# Day 2 – 01 Explore Data (Exercises – Solutions)

Seminar practice worksheet

Use this key after attempting `scripts/01_explore_data_exercises.Rmd`. The code chunks mirror the TODOs but include one possible solution for each task.

## 1. Load and preview the dataset

```
input_path <- file.path('..', 'data', 'dataset2_subset_long.csv')
long_df <- read.csv(input_path, stringsAsFactors = FALSE, check.names = FALSE)
cat('Rows:', nrow(long_df), '\\nColumns:', ncol(long_df), '\\n')
```

```
## Rows: 3072 \nColumns: 7 \n
```

```
head(long_df)
```

```
##                          Genome      snp_id Position    value mouse_id day
## 1 Akkermansia_muciniphila_YL44  239840-C-G   239840 0.000000     1683   0
## 2 Akkermansia_muciniphila_YL44  241793-A-G   241793 0.049587     1683   0
## 3 Akkermansia_muciniphila_YL44  355328-A-T   355328 0.138182     1683   0
## 4 Akkermansia_muciniphila_YL44  356291-C-A   356291 0.000000     1683   0
## 5 Akkermansia_muciniphila_YL44 2351445-C-T  2351445 0.000000     1683   0
## 6   Bacteroides_caecimuris_I48 1601848-T-C  1601848 0.041609     1683   0
##   treatment_group
## 1         Control
## 2         Control
## 3         Control
## 4         Control
## 5         Control
## 6         Control
```

## 2. Enumerate genomes and SNPs

```
unique(long_df$Genome)
```

```
## [1] "Akkermansia_muciniphila_YL44" "Bacteroides_caecimuris_I48"
## [3] "Turicimonas_muris_YL45"
```

```
table(long_df$Genome)
```

```
##
## Akkermansia_muciniphila_YL44   Bacteroides_caecimuris_I48
##                          320                         1216
##       Turicimonas_muris_YL45
##                         1536
```

```
tapply(long_df$snp_id, long_df$Genome, function(x) length(unique(x)))
```

```
## Akkermansia_muciniphila_YL44   Bacteroides_caecimuris_I48
##                            5                           19
##       Turicimonas_muris_YL45
##                           24
```

## 3. Summaries by genome

```
sample_values <- long_df$value[1:10]
summary(sample_values)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.00000 0.00000 0.00000 0.03426 0.04759 0.13818
```

```
aggregate(value ~ Genome, data = long_df, function(x) summary(x))
```

```
##                        Genome value.Min. value.1st Qu. value.Median value.Mean
## 1 Akkermansia_muciniphila_YL44  0.0000000     0.0000000    0.0523090  0.1741893
## 2   Bacteroides_caecimuris_I48  0.0000000     0.0000000    0.0338305  0.1485411
## 3       Turicimonas_muris_YL45  0.0000000     0.0000000    0.2649125  0.4312851
##   value.3rd Qu. value.Max.
## 1     0.2714463  0.8712450
## 2     0.2679232  0.9912180
## 3     0.9090910  1.0000000
```

## 4. Focus on Turicimonas

```
turicimonas_df <- long_df[long_df$Genome == 'Turicimonas_muris_YL45', ]
cat('Rows for Turicimonas:', nrow(turicimonas_df), '\\n')
```

```
## Rows for Turicimonas: 1536 \n
```

```
head(turicimonas_df)
```

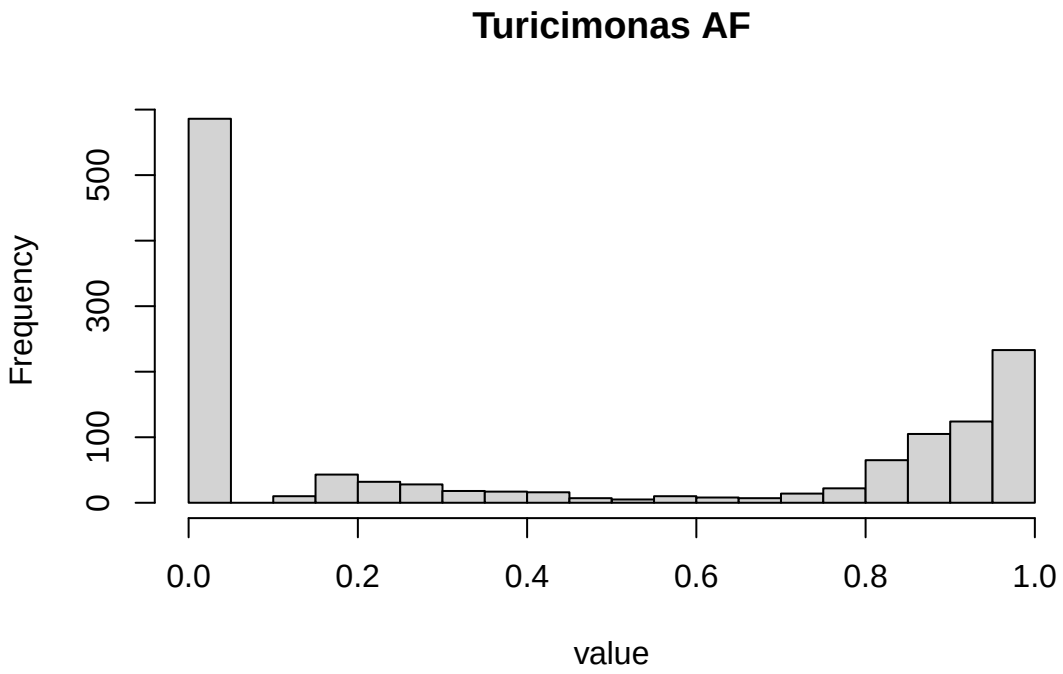
```
##                    Genome      snp_id Position    value mouse_id day
## 25 Turicimonas_muris_YL45  362534-G-A   362534 1.000000     1683   0
## 26 Turicimonas_muris_YL45 1063346-G-A  1063346 0.741935     1683   0
## 27 Turicimonas_muris_YL45 1135479-G-A  1135479 0.000000     1683   0
## 28 Turicimonas_muris_YL45 1364256-G-A  1364256 0.406250     1683   0
## 29 Turicimonas_muris_YL45 1376518-G-A  1376518 0.000000     1683   0
## 30 Turicimonas_muris_YL45 1392383-G-A  1392383 0.461538     1683   0
##    treatment_group
## 25         Control
## 26         Control
## 27         Control
## 28         Control
## 29         Control
## 30         Control
```

```
table(turicimonas_df$mouse_id, turicimonas_df$day)
```

```
##
##         0  4  9 14 18 23 30 37 44 49 53 58 63 67 72 79
##   1683 24 24 24 24 24 24 24 24 24 24 24 24 24 24 24 24
##   1688 24 24 24 24 24 24 24 24 24 24 24 24 24 24 24 24
##   1692 24 24 24 24 24 24 24 24 24 24 24 24 24 24 24 24
##   1699 24 24 24 24 24 24 24 24 24 24 24 24 24 24 24 24
```

## 5. Allele-frequency focus (Turicimonas vs all genomes)

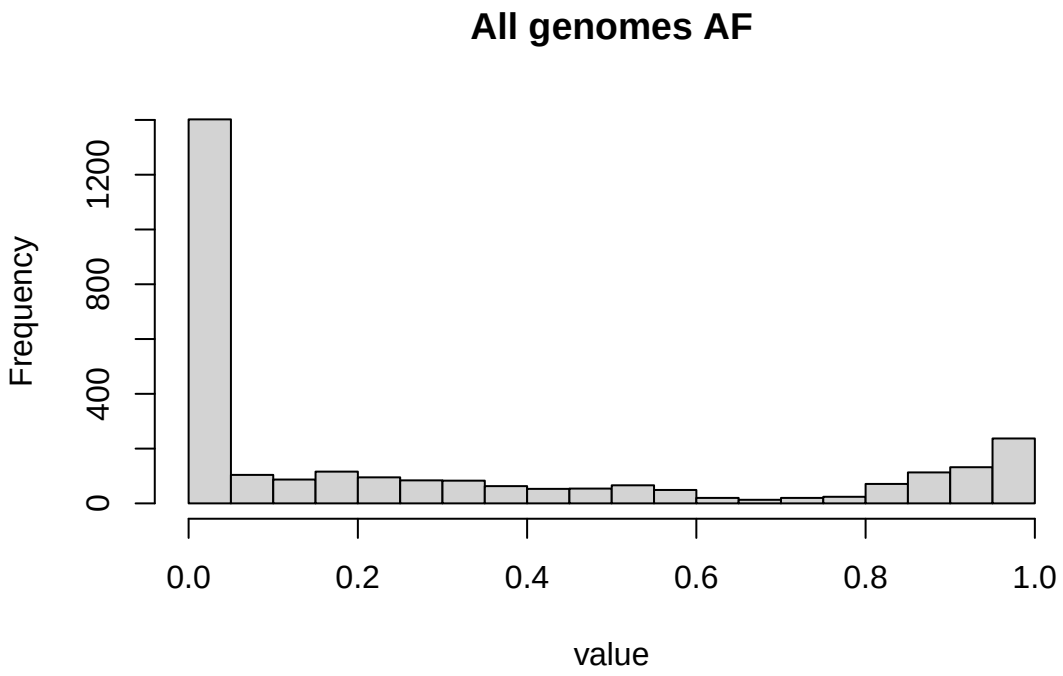
```
turicimonas_values <- long_df$value[long_df$Genome == 'Turicimonas_muris_YL45']
hist(turicimonas_values, breaks = 20, main = 'Turicimonas AF', xlab = 'value')
```




```
summary(turicimonas_values)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##  0.0000  0.0000  0.2649  0.4313  0.9091  1.0000     186
```

```
hist(long_df$value, breaks = 30, main = 'All genomes AF', xlab = 'value')
```



```
summary(long_df$value)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
## 0.00000 0.00000 0.06438 0.28365 0.51995 1.00000     186
```

## 6. Missing values

```
na_total <- sum(is.na(long_df$value))
na_total
```

```
## [1] 186
```

```
na_by_mouse_day <- with(long_df, tapply(value, list(mouse_id, day), function(x) sum(is.na(x))))
na_by_mouse_day
```

```
##       0  4  9 14 18 23 30 37 44 49 53 58 63 67 72 79
## 1683  0  1  0  1  3  2  1  0  0  2  0  1  0  0  0  1
## 1688 15  1  0  1  0  0  0  0  0  0  0  0  0  0  0  1
## 1692  0 24 24  0 24 20  6  0  1  8 16  0  0  6  0  0
## 1699  0  0 24  0  1  0  0  0  1  0  0  0  1  0  0  0
```

In this dataset the counts are all zero, so no genome (including Turicimonas) introduces missing allele-frequency entries.

## 7. Treatment groups

```
unique(long_df$treatment_group)
```

```
## [1] "Control"       "Ciprofloxacin" "Tetracyclin"   "Vancomycin"
```

```
table(long_df$treatment_group)
```

```
##
## Ciprofloxacin       Control   Tetracyclin    Vancomycin
##           768           768           768           768
```

```
table(long_df$mouse_id, long_df$treatment_group)
```

```
##
##        Ciprofloxacin Control Tetracyclin Vancomycin
##   1683             0     768           0          0
##   1688           768       0           0          0
##   1692             0       0         768          0
##   1699             0       0           0        768
```

```
long_df[long_df$day == 30, c('mouse_id','treatment_group')]
```

```
##      mouse_id treatment_group
## 193      1683         Control
## 194      1683         Control
## 195      1683         Control
## 196      1683         Control
## 197      1683         Control
## 198      1683         Control
## 199      1683         Control
## 200      1683         Control
## 201      1683         Control
```

```
## 202      1683         Control
## 203      1683         Control
## 204      1683         Control
## 205      1683         Control
## 206      1683         Control
## 207      1683         Control
## 208      1683         Control
## 209      1683         Control
## 210      1683         Control
## 211      1683         Control
## 212      1683         Control
## 213      1683         Control
## 214      1683         Control
## 215      1683         Control
## 216      1683         Control
## 217      1683         Control
## 218      1683         Control
## 219      1683         Control
## 220      1683         Control
## 221      1683         Control
## 222      1683         Control
## 223      1683         Control
## 224      1683         Control
## 225      1683         Control
## 226      1683         Control
## 227      1683         Control
## 228      1683         Control
## 229      1683         Control
## 230      1683         Control
## 231      1683         Control
## 232      1683         Control
## 233      1683         Control
## 234      1683         Control
## 235      1683         Control
## 236      1683         Control
## 237      1683         Control
## 238      1683         Control
## 239      1683         Control
## 240      1683         Control
## 961      1688   Ciprofloxacin
## 962      1688   Ciprofloxacin
## 963      1688   Ciprofloxacin
## 964      1688   Ciprofloxacin
## 965      1688   Ciprofloxacin
## 966      1688   Ciprofloxacin
## 967      1688   Ciprofloxacin
## 968      1688   Ciprofloxacin
## 969      1688   Ciprofloxacin
## 970      1688   Ciprofloxacin
## 971      1688   Ciprofloxacin
## 972      1688   Ciprofloxacin
## 973      1688   Ciprofloxacin
## 974      1688   Ciprofloxacin
## 975      1688   Ciprofloxacin
```

```
## 976      1688   Ciprofloxacin
## 977      1688   Ciprofloxacin
## 978      1688   Ciprofloxacin
## 979      1688   Ciprofloxacin
## 980      1688   Ciprofloxacin
## 981      1688   Ciprofloxacin
## 982      1688   Ciprofloxacin
## 983      1688   Ciprofloxacin
## 984      1688   Ciprofloxacin
## 985      1688   Ciprofloxacin
## 986      1688   Ciprofloxacin
## 987      1688   Ciprofloxacin
## 988      1688   Ciprofloxacin
## 989      1688   Ciprofloxacin
## 990      1688   Ciprofloxacin
## 991      1688   Ciprofloxacin
## 992      1688   Ciprofloxacin
## 993      1688   Ciprofloxacin
## 994      1688   Ciprofloxacin
## 995      1688   Ciprofloxacin
## 996      1688   Ciprofloxacin
## 997      1688   Ciprofloxacin
## 998      1688   Ciprofloxacin
## 999      1688   Ciprofloxacin
## 1000     1688   Ciprofloxacin
## 1001     1688   Ciprofloxacin
## 1002     1688   Ciprofloxacin
## 1003     1688   Ciprofloxacin
## 1004     1688   Ciprofloxacin
## 1005     1688   Ciprofloxacin
## 1006     1688   Ciprofloxacin
## 1007     1688   Ciprofloxacin
## 1008     1688   Ciprofloxacin
## 1729     1692     Tetracyclin
## 1730     1692     Tetracyclin
## 1731     1692     Tetracyclin
## 1732     1692     Tetracyclin
## 1733     1692     Tetracyclin
## 1734     1692     Tetracyclin
## 1735     1692     Tetracyclin
## 1736     1692     Tetracyclin
## 1737     1692     Tetracyclin
## 1738     1692     Tetracyclin
## 1739     1692     Tetracyclin
## 1740     1692     Tetracyclin
## 1741     1692     Tetracyclin
## 1742     1692     Tetracyclin
## 1743     1692     Tetracyclin
## 1744     1692     Tetracyclin
## 1745     1692     Tetracyclin
## 1746     1692     Tetracyclin
## 1747     1692     Tetracyclin
## 1748     1692     Tetracyclin
## 1749     1692     Tetracyclin
```

```
## 1750     1692     Tetracyclin
## 1751     1692     Tetracyclin
## 1752     1692     Tetracyclin
## 1753     1692     Tetracyclin
## 1754     1692     Tetracyclin
## 1755     1692     Tetracyclin
## 1756     1692     Tetracyclin
## 1757     1692     Tetracyclin
## 1758     1692     Tetracyclin
## 1759     1692     Tetracyclin
## 1760     1692     Tetracyclin
## 1761     1692     Tetracyclin
## 1762     1692     Tetracyclin
## 1763     1692     Tetracyclin
## 1764     1692     Tetracyclin
## 1765     1692     Tetracyclin
## 1766     1692     Tetracyclin
## 1767     1692     Tetracyclin
## 1768     1692     Tetracyclin
## 1769     1692     Tetracyclin
## 1770     1692     Tetracyclin
## 1771     1692     Tetracyclin
## 1772     1692     Tetracyclin
## 1773     1692     Tetracyclin
## 1774     1692     Tetracyclin
## 1775     1692     Tetracyclin
## 1776     1692     Tetracyclin
## 2497     1699      Vancomycin
## 2498     1699      Vancomycin
## 2499     1699      Vancomycin
## 2500     1699      Vancomycin
## 2501     1699      Vancomycin
## 2502     1699      Vancomycin
## 2503     1699      Vancomycin
## 2504     1699      Vancomycin
## 2505     1699      Vancomycin
## 2506     1699      Vancomycin
## 2507     1699      Vancomycin
## 2508     1699      Vancomycin
## 2509     1699      Vancomycin
## 2510     1699      Vancomycin
## 2511     1699      Vancomycin
## 2512     1699      Vancomycin
## 2513     1699      Vancomycin
## 2514     1699      Vancomycin
## 2515     1699      Vancomycin
## 2516     1699      Vancomycin
## 2517     1699      Vancomycin
## 2518     1699      Vancomycin
## 2519     1699      Vancomycin
## 2520     1699      Vancomycin
## 2521     1699      Vancomycin
## 2522     1699      Vancomycin
## 2523     1699      Vancomycin
```

```
## 2524     1699      Vancomycin
## 2525     1699      Vancomycin
## 2526     1699      Vancomycin
## 2527     1699      Vancomycin
## 2528     1699      Vancomycin
## 2529     1699      Vancomycin
## 2530     1699      Vancomycin
## 2531     1699      Vancomycin
## 2532     1699      Vancomycin
## 2533     1699      Vancomycin
## 2534     1699      Vancomycin
## 2535     1699      Vancomycin
## 2536     1699      Vancomycin
## 2537     1699      Vancomycin
## 2538     1699      Vancomycin
## 2539     1699      Vancomycin
## 2540     1699      Vancomycin
## 2541     1699      Vancomycin
## 2542     1699      Vancomycin
## 2543     1699      Vancomycin
## 2544     1699      Vancomycin
```

## 8. Stretch idea (optional)

```
day30 <- long_df[long_df$day == 30, ]
medians_day30 <- tapply(day30$value, day30$Genome, median, na.rm = TRUE)
medians_day30
```

```
## Akkermansia_muciniphila_YL44   Bacteroides_caecimuris_I48
##                     0.124955                     0.030887
##       Turicimonas_muris_YL45
##                     0.250000
```

```
medians_day30[which.max(medians_day30)]
```

```
## Turicimonas_muris_YL45
##                   0.25
```

Feel free to compare your answers with these outputs, then proceed to `scripts/02_simple_heatmap.Rmd`.