12th_april_design_inference_winter_project

Taiwo Ogunkeye

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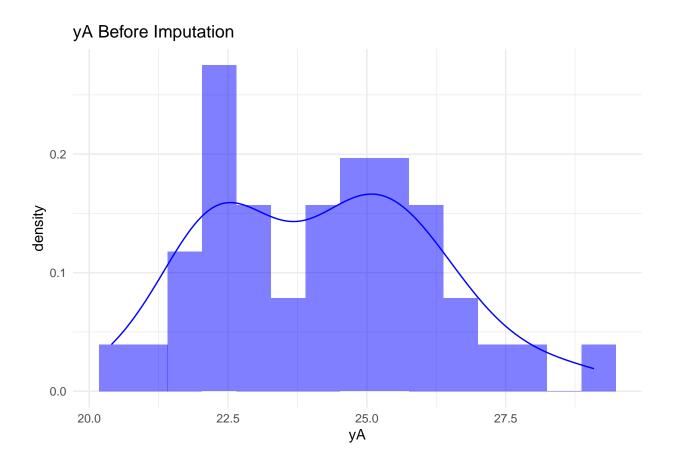
```
# loading libraries
library(mvtnorm)
## Warning: package 'mvtnorm' was built under R version 4.4.3
library(ggplot2)
library(dplyr)
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
       filter, lag
## The following objects are masked from 'package:base':
##
       intersect, setdiff, setequal, union
##
library(MASS)
## Attaching package: 'MASS'
## The following object is masked from 'package:dplyr':
##
##
       select
# Load data with proper column names and whitespace handling
df <- read.table(</pre>
 file = "interexp.dat",
 header = TRUE,
 na.strings = c("NA", ""),
 col.names = c("yA", "yB"), # Explicitly set column names
  strip.white = TRUE, # Remove extra whitespace
  sep = ""
                              # Any whitespace separator
# Check column names
cat("Column names:", colnames(df), "\n")
```

```
## Column names: yA yB
# Check first 6 rows
cat("\nFirst 6 rows:\n")
## First 6 rows:
print(head(df))
##
        уA
## 1 25.33 26.45
## 2 26.77 27.53
## 3 22.76 20.02
## 4 20.94 22.83
## 5 25.40 28.05
## 6 22.49 23.67
# Check missing values
cat("\nMissing values per column:\n")
##
## Missing values per column:
print(colSums(is.na(df)))
## yA yB
## 17 15
# EM Imputation Function that uses bivariate normal data
em_imputation <- function(data, max_iter = 500, tol = 1e-8) {</pre>
    imputed <- data.frame(</pre>
        yA = ifelse(is.na(data$yA),
                    median(data$yA, na.rm = TRUE), # More robust initialization
                    data$yA),
        yB = ifelse(is.na(data$yB),
                    median(data$yB, na.rm = TRUE),
                    data$yB)
    )
    # Convert to matrix for numerical stability
    imputed_mat <- as.matrix(imputed)</pre>
    n <- nrow(imputed_mat)</pre>
    mu <- colMeans(imputed_mat)</pre>
    cov_mat <- cov(imputed_mat)</pre>
    # create initial covariance regularization
    cov_mat <- cov_mat + diag(1e-5, ncol(cov_mat))</pre>
    for (i in 1:max_iter) {
```

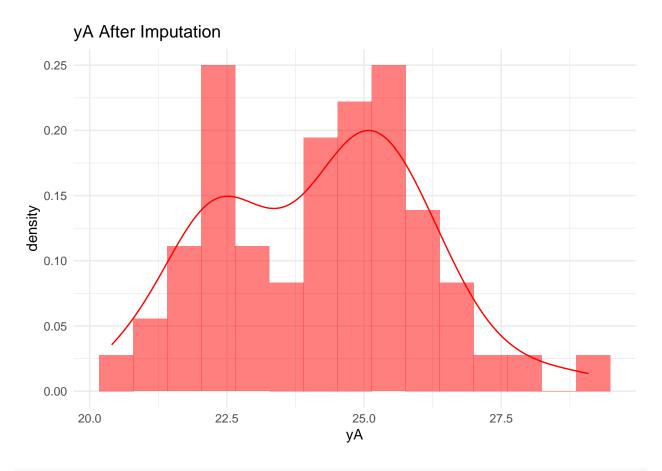
```
sum_z <- matrix(0, 2, 1)</pre>
         sum_zz \leftarrow matrix(0, 2, 2)
        for (j in 1:n) {
             obs <- !is.na(data[j, ])</pre>
             miss <- is.na(data[j, ])</pre>
             if(any(miss)) {
                 cov_sub <- cov_mat[obs, obs, drop = FALSE]</pre>
                  cov_sub_reg <- cov_sub + diag(1e-6, nrow(cov_sub))</pre>
                 cov_inv <- ginv(cov_sub_reg)</pre>
                  #conditional mean calculation
                  mu_cond <- mu[miss] +</pre>
                      (cov_mat[miss, obs, drop = FALSE] %*% cov_inv) %*%
                      (imputed_mat[j, obs] - mu[obs])
                  # Updating the imputation
                  imputed_mat[j, miss] <- mu_cond</pre>
             }
             # collect the statistics by using the updated imputation
             z <- matrix(imputed_mat[j, ], ncol = 1)</pre>
             sum_z <- sum_z + z</pre>
             sum_zz <- sum_zz + tcrossprod(z)</pre>
         # updating the parameters mu and covariance
        new_mu <- sum_z/n</pre>
        new_cov <- (sum_zz/n) - tcrossprod(new_mu)</pre>
        cov_mat <- new_cov + diag(1e-5, 2)</pre>
         # Checking the convergence condition
        if (i > 1 && norm(mu - new_mu, "F") < tol) break
        mu <- new_mu
    }
    list(
         imputed_data = data.frame(imputed_mat),
        mu = mu,
        sigma = cov_mat,
        iterations = i
    )
}
# running the imputation above
set.seed(42) # For reproducibility
result <- em_imputation(df)</pre>
df_imputed <- result$imputed_data</pre>
# creating file called imputed.csv
```

```
write.csv(df_imputed, "imputed_data.csv", row.names = FALSE)
# printing the pre-imputation statistics
cat("Pre-imputation summary:\n")
## Pre-imputation summary:
print(summary(df))
##
         yΑ
                         yВ
## Min.
          :20.40
                          :20.02
                 Min.
                  1st Qu.:23.16
## 1st Qu.:22.41
## Median :24.34 Median :24.99
## Mean
         :24.20
                   Mean
                          :24.81
## 3rd Qu.:25.52
                   3rd Qu.:26.62
## Max. :29.09
                   Max. :28.05
## NA's
                   NA's
         :17
                          :15
#printing the post imputation statistics
cat("\nPost-imputation summary:\n")
##
## Post-imputation summary:
print(summary(df_imputed))
                         yВ
##
         yА
## Min.
         :20.40 Min.
                         :20.02
## 1st Qu.:22.52 1st Qu.:23.50
## Median :24.36 Median :24.98
## Mean :24.21
                 Mean :24.83
## 3rd Qu.:25.38
                   3rd Qu.:26.26
## Max. :29.09 Max.
                          :28.05
# Plotting the distributions in individual density plots
plot_distribution_single <- function(var, dataset, title_text, fill_color) {</pre>
   ggplot() +
       geom histogram(
           data = dataset, aes(x = !!sym(var), y = ..density..),
           bins = 15, fill = fill_color, alpha = 0.5
       geom_density(data = dataset, aes(x = !!sym(var)), color = fill_color) +
       ggtitle(title_text) +
       theme_minimal()
}
# Plotting the distributions in the same plot to check the visual changes
plot_distribution_combined <- function(var) {</pre>
   ggplot() +
       geom_histogram(
```

```
data = df, aes(x = !!sym(var), y = ..density..),
            bins = 15, fill = "blue", alpha = 0.3
        ) +
        geom_histogram(
            data = df_imputed, aes(x = !!sym(var), y = ..density..),
            bins = 15, fill = "red", alpha = 0.3
        ) +
        geom_density(data = df, aes(x = !!sym(var)), color = "blue") +
        geom_density(data = df_imputed, aes(x = !!sym(var)), color = "red") +
        ggtitle(paste("Distribution of", var, "(Combined)")) +
        theme_minimal()
}
plot_distribution_single("yA", df, "yA Before Imputation", "blue")
\mbox{\tt \#\#} Warning: The dot-dot notation ('..density...') was deprecated in ggplot2 3.4.0.
## i Please use 'after_stat(density)' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
## Warning: Removed 17 rows containing non-finite outside the scale range
## ('stat_bin()').
## Warning: Removed 17 rows containing non-finite outside the scale range
## ('stat_density()').
```



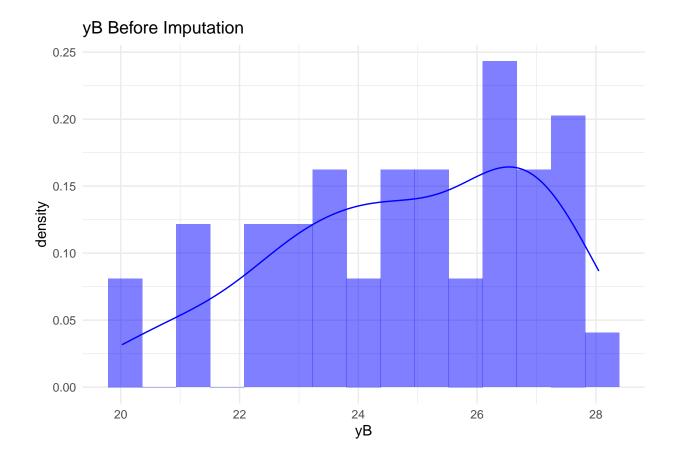
plot_distribution_single("yA", df_imputed, "yA After Imputation", "red")



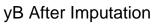
plot_distribution_single("yB", df, "yB Before Imputation", "blue")

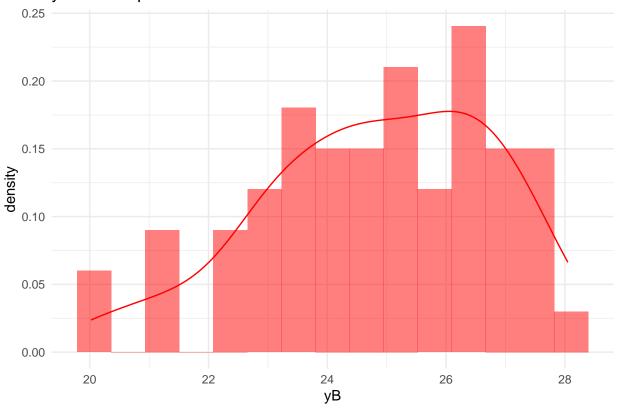
Warning: Removed 15 rows containing non-finite outside the scale range
('stat_bin()').

Warning: Removed 15 rows containing non-finite outside the scale range
('stat_density()').



plot_distribution_single("yB", df_imputed, "yB After Imputation", "red")

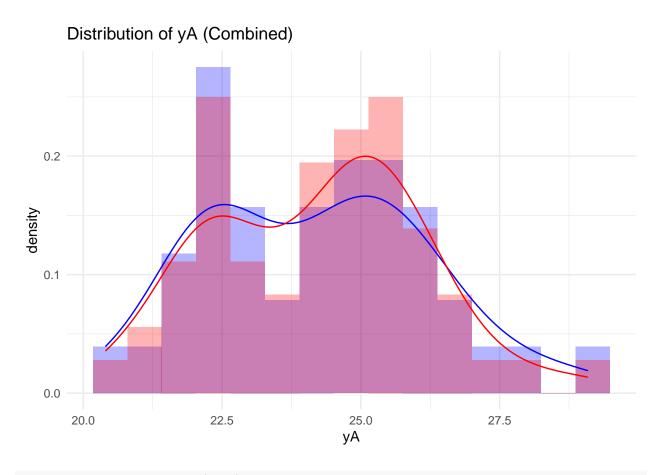




plot_distribution_combined("yA")

Warning: Removed 17 rows containing non-finite outside the scale range
('stat_bin()').

Warning: Removed 17 rows containing non-finite outside the scale range
('stat_density()').

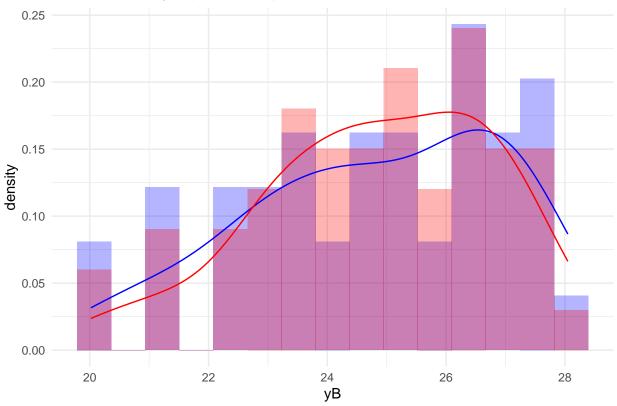


plot_distribution_combined("yB")

Warning: Removed 15 rows containing non-finite outside the scale range
('stat_bin()').

Warning: Removed 15 rows containing non-finite outside the scale range
('stat_density()').





yA 3.576391 2.755524 ## yB 2.755524 3.775615

```
# Statistical test
cat("\nPaired t-test results:\n")
##
## Paired t-test results:
print(t.test(df_imputed$yA, df_imputed$yB, paired = TRUE))
##
## Paired t-test
##
## data: df_imputed$yA and df_imputed$yB
## t = -3.4662, df = 57, p-value = 0.001011
\mbox{\tt \#\#} alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
## -0.9742845 -0.2607698
## sample estimates:
## mean difference
##
        -0.6175271
```