

# Results: cross-experiment analysis

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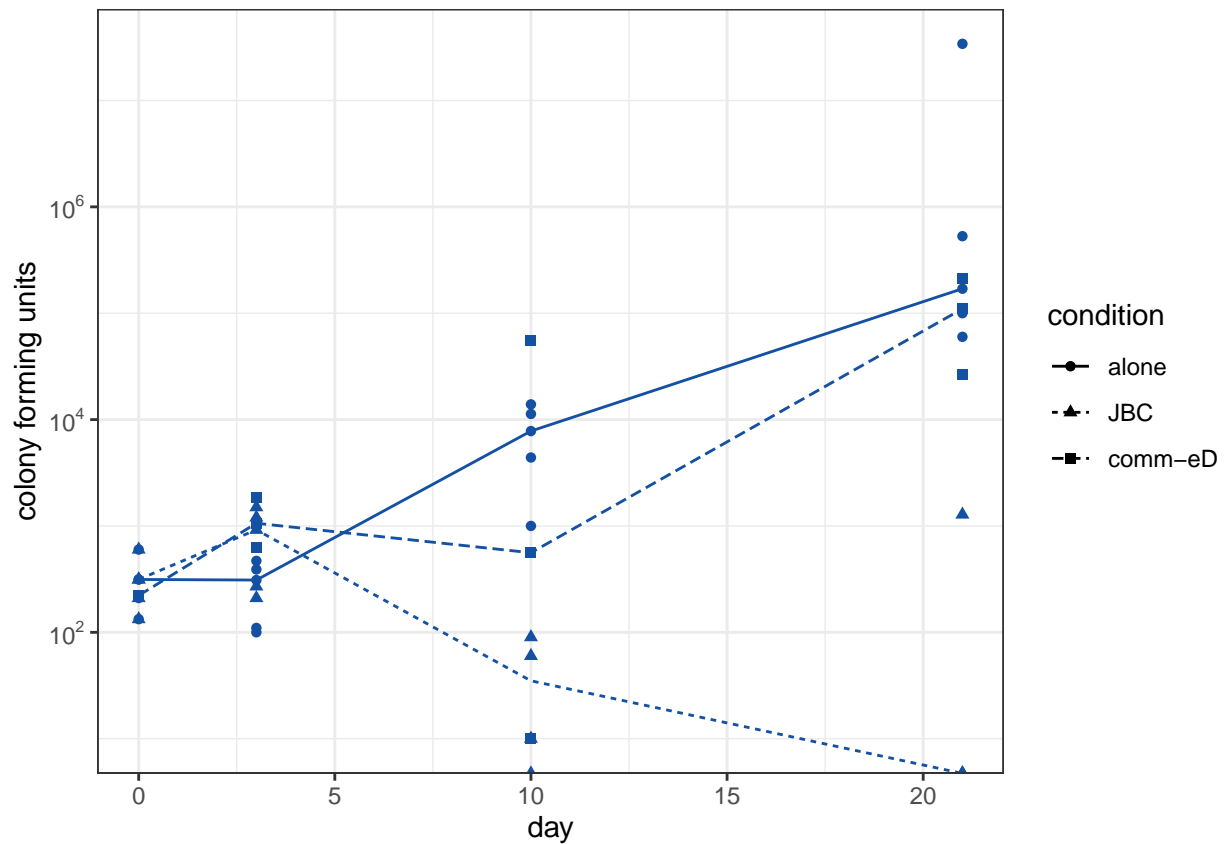
7/16/2021

Compare growth of *Brevibacterium* alone at pH 5, in coculture with *Penicillium*, and in a dropout community excluding *Diutina* and *S. xylosus*

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

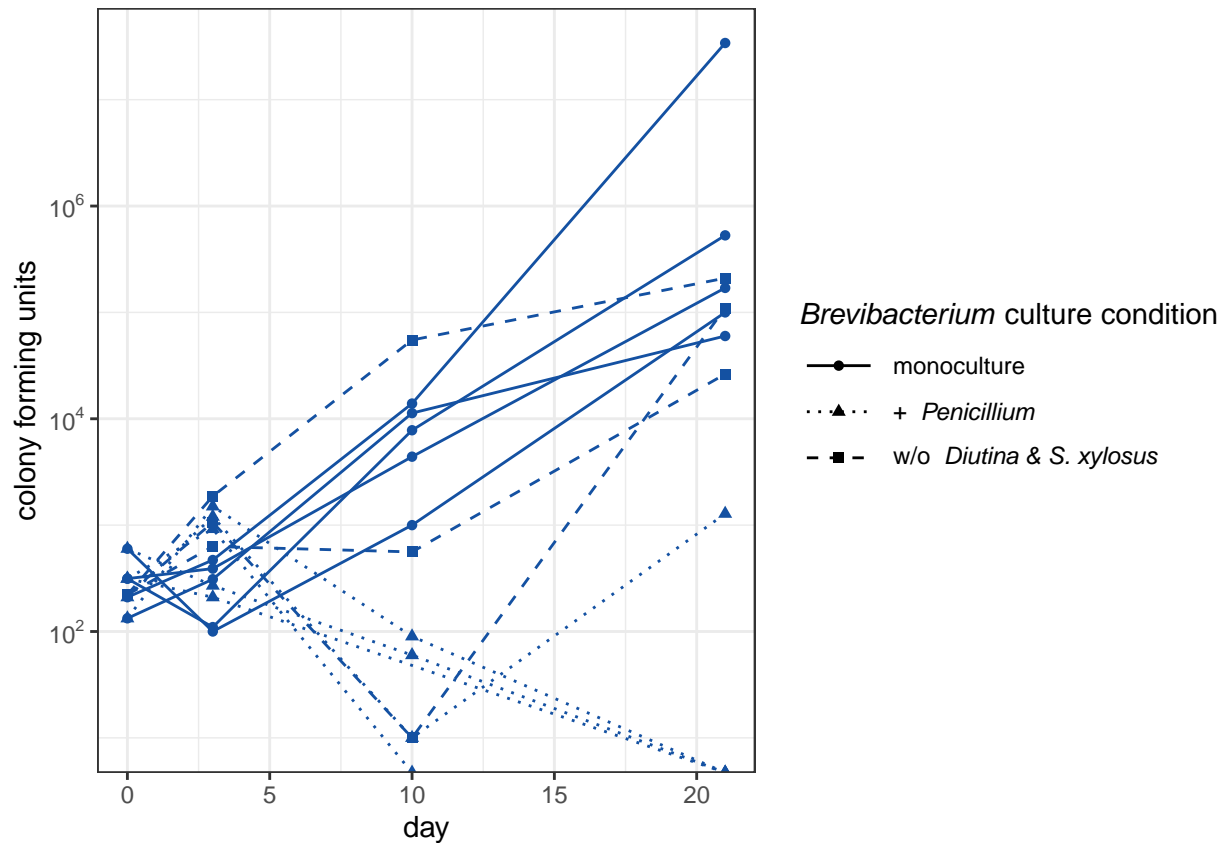
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Let's check all species to see whether inhibition patterns are exacerbated in double dropout, or comparable to the *Penicillium* coculture condition

```
# lines for each replicate within each condition
dat <- rbind(d.18 %>% filter(condition %in% c("alone", "JBC"), pH == 5,
                             !species %in% c("JBC", "BC10", "135E")) %>%
  select(species, condition, replicate, day, total.CFUs),
d.1005 %>% filter(condition == "comm-eD",
                  !species %in% c("JBC", "BC10", "135E")) %>%
  select(species, condition, replicate, day, total.CFUs))

ggplot(dat, aes(x = day, y = total.CFUs,
               color=species, group = interaction(replicate, condition))) +
  geom_point(aes(shape = condition)) +
  geom_line(aes(linetype = condition)) +
  scale_y_log10(breaks = trans_breaks("log10", function(x) 10^x, n=4),
               labels = trans_format("log10", label_math(10^.x))) +
  theme_bw() +
  scale_color_manual(values = species.palette, guide = "none") +
  scale_shape_discrete(labels = c("alone" = "monoculture",
                                "JBC" = expression(paste("+ ", italic(" Penicillium"))),
                                "comm-eD" = expression(paste("w/o ", italic(" Diutina & S. xylosus")))))
  scale_linetype_manual(values = c("alone" = "solid",
                                "JBC" = "dotted",
                                "comm-eD" = "dashed"),
                       labels = c("alone" = "monoculture",
                                "JBC" = expression(paste("+ ", italic(" Penicillium"))),
                                "comm-eD" = expression(paste("w/o ", italic(" Diutina & S. xylosus")))))
```

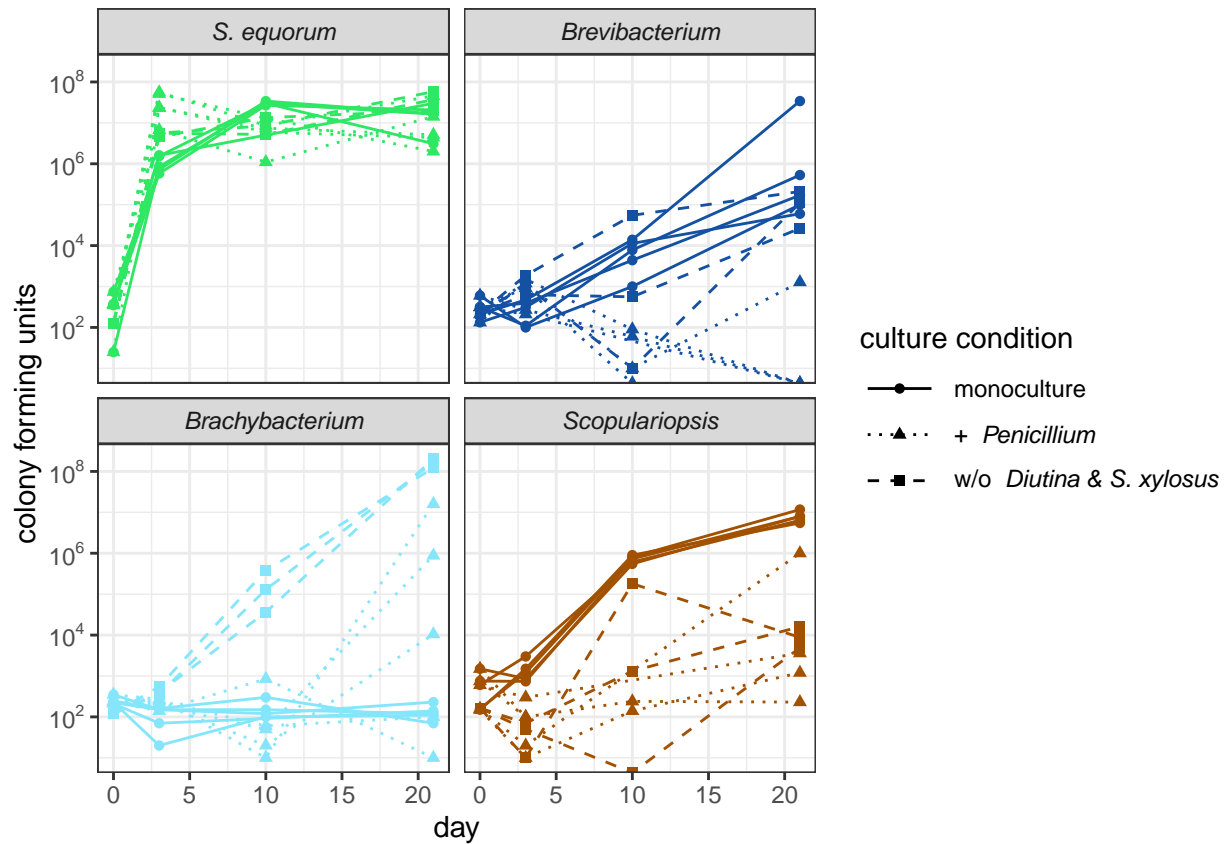
```

"comm-eD"= expression(paste("w/o ", italic(" Diutina & S. xylosus")))
labs(y = "colony forming units",
     shape = "culture condition",
     linetype = "culture condition") +
facet_wrap(~species, nrow = 2, labeller = labeller(species = names)) +
theme(legend.text = element_text(hjust = 0),
      legend.key.width = unit(30, "pt"),
      strip.text = element_text(face = "italic"))

```

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```

ggsave(here("figures/suppl_fig_5.png"), device="png", width = 7, height = 6, units = "in")

```

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```

ggsave(here("figures/suppl_fig_5.svg"), device="svg", width = 7, height = 6, units = "in")

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