

# Function of the Week – `gt::gt()`

*PennCHOP Microbiome Program*

9/18/2019

```
#remotes::install_github("rstudio/gt")
library(gt)
```

## Raw data

```
d0 <- read_tsv("genus_prop.tsv")
dim(d0)

## [1] 10 16

d <- d0 %>%
  mutate(Taxa = fct_relevel(Taxa, "Other", after = Inf)) %>%
  mutate(Phylum = case_when(str_detect(Taxa, "Bacteroidetes") ~ "Bacteroidetes",
                              str_detect(Taxa, "Firmicutes") ~ "Firmicutes",
                              T ~ "Other phyla")) %>%
  arrange(Phylum, Taxa) %>%
  select(Taxa, Phylum, everything())
```

## Final table

```
d %>%
  gt(rowname_col = "Taxa") %>%
  tab_stubhead(label = "Taxonomy") %>%
  cols_hide(columns = "Phylum") %>%
  fmt_percent(columns = contains("DSS")) %>%
  tab_header(title = "Abundance table",
             subtitle = "Genus-level") %>%
  tab_source_note(source_note = "Data from Habtezion project") %>%
  tab_source_note(source_note = md("**E. coli* not found")) %>%
  tab_spanner(label = "LCA DSS",
              columns = starts_with("LCA.DSS")) %>%
  tab_spanner(label = "NO DSS",
              columns = starts_with("NO.DSS")) %>%
  tab_spanner(label = "Water",
              columns = starts_with("Water")) %>%
  tab_row_group(group = "Bacteroidetes",
               rows = Phylum == "Bacteroidetes") %>%
  tab_row_group(group = "Firmicutes",
               rows = Phylum == "Firmicutes") %>%
  tab_row_group(group = "Other phyla",
               rows = Phylum == "Other phyla") %>%
  tab_footnote(footnote = md("**Not observed!**"),
               locations = cells_data(
```

```

        columns = contains("No.DSS"),
        rows = contains("p__Proteobacteria g__Proteus"))
    ) %>%
tab_style(style = cell_fill(color = "cyan"),
  location = cells_data(
    columns = 1:5,
    rows = 1:2)
  ) %>%
gtsave("table_final.pdf")

```

Abundance table																
Taxonomy		LCA DSS					Genus-level					Water				
		LCA.DSS.1	LCA.DSS.2	LCA.DSS.3	LCA.DSS.4	LCA.DSS.5	No.DSS.1	No.DSS.2	No.DSS.3	No.DSS.4	No.DSS.5	Water.DSS.1	Water.DSS.2	Water.DSS.3	Water.DSS.4	Water.DSS.5
Bacteroidetes																
p__Bacteroidetes g__Bacteroides	37.28%	13.42%	26.99%	13.67%	3.20%	20.32%	33.23%	21.78%	17.10%	38.79%	11.03%	19.82%	8.15%	19.65%	23.31%	
p__Bacteroidetes g__Parabacteroides	12.17%	1.07%	3.25%	5.10%	0.32%	10.84%	11.67%	13.08%	7.49%	10.87%	1.34%	4.14%	7.00%	1.84%	1.31%	
Firmicutes																
p__Firmicutes f__Lachnospiraceae	1.07%	13.61%	10.12%	7.44%	3.96%	5.12%	5.94%	8.61%	9.33%	4.90%	8.25%	3.07%	0.48%	7.61%	2.62%	
p__Firmicutes f__Ruminococcaceae	1.23%	2.61%	1.59%	3.69%	3.51%	2.88%	2.10%	2.20%	2.62%	1.64%	3.22%	2.37%	0.21%	2.47%	2.63%	
p__Firmicutes g__Enterococcus	4.53%	0.35%	1.46%	0.10%	8.36%	0.00%	0.00%	0.00%	0.00%	0.00%	0.31%	5.66%	18.70%	0.86%	0.82%	
p__Firmicutes g__Oscillospira	3.72%	12.97%	5.20%	5.43%	6.10%	4.09%	3.63%	3.88%	8.39%	3.53%	7.33%	6.63%	1.31%	6.21%	5.80%	
p__Firmicutes o__Clostridiales	8.71%	25.04%	23.13%	40.95%	29.21%	25.83%	25.59%	33.25%	29.12%	21.74%	41.19%	14.54%	2.82%	29.79%	27.87%	
Other phyla																
p__Deferribacteres g__Mucispirillum	3.50%	9.68%	11.95%	3.39%	28.35%	0.46%	0.09%	0.65%	0.12%	0.09%	11.23%	6.16%	1.97%	16.38%	8.69%	
p__Proteobacteria g__Proteus	16.86%	1.95%	2.81%	0.04%	7.89%	0.00% <sup>†</sup>	0.00% <sup>†</sup>	0.00% <sup>†</sup>	0.00% <sup>†</sup>	0.00% <sup>†</sup>	0.40%	13.21%	56.69%	2.42%	1.52%	
Other	10.94%	19.30%	13.49%	20.20%	9.10%	30.46%	17.74%	16.55%	25.83%	18.44%	15.69%	24.40%	2.67%	12.77%	25.43%	
<sup>†</sup> Not observed!																
Data from Habtezion project																
E. coli not found																