Assignment-4 part-1

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```
# Gene expression file
url_gene <- "https://raw.githubusercontent.com/ghazkha/Assessment4/refs/heads/main/gene_expression.tsv"
download.file(url_gene, destfile = "gene_expression.tsv", mode = "wb")
gene <- read.delim("gene_expression.tsv", row.names = 1, check.names = FALSE)
head(gene)
```

```
##                                GTEX-1117F-0226-SM-5GZZ7 GTEX-1117F-0426-SM-5EGHI
## ENSG00000223972.5_DDX11L1                             0                        0
## ENSG00000227232.5_WASH7P                            187                      109
## ENSG00000278267.1_MIR6859-1                           0                        0
## ENSG00000243485.5_MIR1302-2HG                         1                        0
## ENSG00000237613.2_FAM138A                             0                        0
## ENSG00000268020.3_OR4G4P                              0                        1
##                                GTEX-1117F-0526-SM-5EGHJ
## ENSG00000223972.5_DDX11L1                             0
## ENSG00000227232.5_WASH7P                            143
## ENSG00000278267.1_MIR6859-1                           1
## ENSG00000243485.5_MIR1302-2HG                         0
## ENSG00000237613.2_FAM138A                             0
## ENSG00000268020.3_OR4G4P                              0
```

```
# Growth data file
url_growth <- "https://raw.githubusercontent.com/ghazkha/Assessment4/refs/heads/main/growth_data.csv"
download.file(url_growth, destfile = "growth_data.csv", mode = "wb")
growth <- read.csv("growth_data.csv", check.names = FALSE)
head(growth)
```

```
##        Site TreeID Circumf_2005_cm Circumf_2010_cm Circumf_2015_cm
## 1 northeast   A012             5.2            10.1            19.9
## 2 southwest   A039             4.9             9.6            18.9
## 3 southwest   A010             3.7             7.3            14.3
## 4 northeast   A087             3.8             6.5            10.9
## 5 southwest   A074             3.8             6.4            10.9
## 6 northeast   A008             5.9            10.0            16.8
##   Circumf_2020_cm
## 1            38.9
## 2            37.0
## 3            28.1
## 4            18.5
## 5            18.4
## 6            28.4
```

```
## 1. Show first six genes
# Display the first six rows of the dataset (gene expression counts).
```

```
head(gene)
```

```
##                                GTEX-1117F-0226-SM-5GZZ7 GTEX-1117F-0426-SM-5EGHI
## ENSG00000223972.5_DDX11L1                             0                        0
## ENSG00000227232.5_WASH7P                            187                      109
## ENSG00000278267.1_MIR6859-1                           0                        0
## ENSG00000243485.5_MIR1302-2HG                         1                        0
## ENSG00000237613.2_FAM138A                             0                        0
## ENSG00000268020.3_OR4G4P                              0                        1
##                                GTEX-1117F-0526-SM-5EGHJ
## ENSG00000223972.5_DDX11L1                             0
## ENSG00000227232.5_WASH7P                            143
## ENSG00000278267.1_MIR6859-1                           1
## ENSG00000243485.5_MIR1302-2HG                         0
## ENSG00000237613.2_FAM138A                             0
## ENSG00000268020.3_OR4G4P                              0
```

```
## 2. Add mean column
# Calculate the mean expression across the three samples for each gene.
# Store it in a new column called "mean_expr".
gene$mean_expr <- rowMeans(gene)

# Show the first six rows again, now including the new column.
head(gene)
```

```
##                                GTEX-1117F-0226-SM-5GZZ7 GTEX-1117F-0426-SM-5EGHI
## ENSG00000223972.5_DDX11L1                             0                        0
## ENSG00000227232.5_WASH7P                            187                      109
## ENSG00000278267.1_MIR6859-1                           0                        0
## ENSG00000243485.5_MIR1302-2HG                         1                        0
## ENSG00000237613.2_FAM138A                             0                        0
## ENSG00000268020.3_OR4G4P                              0                        1
##                                GTEX-1117F-0526-SM-5EGHJ   mean_expr
## ENSG00000223972.5_DDX11L1                             0   0.0000000
## ENSG00000227232.5_WASH7P                            143 146.3333333
## ENSG00000278267.1_MIR6859-1                           1   0.3333333
## ENSG00000243485.5_MIR1302-2HG                         0   0.3333333
## ENSG00000237613.2_FAM138A                             0   0.0000000
## ENSG00000268020.3_OR4G4P                              0   0.3333333
```

```
## 3. Top 10 genes by mean expression
# Order the genes by descending mean expression and select the top 10.
top10 <- head(gene[order(-gene$mean_expr), ], 10)
top10
```

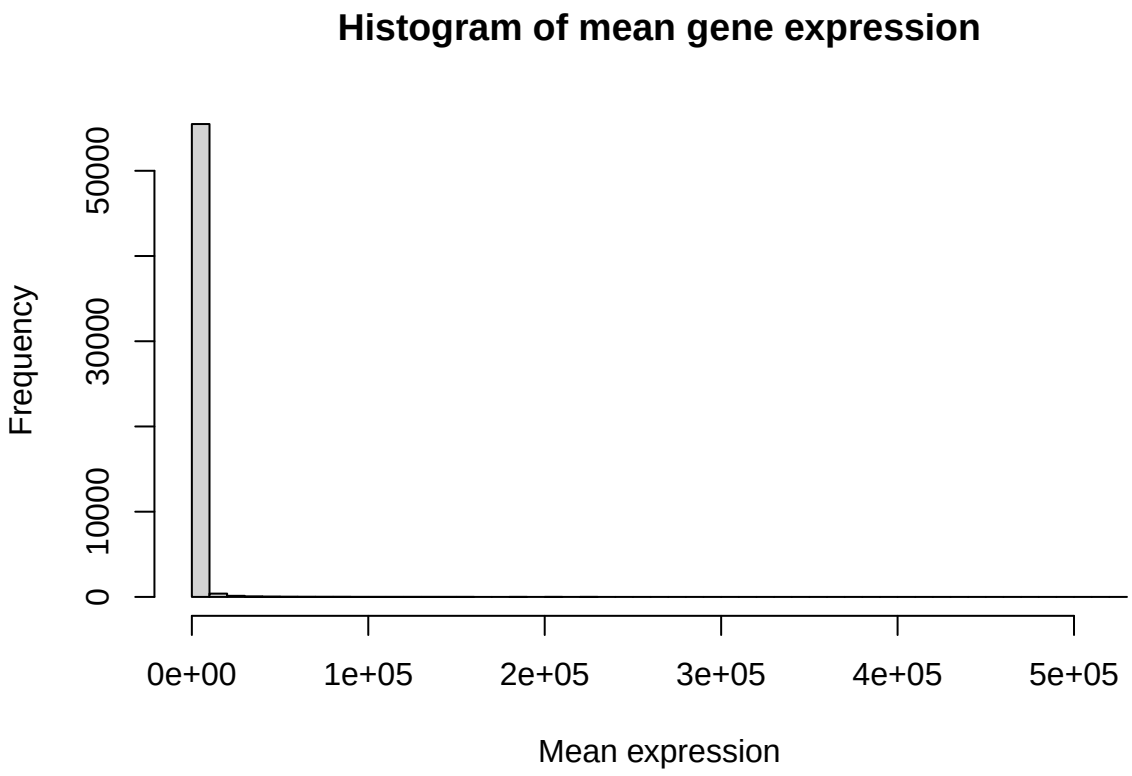
```
##                           GTEX-1117F-0226-SM-5GZZ7 GTEX-1117F-0426-SM-5EGHI
## ENSG00000198804.2_MT-CO1                   267250                  1101779
## ENSG00000198886.2_MT-ND4                   273188                   991891
## ENSG00000198938.2_MT-CO3                   250277                  1041376
## ENSG00000198888.2_MT-ND1                   243853                   772966
## ENSG00000198899.2_MT-ATP6                  141374                   696715
## ENSG00000198727.2_MT-CYB                   127194                   638209
## ENSG00000198763.3_MT-ND2                   159303                   543786
## ENSG00000211445.11_GPX3                    464959                    39396
## ENSG00000198712.1_MT-CO2                   128858                   545360
```

```
## ENSG00000156508.17_EEF1A1                   317642                    39573
##                           GTEX-1117F-0526-SM-5EGHJ mean_expr
## ENSG00000198804.2_MT-CO1                    218923  529317.3
## ENSG00000198886.2_MT-ND4                    277628  514235.7
## ENSG00000198938.2_MT-CO3                    223178  504943.7
## ENSG00000198888.2_MT-ND1                    194032  403617.0
## ENSG00000198899.2_MT-ATP6                   151166  329751.7
## ENSG00000198727.2_MT-CYB                    141359  302254.0
## ENSG00000198763.3_MT-ND2                    149564  284217.7
## ENSG00000211445.11_GPX3                     306070  270141.7
## ENSG00000198712.1_MT-CO2                    122816  265678.0
## ENSG00000156508.17_EEF1A1                   339347  232187.3
```

```r
## 4. Number of genes with mean < 10
# Count how many genes have a mean expression value less than 10.
n_low <- sum(gene$mean_expr < 10)
n_low
```

```
## [1] 35988
```

```r
## 5. Histogram of mean values
# Plot a histogram to visualize the distribution of mean gene expression values.
hist(gene$mean_expr,
     breaks = 40,
     main = "Histogram of mean gene expression",
     xlab = "Mean expression")
```



```r
# Inspect column names
colnames(growth)
```

```
## [1] "Site"            "TreeID"          "Circumf_2005_cm" "Circumf_2010_cm"
## [5] "Circumf_2015_cm" "Circumf_2020_cm"
```

```r
# Define Start and End explicitly from the available columns
growth$Start <- growth$Circumf_2005_cm
growth$End   <- growth$Circumf_2020_cm

## 1) Column names (already printed by colnames)
# colnames(growth)
gene <- read.delim("gene_expression.tsv", row.names = 1, check.names = FALSE)
head(gene)
```

```
##                                GTEX-1117F-0226-SM-5GZZ7 GTEX-1117F-0426-SM-5EGHI
## ENSG00000223972.5_DDX11L1                             0                        0
## ENSG00000227232.5_WASH7P                            187                      109
## ENSG00000278267.1_MIR6859-1                           0                        0
## ENSG00000243485.5_MIR1302-2HG                         1                        0
## ENSG00000237613.2_FAM138A                             0                        0
## ENSG00000268020.3_OR4G4P                              0                        1
##                                GTEX-1117F-0526-SM-5EGHJ
## ENSG00000223972.5_DDX11L1                             0
## ENSG00000227232.5_WASH7P                            143
## ENSG00000278267.1_MIR6859-1                           1
## ENSG00000243485.5_MIR1302-2HG                         0
## ENSG00000237613.2_FAM138A                             0
## ENSG00000268020.3_OR4G4P                              0
```

```r
## --- Prepare convenient Start/End columns (from the year columns) ---
growth$Start <- growth$Circumf_2005_cm
growth$End   <- growth$Circumf_2020_cm

## --- 2) Mean and SD at Start and End by Site (PRINT BOTH) ---
by_start <- aggregate(Start ~ Site, data = growth,
                      FUN = function(x) c(mean = mean(x, na.rm = TRUE),
                                          sd   = sd(x,   na.rm = TRUE)))
by_end   <- aggregate(End ~ Site, data = growth,
                      FUN = function(x) c(mean = mean(x, na.rm = TRUE),
                                          sd   = sd(x,   na.rm = TRUE)))

start_stats <- cbind(Site = by_start$Site, as.data.frame(by_start$Start))
end_stats   <- cbind(Site = by_end$Site,   as.data.frame(by_end$End))
colnames(start_stats)[2:3] <- c("mean_start","sd_start")
colnames(end_stats)[2:3]   <- c("mean_end","sd_end")

start_stats   # <-- keep this printed
```

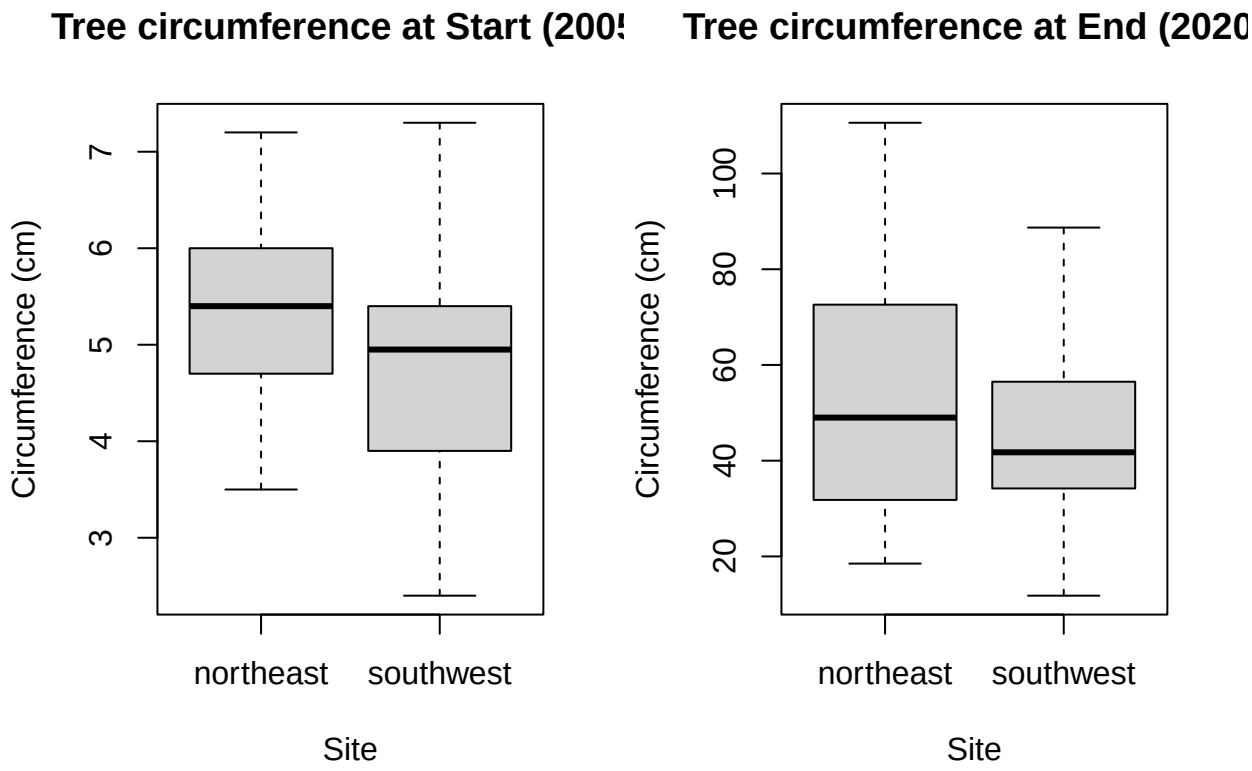
```
##        Site mean_start  sd_start
## 1 northeast      5.292 0.9140267
## 2 southwest      4.862 1.1474710
```

```r
end_stats     # <-- and this printed
```

```
##        Site mean_end   sd_end
```

```
## 1 northeast   54.228 25.22795
## 2 southwest   45.596 17.87345
```

```
## --- 3) Boxplots (Start vs End by Site) ---
par(mfrow = c(1,2))
boxplot(Start ~ Site, data = growth,
        main = "Tree circumference at Start (2005)", ylab = "Circumference (cm)")
boxplot(End   ~ Site, data = growth,
        main = "Tree circumference at End (2020)",  ylab = "Circumference (cm)")
```




```
par(mfrow = c(1,1))
```

```
## --- 4) Mean growth over the LAST 10 YEARS (2010 -> 2020) ---
growth$growth10 <- growth$Circumf_2020_cm - growth$Circumf_2010_cm

## site means (and SD if you want)
tapply(growth$growth10, growth$Site, mean, na.rm = TRUE)
```

```
## northeast southwest
##     42.94     35.49
```

```
# If you also want SD:
tapply(growth$growth10, growth$Site, sd, na.rm = TRUE)
```

```
## northeast southwest
##  22.81510  16.05704
```

```
## --- 5) t-test: is 10-year growth different between sites? ---
t.test(growth$growth10 ~ growth$Site)
```

```
##
##  Welch Two Sample t-test
##
## data:  growth$growth10 by growth$Site
## t = 1.8882, df = 87.978, p-value = 0.06229
## alternative hypothesis: true difference in means between group northeast and group southwest is not e
## 95 percent confidence interval:
##  -0.3909251 15.2909251
## sample estimates:
## mean in group northeast mean in group southwest
##                   42.94                   35.49
```