Plot Model Predictions

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About the data

Collin took alone and pairwise CFU data for each species at day 21, assuming this was the "equilibrium" point (which would be where population size no longer changes, and dn/dt == 0), and used it to fit the Lotka-Volterra competition model to predict cell counts of each species in the complete community.

```
estimates <- rbind(read_csv(here("wrangled_data/model_predictions/coefficient-estimates-pH5.csv")),
                   read_csv(here("wrangled_data/model_predictions/coefficient-estimates-pH7.csv")) %>%
                     mutate(pH = 7)) %>%
  mutate(spec = recode(spec, "X135E" = "135E"), name = recode(name, "X135E" = "135E"))
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   spec = col_character(),
##   name = col_character(),
##   est = col_double(),
##   se = col_double(),
##   pH = col_double()
## )
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   spec = col_character(),
##   name = col_character(),
##   est = col_double(),
##   se = col_double()
## )
```

```
predictions <- rbind(read_csv(here("wrangled_data/model_predictions/predictions-from-pH5.csv")) %>%
                       mutate(pH = 5),
                     read_csv(here("wrangled_data/model_predictions/predictions-from-pH7.csv")) %>%
                       mutate(pH = 7)) %>%
  select(spec, pH, replicate, fit) %>%
  mutate(spec = recode(spec, "X135E" = "135E")) %>%
  na.omit()
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   fit = col_double(),
##   lwr = col_double(),
##   upr = col_double(),
##   replicate = col_double(),
##   spec = col_character(),
##   fam = col_character()
```

```
## )
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   fit = col_double(),
##   lwr = col_double(),
##   upr = col_double(),
##   replicate = col_double(),
##   spec = col_character(),
##   fam = col_character()
## )
```

```
data <- read_csv(here("wrangled_data/model_predictions/community-data-long.csv")) %>%
  mutate(spec = recode(spec, "X135E" = "135E"),
         fit = fit - 1)
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   rep = col_double(),
##   spec = col_character(),
##   fit = col_double()
## )
```

```
colnames(data) <- c("replicate", "spec", "fit")
```

So I have:

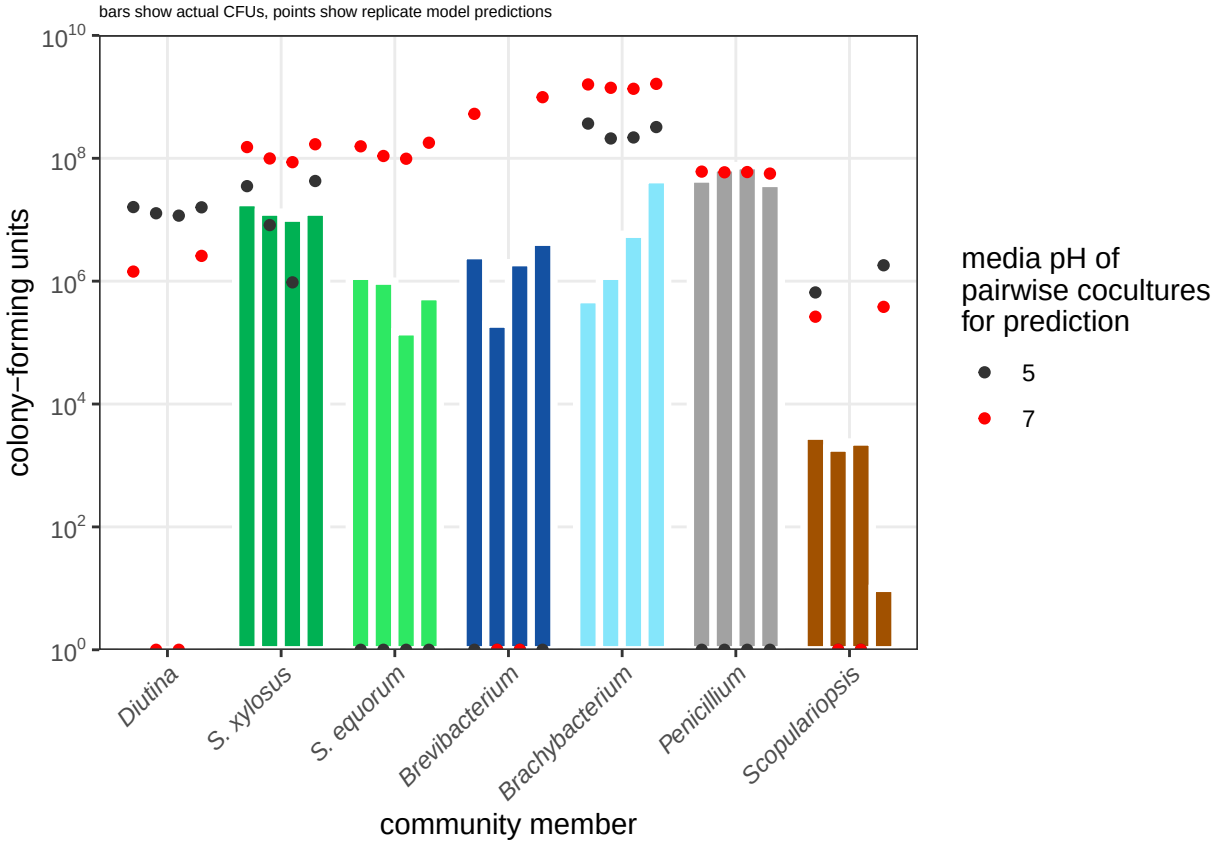
- actual community data,
- predictions of community CFUs from LV modeling of PW/alone growth data, and
- pairwise effect metrics from each pairwise partner species

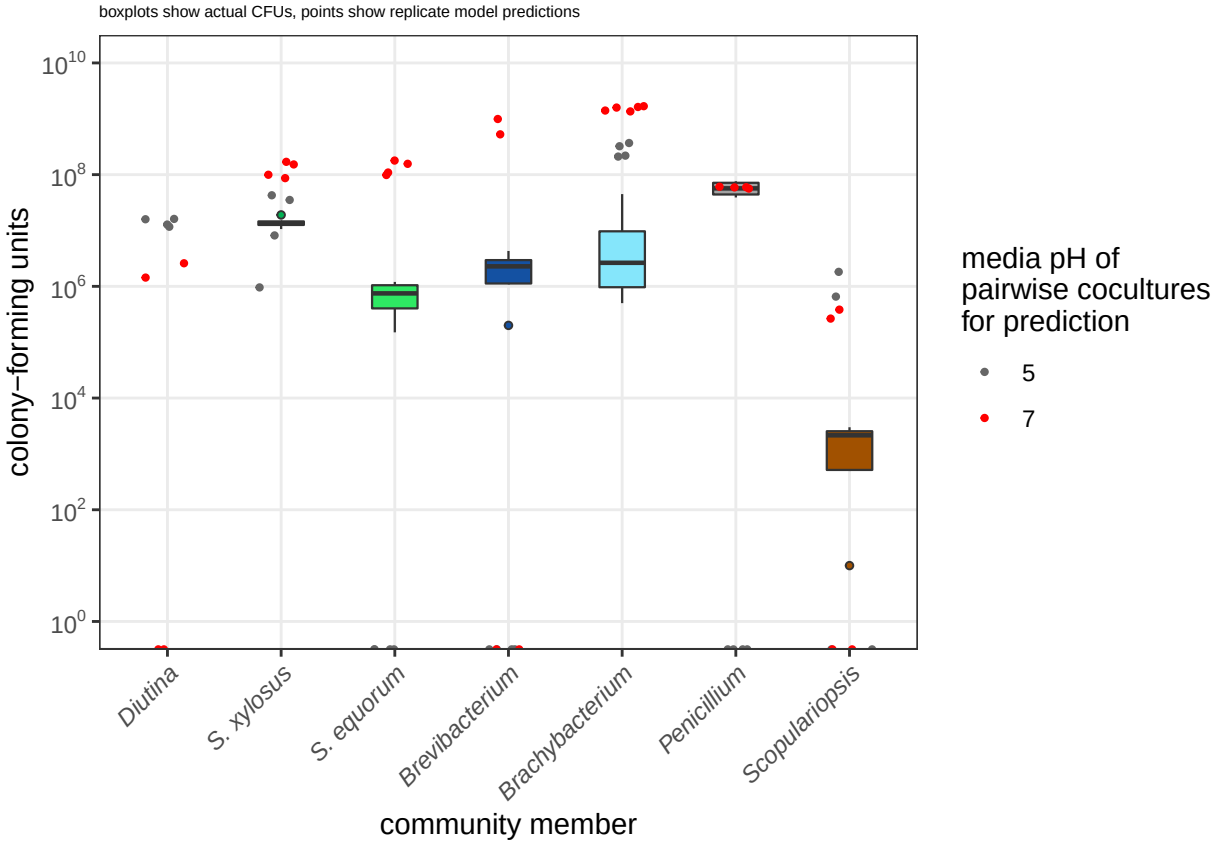
Our main results are that:

- PW growth poorly predicts absolute community composition
- pH 7 PW data better predicts community composition than pH 5 data
- improved predictions from pH 7 pairwise data – coming from Brevi/Brachy pairwise effect metrics?

Let's show these things:

PW growth poorly predicts absolute community composition





Let's focus in on the deviations of predicted population size from actual CFUs when grown in a community:

```
predictions.w <- predictions %>%
  pivot_wider(names_from = "pH", names_prefix = "prediction_pH",
              values_from = "fit")

comparisons <- full_join(data, # %>% mutate(fit = fit+1), # no infinite fold-changes,
                         predictions.w, by = c("spec", "replicate")) %>%
  mutate(diff_ph5_pred = prediction_pH5 - fit,
         diff_ph7_pred = prediction_pH7 - fit,
         perc_ph5_pred = diff_ph5_pred / fit * 100,
         perc_ph7_pred = diff_ph7_pred / fit * 100,
         log_dev_ph5 = ifelse(perc_ph5_pred < 0,
                              -log10(abs(perc_ph5_pred)),
                              log10(perc_ph5_pred)),
         log_dev_ph7 = ifelse(perc_ph7_pred < 0,
                              -log10(abs(perc_ph7_pred)),
                              log10(perc_ph7_pred)))
```

```
## Warning in ifelse(perc_ph5_pred < 0, -log10(abs(perc_ph5_pred)),
## log10(perc_ph5_pred)): NaNs produced
```

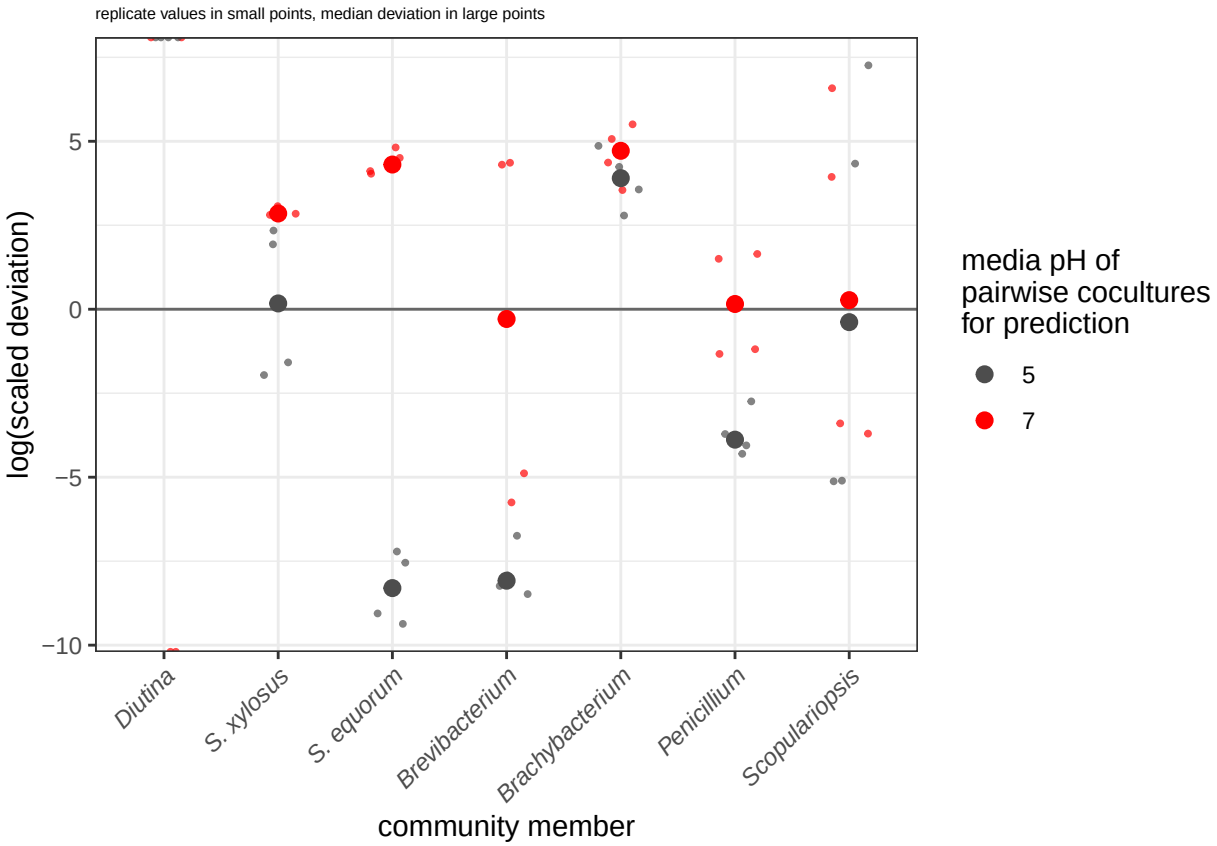
```
## Warning in ifelse(perc_ph7_pred < 0, -log10(abs(perc_ph7_pred)),
## log10(perc_ph7_pred)): NaNs produced
```

```
p.deviations <- ggplot(comparisons %>%
         pivot_longer(cols = c(log_dev_ph5, log_dev_ph7), values_to = "log_deviation",
                      names_to = "pH", names_prefix = "log_dev_ph") %>%
         mutate(spec = factor(spec, levels = names(names)[-c(8:9)])),
       aes(x = spec, y = log_deviation, color = pH)) +
  scale_x_discrete(labels = names) +
  geom_jitter(size = .7, alpha = 0.7, width = .2) +
  scale_color_manual(values = c("gray30", "red")) +
  geom_hline(yintercept = 0, color = "gray40") +
  theme_bw() +
  labs(y = "log(scaled deviation)",
       x = "community member",
       color = paste("media pH of\npairwise cocultures\nfor prediction"),
       subtitle = "replicate log(%difference from actual) in small points") +
  theme(axis.text.x = element_text(angle = 45, face = "italic", hjust = 1),
        plot.subtitle = element_text(size = 6))

p.deviations +
  stat_summary(geom = "point", fun = median, size = 2.5) +
  labs(subtitle = "replicate values in small points, median deviation in large points")
```

```
## Warning: Removed 10 rows containing non-finite values (stat_summary).
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```



For *Diutina* (in that pH 7 predicts it to die off), *S. equorum*, *Brevibacterium*, and *Penicillium*, pH 7 PW data better predicts community composition than pH 5 data:

Can we look back into estimates and peg interactions that might be contributing extra to strong prediction deviations from actual CFUs?

Estimates should be interpreted as a per-capita replacement measurement: for every 1

```
## <list_of<
##   tbl_df<
##     spec : character
##     name : character
##     est_5: double
##     est_7: double
##     se_5 : double
##     se_7 : double
##   >
## >[7]>
## [[1]]
## # A tibble: 7 x 6
##   spec  name     est_5    est_7          se_5          se_7
##   <chr> <chr>    <dbl>    <dbl>         <dbl>         <dbl>
## 1 135E  K      1.80e+7  8.83e+6 2525975.      3057441.
## 2 135E  JB370  1.19e+0 -1.07e+0       1.19          2.83
## 3 135E  BC10  -1.46e-1 -3.06e-3       0.0396        0.0157
## 4 135E  JBC    1.04e-1  1.63e-1       0.0387        0.0919
## 5 135E  BC9   -8.19e-2 -2.04e-2       0.0198        0.0162
## 6 135E  JB5    1.21e-3 -5.38e-4       0.00219       0.00130
## 7 135E  JB7   -8.47e-5 -9.12e-4       0.00172       0.00111
##
```

```
## [[2]]
## # A tibble: 7 x 6
##   spec  name     est_5    est_7          se_5          se_7
##   <chr> <chr>    <dbl>    <dbl>         <dbl>         <dbl>
## 1 BC10  K      8.59e+7  2.55e+8 17395694.     34120612.
## 2 BC10  JB370 -2.10e+1  1.74e+2        4.29         97.8
## 3 BC10  JBC    1.12e+0  2.21e+0        0.536         0.951
## 4 BC10  BC9   -6.09e-1  4.79e-1        0.909         1.26
## 5 BC10  135E  -4.50e-1  1.55e+0        0.805         3.45
## 6 BC10  JB5    4.00e-3 -2.77e-3        0.0112        0.0150
## 7 BC10  JB7   -2.40e-3 -1.68e-2        0.0211        0.0213
##
## [[3]]
## # A tibble: 7 x 6
##   spec  name         est_5    est_7         se_5          se_7
##   <chr> <chr>        <dbl>    <dbl>        <dbl>         <dbl>
## 1 BC9   K     48564127.     2.77e+8 34111561.    38270130.
## 2 BC9   JB7     288927.    -2.83e-2   772340.           0.0257
## 3 BC9   JB5      19682.     4.96e-3    50595.           0.0176
## 4 BC9   JB370      -24.7    1.11e+2        4.15        89.1
## 5 BC9   135E        -4.21  -6.67e-1        1.40         3.03
## 6 BC9   JBC          0.507  2.21e+0        0.868        1.51
## 7 BC9   BC10         0.228  9.41e-1        0.454        0.265
##
## [[4]]
## # A tibble: 7 x 6
##   spec  name          est_5         est_7          se_5          se_7
##   <chr> <chr>         <dbl>         <dbl>         <dbl>         <dbl>
## 1 JB370 K     6450740.      910919.       1092010.      128776.
## 2 JB370 135E        0.197       -0.112          0.160        0.0241
## 3 JB370 JBC         0.128        0.0133         0.0500       0.00392
## 4 JB370 BC9        -0.0145       0.00142        0.00475      0.000874
## 5 JB370 JB5        -0.00928     -0.000171       0.0153       0.000284
## 6 JB370 JB7        -0.00609     -0.000304       0.00627      0.000164
## 7 JB370 BC10       -0.00183      0.00172        0.00906      0.00128
##
## [[5]]
## # A tibble: 7 x 6
##   spec  name         est_5   est_7         se_5          se_7
##   <chr> <chr>        <dbl>   <dbl>        <dbl>         <dbl>
## 1 JB5   K     357069137.   3.73e+9 295783144.   440177922.
## 2 JB5   JB7      289212.   8.35e-1    597239.           0.364
## 3 JB5   135E       -92.8  2.28e+1        32.8         58.4
## 4 JB5   JB370       29.0  2.81e+3        57.2        645.
## 5 JB5   BC10       -17.7  6.25e-1         5.77         2.57
## 6 JB5   BC9         10.5  2.12e+0        16.7          2.07
## 7 JB5   JBC          5.39 6.90e+1         8.18        13.7
##
## [[6]]
## # A tibble: 7 x 6
##   spec  name          est_5    est_7        se_5          se_7
##   <chr> <chr>         <dbl>    <dbl>       <dbl>         <dbl>
## 1 JB7   K     -20627980.     1.88e+9 97255200.   193547405.
## 2 JB7   135E       -148.    -1.91e+2        9.67        22.7
## 3 JB7   JB370       -33.3    2.37e+2       22.0        228.
## 4 JB7   JB5         -28.5    1.13e-2      330.           0.134
```

```
## 5 JB7   BC10        -16.1   -2.48e+0        2.08         0.949
## 6 JB7   BC9          -0.727 -1.27e+0        7.72         0.717
## 7 JB7   JBC          -0.144  7.24e+0        1.04         6.50
##
## [[7]]
## # A tibble: 7 x 6
##   spec  name     est_5    est_7        se_5          se_7
##   <chr> <chr>    <dbl>    <dbl>       <dbl>         <dbl>
## 1 JBC   K      6.96e+7  5.64e+7 8528382.    4605177.
## 2 JBC   135E   5.33e+4 NA         36676.         NA
## 3 JBC   JB5    2.00e+3  1.74e-2   30360.          0.119
## 4 JBC   JB370  3.06e+1 -1.29e+3      38.9      5531.
## 5 JBC   JB7   -1.56e+1  7.04e-3       2.43        0.00558
## 6 JBC   BC10   5.61e-1 -2.81e-2       0.853       0.0721
## 7 JBC   BC9   -4.69e-3  5.02e-2       0.828       0.0453
```

Some of these estimates aren't making sense – e.g. at pH 5 for i = JB5, j = JB7, alpha_ij > 2e5? But neither of these species affect the other in pairwise coculture??

Let's generate a table that we can import into cytoscape to compare to actual effects: