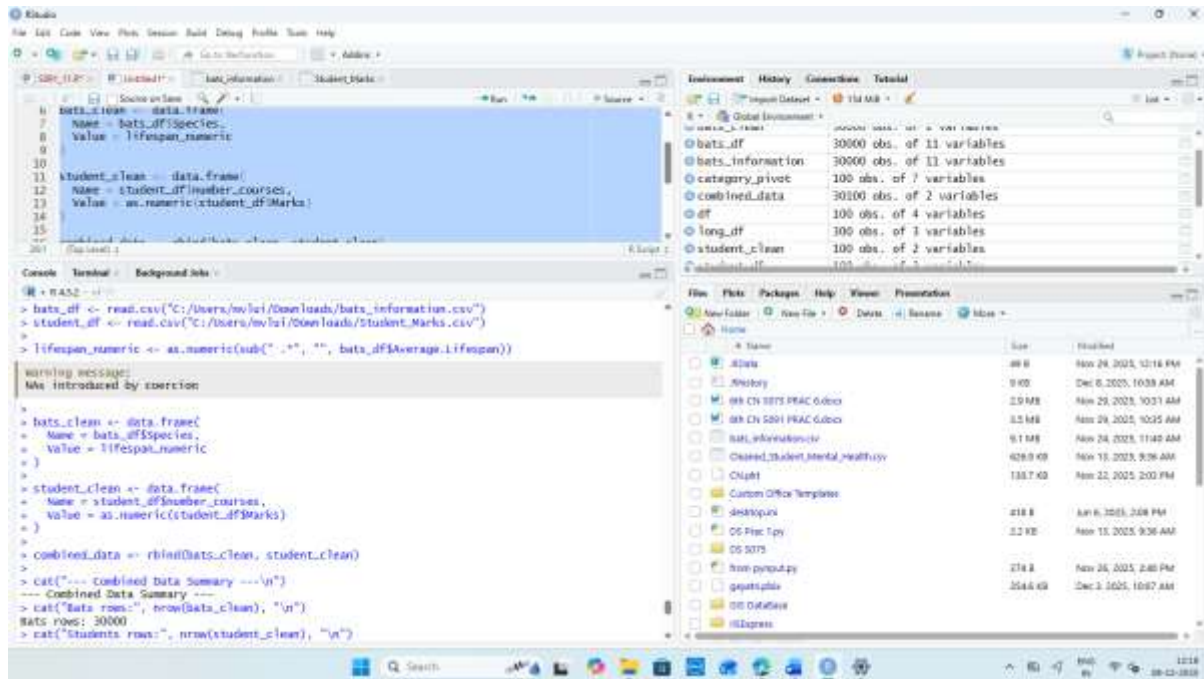
```
cat("--- Preview of Combined Data (Top and Bottom) ---\n")
print(head(combined_data))
```

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print(tail(combined_data))

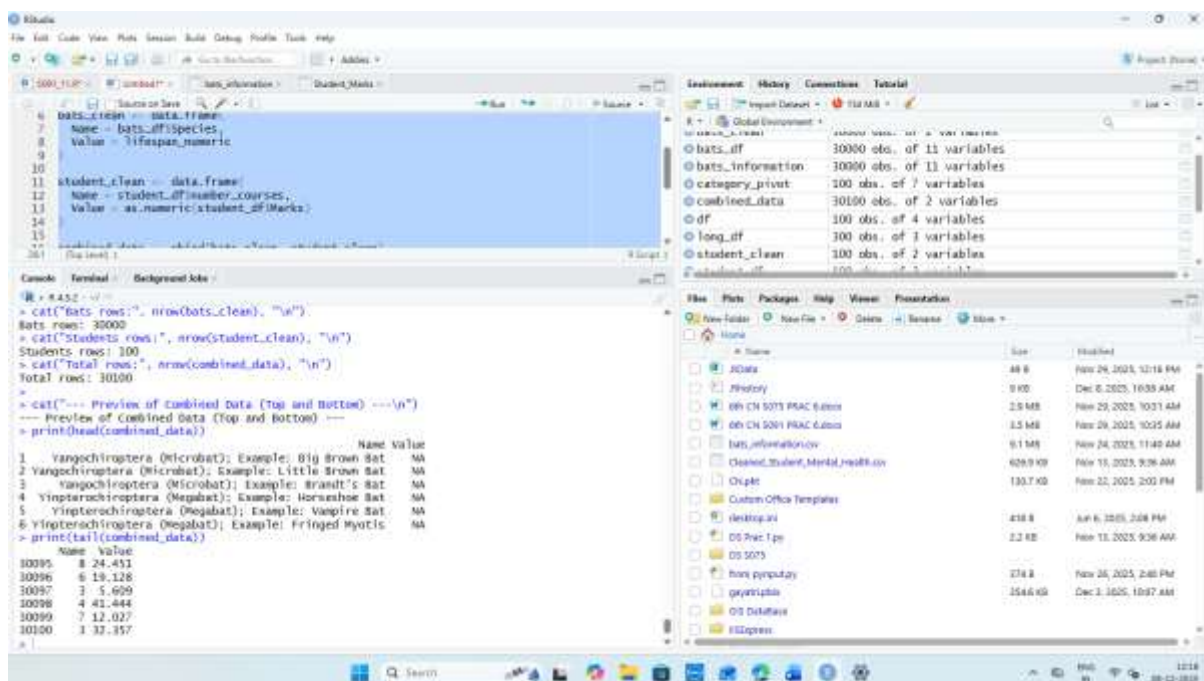
OUTPUT:-



```
RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
[Source] [Console] [Environment] [History] [Connections] [Tutorial]
bats_clean <- data.frame(
  Name = bats_df$Species,
  Value = lifespans_numeric
)
student_clean <- data.frame(
  Name = student_df$number_courses,
  Value = as.numeric(student_df$marks)
)
combined_data <- rbind(bats_clean, student_clean)
cat("---- Combined Data Summary ----\n")
---- Combined Data Summary ----
cat("Bats rows:", nrow(bats_clean), "\n")
Bats rows: 30000
cat("Students rows:", nrow(student_clean), "\n")
Students rows: 100
```

Warning message:
NAs introduced by coercion

Environment: Global Environment, bats_df, bats_information, category_pivot, combined_data, df, long_df, student_clean, student_information



```
RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
[Source] [Console] [Environment] [History] [Connections] [Tutorial]
cat("Bats rows:", nrow(bats_clean), "\n")
Bats rows: 30000
cat("Students rows:", nrow(student_clean), "\n")
Students rows: 100
cat("Total rows:", nrow(combined_data), "\n")
Total rows: 30100
cat("---- Preview of Combined Data (Top and Bottom) ----\n")
---- Preview of Combined Data (Top and Bottom) ----
print(head(combined_data))
      Name value
1  Yangochiroptera (Microbat); Example: Big Brown Bat  NA
2  Yangochiroptera (Microbat); Example: Little Brown Bat  NA
3  Yangochiroptera (Microbat); Example: Brandt's Bat      NA
4  Yinpterochiroptera (Megabat); Example: Horseshoe Bat   NA
5  Yinpterochiroptera (Megabat); Example: Vampire Bat     NA
6  Yinpterochiroptera (Megabat); Example: Fringed Myotis  NA
print(tail(combined_data))
      Name value
10095  8 24.451
10096  6 19.126
10097  3  5.609
10098  4 41.444
10099  7 12.027
10100  3 37.357
```

Environment: Global Environment, bats_df, bats_information, category_pivot, combined_data, df, long_df, student_clean, student_information