

Day 2 – 03 Heatmap + Annotations (Step by Step)

Seminar plotting walk-through

This notebook incrementally builds on the basic heatmap from `02_simple_heatmap.Rmd`. Each step introduces one new detail so students can see how changes affect the final figure.

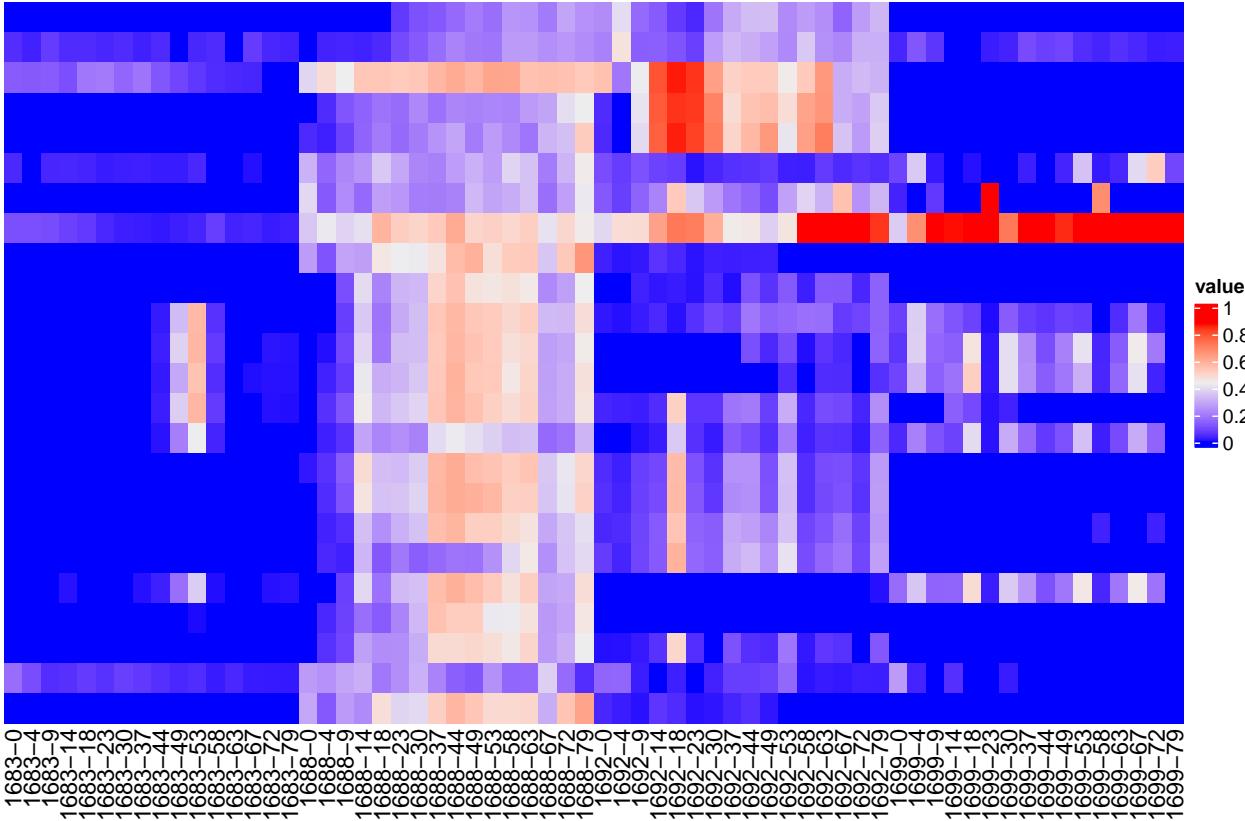
We assume `second_day_part2/data/00_prepare_dataset.Rmd` has already produced the CSVs.

1. Load packages and data

```
library(ComplexHeatmap)
library(circlize)
subset_path <- file.path('..', 'data', 'dataset1_subset.csv')
wide_df <- read.csv(subset_path, check.names = FALSE, stringsAsFactors = FALSE)
sample_cols <- setdiff(names(wide_df), c('Genome', 'snp_id', 'Position'))
mat <- as.matrix(wide_df[, sample_cols])
mode(mat) <- 'numeric'
rownames(mat) <- paste(wide_df$Genome, wide_df$snp_id, sep = ' | ')
```

2. Step 1 – Plain heatmap (same as `02_simple_heatmap`)

```
ht_plain <- Heatmap(
  mat,
  name = 'value',
  cluster_rows = FALSE,
  cluster_columns = FALSE,
  show_row_names = FALSE,
  show_column_names = TRUE
)
draw(ht_plain)
```

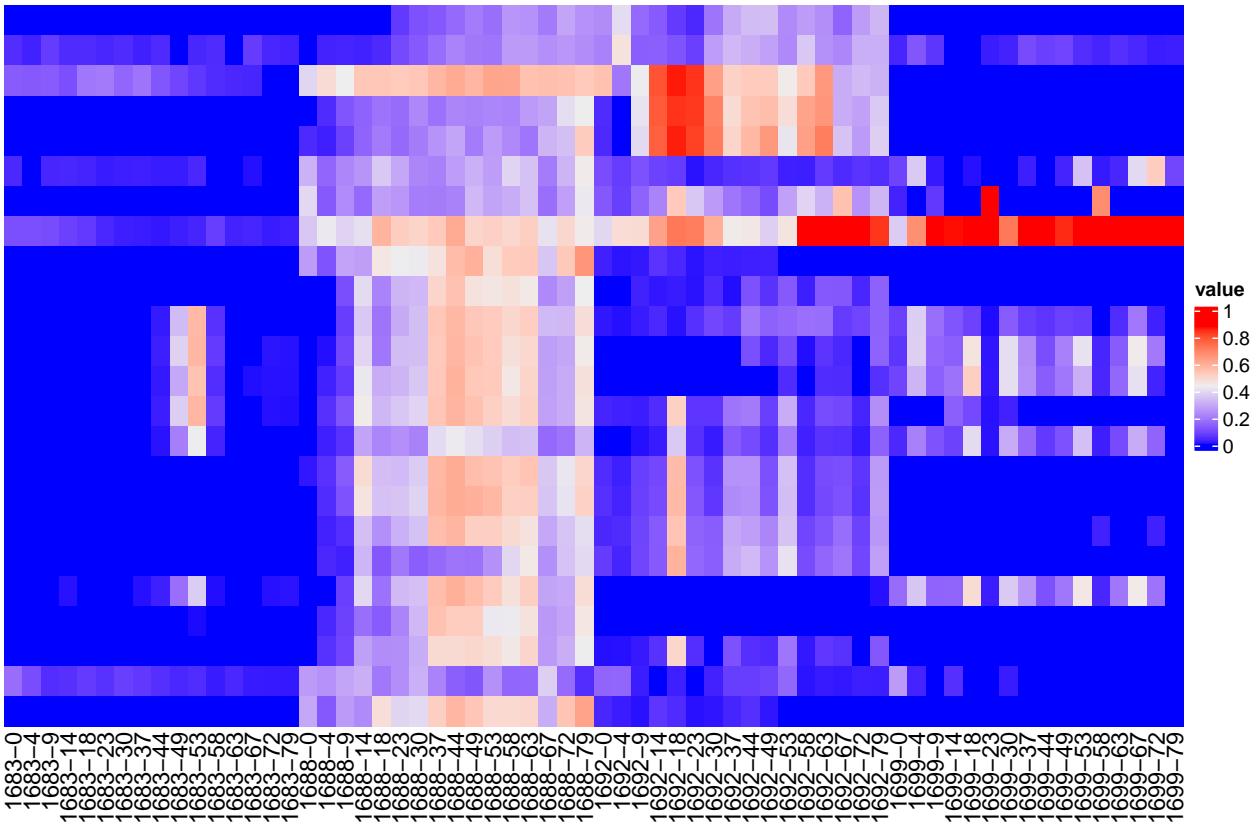


3. Step 2 – Reorder columns (mouse/day ordering)

```

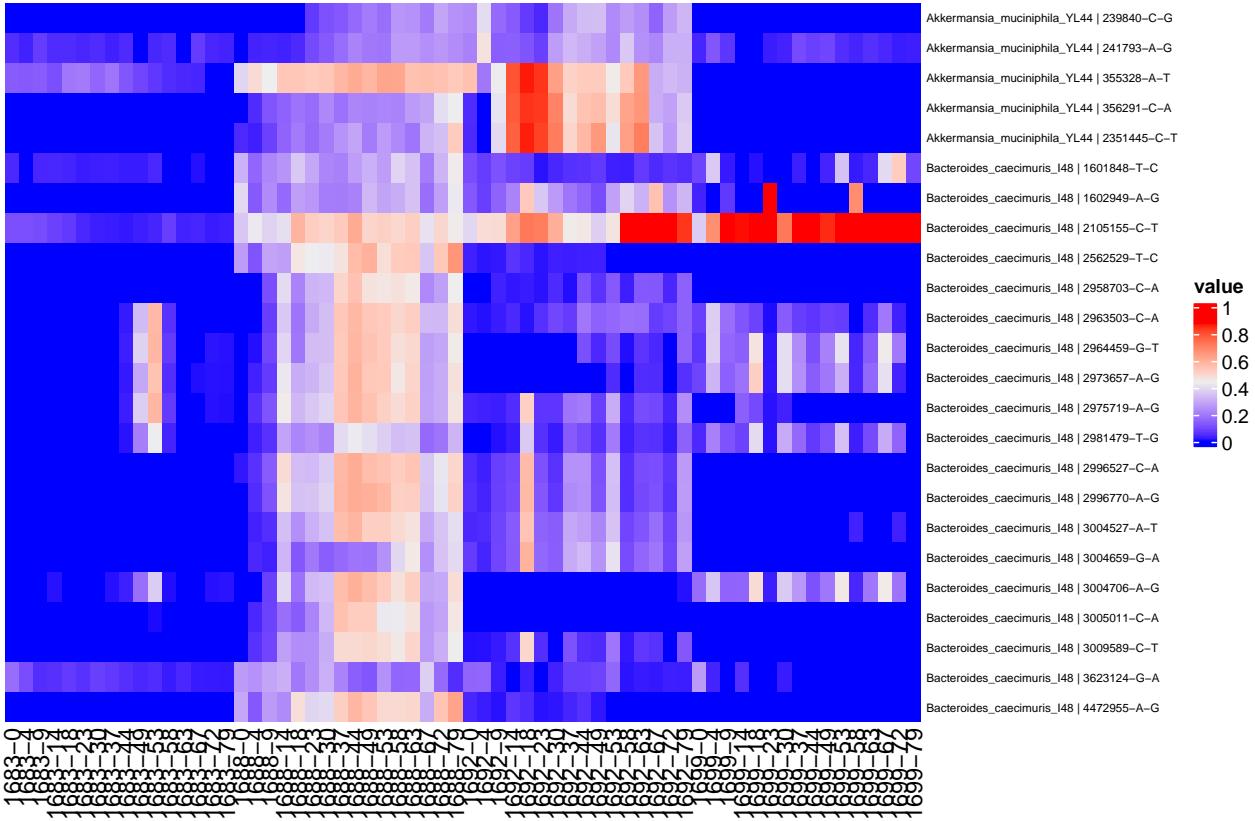
sample_meta <- data.frame(sample_id = sample_cols, stringsAsFactors = FALSE)
split_ids <- strsplit(sample_meta$sample_id, '-', fixed = TRUE)
sample_meta$mouse_id <- vapply(split_ids, `[[`, character(1), 1)
sample_meta$day <- as.integer(vapply(split_ids, function(x) if (length(x) >= 2) x[[2]] else NA_character))
order_idx <- order(sample_meta$mouse_id, sample_meta$day, sample_meta$sample_id)
mat_ordered <- mat[, order_idx, drop = FALSE]
ht_ordered <- Heatmap(
  mat_ordered,
  name = 'value',
  cluster_rows = FALSE,
  cluster_columns = FALSE,
  show_row_names = FALSE,
  show_column_names = TRUE
)
draw(ht_ordered)

```



4. Step 3 – Add row labels (Genome | SNP)

```
ht_rows <- Heatmap(
  mat_ordered,
  name = 'value',
  cluster_rows = FALSE,
  cluster_columns = FALSE,
  show_row_names = TRUE,
  show_column_names = TRUE,
  row_names_gp = grid::gpar(fontsize = 6)
)
draw(ht_rows)
```

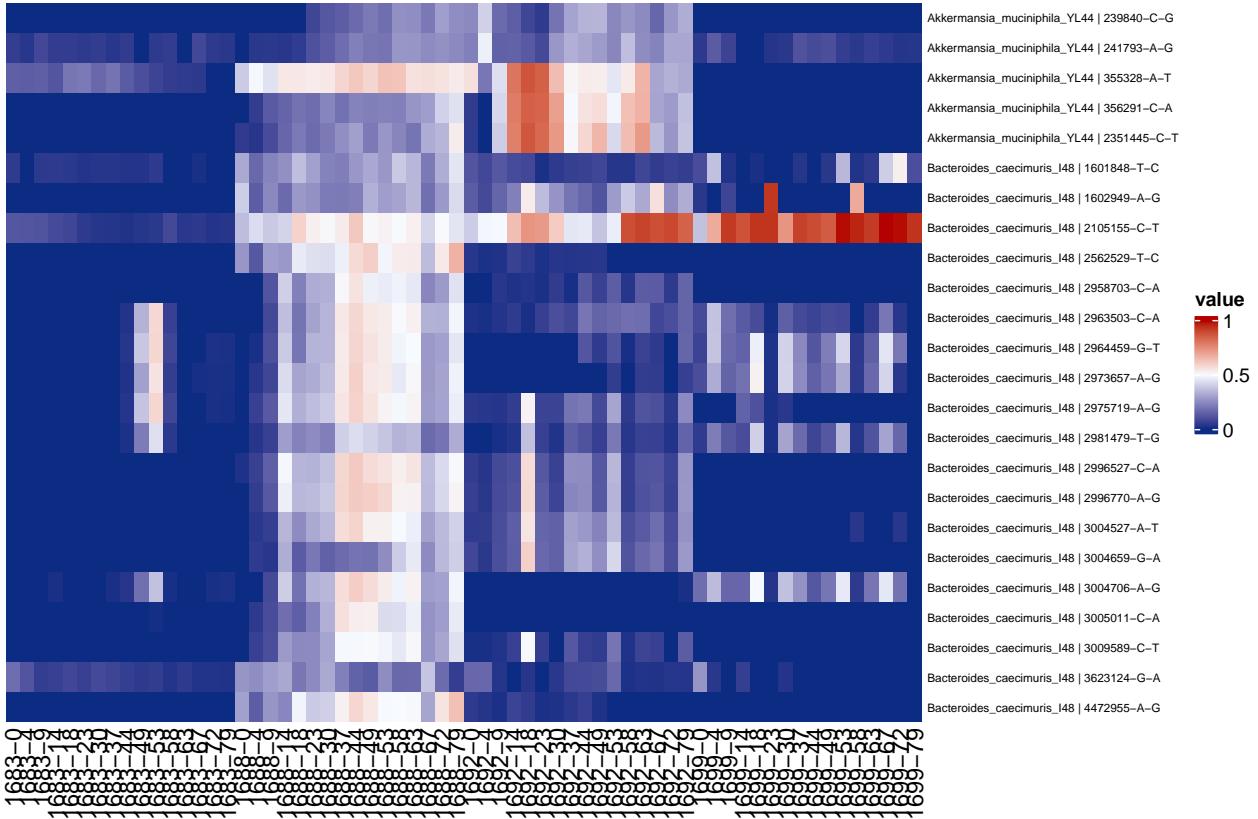


5. Step 4 – Add simple color control

```

min_val <- min(mat_ordered, na.rm = TRUE)
max_val <- max(mat_ordered, na.rm = TRUE)
mid_val <- (min_val + max_val) / 2
col_fun <- circlize::colorRamp2(c(min_val, mid_val, max_val), c('#0c2c84', '#f7fbff', '#b30000'))
ht_colors <- Heatmap(
  mat_ordered,
  name = 'value',
  col = col_fun,
  cluster_rows = FALSE,
  cluster_columns = FALSE,
  show_row_names = TRUE,
  show_column_names = TRUE,
  row_names_gp = grid::gpar(fontsize = 6)
)
draw(ht_colors)

```

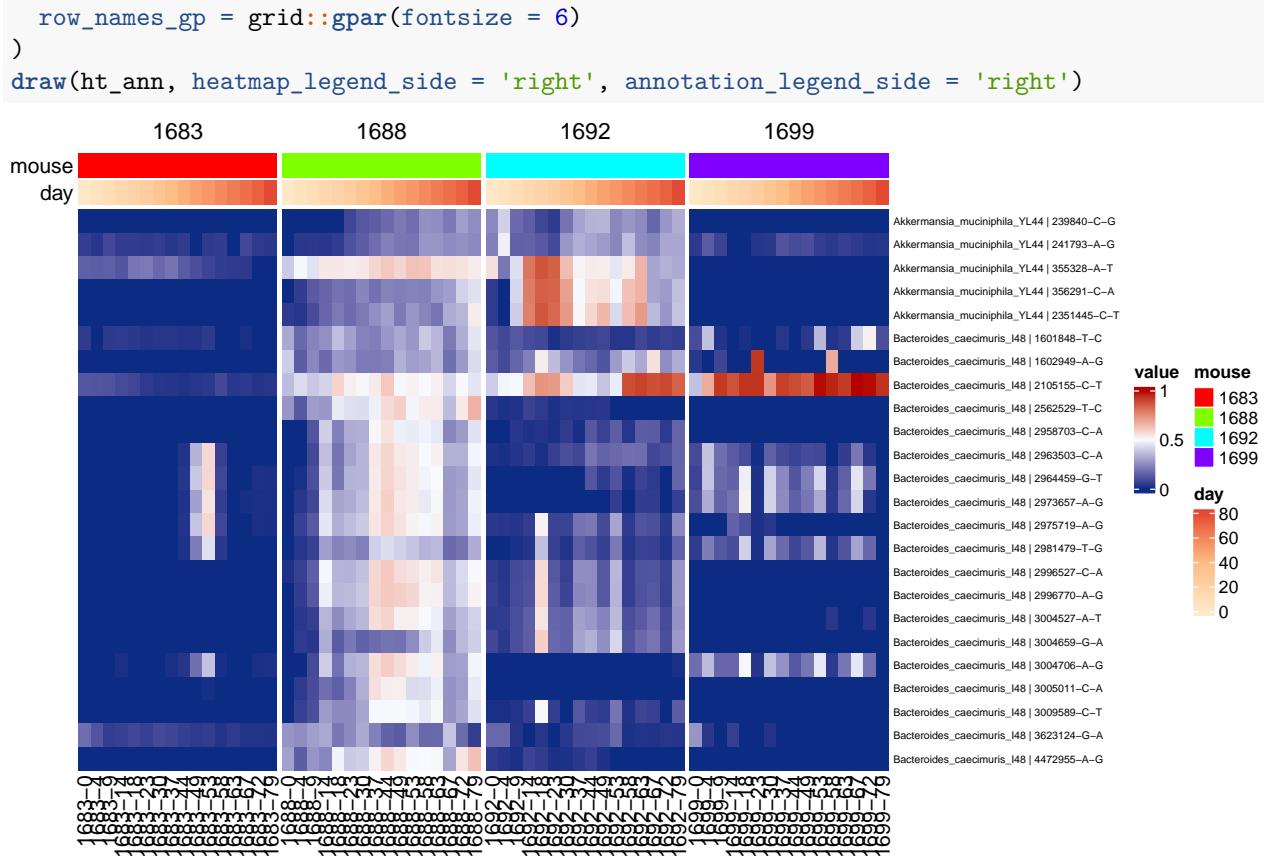


6. Step 5 – Add column annotations (mouse ID, day)

```

mouse_levels <- unique(sample_meta$mouse_id)
mouse_colors <- setNames(grDevices::rainbow(length(mouse_levels)), mouse_levels)
min_day <- min(sample_meta$day, na.rm = TRUE)
max_day <- max(sample_meta$day, na.rm = TRUE)
if (min_day == max_day) {
  day_colors <- circlize::colorRamp2(c(min_day, min_day + 1), c('#fee8c8', '#e34a33'))
} else {
  day_colors <- circlize::colorRamp2(seq(min_day, max_day, length.out = 3), c('#fee8c8', '#fdbb84', '#e34a33'))
}
col_ann <- HeatmapAnnotation(
  mouse = factor(sample_meta$mouse_id, levels = mouse_levels),
  day = sample_meta$day,
  col = list(mouse = mouse_colors, day = day_colors),
  annotation_name_side = 'left'
)
ht_ann <- Heatmap(
  mat_ordered,
  name = 'value',
  col = col_fun,
  top_annotation = col_ann,
  column_split = factor(sample_meta$mouse_id, levels = mouse_levels),
  cluster_rows = FALSE,
  cluster_columns = FALSE,
  show_row_names = TRUE,
  show_column_names = TRUE,
)

```



7. Step 6 – Export to PDF

```

pdf(file.path('..', 'pdf', '02_simple_heatmap_with_annotations.pdf'), width = 10, height = 7)
draw(ht_ann, heatmap_legend_side = 'right', annotation_legend_side = 'right')
dev.off()

```

You can extend this notebook further by experimenting with row splits, additional color control, or integrating external annotations. Compare this result with the minimalist `02_simple_heatmap.Rmd` to emphasize how each step adds clarity.