Transforming raw data

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Pairwise data

All PW combinations of 7 species, plus the alone condition & the complete 7-member community condition; all these assemblages repeated 5 times for experiments started on CCA pH 5 and CCA pH 7.

```
# pH-factored growth data of alone, pairwise, and full communities
d.18 <- read.csv(file = here("raw_data/2018_08_21_Bayley_allPW.csv"))
d.18$pH <- as.factor(d.18$pH)
colnames(d.18)[c(1,2,4,8)] <- c("species", "condition", "replicate", "total.CFUs")
d.18$condition <- factor(d.18$condition, levels = c("alone", "135E", "BC10", "BC9", "JB5", "JB7", "JBC"
d.18$species <- factor(d.18$species, levels = c("135E", "BC10", "BC9", "JB5", "JB7", "JBC", "JB370"))
d.18 <- d.18 %>% mutate(log.CFUs = log10(total.CFUs))

# get means & medians from replicates
d.18.summ <- d.18 %>%
  group_by(species, condition, day, pH, class) %>%
  summarize(mean.CFUs = mean(total.CFUs, na.rm = TRUE),
            mean.measured.pH = mean(measured.pH, na.rm = TRUE),
            med.CFUs = median(total.CFUs, na.rm = TRUE),
            med.measured.pH = median(measured.pH, na.rm = TRUE)) %>%
  mutate(mean.log.CFUs = log10(mean.CFUs),
         med.log.CFUs = log10(med.CFUs),
         dayChar = as.factor(day))
```

```
## `summarise()` has grouped output by 'species', 'condition', 'day', 'pH'. You can override using the
```

```
write_csv(d.18, file = here("wrangled_data/all_pairwise.csv"))
saveRDS(d.18, file = here("wrangled_data/all_pairwise.rds"))

write_csv(d.18.summ, file = here("wrangled_data/pairwise_summary_stats.csv"))
saveRDS(d.18.summ, file = here("wrangled_data/pairwise_summary_stats.rds"))
```

Leave-one-out communities on CCA pH 5

The objective of this experiment was to assess the net contributions of key Bayley species, as identified by strong roles in pairwise interaction assays. To assess their overall contribution in the community, each of the following species was left out of the community when plates in equal ratio on cheese curd agar, pH 5.

Species left out * none (“community” or “comm”) * Penicillium JBC (“comm-JBC”) * Candida/Diutina 135E (“comm-135E”) * Staphyloccocus xylosus BC10 (“comm-BC10”) * Candida/Diutina 135E & S. xylosus BC10 (“community minus early deacidifiers” or “comm-eD”)

```
d.loo5 <- read_csv(file = here("raw_data/2020_11_09_LeaveOneOut - Data.csv"), col_types = "ffffddddd")

# calculate change in pH from beginning
average.start.pH <- d.loo5 %>% filter(day == 0) %>% pull(pH) %>% mean(na.rm = T)
d.loo5 <- d.loo5 %>% mutate(delta.pH.fromDay0 = ifelse(day == 0, 0, pH-average.start.pH))
```

```
write_csv(d.loo5, file = here("wrangled_data/leave-one-out_pH5.csv"))
saveRDS(d.loo5, file = here("wrangled_data/leave-one-out_pH5.rds"))
```

Leave-one-out communities on CCA pH 7

The objective of this experiment was to reconstruct the Bayley community to have no (or rather minimized) net growth effects. This community eliminates stimulatory effects of deacidification by growing the community at pH 7 and also eliminated inhibitory effects due to *Penicillium* JBC by removing it from the community. Comparison of the growth each species grown alone at pH 7 to growth in the community lacking Penicillium will reveal any additional interactions not accounted for by these two growth affectors.

Community conditions

- none ("community" or "comm")
- Penicillium JBC ("comm-JBC")
- each of 7 Bayley species grown alone

```
d.loo7 <- read_csv(file = here("raw_data/2020_11_17_pH7LOO - Data.csv"), col_types = "ffffdddddd")
```

```
write_csv(d.loo7, file = here("wrangled_data/leave-one-out_pH7.csv"))
saveRDS(d.loo7, file = here("wrangled_data/leave-one-out_pH7.rds"))
```

```
save(d.18, d.18.summ, d.loo5, d.loo7, file = here("wrangled_data/all_data.RData"))
```