experiment 1

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This experiment supercedes all previous ones. It is a factorial manipulation of diversity of the three groups. It takes about 50 hours to run while using 12 cores.

Setup

R

```
rm(list = ls())

knitr::opts_knit$set(progress = TRUE, verbose = FALSE, cache = TRUE)

microxanox_release <- "0.2"

#tmplib <- tempfile()
#dir.create(tmplib)


### From '?remotes::install_github`:
# auth_token
#   To install from a private repo, generate a personal access token (PAT) in
#   "https://github.com/settings/tokens" and supply to this argument. This is
#   safer than using a password because you can easily delete a PAT without
#   affecting any others. Defaults to the GITHUB_PAT environment variable.

# remotes::install_github(
#   "opetchey/microxanox",
#   ref = microxanox_release,
#   # auth_token = "ENTER YOUR TOKEN or PROVED AS ENVIRONMENT VARIABLE",
#   build_vignettes = FALSE,
#   force = TRUE,
#   upgrade = FALSE,
#   lib = tmplib
# )

#library(microxanox, lib.loc = tmplib)

library(microxanox)
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --

## v ggplot2 3.3.4     v purrr   0.3.4
## v tibble  3.1.2     v dplyr   1.0.7
## v tidyr   1.1.3     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.1

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(patchwork)
library(here)
```

```
## here() starts at /Users/owenpetchey/Desktop/microxanox/diversity_envresp1
```

```
source(here("experiments/r functions/various_useful_functions.r"))
zero <- 0 ## don't change
unity <- 1 ## don't change!!!
#options(mc.cores = 8)
eval_dynamics_flag <- FALSE
```

Version of `microxanox` package used: 0.2.1

General simulation conditions

```
default_dynamic_model <- bushplus_dynamic_model
default_event_definition <- event_definition_1
default_event_interval <- 100
default_noise_sigma <- 0
default_minimum_abundances <- rep(1, 3)
names(default_minimum_abundances) <- c("CB", "PB", "SB")
default_sim_duration <- 80000
default_sim_sample_interval <- 100
initial_pars_from <- "bush_ssfig3"
## note that next line (log10a_series is over-ridden with getting stable states)
#default_log10a_series <- c(-2, -2, -2, -2, -10, -10, -10, -10, -10)
```

Define diversity

```
num_CB_strains <- 9
num_SB_strains <- 9
num_PB_strains <- 9
CB_gmax_div <- 0.015789474 * 0
CB_h_div <- -0.08 * 0
SB_gmax_div <- 0.015789474 * 5
SB_h_div <- -0.323  * 5
PB_gmax_div <- 0.015789474  * 5
```

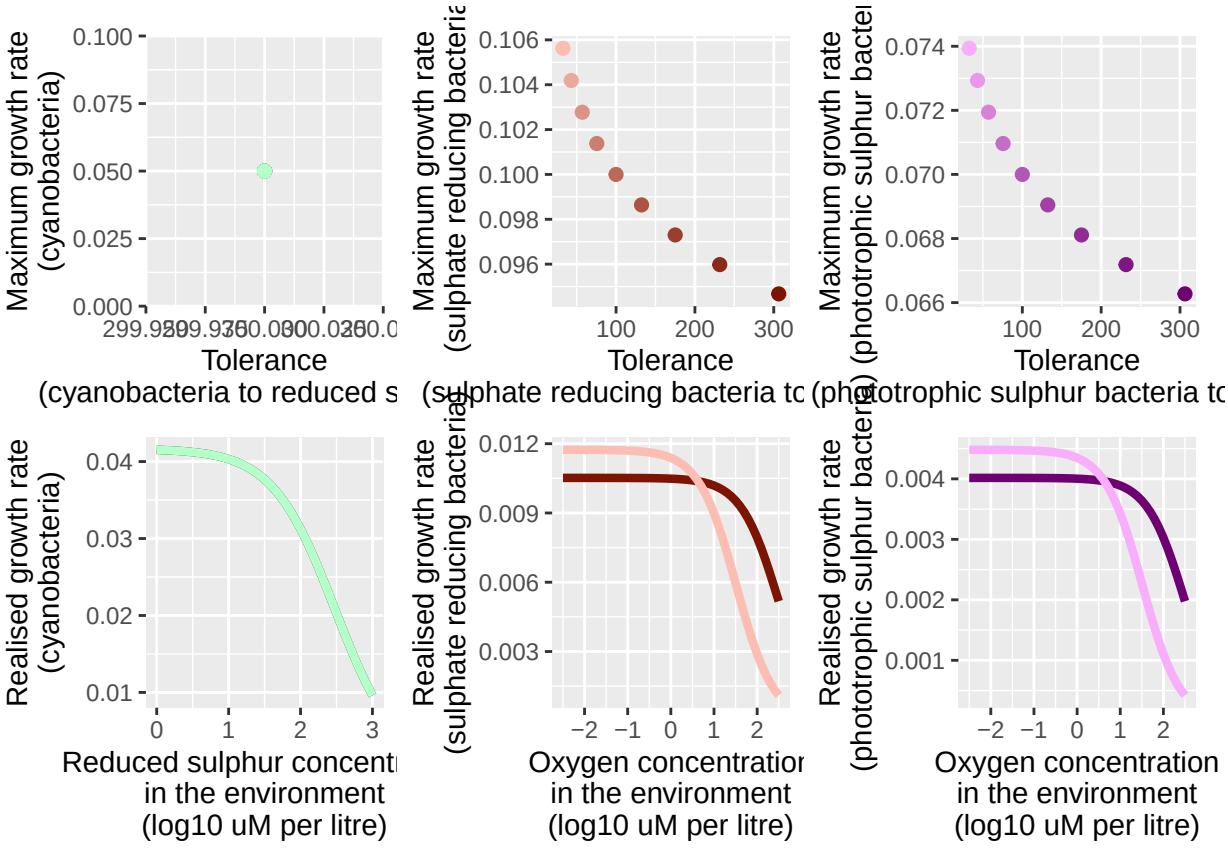
```
PB_h_div <- -0.323  * 5

num_div_treatment_levels <- 20
```

Create diversity

```
var_expt <- create_diversity_factorial()
```

Display diversity

```
display_diversity(20)
```



Temporal switching

```
var_expt_levels <- var_expt[,1:6]

no_diversity <- which(rowSums(abs(var_expt_levels))==0)
max_diversty_all <- which(max(rowSums(abs(var_expt_levels))) ==
```

```
                            rowSums(abs(var_expt_levels)))
max_only_CB_diversity <- which(max(rowSums(abs(var_expt_levels[,1:2]))) ==
                            rowSums(abs(var_expt_levels[,1:2])) &
                              rowSums(abs(var_expt_levels[,3:6]))==0)
#var_expt_levels[381,]

max_only_SBPB_diversity <- which(max(rowSums(abs(var_expt_levels[,3:6]))) ==
                            rowSums(abs(var_expt_levels[,3:6])) &
                              rowSums(abs(var_expt_levels[,1:2]))==0)
#var_expt_levels[20,]
```

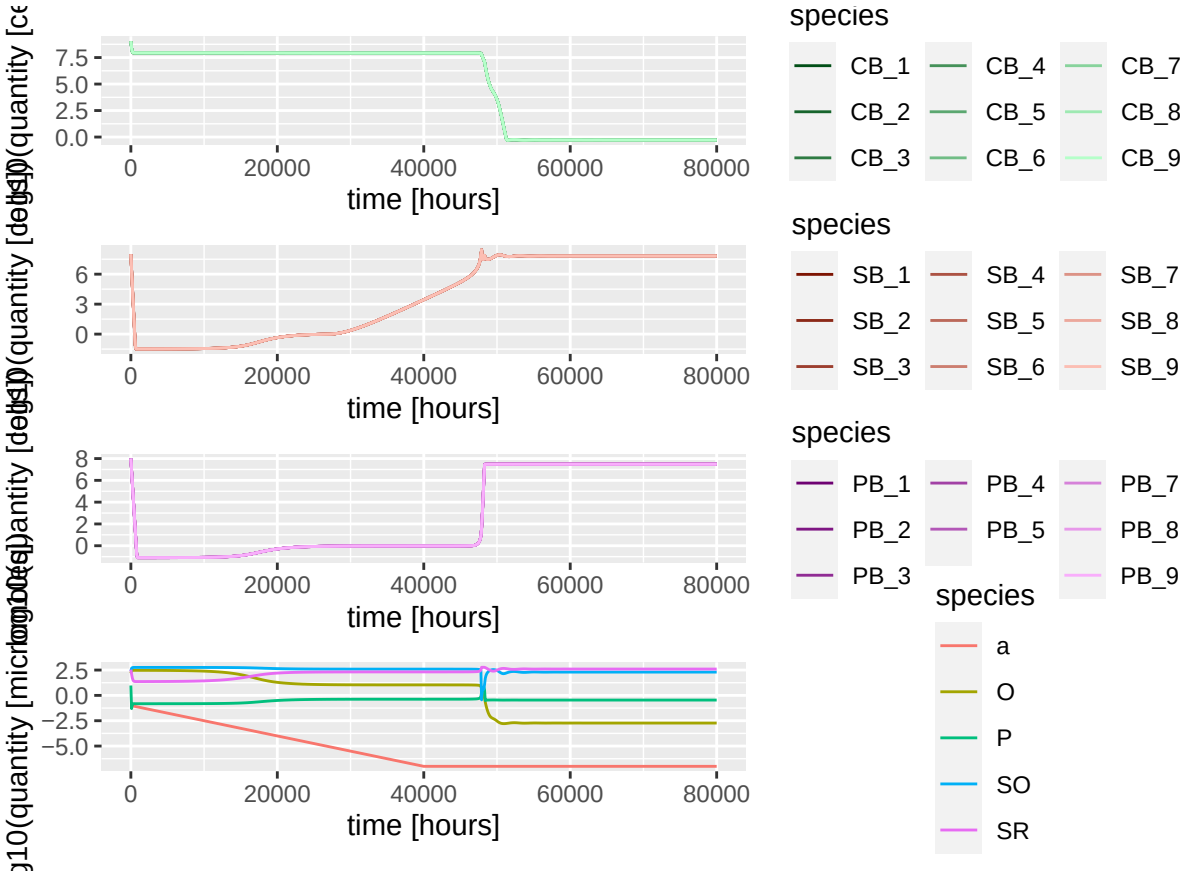
Oxic to anoxic

No diversity

```
default_sim_duration <- 80000
```

```
default_log10a_series <- c(-1, -7, -7)
initial_state <- new_initial_state(num_CB_strains,
                                   num_PB_strains,
                                   num_SB_strains,
                                   values = "bush_ssfig3")
initial_state[grep("CB_", names(initial_state))] <- 10^10/num_CB_strains
sim_res_novar1 <- run_simulation(parameter_values = var_expt$pars[[no_diversity]],
                           initial_state = initial_state)
saveRDS(sim_res_novar1, here("experiments/experiment 1/data/sim_res_novar1.RDS"))
```

```
sim_res_novar1 <- readRDS(here("experiments/experiment 1/data/sim_res_novar1.RDS"))
plot_dynamics(sim_res_novar1)
```

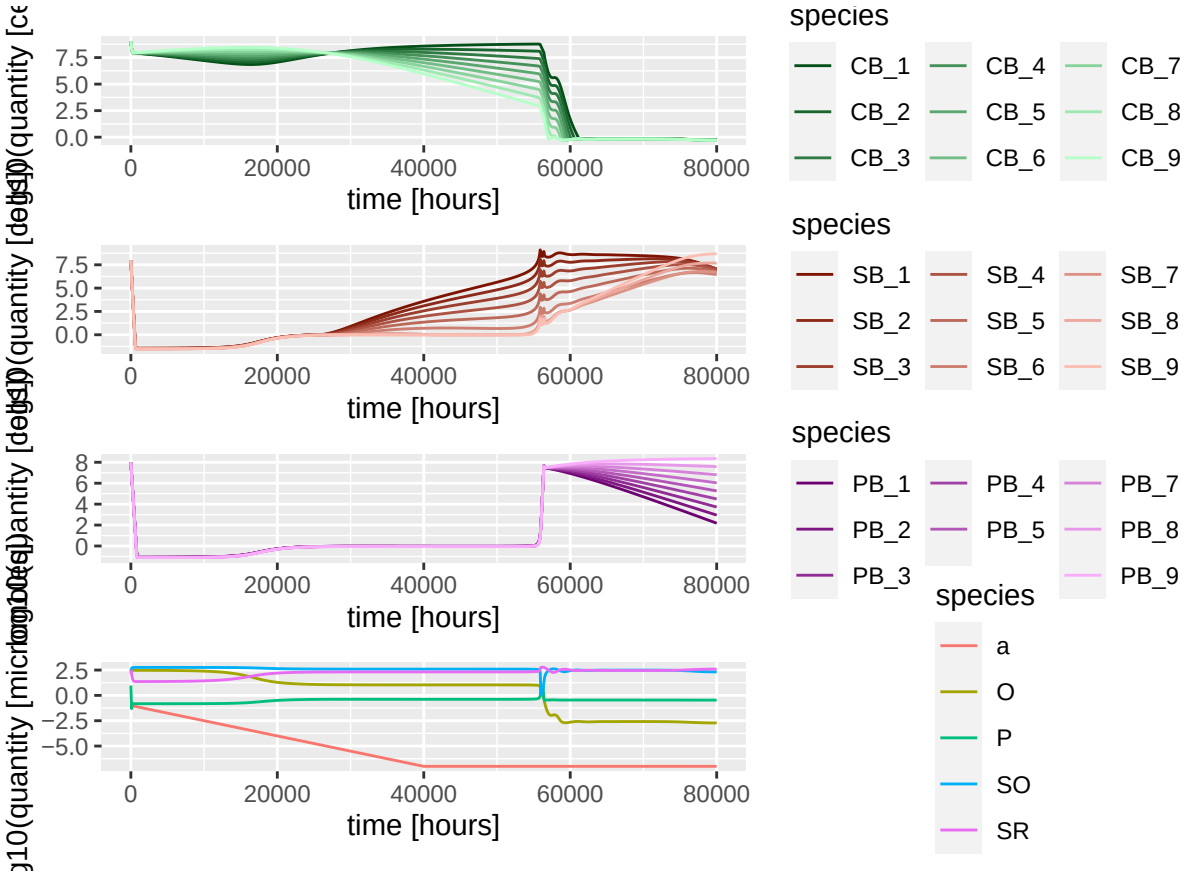



```
#ggsave(here("simulations/expt2/figures/switching_novar.pdf"), width = 10)
```

Maximum diversity

```
sim_number <- num_div_treatment_levels
sim_res_highvar1 <- run_simulation(parameter_values = var_expt$pars[[max_diversty_all]],
                           initial_state = initial_state)
saveRDS(sim_res_highvar1, here("experiments/experiment 1/data/sim_res_highvar1.RDS"))
```

```
sim_res_highvar1 <- readRDS(here("experiments/experiment 1/data/sim_res_highvar1.RDS"))
plot_dynamics(sim_res_highvar1)
```




```
#ggsave(here("simulationsexpt2/figures/switching_highvar.pdf"), width = 10)
```

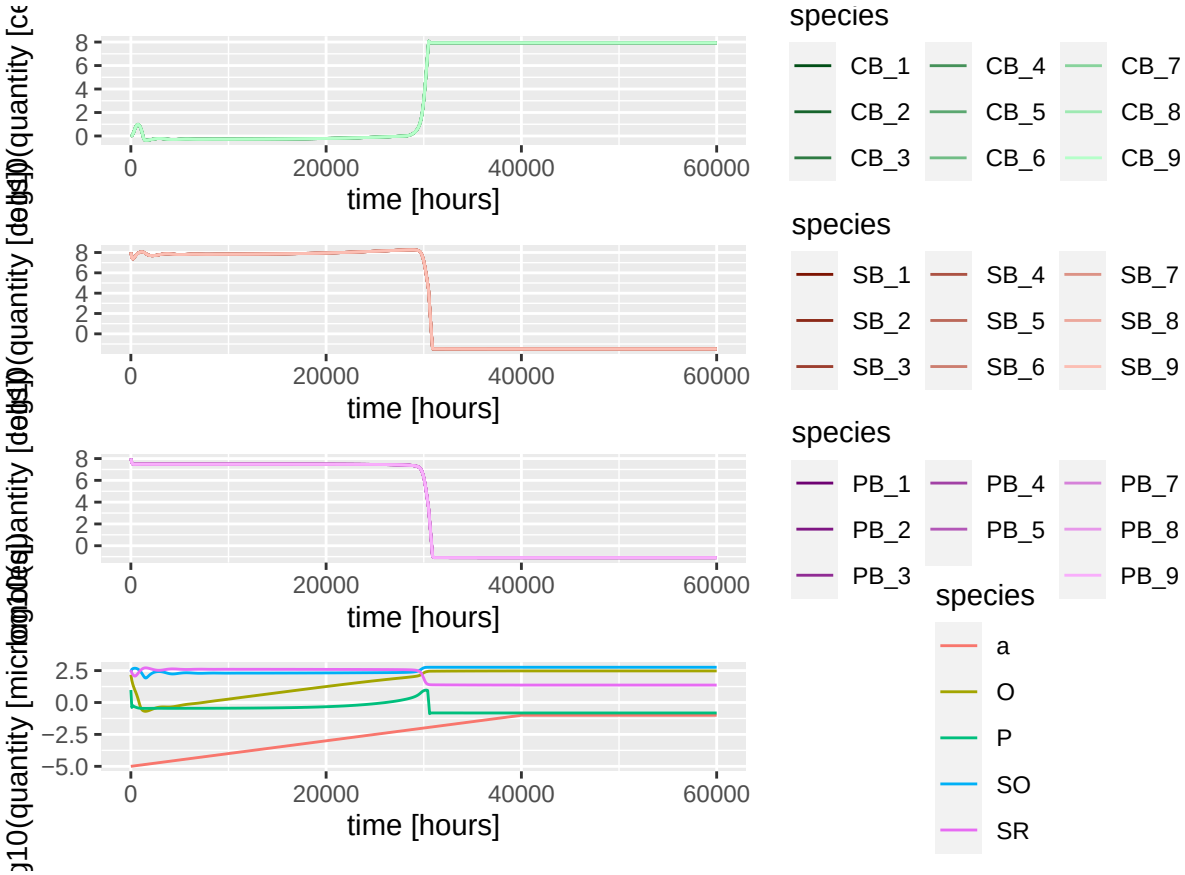
Anoxic to oxic

No diversity

```
default_sim_duration <- 60000
```

```
sim_number <- 1
default_log10a_series <- c(-5, -3, -1, -1)
initial_state <- new_initial_state(num_CB_strains,
                                   num_PB_strains,
                                   num_SB_strains,
                                   values = "bush_ssfig3")
initial_state[grep("CB_", names(initial_state))] <- 10/num_CB_strains
sim_res_novar2 <- run_simulation(parameter_values = var_expt$pars[[no_diversity]],
                           initial_state = initial_state)
saveRDS(sim_res_novar2, here("experiments/experiment 1/data/sim_res_novar2.RDS"))
```

```
sim_res_novar2 <- readRDS(here("experiments/experiment 1/data/sim_res_novar2.RDS"))
plot_dynamics(sim_res_novar2)
```

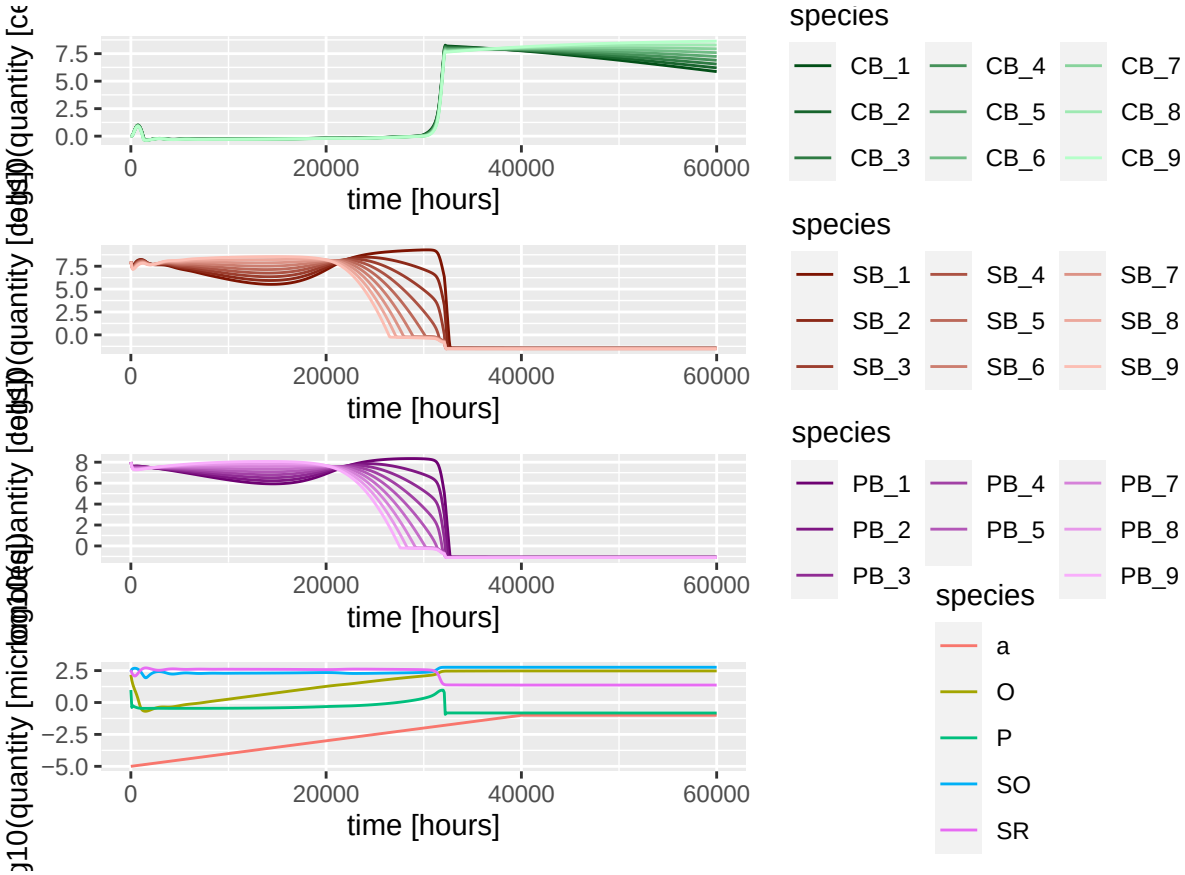



```
#ggsave(here("simulations/expt2/figures/switching_novar.pdf"), width = 10)
```

Maximum diversity

```
sim_number <- num_div_treatment_levels
sim_res_highvar2 <- run_simulation(parameter_values = var_expt$pars[[max_diversty_all]],
                          initial_state = initial_state)
saveRDS(sim_res_highvar2, here("experiments/experiment 1/data/sim_res_highvar2.RDS"))
```

```
sim_res_highvar2 <- readRDS(here("experiments/experiment 1/data/sim_res_highvar2.RDS"))
plot_dynamics(sim_res_highvar2)
```




```
#ggsave(here("simulationsexpt2/figures/switching_highvar.pdf"), width = 10)
```

Anoxic to oxic to anoxic

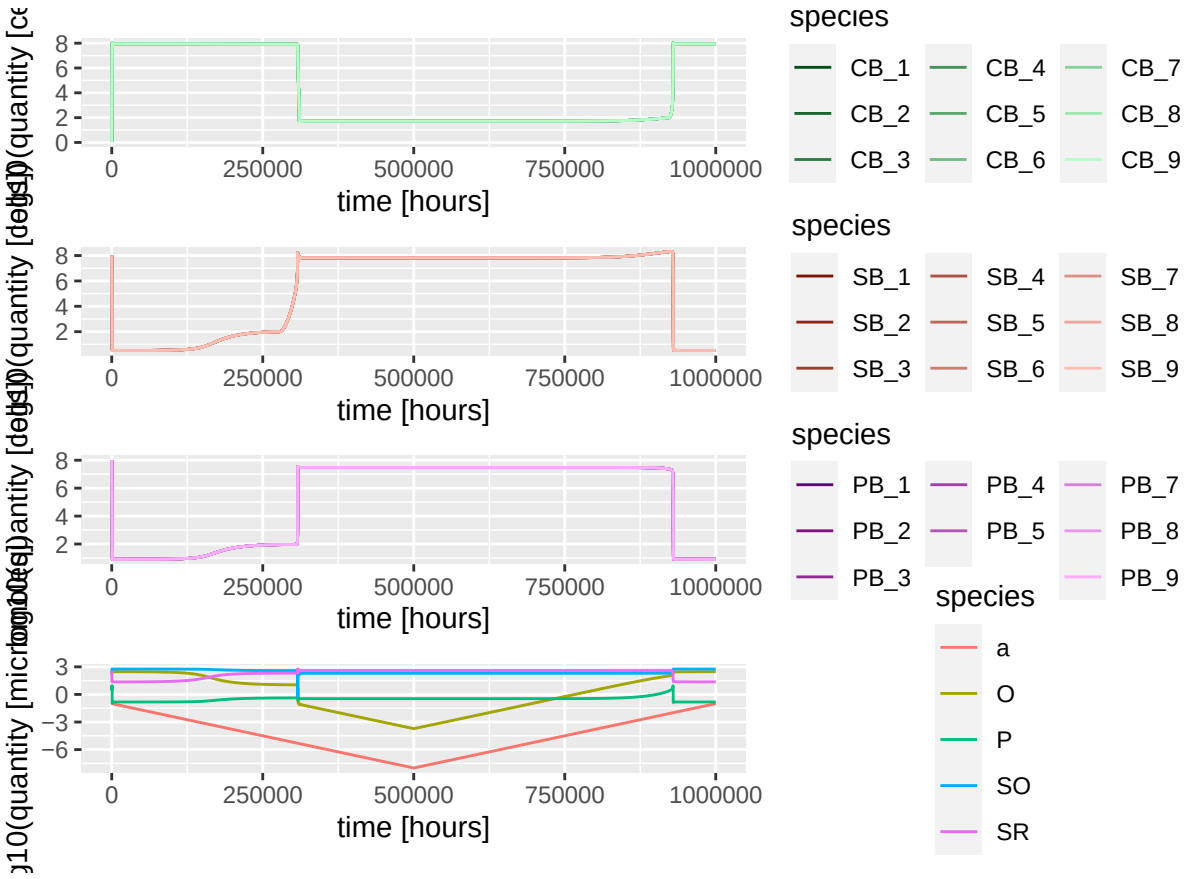
No diversity

```
default_sim_duration <- 1000000
```

```
default_minimum_abundances <- rep(100, 3)
names(default_minimum_abundances) <- c("CB", "PB", "SB")
```

```
sim_number1 <- 1
default_log10a_series <- c(-1, -8, -1)
initial_state <- new_initial_state(num_CB_strains,
                                   num_PB_strains,
                                   num_SB_strains,
                                   values = "bush_ssfig3")
initial_state[grep("CB_", names(initial_state))] <- 10/num_CB_strains
sim_res_novar3 <- run_simulation(parameter_values = var_expt$pars[[no_diversity]],
                           initial_state = initial_state)
saveRDS(sim_res_novar3, here("experiments/experiment 1/data/sim_res_novar3.RDS"))
```

```
sim_res_novar3 <- readRDS(here("experiments/experiment 1/data/sim_res_novar3.RDS"))
plot_dynamics(sim_res_novar3)
```

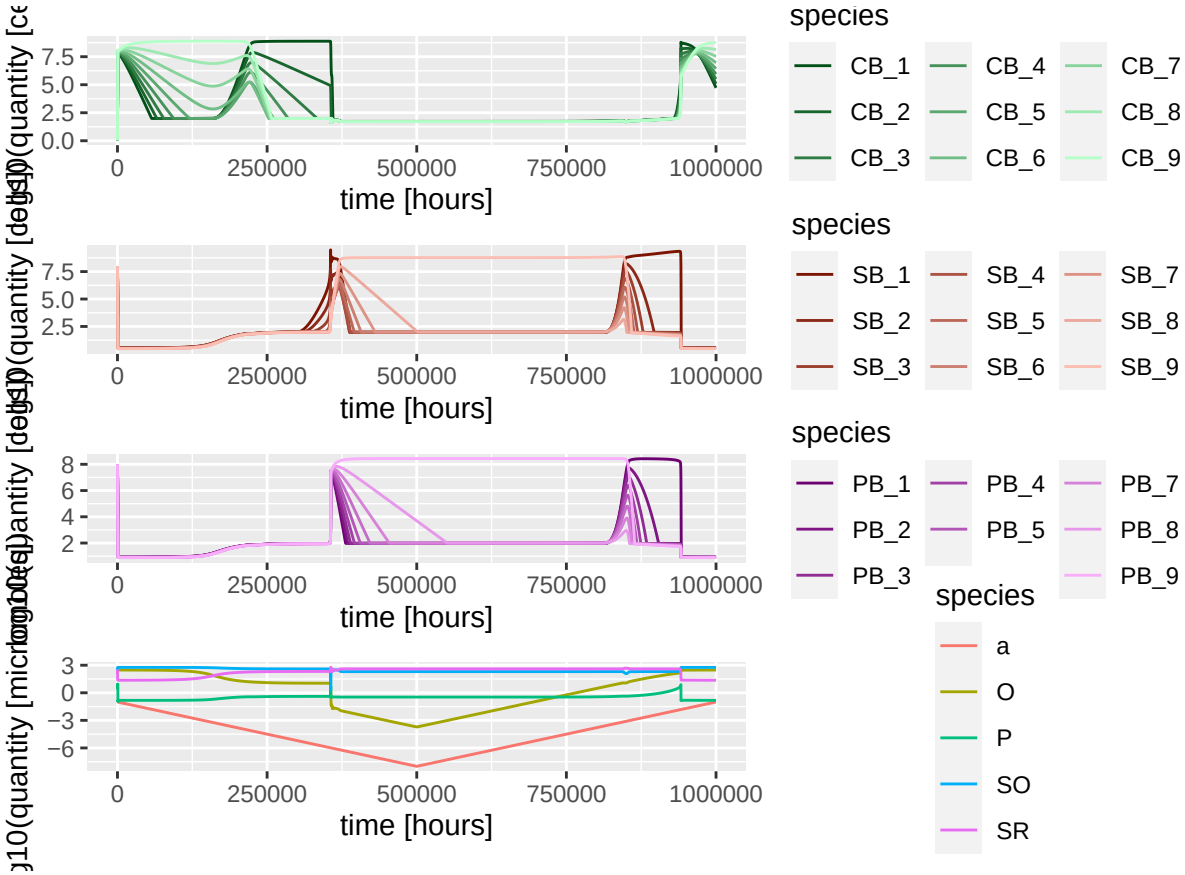



```
#ggsave(here("simulations/expt2/figures/switching_novar.pdf"), width = 10)
```

Maximum diversity

```
sim_number2 <- num_div_treatment_levels
sim_res_highvar3 <- run_simulation(parameter_values = var_expt$pars[[max_diversty_all]],
                           initial_state = initial_state)
saveRDS(sim_res_highvar3, here("experiments/experiment 1/data/sim_res_highvar3.RDS"))
```

```
sim_res_highvar3 <- readRDS(here("experiments/experiment 1/data/sim_res_highvar3.RDS"))
plot_dynamics(sim_res_highvar3)
```




```
#ggsave(here("simulationsexpt2/figures/switching_highvar.pdf"), width = 10)
```

Visualise

```
visualise_temporal_env_eco()
```

Stable state finding

Finding

```
options(mc.cores = 12)
```

```
default_sim_duration <- 1000000
ssfind_minimum_abundances <- rep(0, 3)
names(ssfind_minimum_abundances) <- c("CB", "PB", "SB")
ssfind_simulation_duration <- default_sim_duration
ssfind_simulation_sampling_interval <- ssfind_simulation_duration
ssfind_event_interval <- ssfind_simulation_duration
grid_num_a <- 1000 #usually 1000 ## number of a_0 values
a_0s <- 10^seq(-7, -1, length=grid_num_a) ## sequence of a_0 values
```

```
grid_num_N <- 2 ## number of N values
initial_CBs <- 10^seq(0, 10, length=grid_num_N) ## sequence of N values
initial_PBs <- 1e8 ## not varied
initial_SBs <- 1e8 ## not varied
# next line creates all possible combinations
ss_expt <- expand.grid(N_CB = initial_CBs,
                       N_PB = initial_PBs,
                       N_SB = initial_SBs,
                       a_0 = a_0s)
```

Run stable state finding

*Careful, this simulation takes about 600 hours on a single core

```
#var_expt <- run_ss_var_experiment()
#saveRDS(var_expt, here("experiments/experiment 1/data/ss_data_1e6_noCB_5xSBPB_.RDS"))
```

Process the stable state data

Bring in various stable state datasets

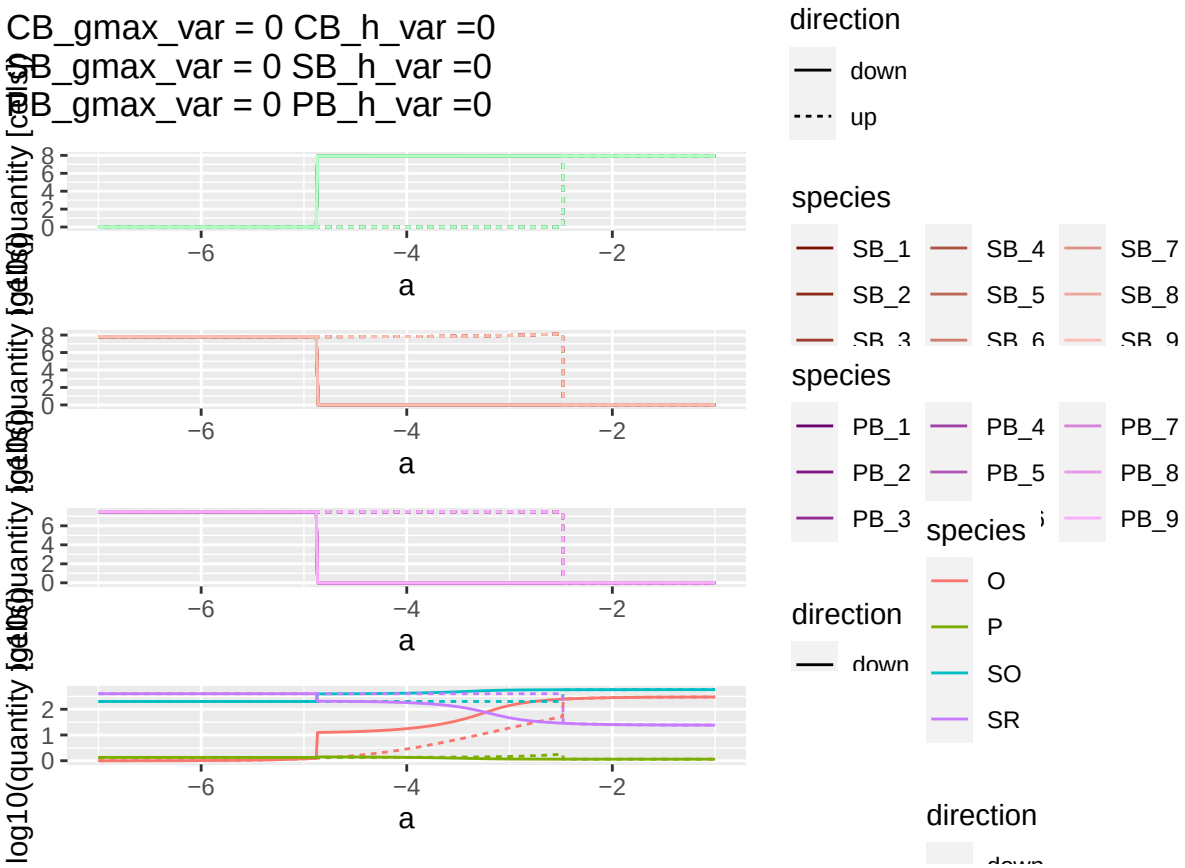
```
## sim length 80'000, 20 x 20 factorial, reference maximum diversity
var_expt1 <- readRDS(here("experiments/experiment 1/data/ss_data_80000.RDS")) %>%
  mutate(sim_length = 80000)
stab_data1 <- var_expt1 %>%
  group_by(CB_var_gmax_s, CB_var_h_s,
           SB_var_gmax_s, SB_var_h_s,
           PB_var_gmax_s, PB_var_h_s, sim_length) %>%
  do(stability_measures = get_stability_measures(.$ss_res[[1]]))
stab_data1 <- unnest(stab_data1, cols = c(stability_measures))
saveRDS(stab_data1, here("experiments/experiment 1/data/stab_data_80000.RDS"))



## sim length 1'000'000, 20 x 20 factorial, reference maximum diversity
var_expt2 <- readRDS(here("experiments/experiment 1/data/ss_data_1000000_20factorial.RDS")) %>%
  mutate(sim_length = 1000000)
stab_data2 <- var_expt2 %>%
  group_by(CB_var_gmax_s, CB_var_h_s,
           SB_var_gmax_s, SB_var_h_s,
           PB_var_gmax_s, PB_var_h_s, sim_length) %>%
  do(stability_measures = get_stability_measures(.$ss_res[[1]]))
stab_data2 <- unnest(stab_data2, cols = c(stability_measures))
saveRDS(stab_data2, here("experiments/experiment 1/data/stab_data_1000000_20factorial.RDS"))


## sim length 1'000'000, 20 SBPBgrad, 5x maximum diversity
var_expt3 <- readRDS(here("experiments/experiment 1/data/ss_data_1e6_noCB_5xSBPB_.RDS")) %>%
  mutate(sim_length = 1000000)
stab_data3 <- var_expt3 %>%
  group_by(CB_var_gmax_s, CB_var_h_s,
           SB_var_gmax_s, SB_var_h_s,
           PB_var_gmax_s, PB_var_h_s, sim_length) %>%
  do(stability_measures = get_stability_measures(.$ss_res[[1]]))
```

```
stab_data3 <- unnest(stab_data3, cols = c(stability_measures))
saveRDS(stab_data3, here("experiments/experiment 1/data/stab_data_1e6_noCB_5xSBPB_.RDS"))


## sim length 300'000, 20 SBPBgrad, reference maximum diversity
var_expt4 <- readRDS(here("experiments/experiment 1/data/ss_data_300000_small.RDS")) %>%
  mutate(sim_length = 300000)
stab_data4 <- var_expt4 %>%
  group_by(CB_var_gmax_s, CB_var_h_s,
           SB_var_gmax_s, SB_var_h_s,
           PB_var_gmax_s, PB_var_h_s, sim_length) %>%
  do(stability_measures = get_stability_measures(.$ss_res[[1]]))
stab_data4 <- unnest(stab_data4, cols = c(stability_measures))
saveRDS(stab_data4, here("experiments/experiment 1/data/stab_data_300000.RDS"))
```

SS, no diversity, all diversity, CB only, and SBPB only

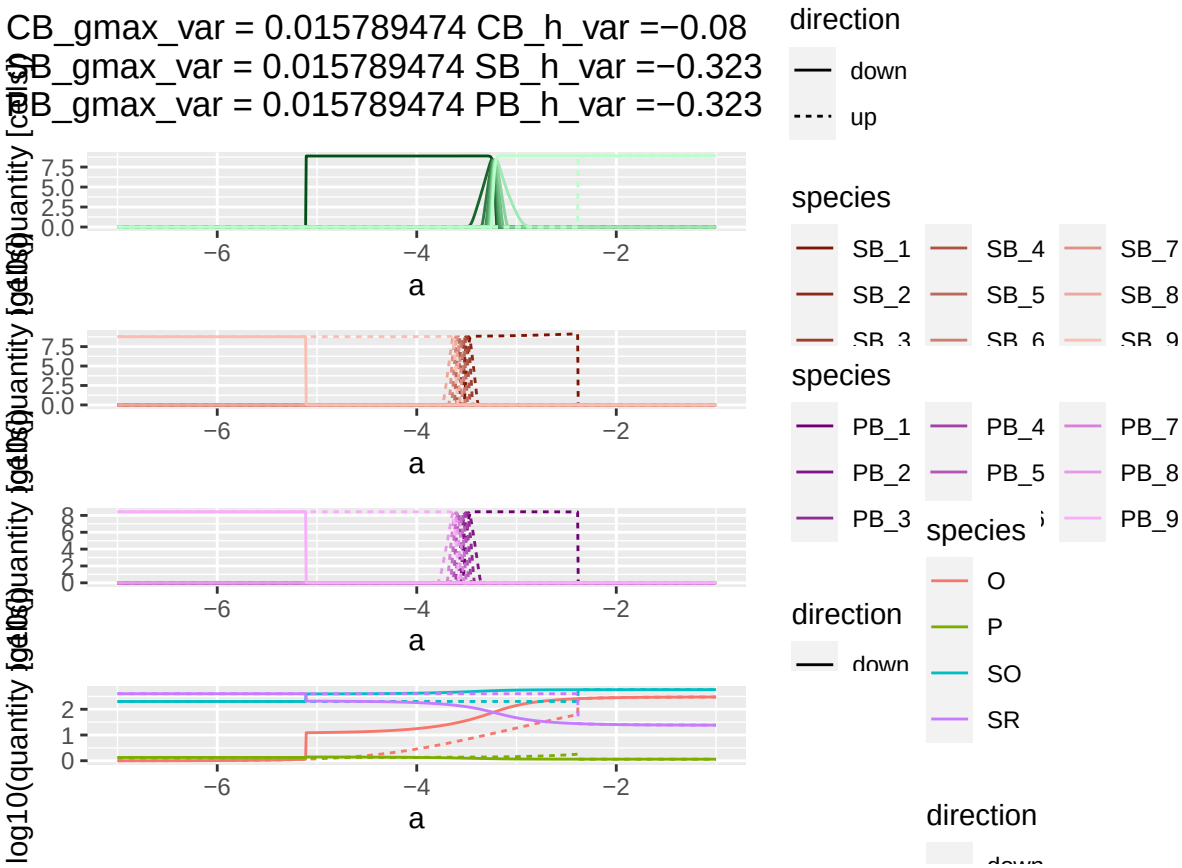
```
## find various combinations of diversity
var_expt <- readRDS(here("experiments/experiment 1/data/ss_data_1000000_20factorial.RDS"))

var_expt_levels <- var_expt[,1:6]

no_diversity <- which(rowSums(abs(var_expt_levels))==0)
max_diversty_all <- which(max(rowSums(abs(var_expt_levels))) ==
                            rowSums(abs(var_expt_levels)))
max_only_CB_diversity <- which(max(rowSums(abs(var_expt_levels[,1:2]))) ==
                            rowSums(abs(var_expt_levels[,1:2])) &
                              rowSums(abs(var_expt_levels[,3:6]))==0)
#var_expt_levels[381,]

max_only_SBPB_diversity <- which(max(rowSums(abs(var_expt_levels[,3:6]))) ==
                            rowSums(abs(var_expt_levels[,3:6])) &
                              rowSums(abs(var_expt_levels[,1:2]))==0)
#var_expt_levels[20,]
```

```
p1  <- plot_ss_result1(var_expt,
                result_index = no_diversity,
                filename_prefix = NULL,
                save_image_file = FALSE)
p1
```

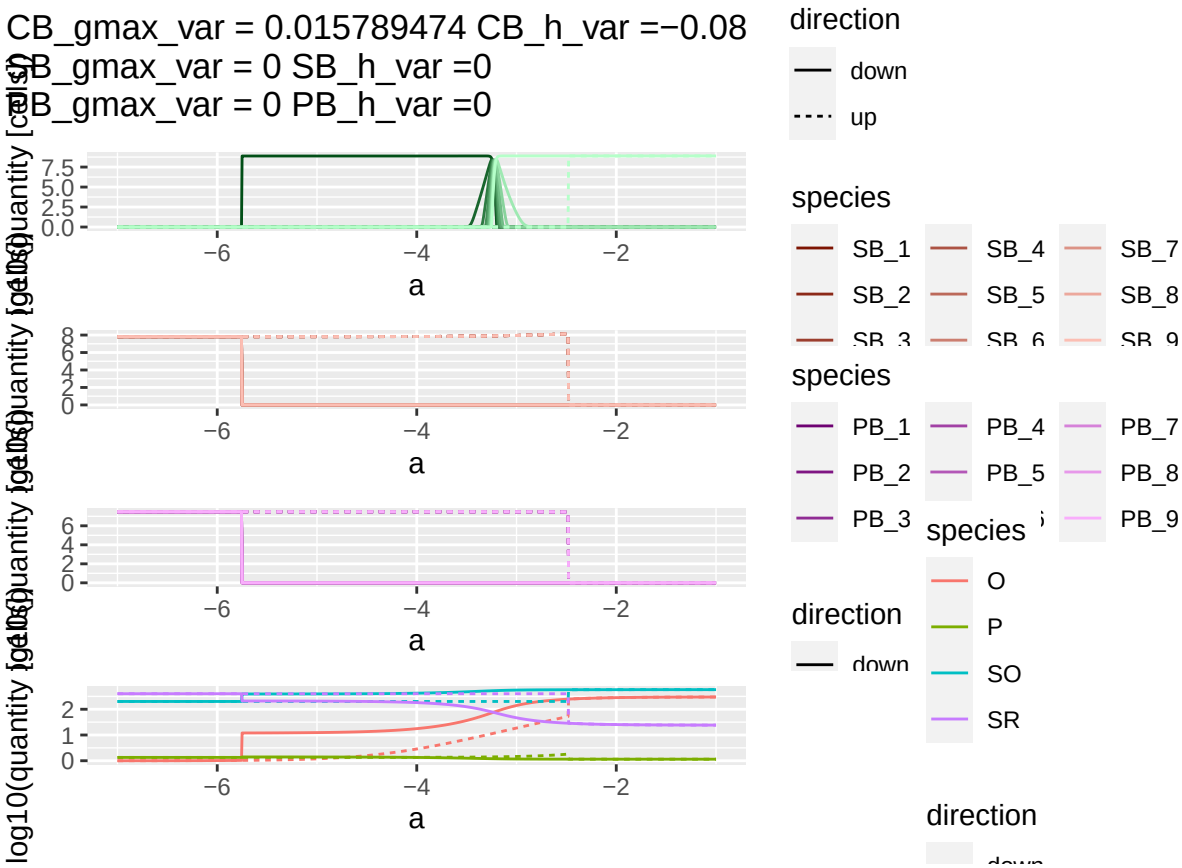



```
#junk1 <- var_expt[no_diversity,]$ss_res[[1]]
```

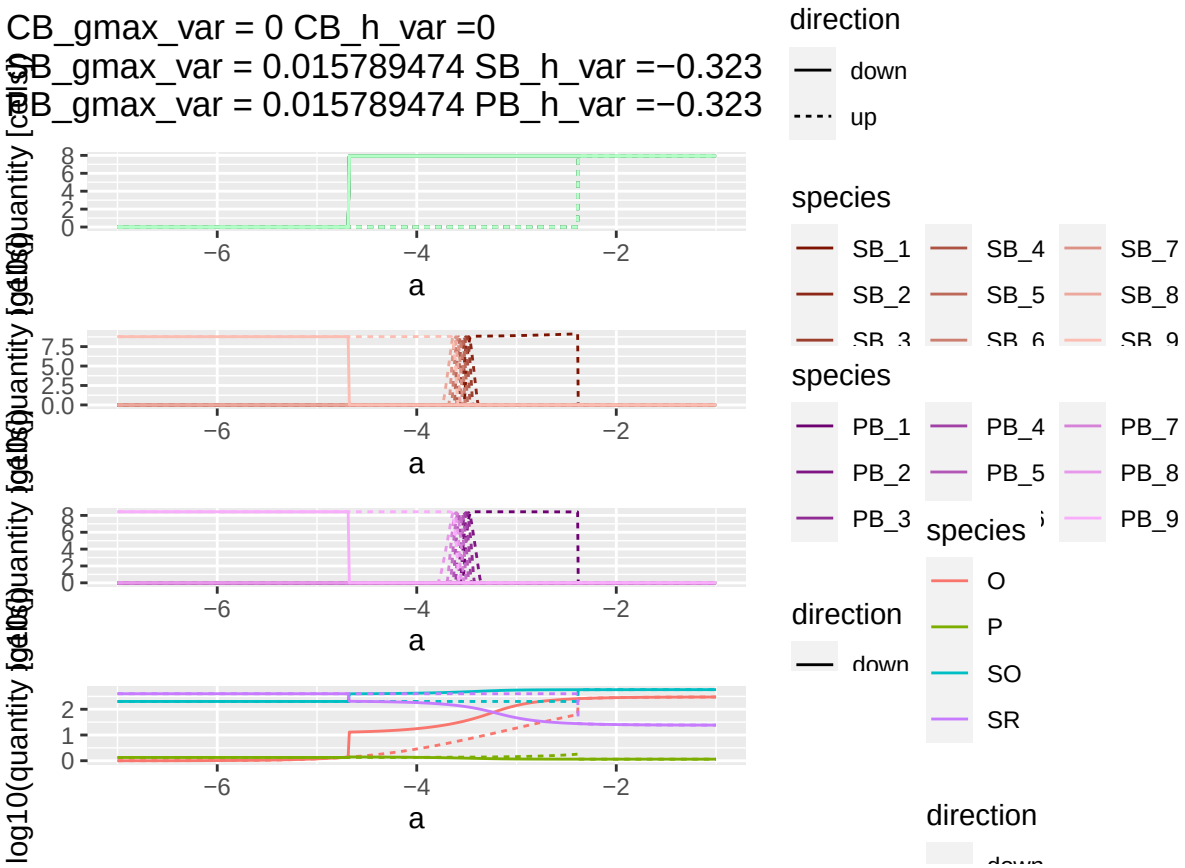
```
p2  <- plot_ss_result1(var_expt,
                result_index = max_diversty_all,
                filename_prefix = NULL,
                save_image_file = FALSE)
p2
```




```
p3  <- plot_ss_result1(var_expt,
                result_index = max_only_CB_diversity,
                filename_prefix = NULL,
                save_image_file = FALSE)
p3
```



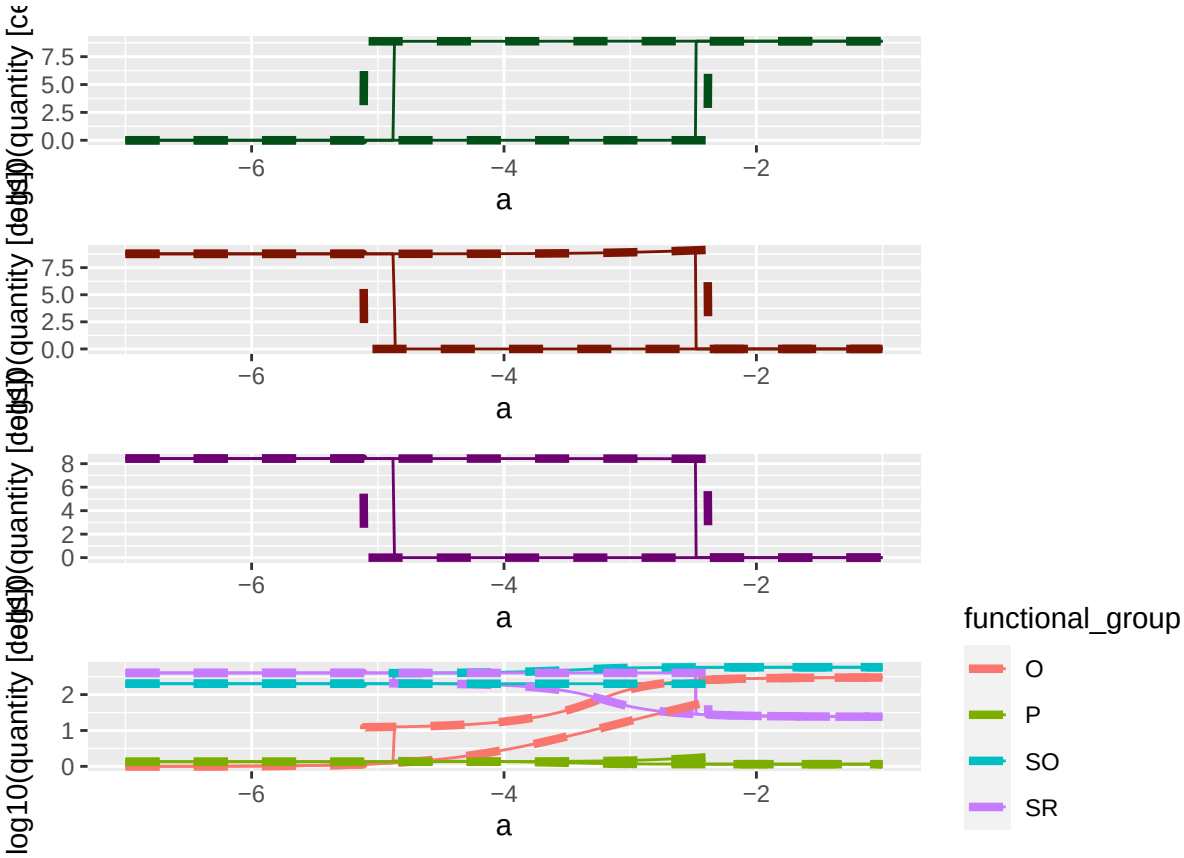

```
p4  <- plot_ss_result1(var_expt,
                result_index = max_only_SBPB_diversity,
                filename_prefix = NULL,
                save_image_file = FALSE)
p4
```




```
p_overlay1 <- plot_ss_result2(var_expt[no_diversity,]$ss_res[[1]],
                              var_expt[max_diversty_all,]$ss_res[[1]],
                              xlims = c(-7, -1))
```

```
## `summarise()` has grouped output by 'a', 'direction', 'var_type'. You can override using the `.groups
## `summarise()` has grouped output by 'a', 'direction', 'var_type'. You can override using the `.groups
```

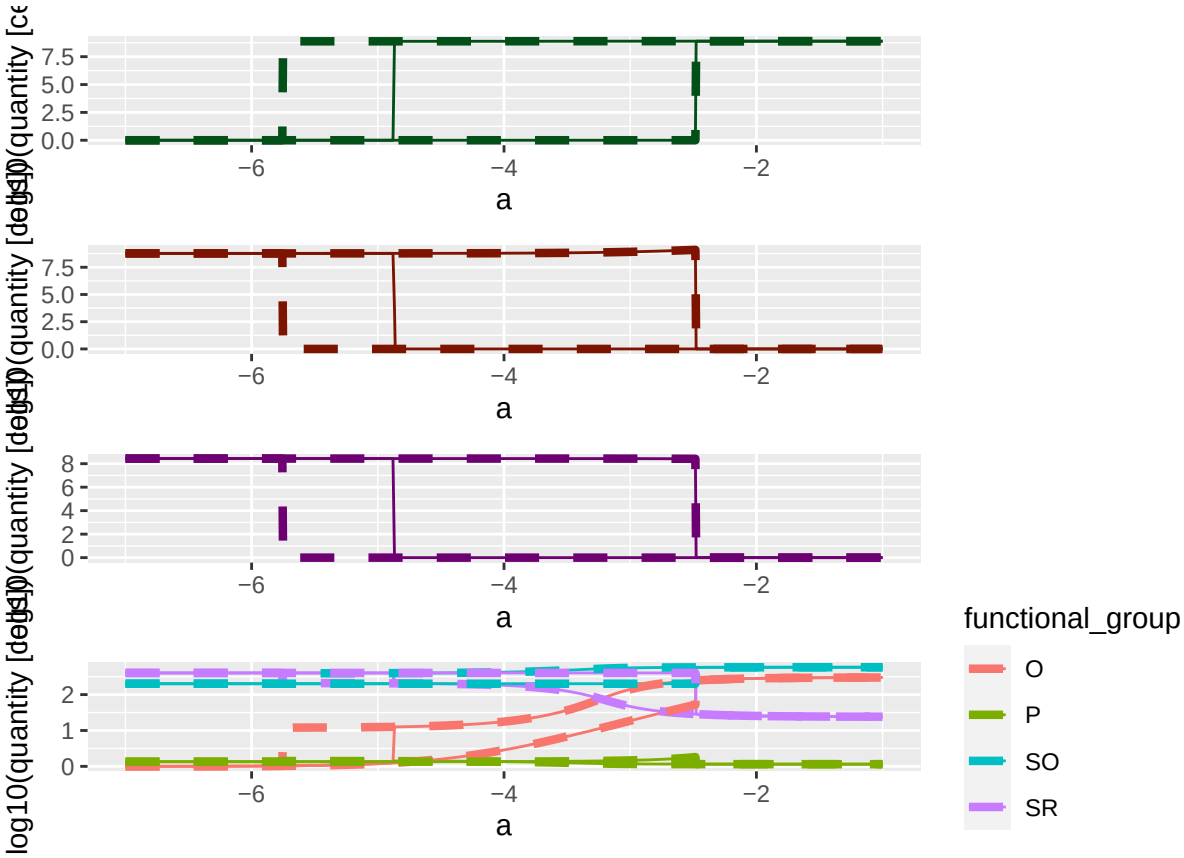
```
p_overlay1
```




```
p_overlay2 <- plot_ss_result2(var_expt[no_diversity,]$ss_res[[1]],
                              var_expt[max_only_CB_diversity,]$ss_res[[1]],
                              xlims = c(-7, -1))
```

```
## `summarise()` has grouped output by 'a', 'direction', 'var_type'. You can override using the `.groups
## `summarise()` has grouped output by 'a', 'direction', 'var_type'. You can override using the `.groups
```

```
p_overlay2
```

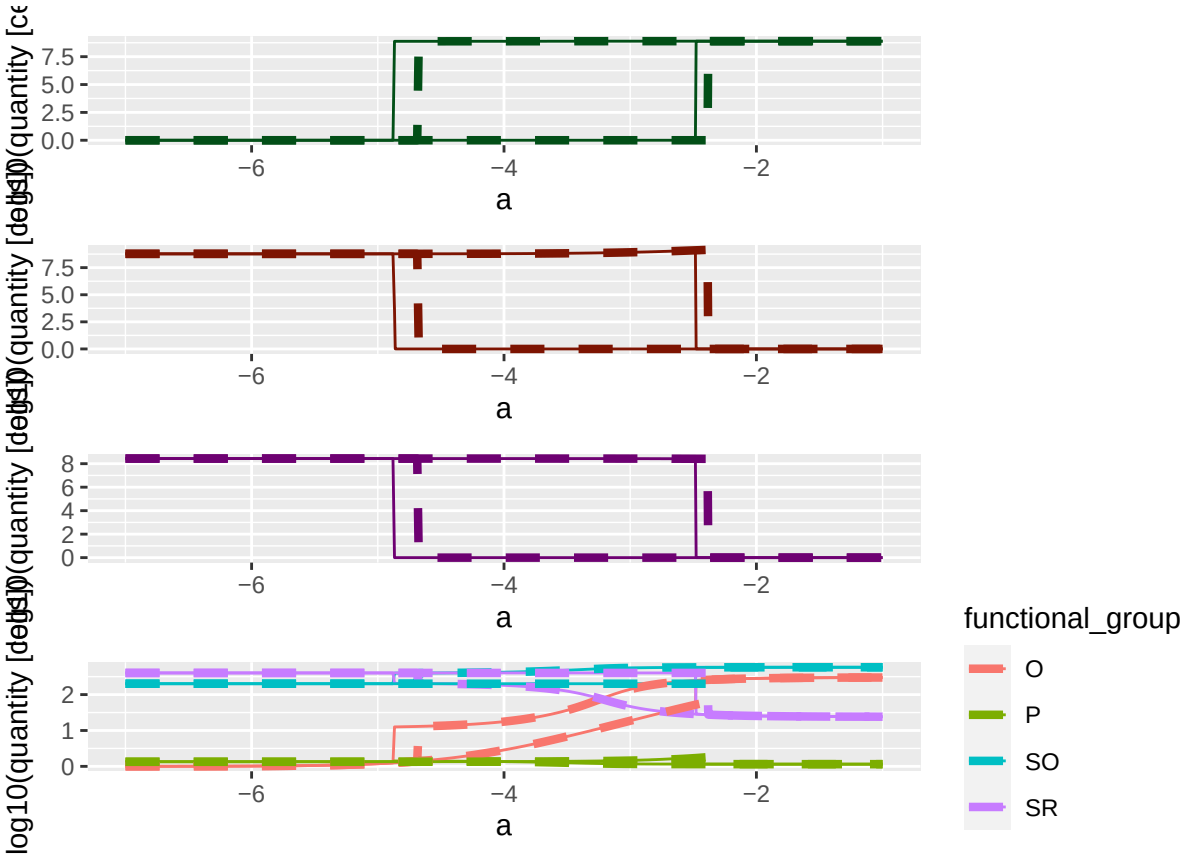



```
#ss_result1 <- var_expt[no_diversity,]$ss_res[[1]]
#ss_result2 <- var_expt[max_only_CB_diversity,]$ss_res[[1]]
```

```
p_overlay3 <- plot_ss_result2(var_expt[no_diversity,]$ss_res[[1]],
                              var_expt[max_only_SBPB_diversity,]$ss_res[[1]],
                              xlims = c(-7, -1))
```

```
## `summarise()` has grouped output by 'a', 'direction', 'var_type'. You can override using the `.groups
## `summarise()` has grouped output by 'a', 'direction', 'var_type'. You can override using the `.groups
```

```
p_overlay3
```




```
#ss_result3 <- var_expt[max_only_SBPB_diversity,]$ss_res[[1]]
```

Look at stability measures

```
stab_data1 <- readRDS(here("experiments/experiment 1/data/stab_data_1000000_20factorial.RDS"))
stab_data2 <- readRDS(here("experiments/experiment 1/data/stab_data_80000.RDS"))
stab_data <- bind_rows(stab_data1, stab_data2)

CB_vars <- unique(stab_data$CB_var_gmax_s)
SB_vars <- unique(stab_data$CB_var_gmax_s)

CB_stab_data <- stab_data %>%
  filter(SB_var_gmax_s == 0) %>%
  mutate(var_treat = "CB",
         var_gmax = CB_var_gmax_s)

SBPB_stab_data <- stab_data %>%
  filter(CB_var_gmax_s == 0) %>%
  mutate(var_treat = "SB-PB",
         var_gmax = SB_var_gmax_s)

for_join <- tibble(CB_var_gmax_s = CB_vars,
                   SB_var_gmax_s = SB_vars)
```

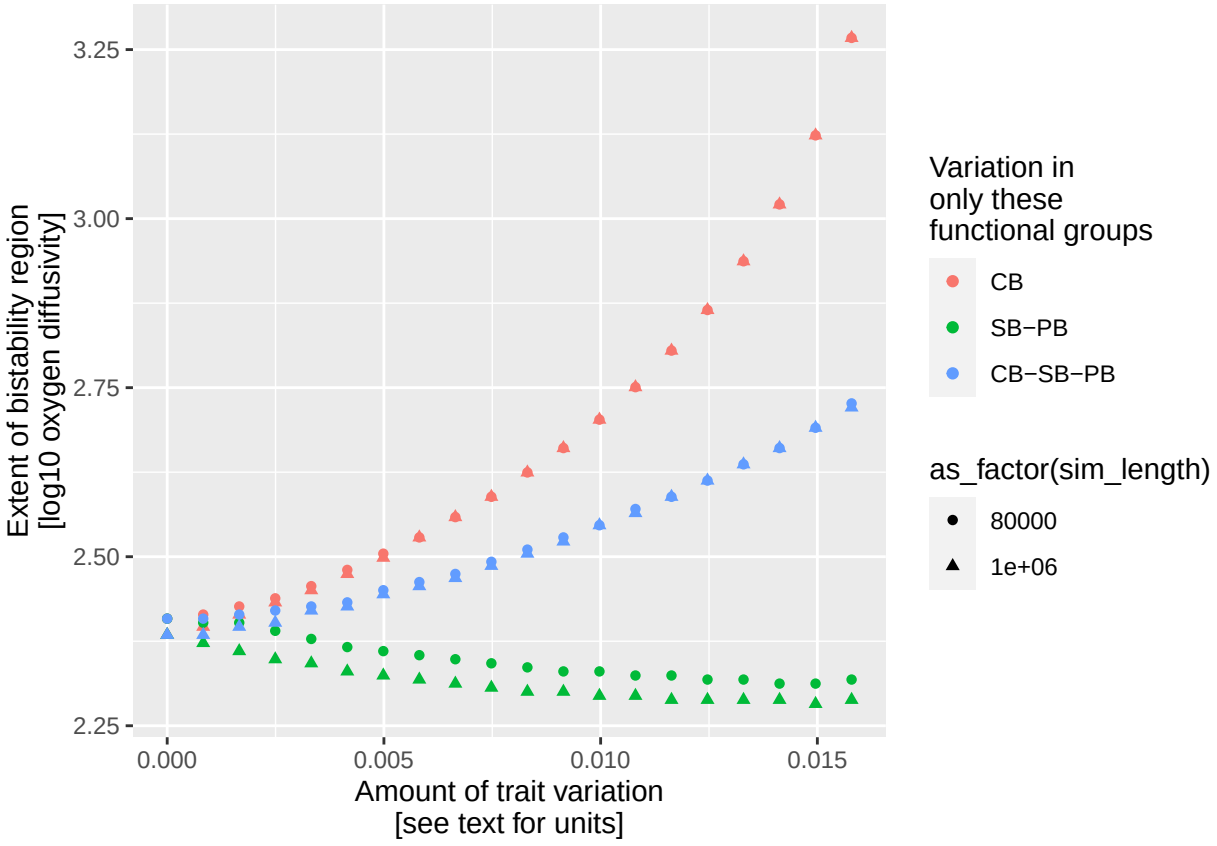
```
CBSBPB_stab_data <- stab_data %>%
  right_join(for_join) %>%
  mutate(var_treat = "CB-SB-PB",
         var_gmax = CB_var_gmax_s)
```

```
## Joining, by = c("CB_var_gmax_s", "SB_var_gmax_s")
```

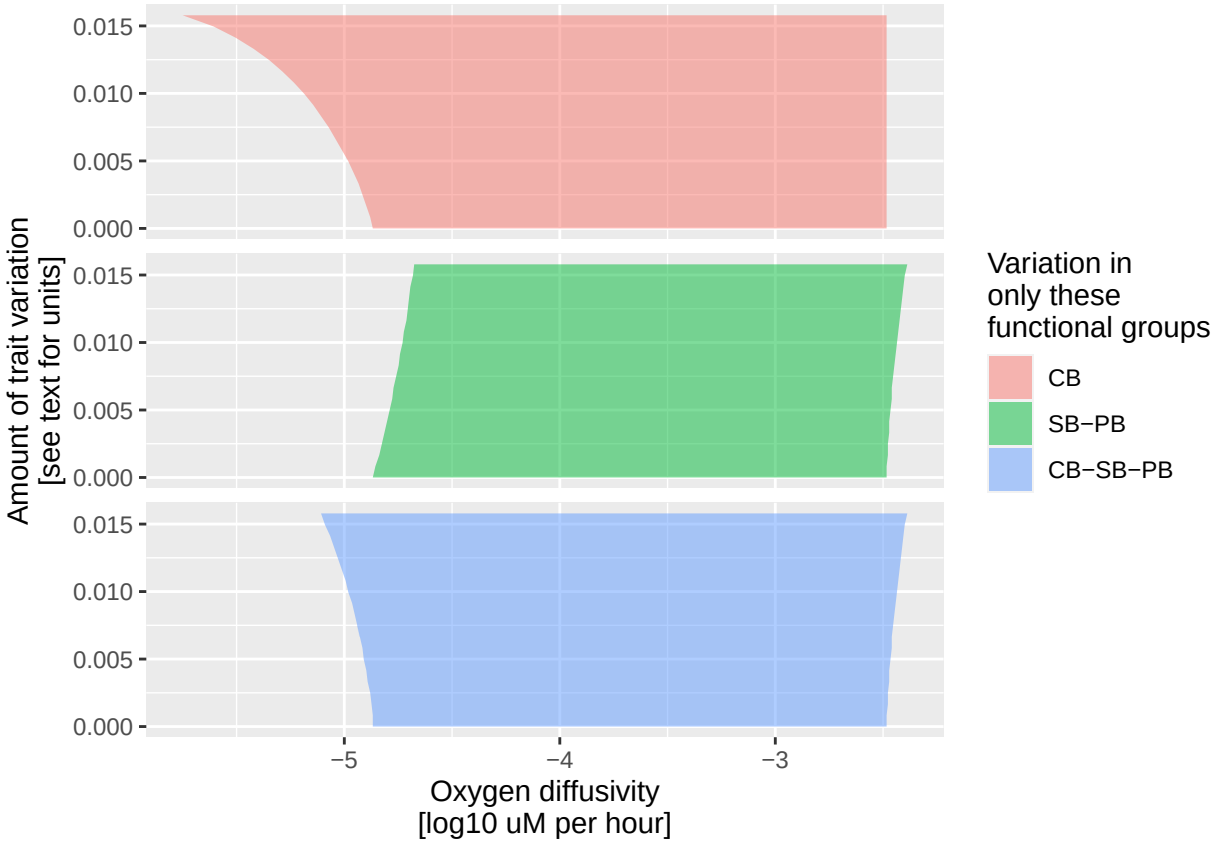
```
all_stab_results <- CB_stab_data %>%
  bind_rows(SBPB_stab_data) %>%
#  bind_rows(results3) %>%
 # bind_rows(results4) %>%
  bind_rows(CBSBPB_stab_data)

all_stab_results<- all_stab_results %>%
    mutate(var_treat = forcats::fct_relevel(var_treat, levels = c("CB", "SB-PB", "CB-SB-PB")))
```

```
## Warning: Outer names are only allowed for unnamed scalar atomic inputs
```

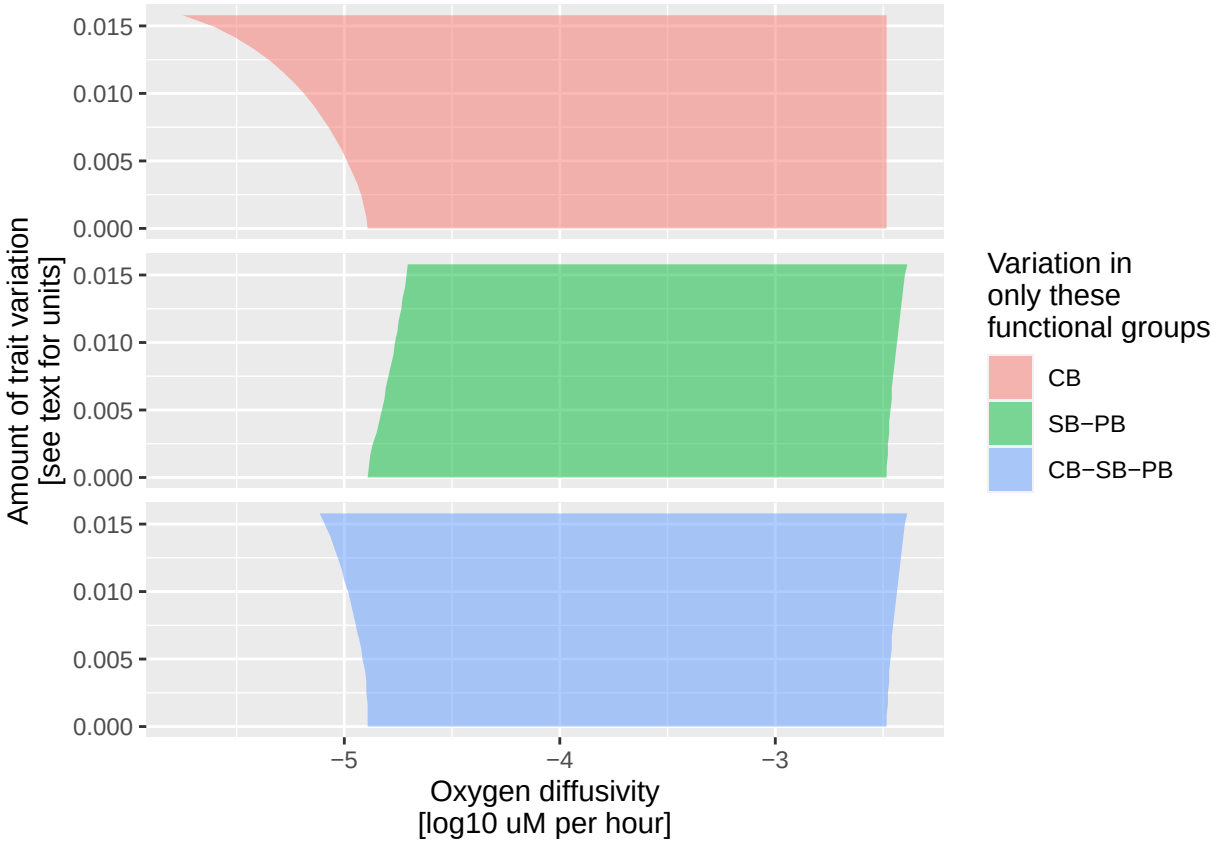
```
#saveRDS(all_stab_results, here("experiments/experiment summary/all_stab.RDS"))


#all_stab_results <- readRDS(here("experiments/experiment summary/all_stab.RDS"))

all_stab_results %>%
  filter(Species == "O") %>%
  ggplot(aes(x = var_gmax, y = hyst_range, col=var_treat, shape = as_factor(sim_length))) +
  geom_point() +
  xlab("Amount of trait variation\n[see text for units]") +
  ylab("Extent of bistability region\n[log10 oxygen diffusivity]") +
  labs(col = "Variation in\nonly these\nfunctional groups")
```




```
##ggsave("manuscript/figures/extent_of_bistab1.pdf", height = 4)

all_stab_results %>%
  #filter(var_treat == "CB") %>%
  filter(Species == "O",
         sim_length == 1e6) %>%
  ggplot(aes(x = var_gmax,
             ymin = hyst_min,
             ymax = hyst_max,
             fill=var_treat)) +
  geom_ribbon(alpha = 0.5) +
  facet_wrap( ~ var_treat, nrow = 3) +
  xlab("Amount of trait variation\n[see text for units]") +
  ylab("Oxygen diffusivity\n[log10 uM per hour]") +
  labs(fill = "Variation in\nonly these\nfunctional groups") +
  coord_flip() +
  theme(
    strip.background = element_blank(),
    strip.text.x = element_blank()
  )
```



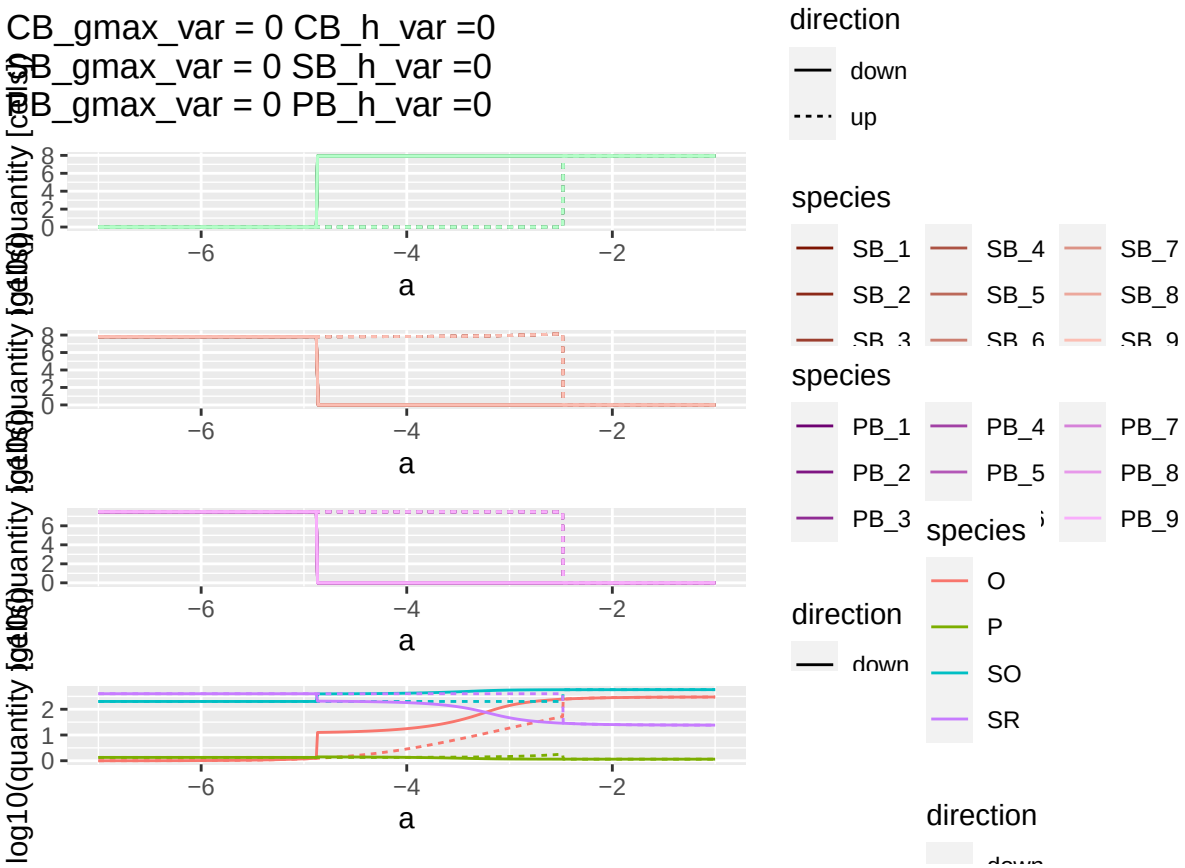

```
all_stab_results %>%
  #filter(var_treat == "CB") %>%
  filter(Species == "O",
         sim_length == 8e4) %>%
  ggplot(aes(x = var_gmax,
             ymin = hyst_min,
             ymax = hyst_max,
             fill=var_treat)) +
  geom_ribbon(alpha = 0.5) +
  facet_wrap( ~ var_treat, nrow = 3) +
  xlab("Amount of trait variation\n[see text for units]") +
  ylab("Oxygen diffusivity\n[log10 uM per hour]") +
  labs(fill = "Variation in\nonly these\nfunctional groups") +
  coord_flip() +
  theme(
    strip.background = element_blank(),
    strip.text.x = element_blank()
  )
```



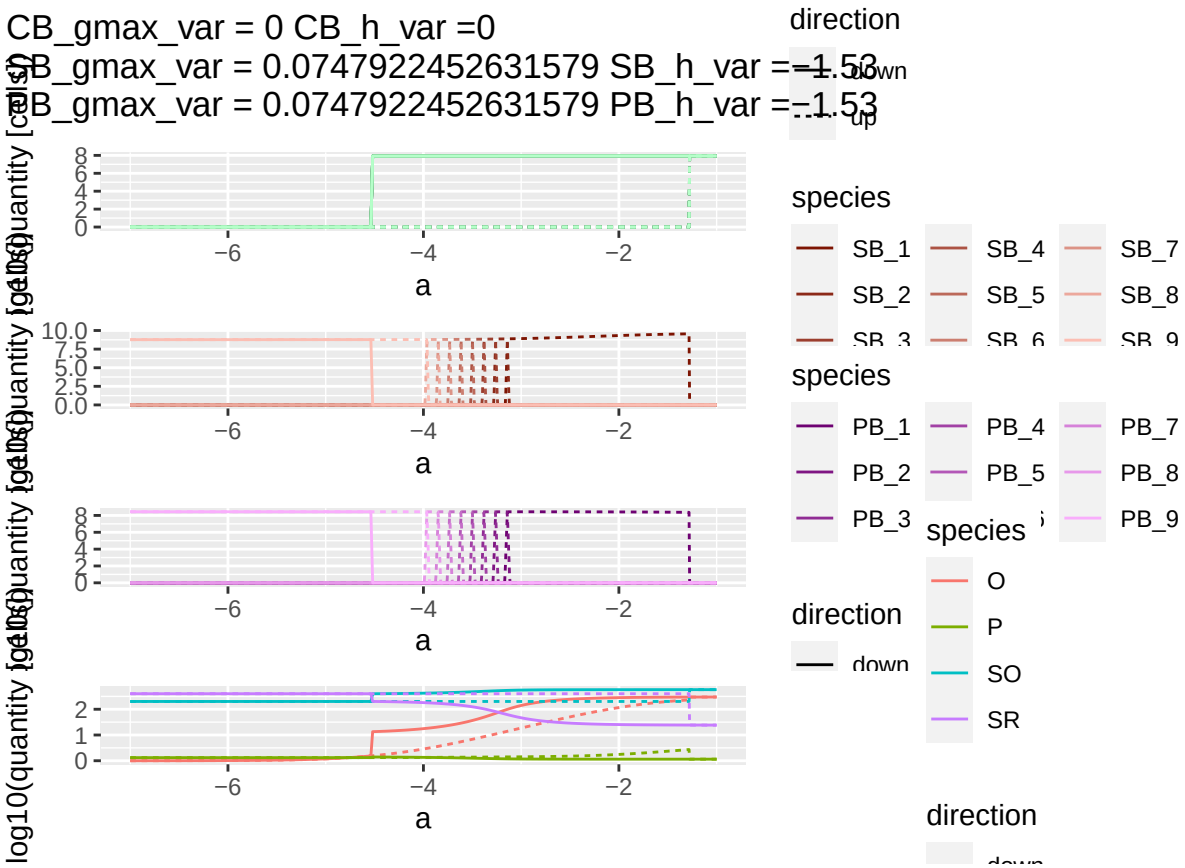

```
##ggsave("manuscript/figures/extent_of_bistab2.pdf", height = 4)
```

Extra SBPB diversity

```
var_expt_x <- readRDS(here("experiments/experiment 1/data/ss_data_1e6_noCB_5xSBPB_.RDS"))
stab_data_x <- readRDS(here("experiments/experiment 1/data/stab_data_1e6_noCB_5xSBPB_.RDS"))

p1  <- plot_ss_result1(var_expt_x,
                result_index = 1,
                filename_prefix = NULL,
                save_image_file = FALSE)
p1
```



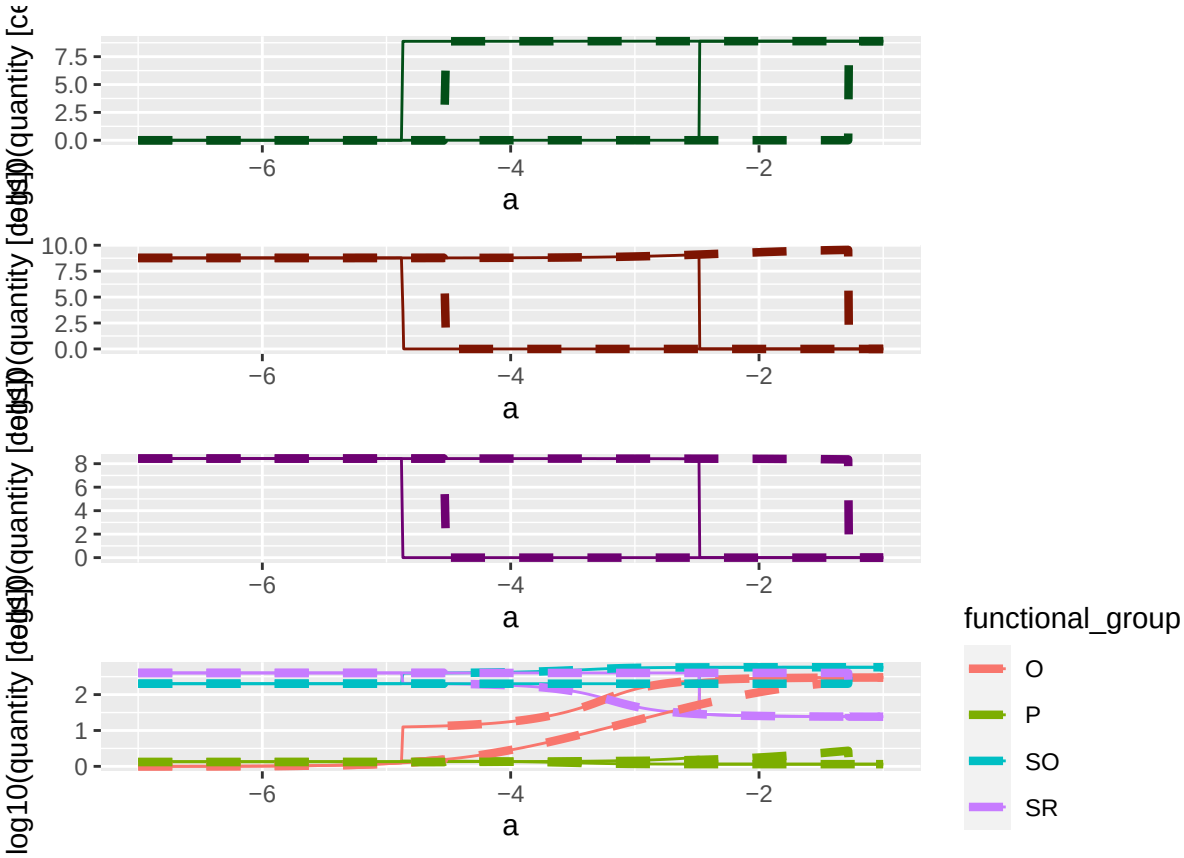

```
p1  <- plot_ss_result1(var_expt_x,
                result_index = 19,
                filename_prefix = NULL,
                save_image_file = FALSE)
p1
```



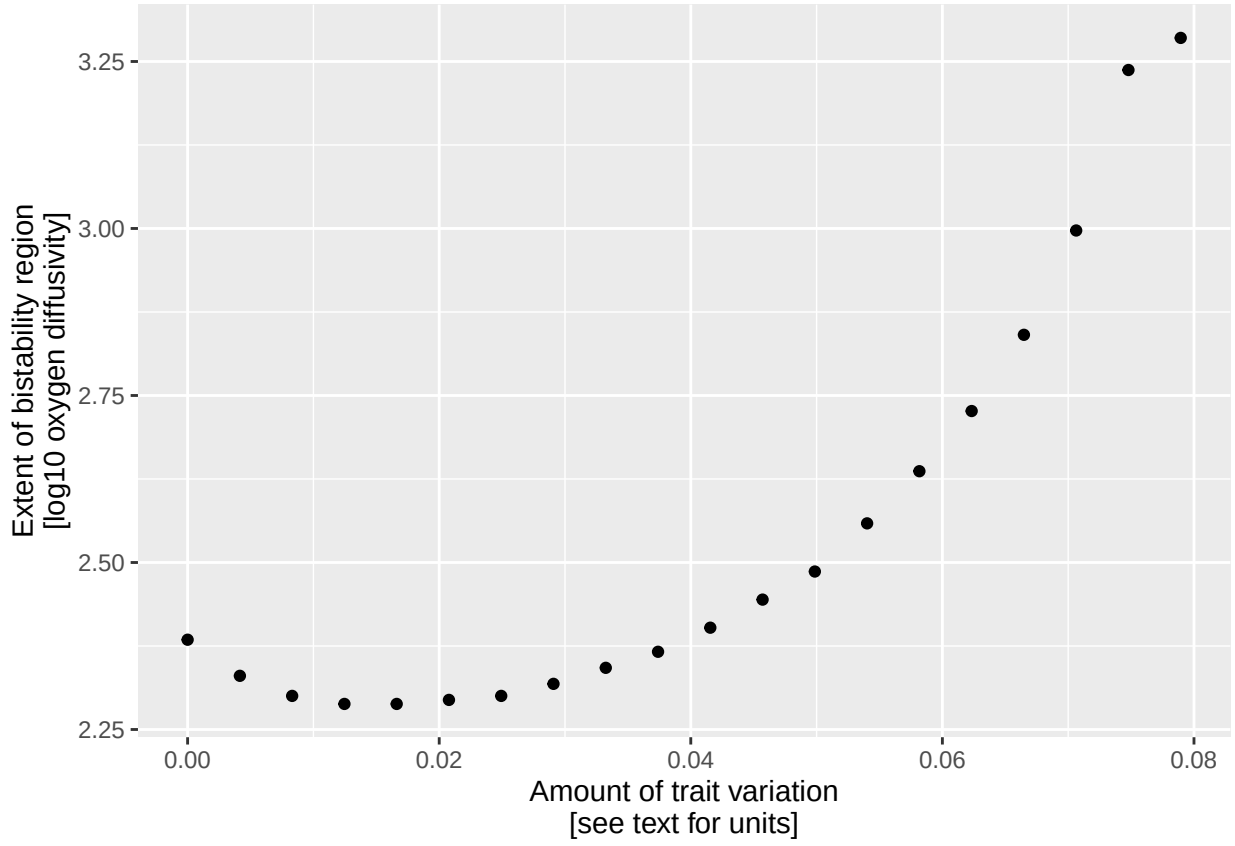

```
p_overlay1 <- plot_ss_result2(var_expt_x[1,]$ss_res[[1]],
                              var_expt_x[19,]$ss_res[[1]],
                              xlims = c(-7, -1))
```

```
## `summarise()` has grouped output by 'a', 'direction', 'var_type'. You can override using the `.groups
## `summarise()` has grouped output by 'a', 'direction', 'var_type'. You can override using the `.groups
```

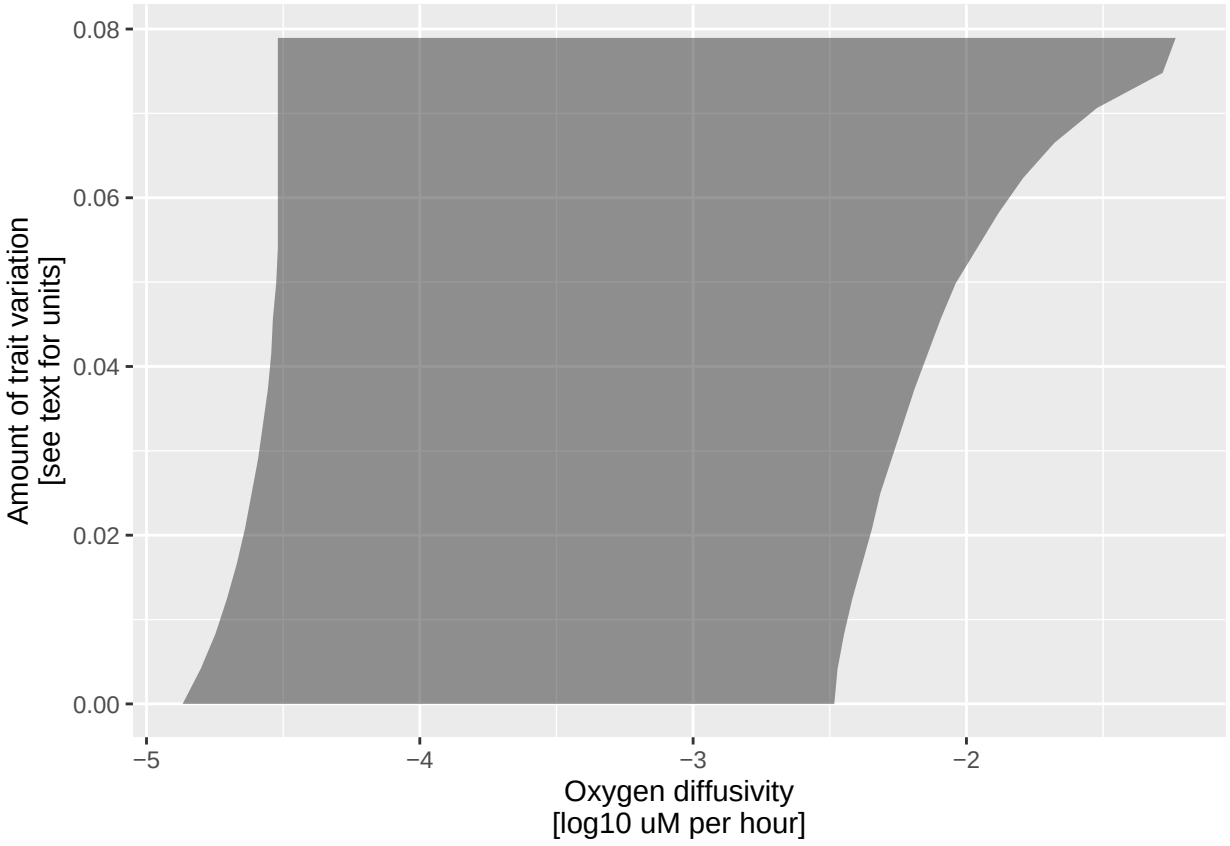
```
p_overlay1
```




```
stab_data_x %>%
  filter(Species == "O") %>%
  ggplot(aes(x = SB_var_gmax_s, y = hyst_range)) +
  geom_point() +
  xlab("Amount of trait variation\n[see text for units]") +
  ylab("Extent of bistability region\n[log10 oxygen diffusivity]") +
  labs(col = "Variation in\nonly these\nfunctional groups")
```

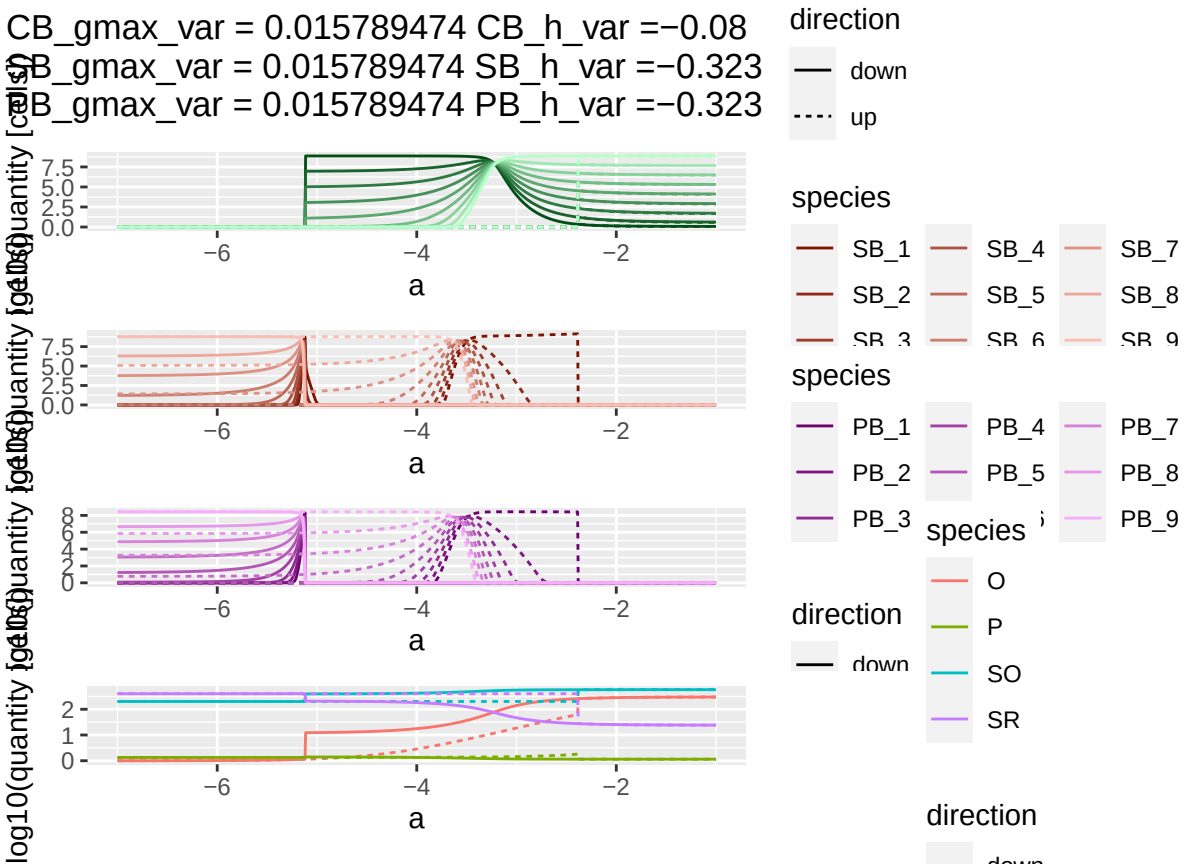



```
##ggsave("manuscript/figures/extent_of_bistab1.pdf", height = 4)

stab_data_x %>%
  #filter(var_treat == "CB") %>%
  filter(Species == "O") %>%
  ggplot(aes(x = SB_var_gmax_s,
             ymin = hyst_min,
             ymax = hyst_max)) +
  geom_ribbon(alpha = 0.5) +
  xlab("Amount of trait variation\n[see text for units]") +
  ylab("Oxygen diffusivity\n[log10 uM per hour]") +
  coord_flip() +
  theme(
    strip.background = element_blank(),
    strip.text.x = element_blank()
  )
```

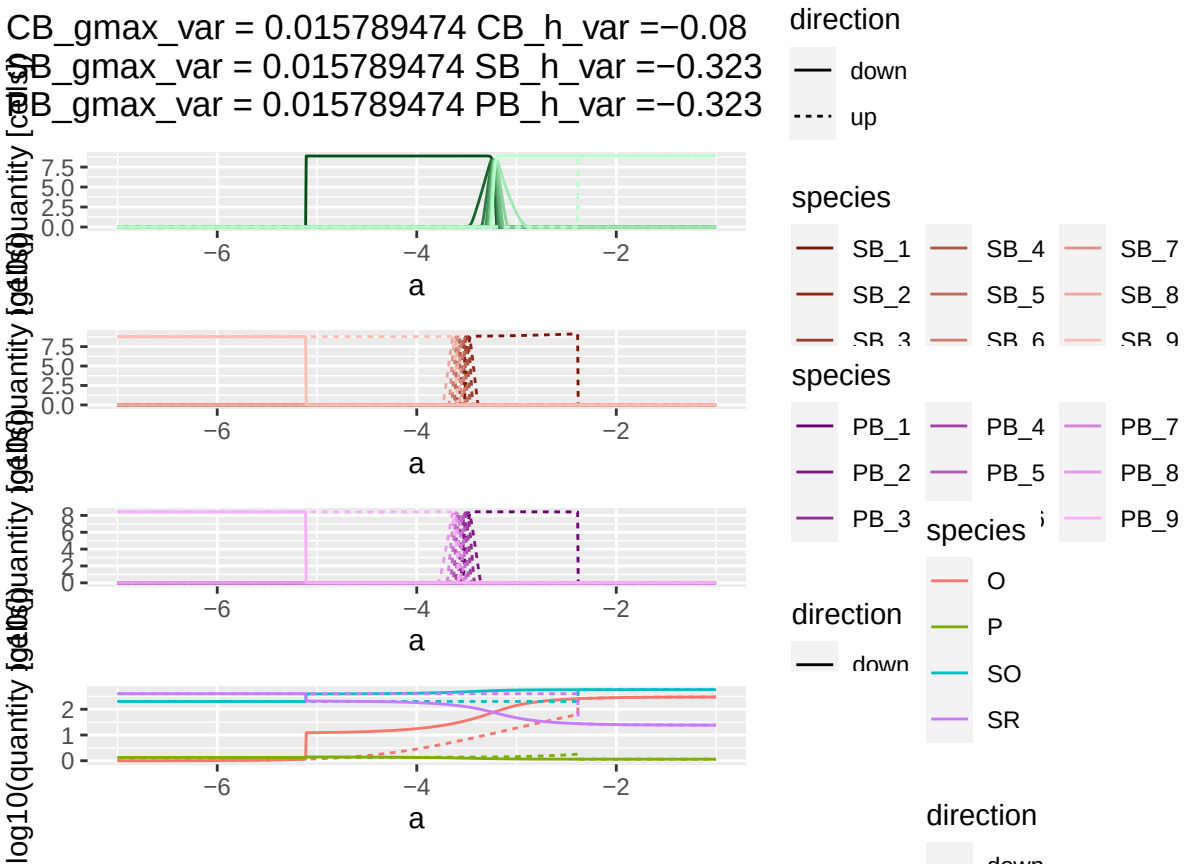


What effect of changing the length of the simulations

```
var_expt1 <- readRDS(here("experiments/experiment 1/data/ss_data_1000000_20factorial.RDS"))
var_expt2 <- readRDS(here("experiments/experiment 1/data/ss_data_80000.RDS"))

p1_short  <- plot_ss_result1(var_expt2,
                result_index = max_diversty_all,
                filename_prefix = NULL,
                save_image_file = FALSE)
p1_short
```




```
p1_long  <- plot_ss_result1(var_expt1,
                result_index = max_diversty_all,
                filename_prefix = NULL,
                save_image_file = FALSE)
p1_long
```



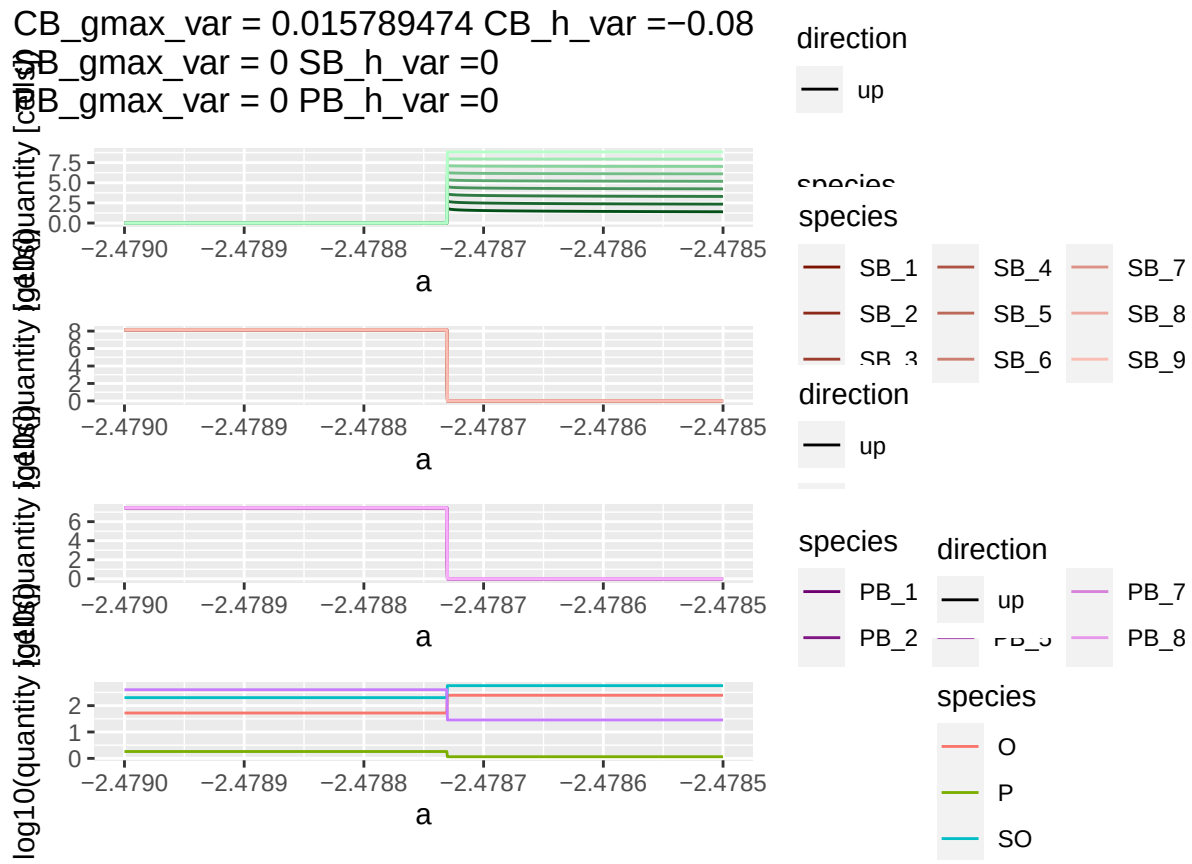
Zoom in on SS

```
a_Os <- 10^seq(-2.479, -2.4785, length=grid_num_a) ## sequence of a_O values
initial_CBs <- 1#10^seq(0, 0, length=grid_num_N) ## sequence of N values
initial_PBs <- 1e8 ## not varied
initial_SBs <- 1e8 ## not varied
# next line creates all possible combinations
ss_expt <- expand.grid(N_CB = initial_CBs,
                       N_PB = initial_PBs,
                       N_SB = initial_SBs,
                       a_O = a_Os)
var_expt_master <- var_expt
var_expt <- var_expt_master[381,]
```

```
#var_expt <- run_ss_var_experiment()
#saveRDS(var_expt, here("experiments/experiment 1/data/ss_data_zoom.RDS"))
```

```
library(here)
zoom <- readRDS(here("experiments/experiment 1/data/ss_data_zoom.RDS"))

p1  <- plot_ss_result1(zoom,
                result_index = 1,
```

```
                filename_prefix = NULL,
                save_image_file = FALSE)
p1
```



Negative abundance investigation

I (Owen) found that the sampling interval had an effect on the stability of the simulation. If the sampling interval was long, then in some rare cases (see below) the odesolver failed, with negative abundances occuring. I think this is due to abundances becoming very small, and then the computer having trouble with precision. I guess that when a sample is taken, the abundance is somehow altered if it is very low, probably by some rounding.

```
var_expt$pars[[1]]
dd <- var_expt$ss_res[[1]]
dd1 <- filter(dd, PB_1<(-0.0001))
dd1$a_0

ss_expt_master <- ss_expt
ss_expt <- ss_expt_master[abs(ss_expt_master$a_0 - 1.336984e-05)<1e-10,]

var_expt_master <- var_expt
#var_expt <- var_expt[1,]
var_expt_test <- run_ss_var_experiment()
```

```
res <- var_expt_test$ss_res[[1]]

test1 <- ss_by_a_N(ss_expt, var_expt$pars[[1]])
x <- ss_expt[2,]
param <- var_expt$pars[[1]]
get_final_states_a_N(x, param)
ssfind_parameters <- param
ssfind_simulation_sampling_interval <- 1000
## now run inside the function "get_final_states_a_N"
simres1 <- simres
ssfind_simulation_sampling_interval <- 5000
## now run inside the function "get_final_states_a_N"
simres2 <- simres  # this fails

## now run inside the function "get_final_states_a_N"
plot_dynamics(simres2)

ggplot() +
  geom_line(data = simres1$result,
            mapping = aes(x = time, y = log10(PB_1))) +
  geom_point(data = simres2$result,
            mapping = aes(x = time, y = log10(PB_1))) +
  xlim(c(0, 250000))

ccc <- simres2$result

simres2$result$PB_1
simres2$result$time


log10_a <- log10(ss_expt$a_0[1]) ## very slowly goes anoxic
#log10_a <- log10(a_Os[354]) ## very slowly goes anoxic
#log10_a <- log10(a_Os[356]) ## very very very  slowly goes anoxic
#log10_a <- log10(a_Os[357]) ## does not go anoxic



default_dynamic_model <- bushplus_dynamic_model
default_event_definition <- event_definition_1
default_event_interval <- ssfind_simulation_duration
default_noise_sigma <- 0
default_minimum_abundances <- ssfind_minimum_abundances
default_sim_duration <- ssfind_simulation_duration
default_sim_sample_interval <- ssfind_simulation_duration
#initial_pars_from <- "bush_ssfig3"


default_log10a_series <- c(log10_a, log10_a)
initial_state <- new_initial_state(num_CB_strains,
                                   num_PB_strains,
                                   num_SB_strains,
                                   values = "bush_ssfig3")
initial_state[grep("CB_", names(initial_state))] <- 10^10/num_CB_strains
```

```r
sim_res_novar <- run_simulation(parameter_values = var_expt$pars[[1]],
                          initial_state = initial_state)
plot_dynamics(sim_res_novar)

simulation_result <- sim_res_novar
every_n <- 1

chk <- sim_res_novar$result

sim_res_novar$result %>%
  ggplot() +
  geom_line(mapping = aes(x = time, y = PB_1))

#ggsave(here("simulations/expt2/figures/switching_novar.pdf"), width = 10)
```