

Results and Assessment of pH 5 Leave-One-Out data

Brooke Anderson

7/13/2021

Background info

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”) * *Staphylococcus xylosus* BC10 (“comm-BC10”) * *Candida*/*Diutina* 135E & *S. xylosus* BC10 (“community minus early deacidifiers” or “comm-eD”)

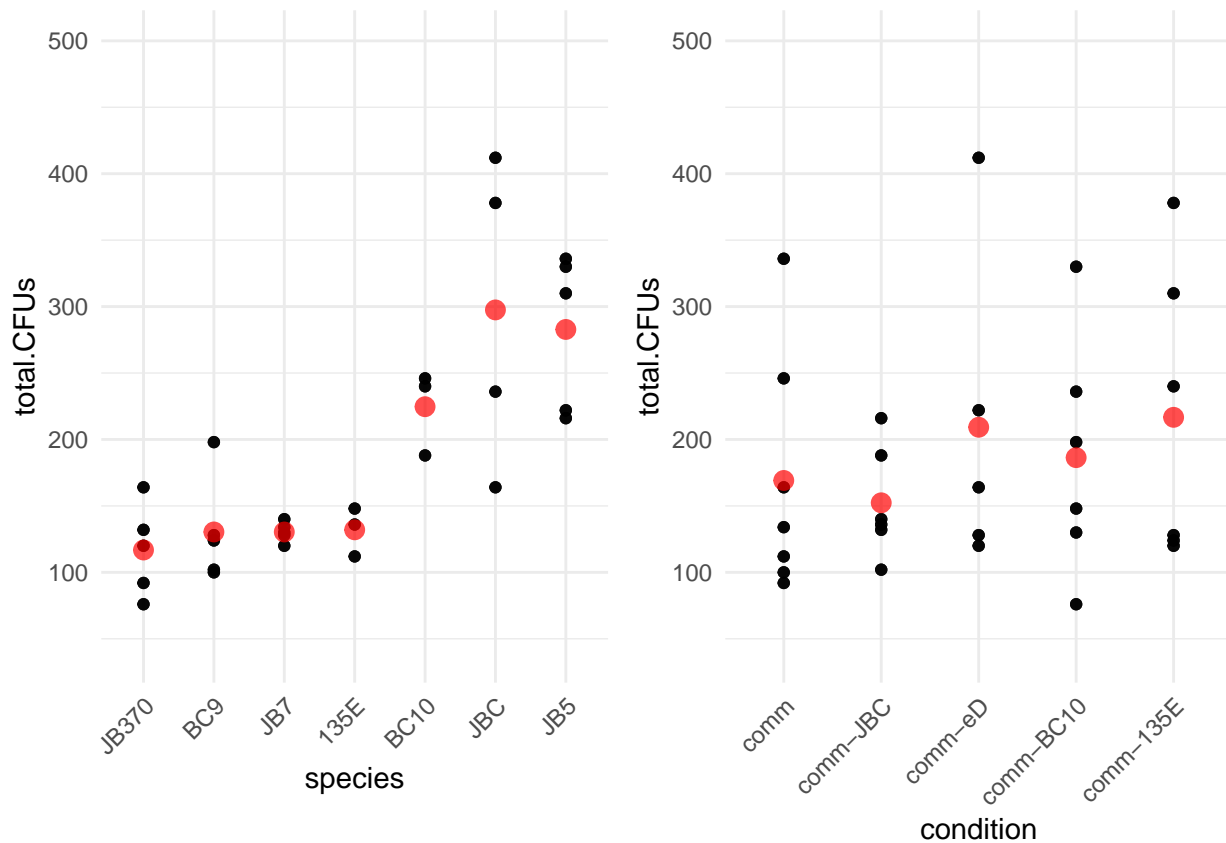
```
d.1005 <- readRDS(here("wrangled_data/leave-one-out_pH5.rds"))  
d.18 <- readRDS(here("wrangled_data/all_pairwise.rds"))  
load(here("figures/plotting_objects.RData"))
```

Inoculation quality assessment

Are the inoculations around 200 CFUs each? Any notable biases?

```
## Warning: `fun.y` is deprecated. Use `fun` instead.
```

```
## Warning: `fun.y` is deprecated. Use `fun` instead.
```



Representative inoculation of each species in each condition in black, and the mean within species (left) or within condition (right) in red.

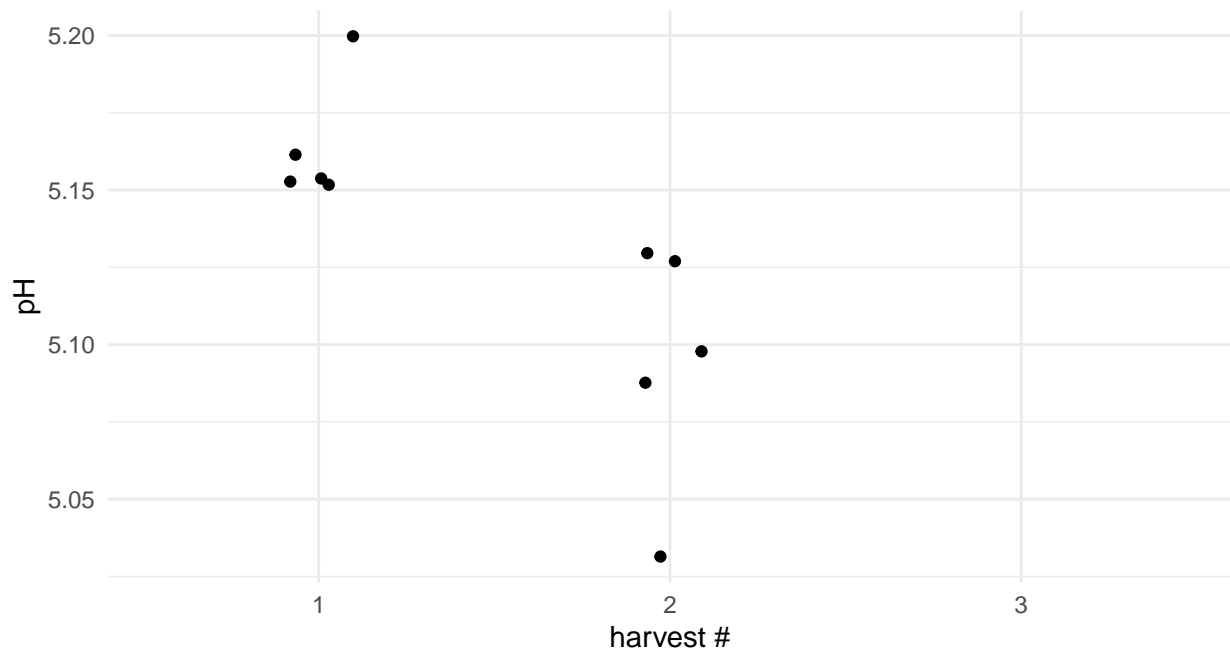
So there's definitely some species that were inoculated lower than target (mean ~130 CFUs), and some species that were inoculated higher than target, namely *Brevibacterium* JB5 with average ~300 CFUs. *S. xylosus* BC10 was right about on target, and then *Penicillium* JBC was all over the place, from 150 - 400 CFUs inoculated.

However, overall the average inoculation within each community was right about at 200, or at least between 150 - 220 CFUs, which is pretty good.

pH probe variability

Interested in seeing whether pH of "control" (uninoculated but from same 96-well plate as community samples) cheese at time of harvest is changing at different timepoints, given that I've found strong ability of some Bayley species to raise the pH of the media through volatiles alone (namely, *Penicillium*, *Brevibacterium*, and *Scopulariopsis*, and this effect gets stronger between 7 & 10 days of growth).

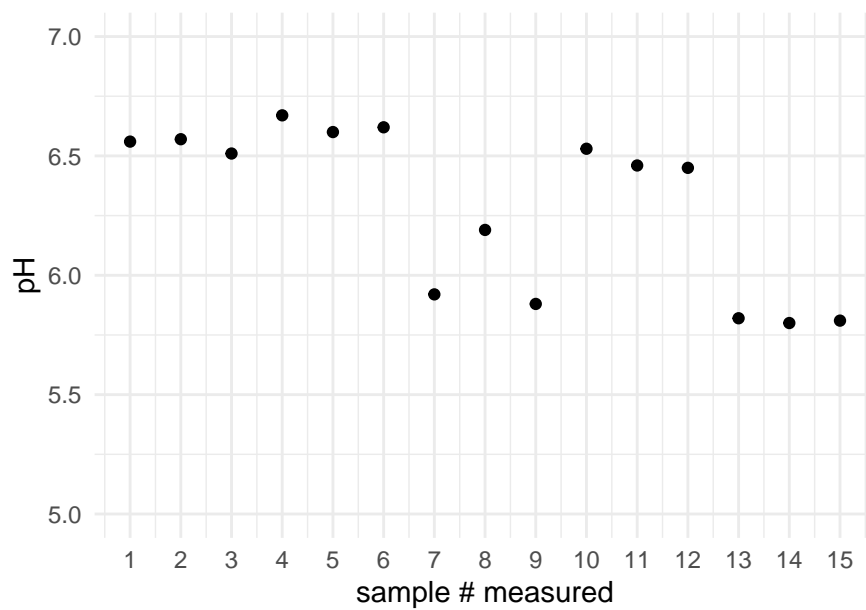
Note that each "replicate" was the pH of uninoculated cheese at harvest day 3 (rep./harvest # 1), day 10 (rep./harvest # 2), and day 21 (rep./harvest # 3).



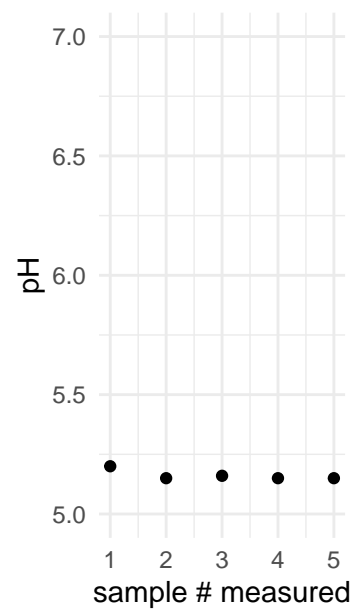
So what I'm really seeing here is just a bias according to harvest date (note, pH probe re-calibrated at day 3 and day 10).

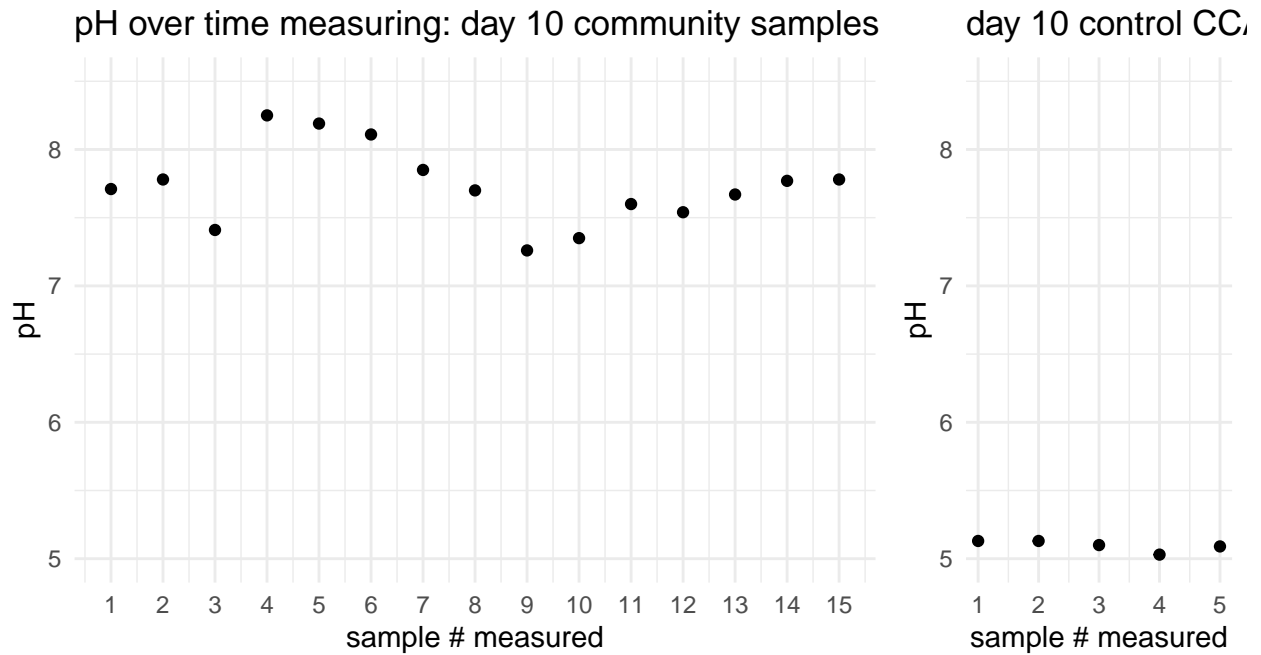
I also want to check that there isn't some systematic pH change over time of use.

pH over time measuring: day 3 community samples



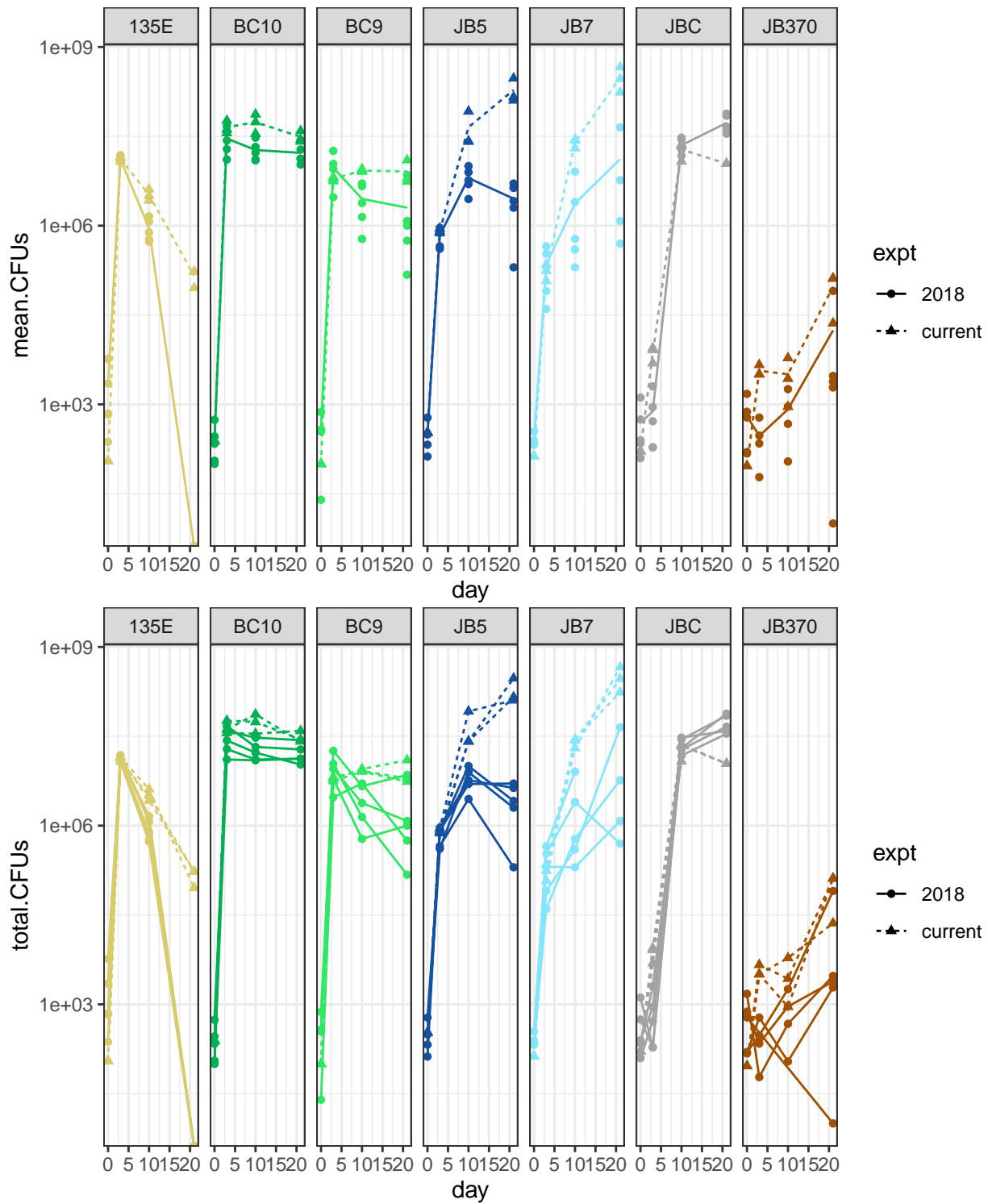
day 3 control CC





I can't help but feel there is like some smalllllll bias towards pH measurement decline over time. But even if so, from looking at any trend in the control (uninocuated) data and comparing it to the scale of differences in the community sample data, I don't think it's going to have an effect in the analysis. (could do a linear model assessment if I really cared to eliminate this).

Is complete community data replicating what has been seen before
(i.e. 08_2018)



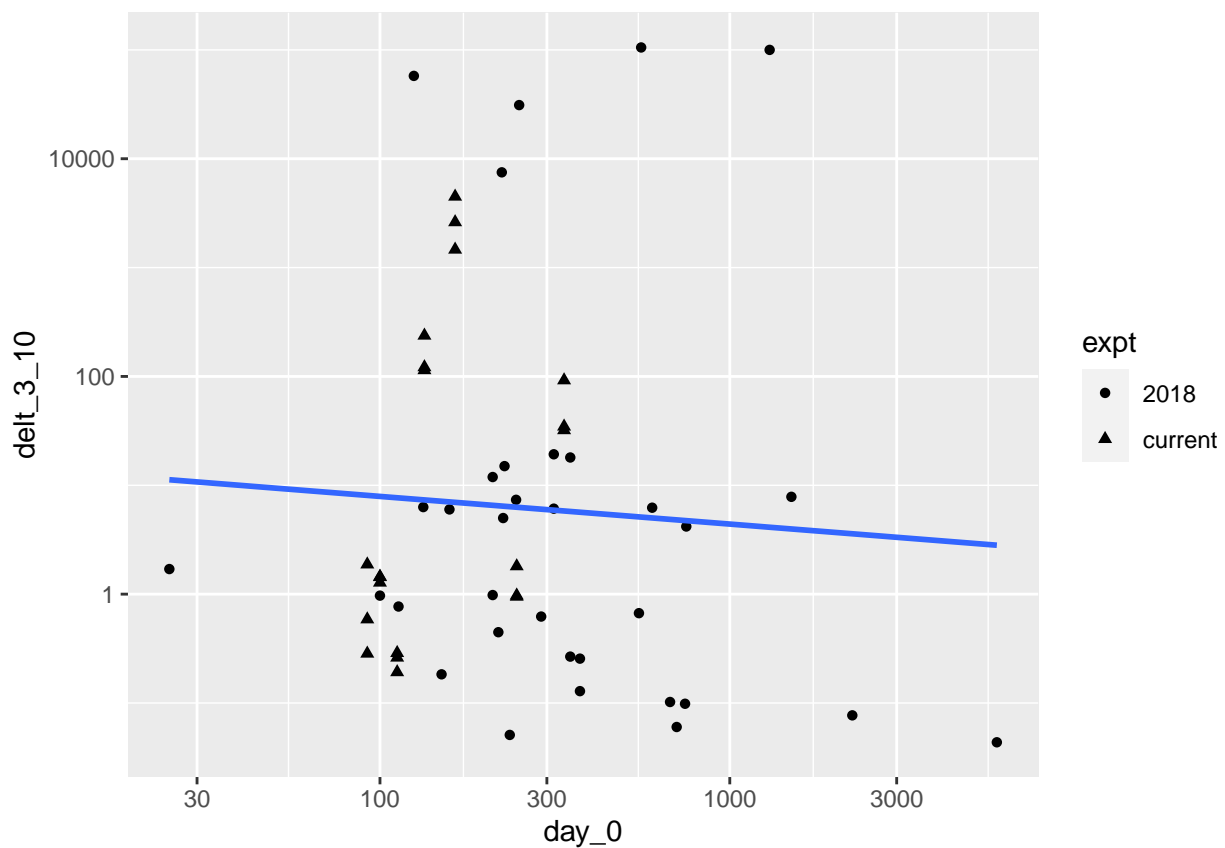
See if there's something predictive about the difference in growth patterns between day3 & day10

A tibble: 0 x 3

```
## # ... with 3 variables: species <fct>, growth_period <fct>, p.value <dbl>
```

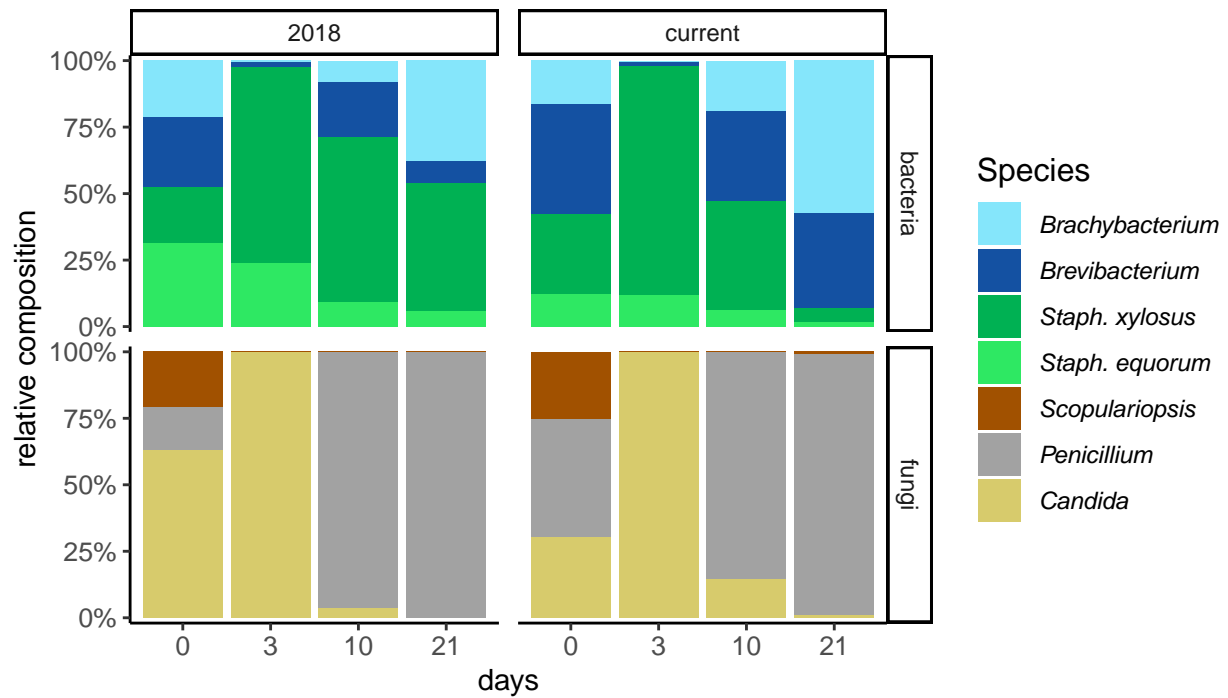
```
## # A tibble: 10 x 4
```

	species	growth_period	term	p.value
	<fct>	<fct>	<chr>	<dbl>
## 1	BC9	0-3	day_0	0.00851
## 2	BC9	3-10	day_0	0.0289
## 3	JB5	3-10	exptcurrent	0.0447
## 4	JB5	0-3	day_0	0.0203
## 5	JB7	3-10	exptcurrent	0.0353
## 6	135E	0-3	exptcurrent	0.000399
## 7	135E	3-10	exptcurrent	0.00237
## 8	135E	10-21	exptcurrent	0.00991
## 9	JBC	0-3	exptcurrent	0.00215
## 10	JB370	0-3	exptcurrent	0.00293



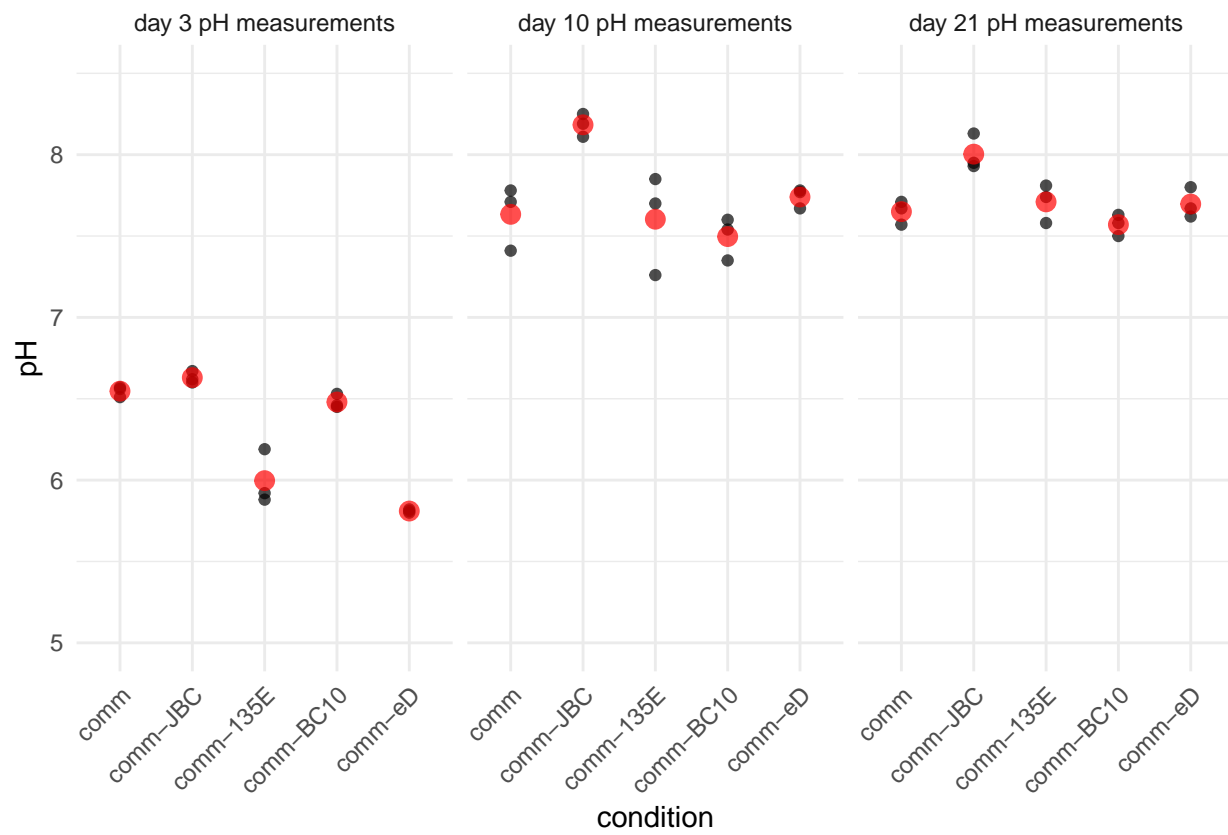
Compare community succession pattern

Relative composition of Bayley community bacteria and fungi



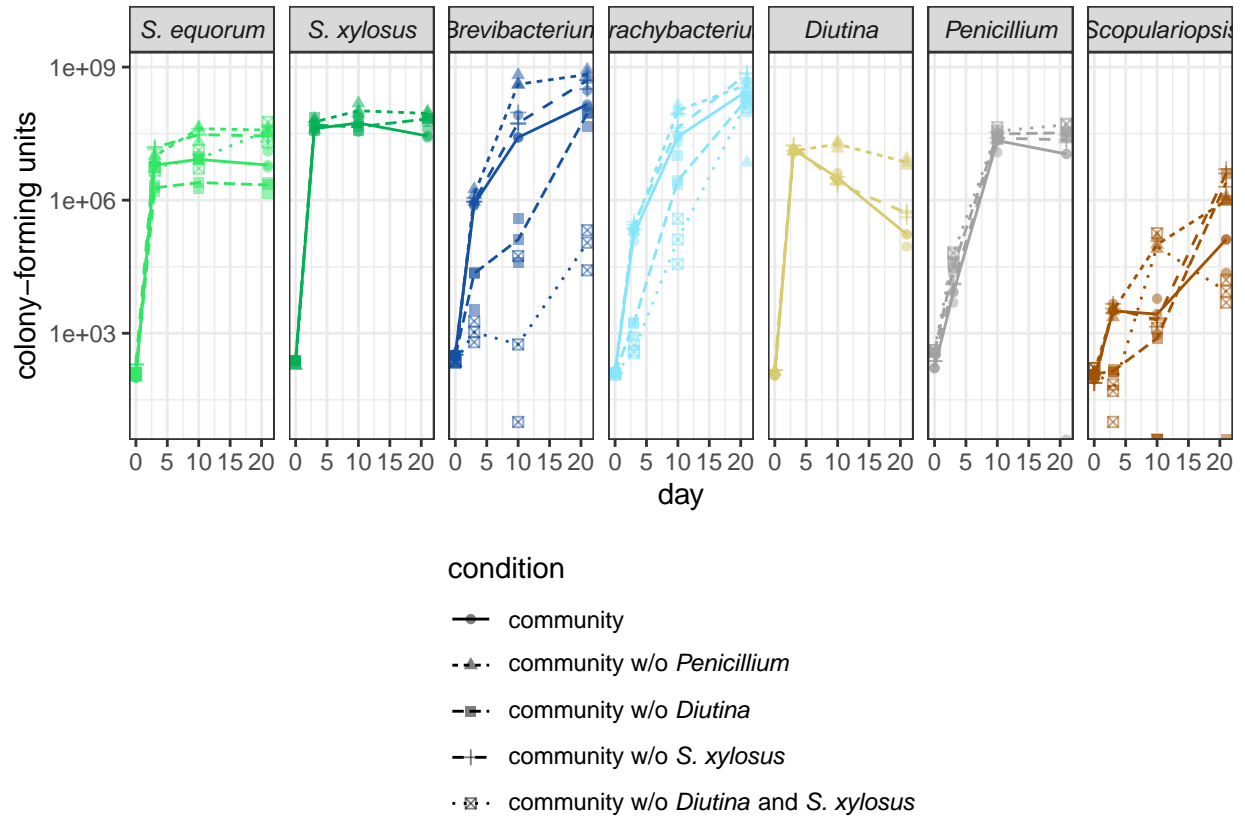
pH data

First let's plot the data to know what we're working with:

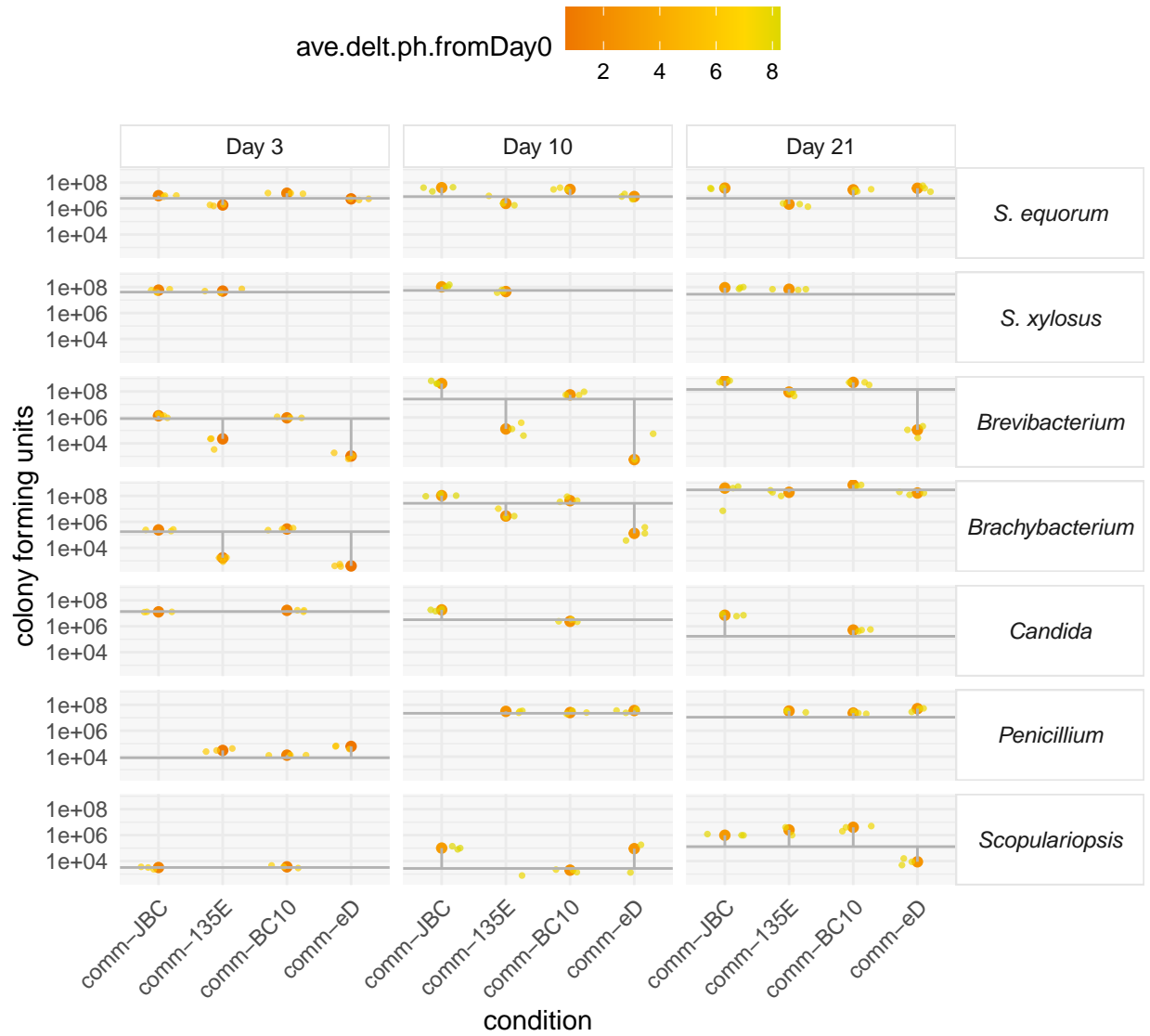


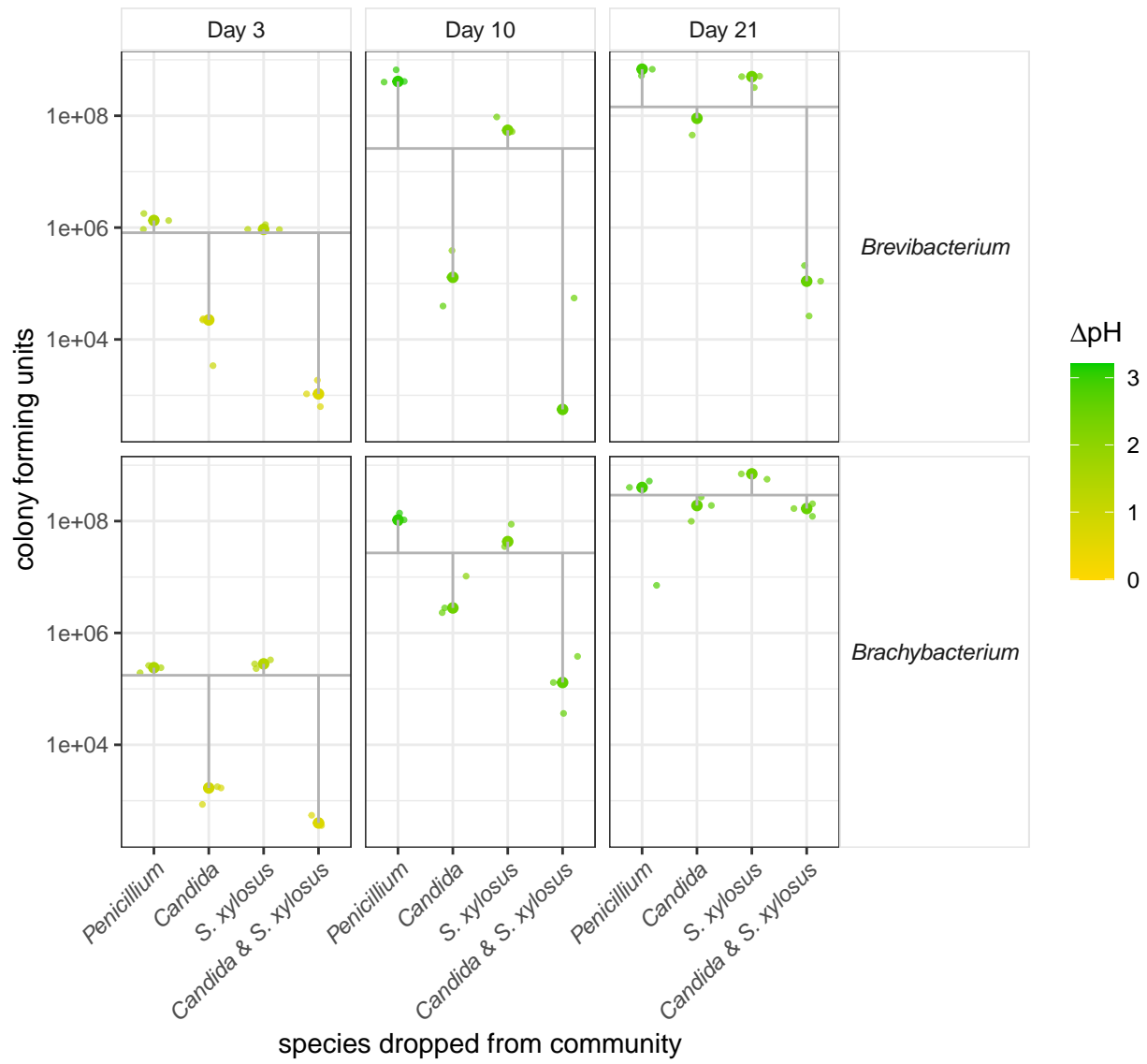
growth data & ttests

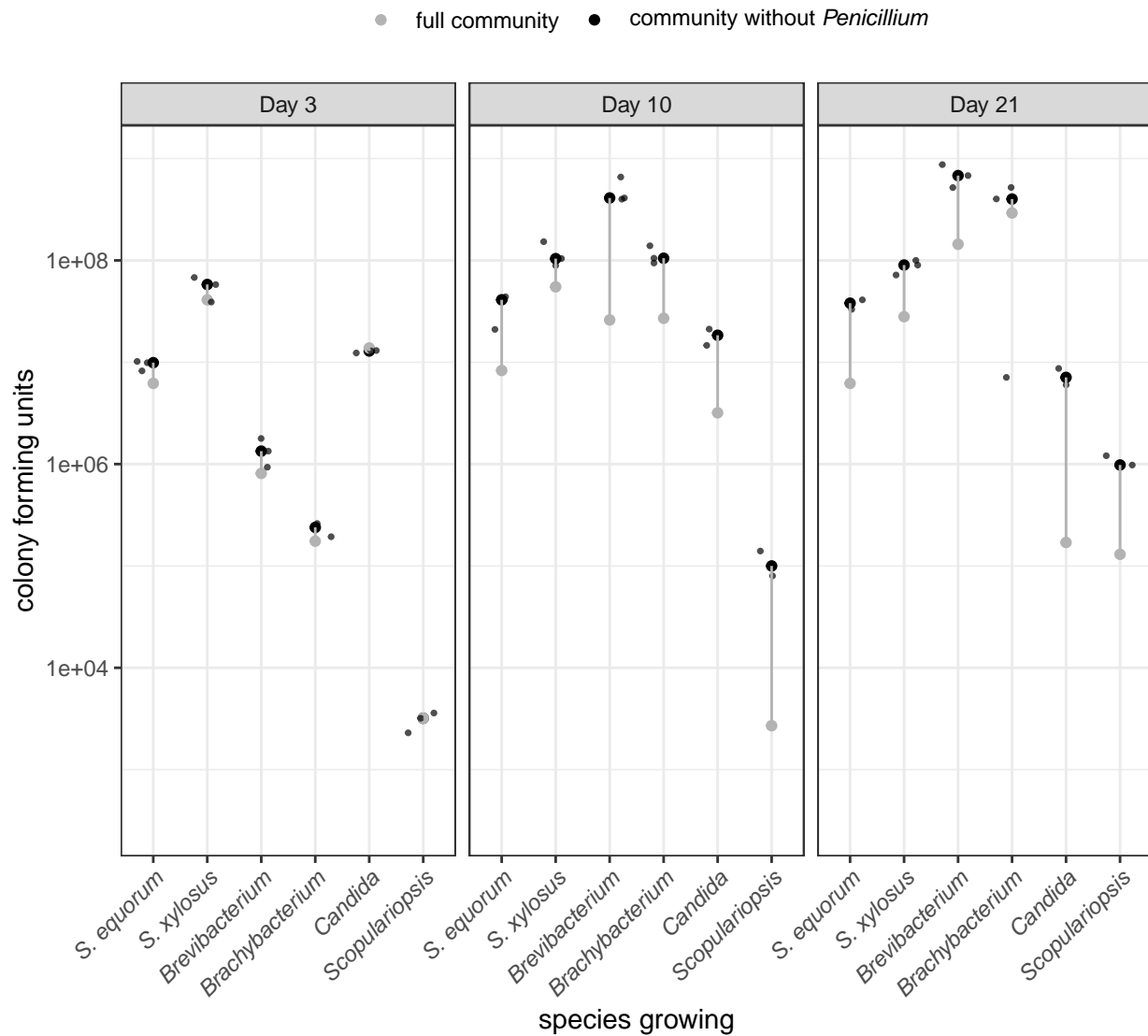
Comparing growth curves for each species in each condition:



Assess how dropping certain community members from the community affects growth, using growth in the full community as a baseline for comparison (indicated by horizontal gray bar, CFUs of the species in full community at that timepoint). Each large dot is the average of the smaller dots, which show the growth of that species in that community at that time point, and the vertical line connecting the dots to the horizontal gray line highlights the difference in growth between the dropout community and the full community. Points are colored by sample pH.







Statistical tests on differences in growth

```
## # A tibble: 21 x 4
##   species   day   `p-value` sig.by.condition
##   <chr>    <dbl>     <dbl>    <chr>
## 1 BC9      3 0.0000000116 "*"
## 2 BC9     10 0.000367    "*"
## 3 BC9     21 0.00164     "*"
## 4 BC10     3 0.706         ""
## 5 BC10     10 0.0230        "*"
## 6 BC10     21 0.00109       "*"
## 7 JB5      3 0.0000233     "*"
## 8 JB5     10 0.0000209     "*"
## 9 JB5     21 0.0000465     "*"
## 10 JB7     3 0.00000415    "*"
## # ... with 11 more rows

## [1] "Contrasts for BC9 on day 3"
##
##               Df   Sum Sq  Mean Sq F value
## condition      4 2.959e+14 7.399e+13 135.34
```

```

## condition: minus Penicillium versus full 1 1.204e+14 1.204e+14 220.32
## condition: minus Candida versus full 1 1.464e+14 1.464e+14 267.75
## condition: minus S. xylosus versus full 1 1.247e+13 1.247e+13 22.80
## condition: minus eD versus full 1 1.667e+13 1.667e+13 30.49
## Residuals 10 5.467e+12 5.467e+11
## Pr(>F)
## condition 1.16e-08 ***
## condition: minus Penicillium versus full 3.87e-08 ***
## condition: minus Candida versus full 1.51e-08 ***
## condition: minus S. xylosus versus full 0.000751 ***
## condition: minus eD versus full 0.000254 ***
## Residuals
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for BC9 on day 10"
## Df Sum Sq Mean Sq F value
## condition 4 2.689e+15 6.722e+14 14.456
## condition: minus Penicillium versus full 1 6.922e+14 6.922e+14 14.888
## condition: minus Candida versus full 1 5.808e+14 5.808e+14 12.491
## condition: minus S. xylosus versus full 1 3.302e+14 3.302e+14 7.102
## condition: minus eD versus full 1 1.085e+15 1.085e+15 23.344
## Residuals 10 4.650e+14 4.650e+13
## Pr(>F)
## condition 0.000367 ***
## condition: minus Penicillium versus full 0.003168 **
## condition: minus Candida versus full 0.005408 **
## condition: minus S. xylosus versus full 0.023693 *
## condition: minus eD versus full 0.000690 ***
## Residuals
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for BC9 on day 21"
## Df Sum Sq Mean Sq F value
## condition 4 3.343e+15 8.357e+14 9.934
## condition: minus Penicillium versus full 1 1.570e+15 1.570e+15 18.660
## condition: minus Candida versus full 1 3.547e+12 3.547e+12 0.042
## condition: minus S. xylosus versus full 1 4.878e+14 4.878e+14 5.798
## condition: minus eD versus full 1 1.282e+15 1.282e+15 15.238
## Residuals 10 8.413e+14 8.413e+13
## Pr(>F)
## condition 0.00164 **
## condition: minus Penicillium versus full 0.00151 **
## condition: minus Candida versus full 0.84143
## condition: minus S. xylosus versus full 0.03682 *
## condition: minus eD versus full 0.00294 **
## Residuals
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for BC10 on day 3"
## Df Sum Sq Mean Sq F value
## condition 2 1.642e+14 8.211e+13 0.370
## condition: minus Penicillium versus full 1 1.422e+13 1.422e+13 0.064
## condition: minus Candida versus full 1 1.500e+14 1.500e+14 0.675
## condition: minus S. xylosus versus full 1

```

```

## condition: minus eD versus full 1
## Residuals 6 1.333e+15 2.221e+14
## Pr(>F)
## condition 0.706
## condition: minus Penicillium versus full 0.809
## condition: minus Candida versus full 0.443
## condition: minus S. xylosus versus full
## condition: minus eD versus full
## Residuals
## [1] "Contrasts for BC10 on day 10"
## Df Sum Sq Mean Sq F value
## condition 2 8.308e+15 4.154e+15 7.553
## condition: minus Penicillium versus full 1 2.788e+15 2.788e+15 5.068
## condition: minus Candida versus full 1 5.521e+15 5.521e+15 10.038
## condition: minus S. xylosus versus full 1
## condition: minus eD versus full 1
## Residuals 6 3.300e+15 5.500e+14
## Pr(>F)
## condition 0.0230 *
## condition: minus Penicillium versus full 0.0653 .
## condition: minus Candida versus full 0.0194 *
## condition: minus S. xylosus versus full
## condition: minus eD versus full
## Residuals
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for BC10 on day 21"
## Df Sum Sq Mean Sq F value
## condition 2 4.828e+15 2.414e+15 26.114
## condition: minus Penicillium versus full 1 6.806e+13 6.806e+13 0.736
## condition: minus Candida versus full 1 4.760e+15 4.760e+15 51.492
## condition: minus S. xylosus versus full 1
## condition: minus eD versus full 1
## Residuals 6 5.547e+14 9.244e+13
## Pr(>F)
## condition 0.00109 **
## condition: minus Penicillium versus full 0.42383
## condition: minus Candida versus full 0.00037 ***
## condition: minus S. xylosus versus full
## condition: minus eD versus full
## Residuals
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for JB5 on day 3"
## Df Sum Sq Mean Sq F value
## condition 4 4.375e+12 1.094e+12 27.267
## condition: minus Penicillium versus full 1 1.441e+12 1.441e+12 35.918
## condition: minus Candida versus full 1 1.635e+11 1.635e+11 4.077
## condition: minus S. xylosus versus full 1 2.349e+12 2.349e+12 58.569
## condition: minus eD versus full 1 4.214e+11 4.214e+11 10.504
## Residuals 10 4.011e+11 4.011e+10
## Pr(>F)
## condition 2.33e-05 ***
## condition: minus Penicillium versus full 0.000133 ***

```

```

## condition: minus Candida versus full 0.071074 .
## condition: minus S. xylosus versus full 1.73e-05 ***
## condition: minus eD versus full 0.008854 **
## Residuals
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for JB5 on day 10"
##
## Df Sum Sq Mean Sq F value
## condition 4 5.221e+17 1.305e+17 27.941
## condition: minus Penicillium versus full 1 5.429e+16 5.429e+16 11.621
## condition: minus Candida versus full 1 2.773e+16 2.773e+16 5.935
## condition: minus S. xylosus versus full 1 1.431e+17 1.431e+17 30.629
## condition: minus eD versus full 1 2.970e+17 2.970e+17 63.580
## Residuals 10 4.672e+16 4.672e+15
## Pr(>F)
## condition 2.09e-05 ***
## condition: minus Penicillium versus full 0.00667 **
## condition: minus Candida versus full 0.03508 *
## condition: minus S. xylosus versus full 0.00025 ***
## condition: minus eD versus full 1.21e-05 ***
## Residuals
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for JB5 on day 21"
##
## Df Sum Sq Mean Sq F value
## condition 4 9.679e+17 2.420e+17 23.371
## condition: minus Penicillium versus full 1 1.550e+17 1.550e+17 14.969
## condition: minus Candida versus full 1 5.067e+16 5.067e+16 4.895
## condition: minus S. xylosus versus full 1 3.867e+17 3.867e+17 37.351
## condition: minus eD versus full 1 3.755e+17 3.755e+17 36.269
## Residuals 10 1.035e+17 1.035e+16
## Pr(>F)
## condition 4.65e-05 ***
## condition: minus Penicillium versus full 0.003114 **
## condition: minus Candida versus full 0.051355 .
## condition: minus S. xylosus versus full 0.000114 ***
## condition: minus eD versus full 0.000128 ***
## Residuals
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for JB7 on day 3"
##
## Df Sum Sq Mean Sq F value
## condition 4 2.027e+11 5.068e+10 39.725
## condition: minus Penicillium versus full 1 6.888e+10 6.888e+10 53.993
## condition: minus Candida versus full 1 4.765e+10 4.765e+10 37.347
## condition: minus S. xylosus versus full 1 8.085e+10 8.085e+10 63.375
## condition: minus eD versus full 1 5.340e+09 5.340e+09 4.186
## Residuals 10 1.276e+10 1.276e+09
## Pr(>F)
## condition 4.15e-06 ***
## condition: minus Penicillium versus full 2.46e-05 ***
## condition: minus Candida versus full 0.000114 ***
## condition: minus S. xylosus versus full 1.23e-05 ***
## condition: minus eD versus full 0.067971 .

```

```

## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for JB7 on day 10"
##
##              Df      Sum Sq   Mean Sq F value
## condition          4 2.562e+16 6.404e+15 22.769
##   condition: minus Penicillium versus full 1 4.464e+15 4.464e+15 15.872
##   condition: minus Candida versus full     1 1.981e+14 1.981e+14  0.704
##   condition: minus S. xylosus versus full  1 9.426e+15 9.426e+15 33.513
##   condition: minus eD versus full          1 1.153e+16 1.153e+16 40.988
## Residuals          10 2.813e+15 2.813e+14
##
##              Pr(>F)
## condition          5.22e-05 ***
##   condition: minus Penicillium versus full 0.002584 **
##   condition: minus Candida versus full     0.420917
##   condition: minus S. xylosus versus full  0.000176 ***
##   condition: minus eD versus full          7.81e-05 ***
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for JB7 on day 21"
##
##              Df      Sum Sq   Mean Sq F value
## condition          4 4.866e+17 1.217e+17  5.510
##   condition: minus Penicillium versus full 1 7.407e+16 7.407e+16  3.354
##   condition: minus Candida versus full     1 3.713e+17 3.713e+17 16.814
##   condition: minus S. xylosus versus full  1 4.129e+16 4.129e+16  1.870
##   condition: minus eD versus full          1 2.802e+12 2.802e+12  0.000
## Residuals          10 2.208e+17 2.208e+16
##
##              Pr(>F)
## condition          0.01315 *
##   condition: minus Penicillium versus full 0.09694 .
##   condition: minus Candida versus full     0.00214 **
##   condition: minus S. xylosus versus full  0.20143
##   condition: minus eD versus full          0.99123
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for 135E on day 3"
##
##              Df      Sum Sq   Mean Sq F value
## condition          2 1.489e+13 7.444e+12  3.234
##   condition: minus Penicillium versus full 1 1.422e+13 1.422e+13  6.178
##   condition: minus Candida versus full     1 6.667e+11 6.667e+11  0.290
##   condition: minus S. xylosus versus full  1
##   condition: minus eD versus full          1
## Residuals          6 1.381e+13 2.302e+12
##
##              Pr(>F)
## condition          0.1115
##   condition: minus Penicillium versus full 0.0475 *
##   condition: minus Candida versus full     0.6099
##   condition: minus S. xylosus versus full
##   condition: minus eD versus full
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```



```

## [1] "Contrasts for 135E on day 10"
##
##          Df      Sum Sq   Mean Sq F value
## condition      2 4.555e+14 2.278e+14   57.64
##   condition: minus Penicillium versus full      1 1.289e+14 1.289e+14   32.62
##   condition: minus Candida versus full          1 3.266e+14 3.266e+14   82.65
##   condition: minus S. xylosus versus full          1
##   condition: minus eD versus full                1
## Residuals      6 2.371e+13 3.952e+12
##          Pr(>F)
## condition      0.000121 ***
##   condition: minus Penicillium versus full      0.001247 **
##   condition: minus Candida versus full          9.94e-05 ***
##   condition: minus S. xylosus versus full
##   condition: minus eD versus full
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for 135E on day 21"
##
##          Df      Sum Sq   Mean Sq F value
## condition      2 9.670e+13 4.835e+13   78.35
##   condition: minus Penicillium versus full      1 2.059e+13 2.059e+13   33.36
##   condition: minus Candida versus full          1 7.611e+13 7.611e+13  123.34
##   condition: minus S. xylosus versus full          1
##   condition: minus eD versus full                1
## Residuals      6 3.703e+12 6.171e+11
##          Pr(>F)
## condition      5.01e-05 ***
##   condition: minus Penicillium versus full      0.00118 **
##   condition: minus Candida versus full          3.18e-05 ***
##   condition: minus S. xylosus versus full
##   condition: minus eD versus full
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for JBC on day 3"
##
##          Df      Sum Sq   Mean Sq F value
## condition      3 4.321e+09 1.440e+09  17.867
##   condition: minus Penicillium versus full      1 1.117e+08 1.117e+08   1.385
##   condition: minus Candida versus full          1 6.907e+08 6.907e+08   8.568
##   condition: minus S. xylosus versus full          1 3.519e+09 3.519e+09  43.648
##   condition: minus eD versus full                1
## Residuals      8 6.449e+08 8.062e+07
##          Pr(>F)
## condition      0.000663 ***
##   condition: minus Penicillium versus full      0.273072
##   condition: minus Candida versus full          0.019084 *
##   condition: minus S. xylosus versus full          0.000168 ***
##   condition: minus eD versus full
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for JBC on day 10"
##
##          Df      Sum Sq   Mean Sq F value
## condition      3 3.889e+14 1.296e+14   2.412

```

```

## condition: minus Penicillium versus full 1 2.025e+13 2.025e+13 0.377
## condition: minus Candida versus full 1 5.000e+11 5.000e+11 0.009
## condition: minus S. xylosus versus full 1 3.682e+14 3.682e+14 6.850
## condition: minus eD versus full 1
## Residuals 8 4.300e+14 5.375e+13
## Pr(>F)
## condition 0.1421
## condition: minus Penicillium versus full 0.5564
## condition: minus Candida versus full 0.9255
## condition: minus S. xylosus versus full 0.0308 *
## condition: minus eD versus full
## Residuals
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for JBC on day 21"
## Df Sum Sq Mean Sq F value
## condition 3 2.070e+15 6.900e+14 10.024
## condition: minus Penicillium versus full 1 8.711e+13 8.711e+13 1.266
## condition: minus Candida versus full 1 2.722e+12 2.722e+12 0.040
## condition: minus S. xylosus versus full 1 1.980e+15 1.980e+15 28.768
## condition: minus eD versus full 1
## Residuals 8 5.507e+14 6.883e+13
## Pr(>F)
## condition 0.004375 **
## condition: minus Penicillium versus full 0.293222
## condition: minus Candida versus full 0.847328
## condition: minus S. xylosus versus full 0.000675 ***
## condition: minus eD versus full
## Residuals
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for JB370 on day 3"
## Df Sum Sq Mean Sq F value
## condition 4 41866933 10466733 28.634
## condition: minus Penicillium versus full 1 14652042 14652042 40.083
## condition: minus Candida versus full 1 4745136 4745136 12.981
## condition: minus S. xylosus versus full 1 21868089 21868089 59.824
## condition: minus eD versus full 1 601667 601667 1.646
## Residuals 10 3655400 365540
## Pr(>F)
## condition 1.87e-05 ***
## condition: minus Penicillium versus full 8.56e-05 ***
## condition: minus Candida versus full 0.00482 **
## condition: minus S. xylosus versus full 1.58e-05 ***
## condition: minus eD versus full 0.22845
## Residuals
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for JB370 on day 10"
## Df Sum Sq Mean Sq F value
## condition 4 2.729e+10 6.823e+09 2.926
## condition: minus Penicillium versus full 1 4.394e+09 4.394e+09 1.884
## condition: minus Candida versus full 1 6.782e+09 6.782e+09 2.908
## condition: minus S. xylosus versus full 1 6.061e+07 6.061e+07 0.026

```

```

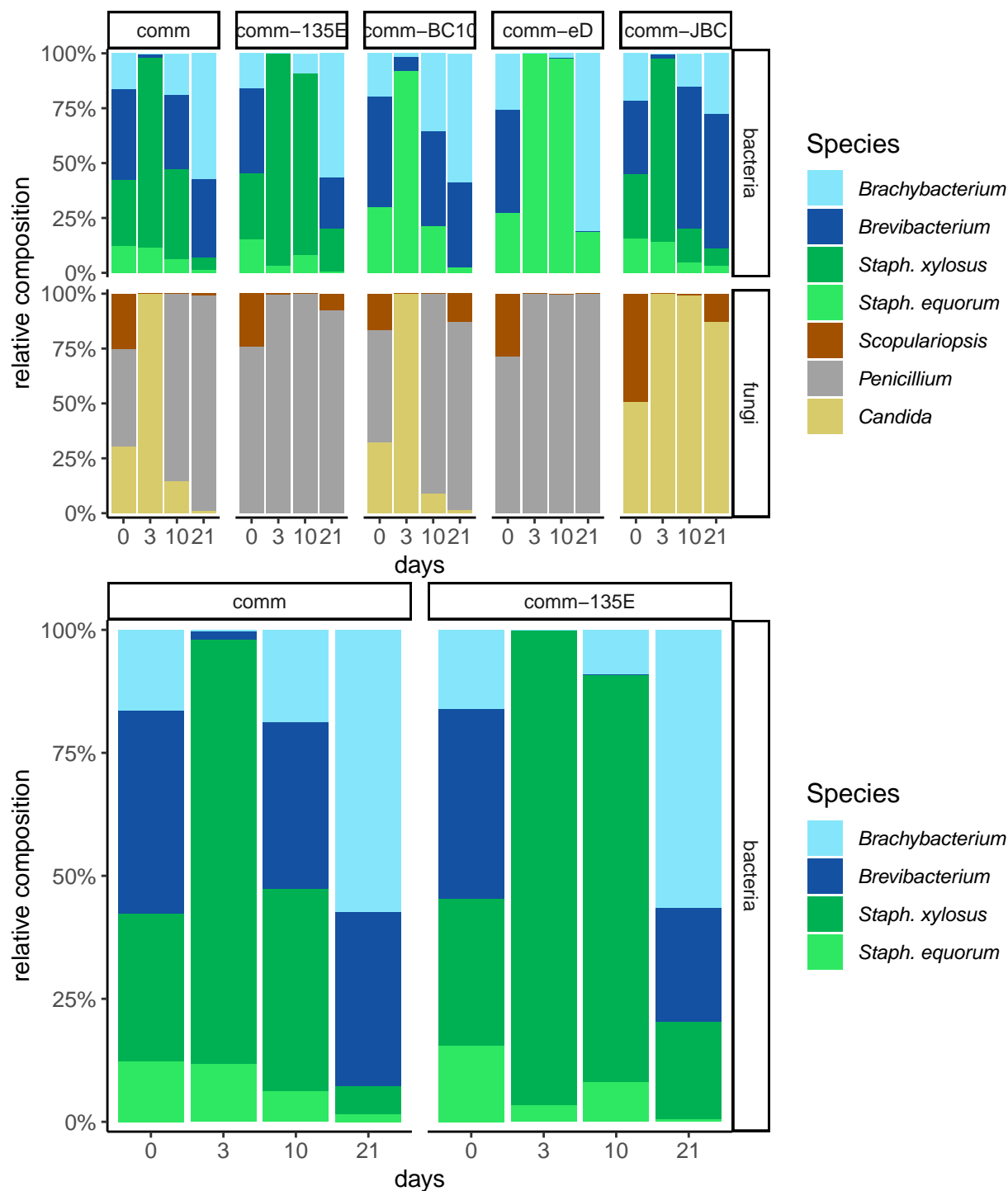
## condition: minus eD versus full      1 1.606e+10 1.606e+10 6.884
## Residuals                          10 2.332e+10 2.332e+09
##                                     Pr(>F)
## condition                          0.0768 .
## condition: minus Penicillium versus full 0.1999
## condition: minus Candida versus full 0.1190
## condition: minus S. xylosus versus full 0.8751
## condition: minus eD versus full      0.0254 *
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Contrasts for JB370 on day 21"
##                                     Df      Sum Sq   Mean Sq F value
## condition                          4 2.674e+13 6.686e+12 4.998
## condition: minus Penicillium versus full 1 5.092e+11 5.092e+11 0.381
## condition: minus Candida versus full 1 2.422e+13 2.422e+13 18.103
## condition: minus S. xylosus versus full 1 6.360e+11 6.360e+11 0.475
## condition: minus eD versus full      1 1.380e+12 1.380e+12 1.031
## Residuals                          10 1.338e+13 1.338e+12
##                                     Pr(>F)
## condition                          0.01786 *
## condition: minus Penicillium versus full 0.55106
## condition: minus Candida versus full 0.00168 **
## condition: minus S. xylosus versus full 0.50618
## condition: minus eD versus full      0.33382
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

patterns of succession

Compare patterns of succession when certain species are dropped from the community

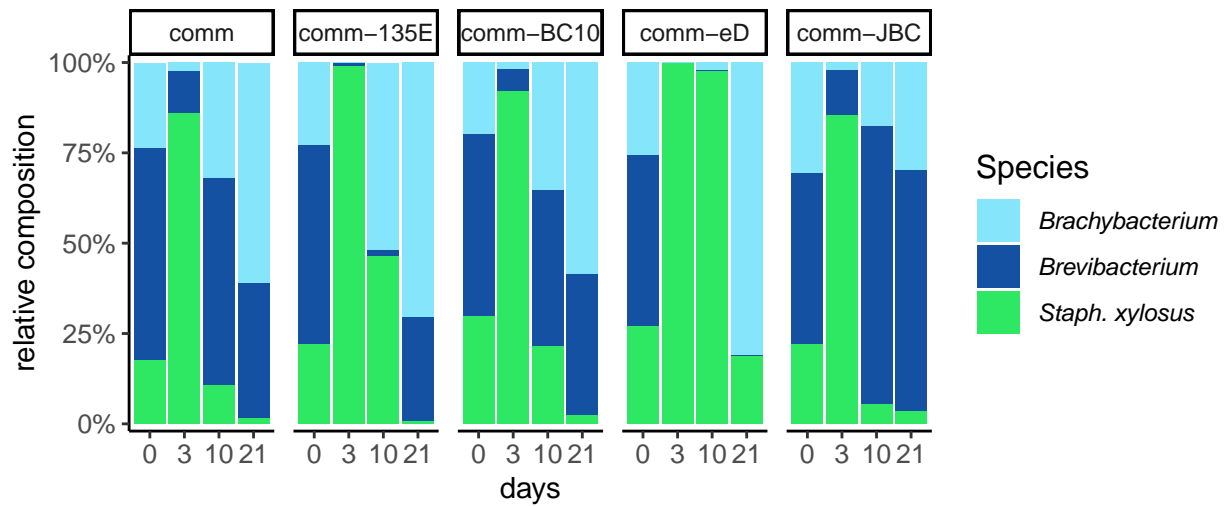
Relative composition of Bayley community bacteria and fungi



Obviously this is a little hard to interpret because, e.g. in the community minus BC10, there is no bar for BC10 anymore and so the percent abundance of the remaining bacteria can't be directly compared to conditions that also have BC10.

Let's first look at just the bacteria that are in all the community conditions – BC9, JB5, and JB7:

Relative composition of Bayley community bacteria and fungi



Let's also look at the balance between fungi and bacteria, although I suppose it's a little funny to consider this since the dropout of any one fungus or bacterium necessitates that the amount of fungi vs. bacteria from the start is different as compared to the complete community.

Relative composition of Bayley community bacteria and fungi

