

# 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 0.00000000    0.0000000    0.0523090 0.1741893
## 2 Bacteroides_caecimuris_I48 0.00000000    0.0000000    0.0338305 0.1485411
## 3 Turicimonas_muris_YL45 0.00000000    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
```

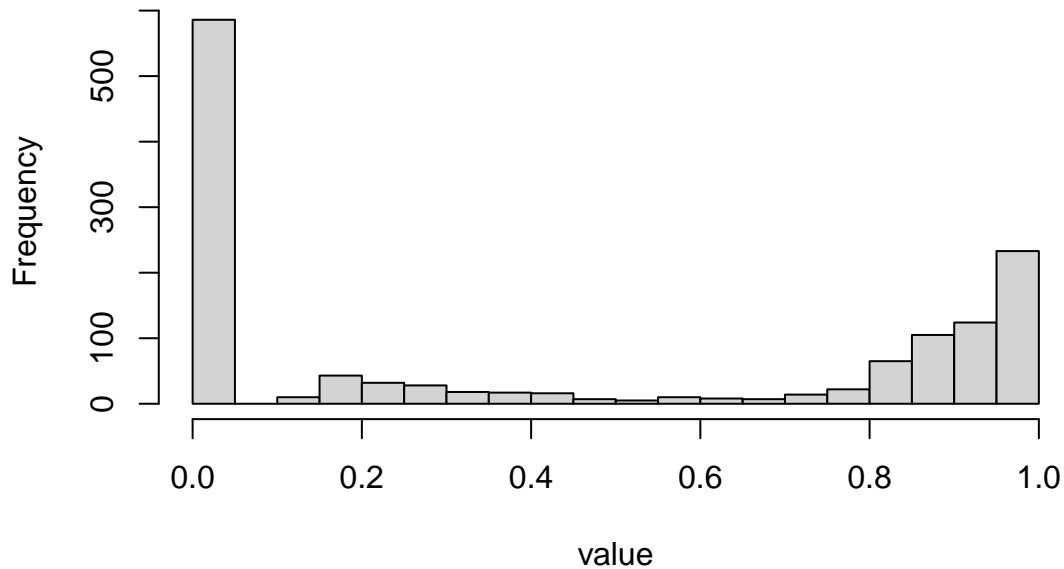
```
table(turicimonas_df$mouse_id, turicimonas_df$day)
```

```
##
##      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
## 1688 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
## 1699 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')
```

**Turicimonas AF**

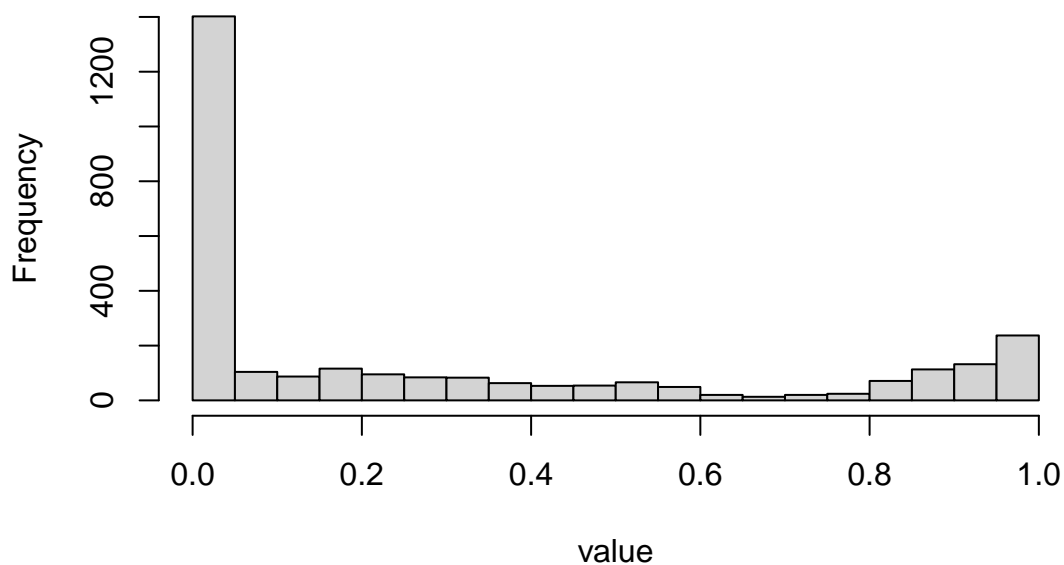


```
summary(turicimonas_values)
```

```
##      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')
```

**All genomes AF**



```
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`.