9 strains

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This experiment supersedes 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

```r
# rm(list = ls())

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

microxanox_release <- "0.3.1"

#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)
```

```r
library(microxanox)
if (packageVersion("microxanox") < package_version("0.3.0")) {
  stop("microxanox version needs to be at least 0.3.0!")
}
library(tidyverse)
```

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


## v ggplot2 3.3.5     v purrr   0.3.4
## v tibble  3.1.4     v dplyr   1.0.7
## v tidyr   1.1.3     v stringr 1.4.0
## v readr   2.0.1     v forcats 0.5.1


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

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

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

```r
source(here("R/various_useful_functions.r"))
zero <- 0 ## don't change
unity <- 1 ## don't change!!!
options(mc.cores = 7)
eval_dynamics_flag <- FALSE
plot_ss_results <- TRUE
```

Version of `microxanox` package used: 0.3.1

General simulation conditions

```r
num_CB_strains <- 9
num_SB_strains <- 9
num_PB_strains <- 9

sp <- new_strain_parameter(
  n_CB = num_CB_strains,
  n_PB = num_SB_strains,
  n_SB = num_PB_strains,
  values_initial_state = "bush_ssfig3"
)

parameter <- new_runsim_parameter(
  dynamic_model = bushplus_dynamic_model,
  event_definition = event_definition_1,
  event_interval = 100,
```

```
  noise_sigma = 0,
  minimum_abundances = rep(1, 3),
  sim_duration = 2000,
  sim_sample_interval = 100,
  strain_parameter = sp,
  log10a_series = c(
    log10(sp$a_0),
    log10(sp$a_0)
  )
)
names(parameter$minimum_abundances) <- c("CB", "PB", "SB")
rm(sp)
```

Define diversity

```
## multiplier of SBPB variation
CB_var_multiplier <- 2
SBPB_var_multiplier <- 6


CB_gmax_div <- 0.015789474 * CB_var_multiplier
CB_h_div <- -0.08 * CB_var_multiplier
SB_gmax_div <- 0.015789474 * SBPB_var_multiplier
SB_h_div <- -0.323  * SBPB_var_multiplier
PB_gmax_div <- 0.015789474  * SBPB_var_multiplier
PB_h_div <- -0.323  * SBPB_var_multiplier


num_div_treatment_levels <- 20
```

Create diversity

```
var_expt <- create_diversity_factorial(
  zero = zero, unity = unity,
  num_div_treatment_levels = num_div_treatment_levels,
  CB_gmax_div = CB_gmax_div, CB_h_div = CB_h_div,
  SB_gmax_div = SB_gmax_div, SB_h_div = SB_h_div,
  PB_gmax_div = PB_gmax_div, PB_h_div = PB_h_div,
  default_9strain = new_strain_parameter(
    n_CB = num_CB_strains,
    n_SB = num_SB_strains,
    n_PB = num_PB_strains,
    values_initial_state =  "bush_ssfig3"
  )
)
```

Display diversity

```
display_diversity(
  400,
  var_expt = var_expt,
  num_CB_strains = num_CB_strains,
  num_SB_strains = num_SB_strains,
  num_PB_strains = num_PB_strains
)
```
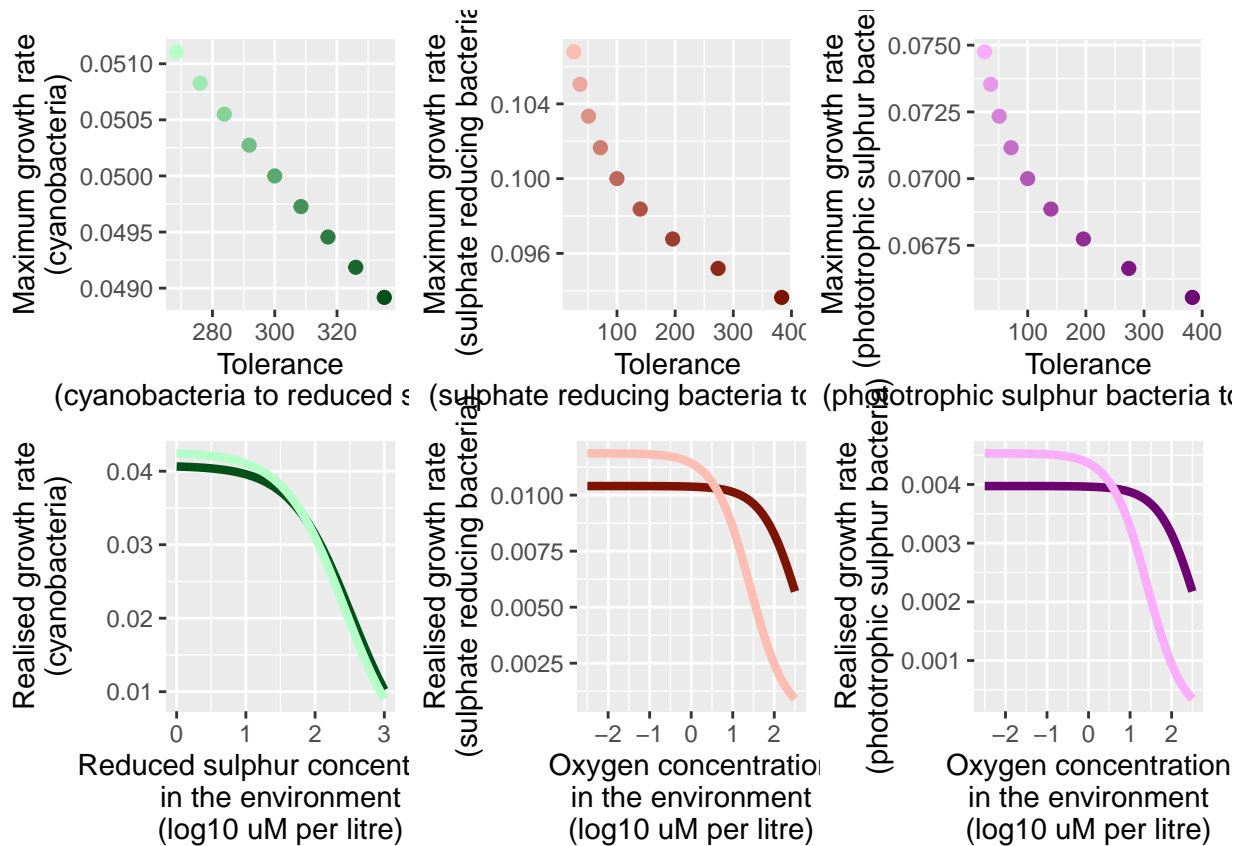

Temporal switching

```
## Here we get some rows of var_expt that correspond with particular diversity levels

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
)
```

4

```r
# 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,]

medium_diverity_varexp_row <- 311
```

Oxic to anoxic
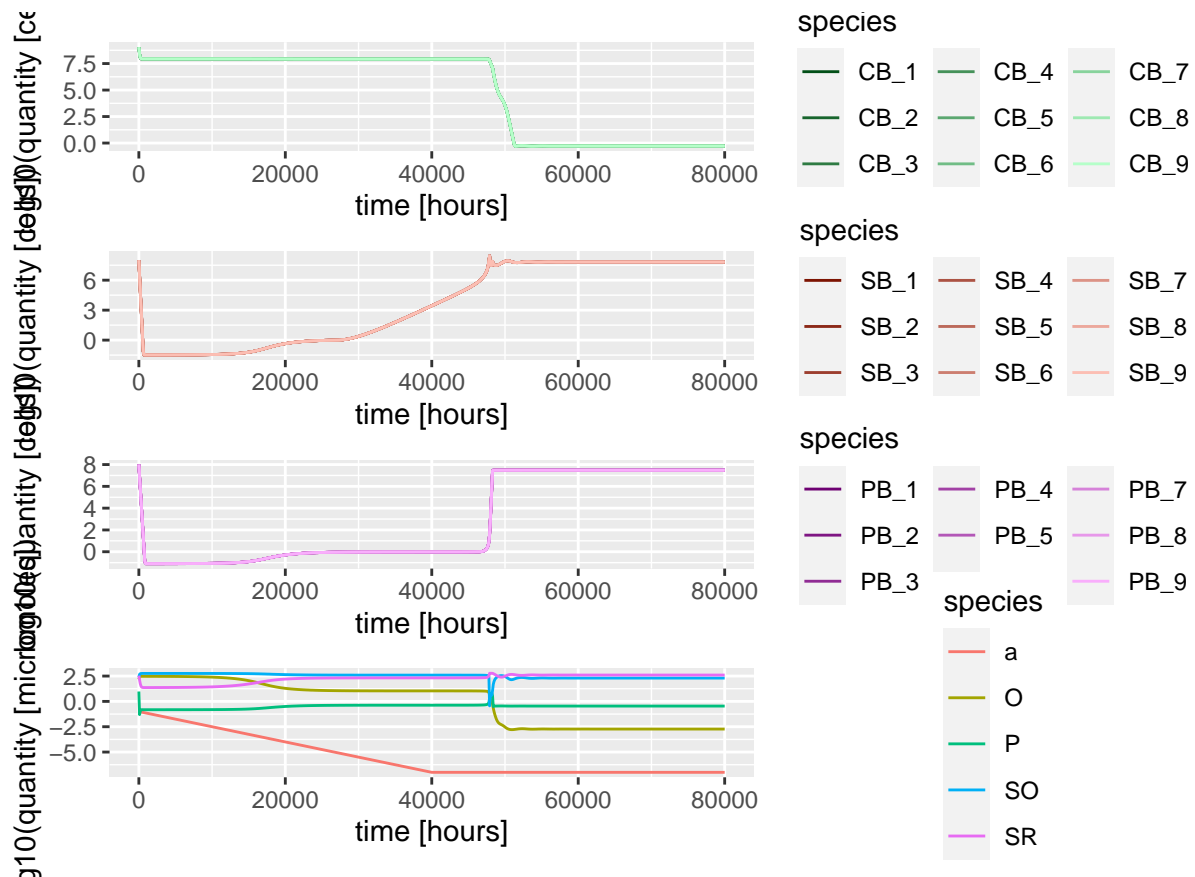
No diversity

```r
parameter$sim_duration <- 80000
```

```r
parameter$log10a_series <- c(-1, -7, -7)
parameter$strain_parameter <- var_expt$pars[[no_diversity]]
parameter$strain_parameter$initial_state <- new_initial_state(
  num_CB_strains,
  num_PB_strains,
  num_SB_strains,
  values = "bush_ssfig3"
)
parameter$strain_parameter$initial_state[grep("CB_", names(parameter$strain_parameter$initial_state))]
sim_res_novar1 <- run_simulation(parameter)
saveRDS(sim_res_novar1, here("experiments/9_strains/data/sim_res_novar1.RDS"))
```

```r
sim_res_novar1 <- readRDS(here("experiments/9_strains/data/sim_res_novar1.RDS"))
plot_dynamics(sim_res_novar1)
```
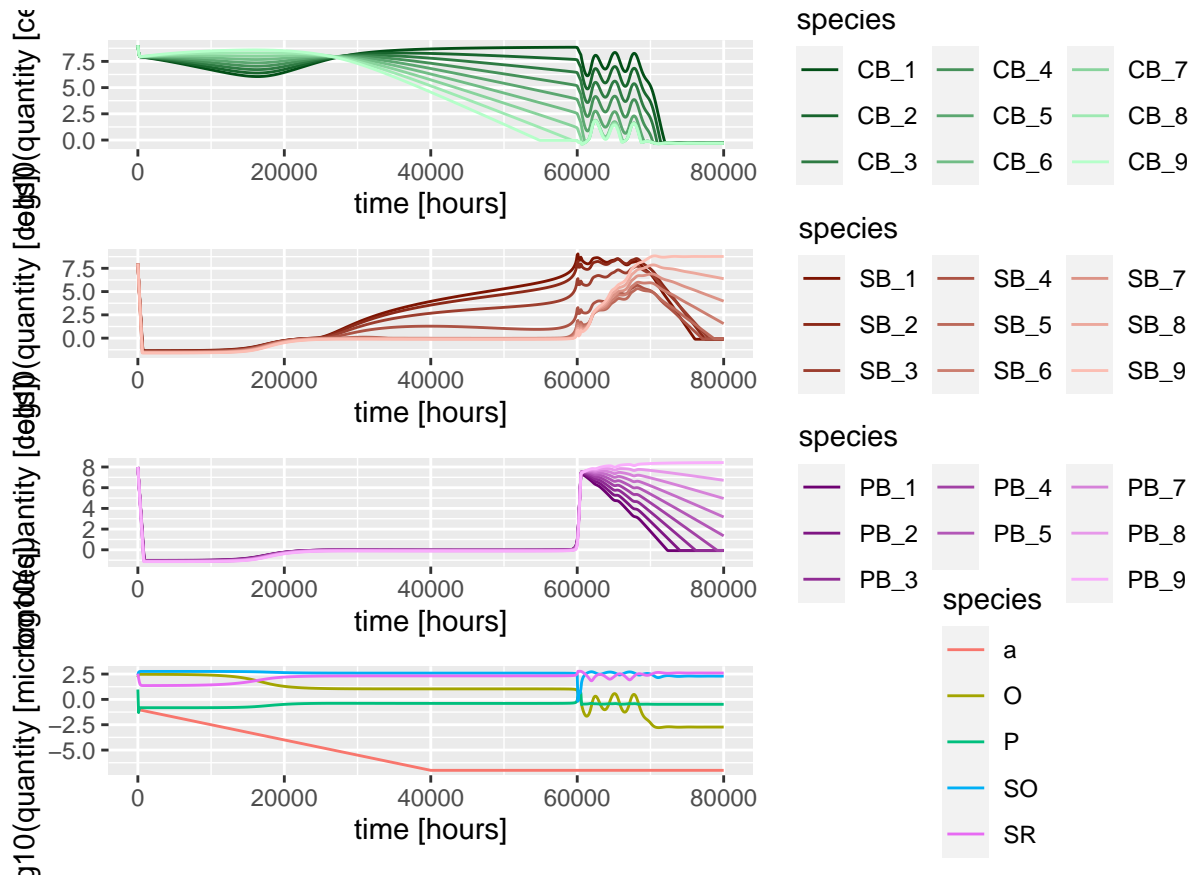
```
#ggsave(here("simulations/expt2/figures/switching_novar.pdf"), width = 10)
```

With diversity

```
parameter$strain_parameter <- var_expt$pars[[medium_diverity_varexp_row]]
parameter$strain_parameter$initial_state <- sim_res_novar1$strain_parameter$initial_state
sim_res_highvar1 <- run_simulation(parameter)
saveRDS(sim_res_highvar1, here("experiments/9_strains/data/sim_res_highvar1.RDS"))
```

```
sim_res_highvar1 <- readRDS(here("experiments/9_strains/data/sim_res_highvar1.RDS"))
plot_dynamics(sim_res_highvar1)
```

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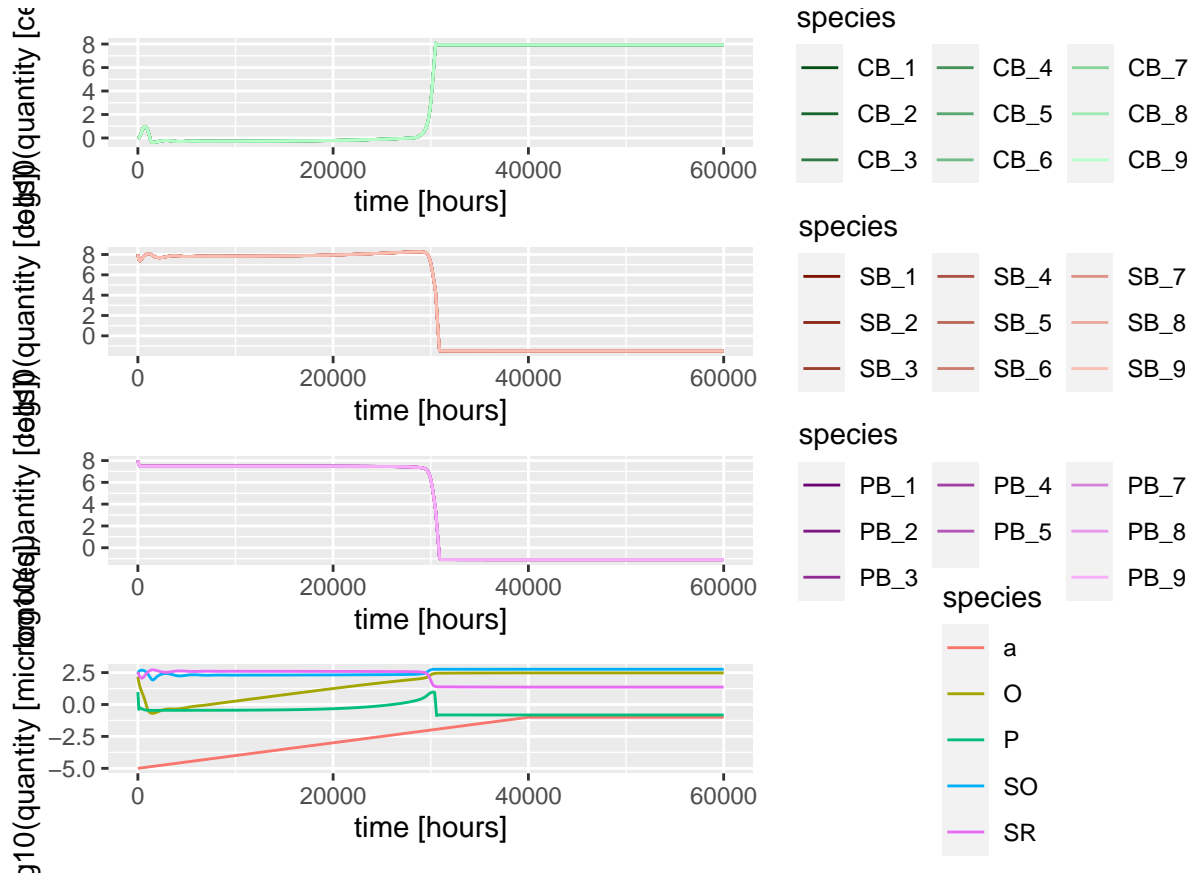
Anoxic to oxic

No diversity

```
parameter$sim_duration <- 60000
```

```
parameter$log10a_series <- c(-5, -3, -1, -1)
parameter$strain_parameter <- var_expt$pars[[no_diversity]]
parameter$strain_parameter$initial_state <- new_initial_state(
  num_CB_strains,
  num_PB_strains,
  num_SB_strains,
  values = "bush_ssfig3"
)
parameter$strain_parameter$initial_state[grep("CB_", names(parameter$strain_parameter$initial_state))] <-
sim_res_novar2 <- run_simulation(parameter)
saveRDS(sim_res_novar2, here("experiments/9_strains/data/sim_res_novar2.RDS"))
```

```
sim_res_novar2 <- readRDS(here("experiments/9_strains/data/sim_res_novar2.RDS"))
plot_dynamics(sim_res_novar2)
```
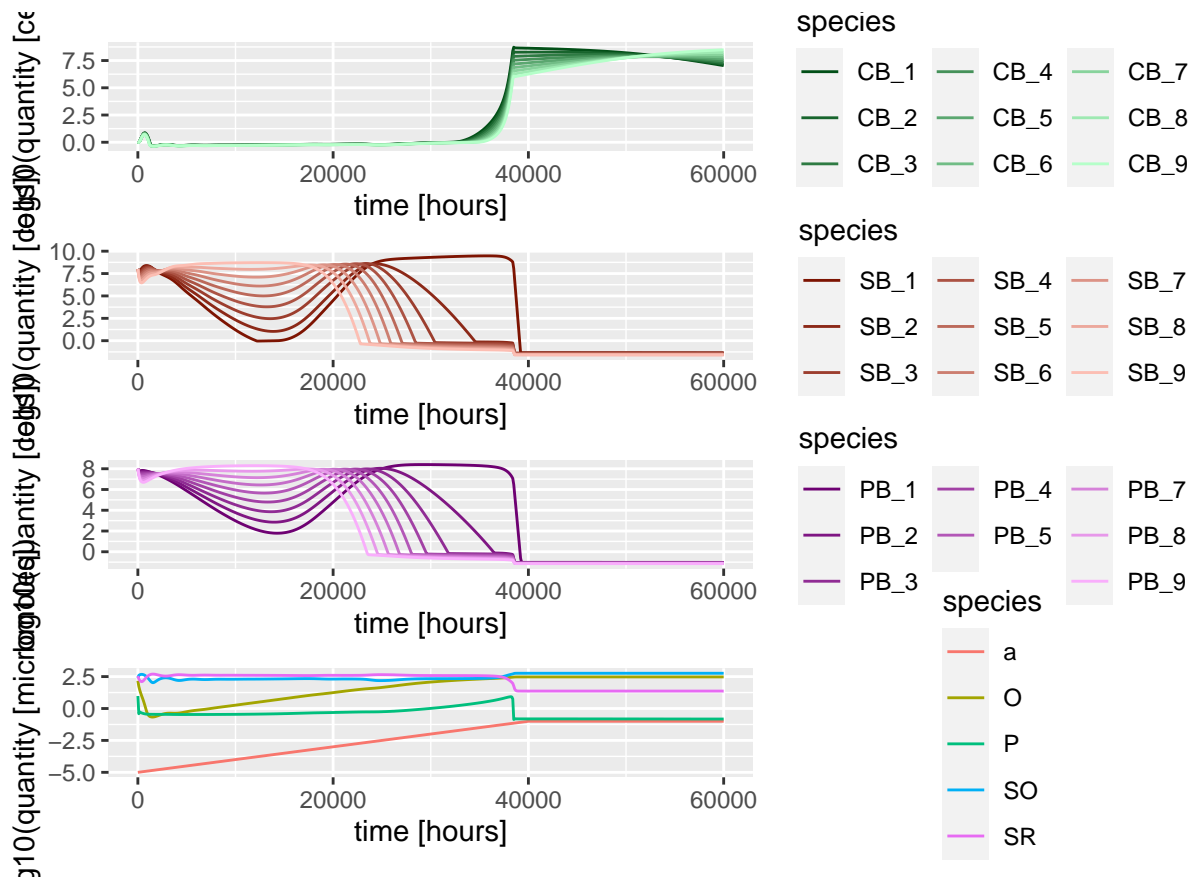
```
#ggsave(here("simulations/expt2/figures/switching_novar.pdf"), width = 10)
```

With diversity

```
parameter$strain_parameter <- var_expt$pars[[medium_diverity_varexp_row]]
parameter$strain_parameter$initial_state <- sim_res_novar2$strain_parameter$initial_state
sim_res_highvar2 <- run_simulation(parameter)
saveRDS(sim_res_highvar2, here("experiments/9_strains/data/sim_res_highvar2.RDS"))
```

```
sim_res_highvar2 <- readRDS(here("experiments/9_strains/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

```
parameter$sim_duration <- 1000000
```

```
parameter$minimum_abundances <- rep(100, 3)
names(parameter$minimum_abundances) <- c("CB", "PB", "SB")
```

```
parameter$log10a_series <- c(-1, -8, -1)
parameter$strain_parameter <- var_expt$pars[[no_diversity]]
parameter$strain_parameter$initial_state <- new_initial_state(
  num_CB_strains,
  num_PB_strains,
  num_SB_strains,
  values = "bush_ssfig3"
)
parameter$strain_parameter$initial_state[grep("CB_", names(parameter$strain_parameter$initial_state))] <-
sim_res_novar3 <- run_simulation(parameter)
saveRDS(sim_res_novar3, here("experiments/9_strains/data/sim_res_novar3.RDS"))
```

```
sim_res_novar3 <- readRDS(here("experiments/9_strains/data/sim_res_novar3.RDS"))
plot_dynamics(sim_res_novar3)
```
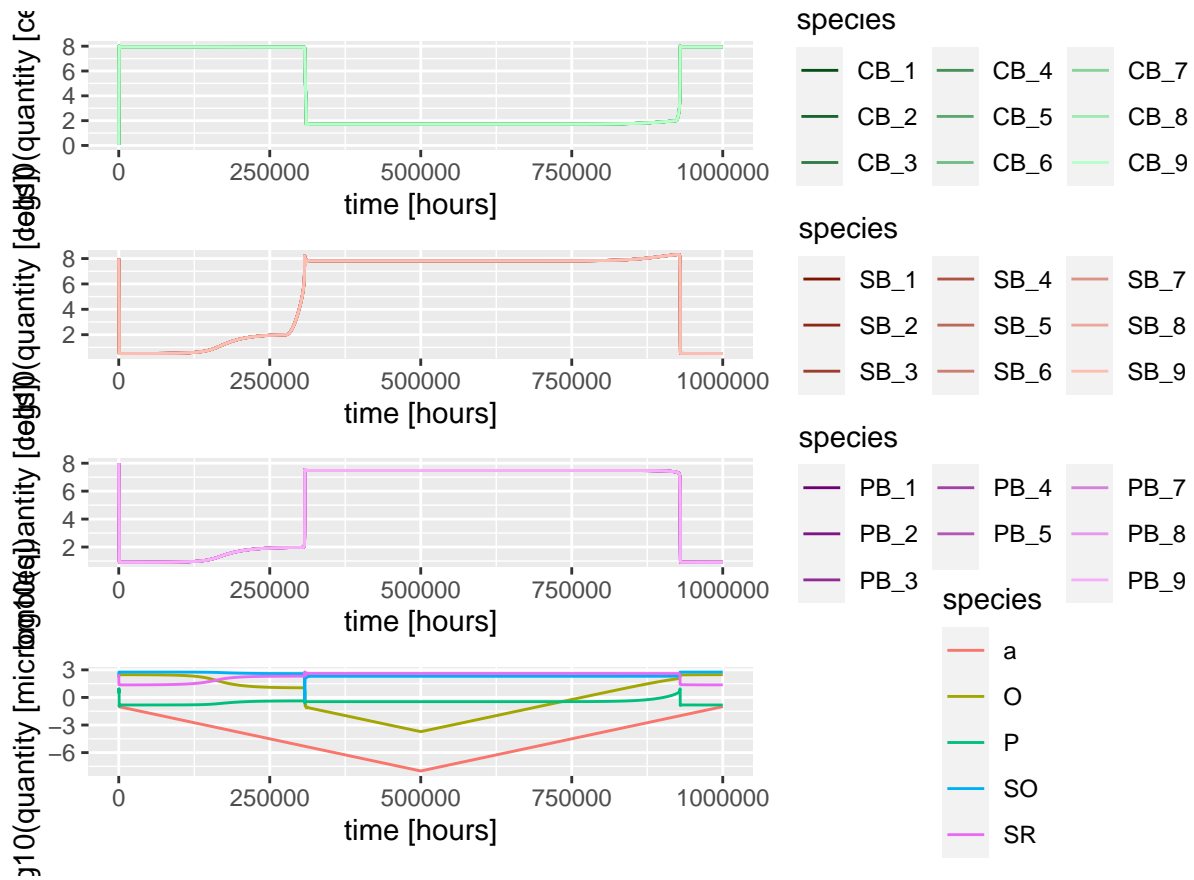
With diversity

```
parameter$strain_parameter <- var_expt$pars[[medium_diverity_varexp_row]]
parameter$strain_parameter$initial_state <- sim_res_novar3$strain_parameter$initial_state
sim_res_highvar3 <- run_simulation(parameter)
saveRDS(sim_res_highvar3, here("experiments/9_strains/data/sim_res_highvar3.RDS"))
```

```
sim_res_highvar3 <- readRDS(here("experiments/9_strains/data/sim_res_highvar3.RDS"))
plot_dynamics(sim_res_highvar3)
```
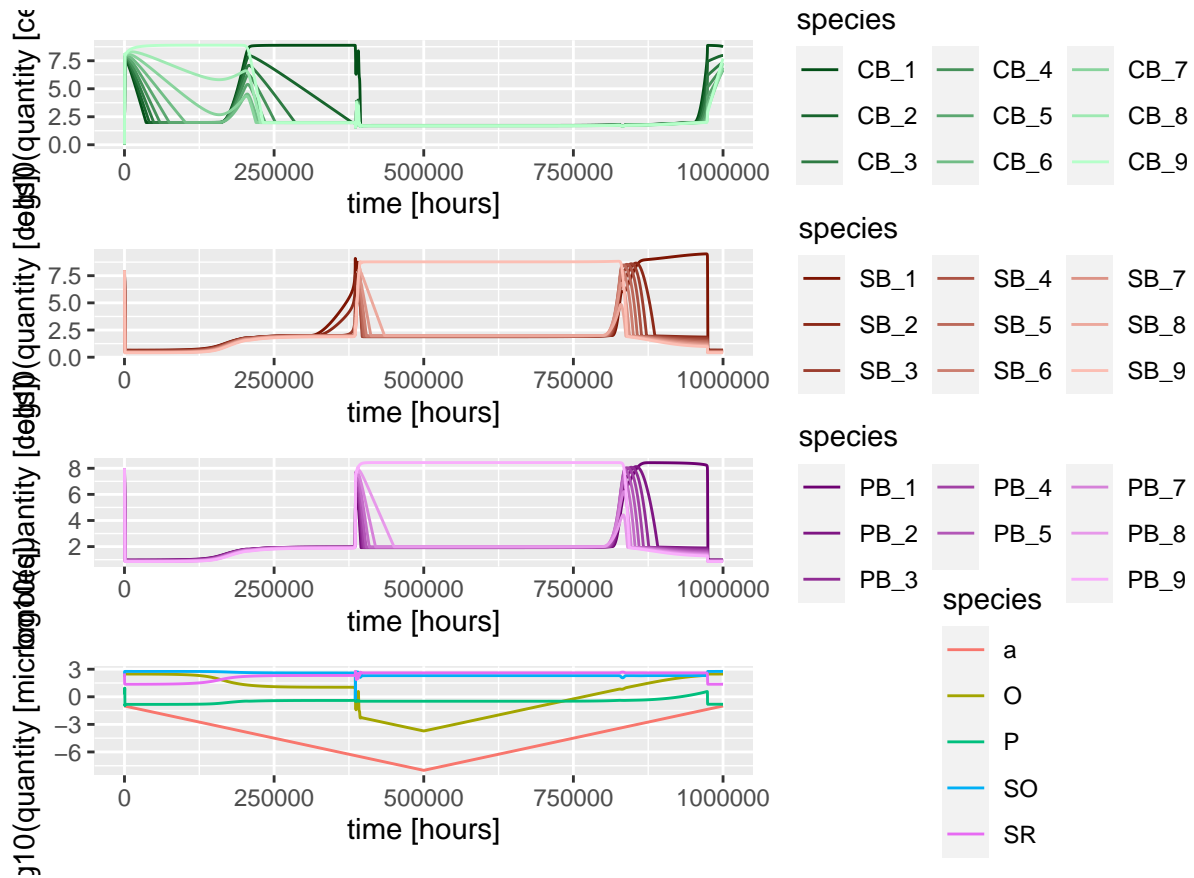
```
#ggsave(here("simulationsexpt2/figures/switching_highvar.pdf"), width = 10)
```

Ecosystem-environment relationship

Stable state finding

Finding

Setup parameter

```
options(mc.cores = 7)
```

```
minimum_abundances <- rep(0, 3)
names(minimum_abundances) <- c("CB", "PB", "SB")
```

```
grid_num_a <- 1000 #usually 1000 ## number of a_O values
#grid_num_a <- 10 ## FOR TEST
a_Os <- 10^seq(-8, 0, length=grid_num_a) ## sequence of a_O 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
```

```r
# 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)

parameter <- new_ss_by_a_N_parameter(
  dynamic_model = parameter$dynamic_model,
  event_definition = parameter$event_definition,
  event_interval = 1000000,
  noise_sigma = parameter$noise_sigma,
  minimum_abundances = minimum_abundances,
  sim_duration = 1000000,
  sim_sample_interval = 1000000,
  log10a_series = parameter$log10a_series,
  solver_method = parameter$solver_method,
  ss_expt = ss_expt
)
rm(minimum_abundances, grid_num_a, a_Os, grid_num_N, initial_CBs, initial_PBs, initial_SBs, ss_expt)

saveRDS(parameter, here("experiments/9_strains/data/parameter_1e6_x2x6_factorial.RDS"))
saveRDS(var_expt, here("experiments/9_strains/data/var_expt_1e6_x2x6_factorial.RDS"))
```

Run stable state finding

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

```r
run_ss_var_experiment(
  parameter = readRDS(here("experiments/9_strains/data/parameter_1e6_x2x6_factorial.RDS")),
  var_expt = readRDS(here("experiments/9_strains/data/var_expt_1e6_x2x6_factorial.RDS"))) %>%
saveRDS(here("experiments/9_strains/data/ss_data_1e6_x2x6_factorial.RDS"))
```

Process the stable state data

Bring in various stable state datasets

```r
cluster <- multidplyr::new_cluster(7)
multidplyr::cluster_library(cluster, c("microxanox", "dplyr"))

## sim length 1'000'000, 20 SBPBgrad, 2xCB variation, 6xSBPB variation
readRDS(here("experiments/9_strains/data/ss_data_1e6_x2x6_factorial_small.RDS")) %>%
  mutate(sim_length = 1000000) %>%
  multidplyr::partition(cluster) %>%
  mutate(stability_measures = list(get_stability_measures(ss_res))) %>%
  collect() %>%
  unnest(cols = c(stability_measures)) %>%
  saveRDS(here("experiments/9_strains/data/stab_data_1e6_x2x6_factorial_small.RDS"))

## find various combinations of diversity
var_expt <- readRDS(here("experiments/9_strains/data/ss_data_1e6_x2x6_factorial.RDS"))
#stab_data <- readRDS(here("experiments/9_strains/data/stab_data_1e6_x2x6_factorial.RDS"))
```

```r
#stab_data_smaller <- stab_data %>%
#  mutate(num_strains = 9) %>%
#  select(1:6, 11:25)
#saveRDS(stab_data_smaller, here("experiments/9_strains/data/small_stab_1e6_x2x6_factorial.RDS"))

#var_expt$pars

stab_data <- readRDS(here("experiments/9_strains/data/small_stab_data_1e6_x2x6_factorial.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,]

medium_diverity_varexp_row <- 311
```
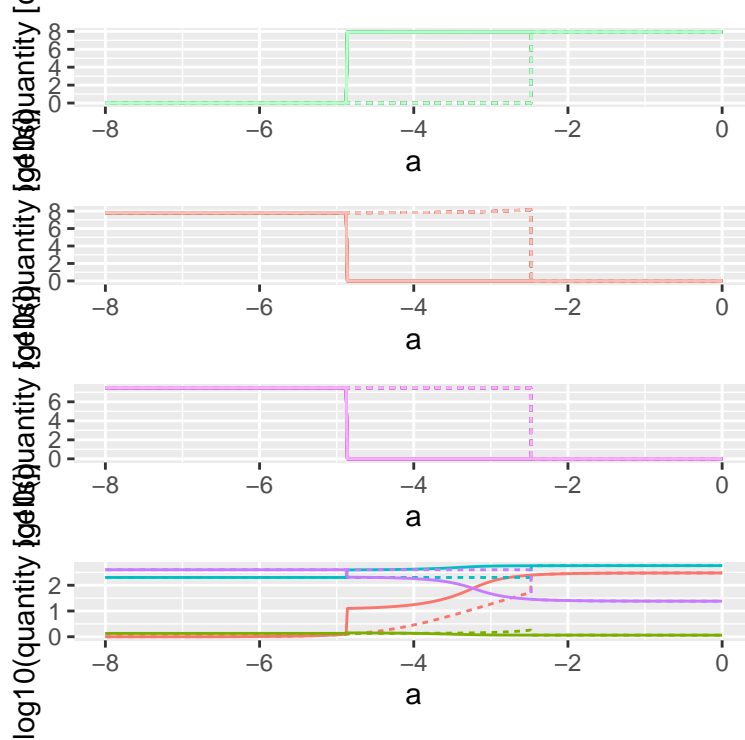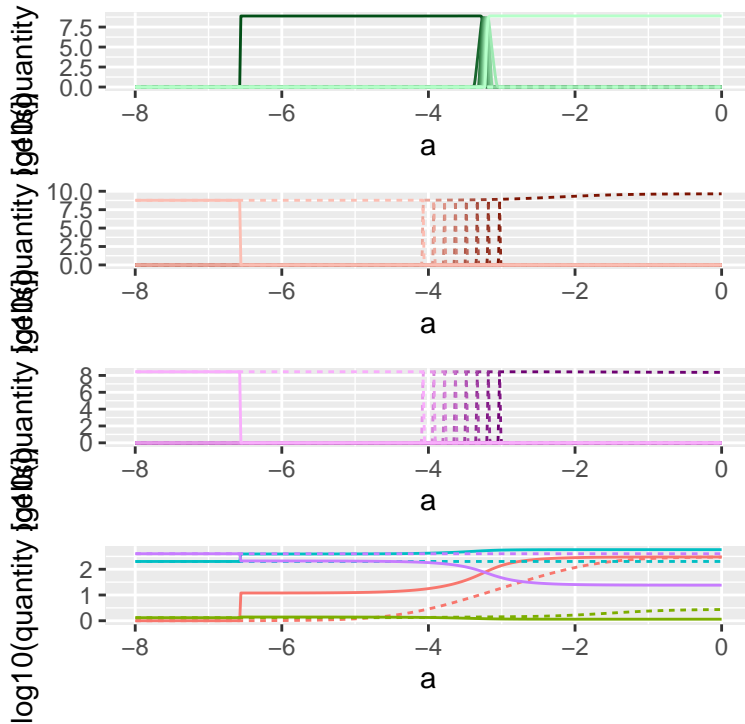
Display results

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

CB_gmax_var = 0 CB_h_var =0
SB_gmax_var = 0 SB_h_var =0
PB_gmax_var = 0 PB_h_var =0


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

CB_gmax_var = 0.031578948 CB_h_var =−0.16
SB_gmax_var = 0.094736844 SB_h_var =−1.938
PB_gmax_var = 0.094736844 PB_h_var =−1.938
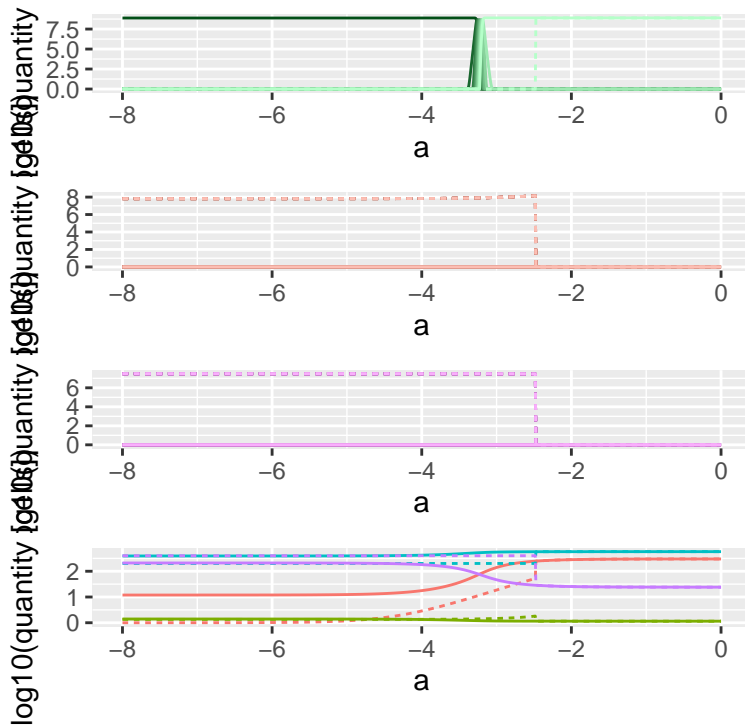


```
p3  <- plot_ss_result1(var_expt,
              result_index = max_only_CB_diversity,
              filename_prefix = NULL,
              save_image_file = FALSE)
p3
```

CB_gmax_var = 0.031578948 CB_h_var =−0.16
SB_gmax_var = 0 SB_h_var =0
PB_gmax_var = 0 PB_h_var =0
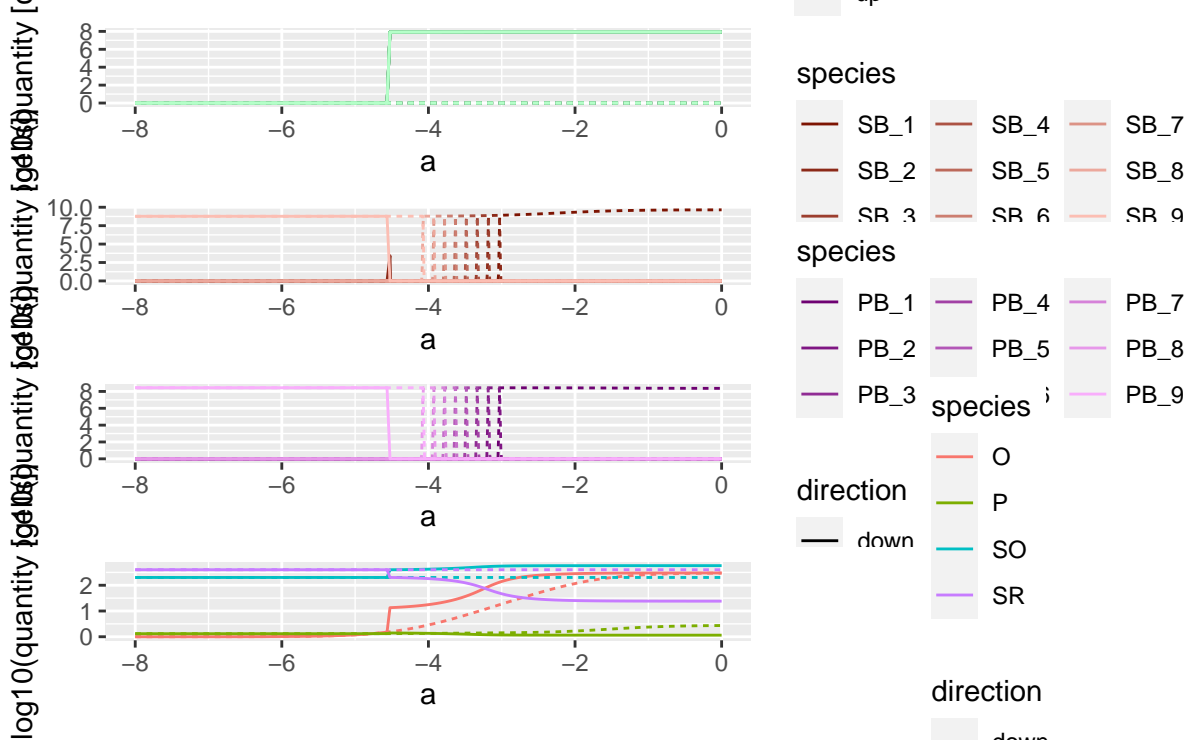
```
p4  <- plot_ss_result1(var_expt,
              result_index = max_only_SBPB_diversity,
              filename_prefix = NULL,
              save_image_file = FALSE)
p4
```

CB_gmax_var = 0 CB_h_var =0
SB_gmax_var = 0.094736844 SB_h_var =−1.938
PB_gmax_var = 0.094736844 PB_h_var =−1.938

direction
— down
.... up

species
— SB_1 — SB_4 — SB_7
— SB_2 — SB_5 — SB_8
— SB_3 — SB_6 — SB_9

species
— PB_1 — PB_4 — PB_7
— PB_2 — PB_5 — PB_8
— PB_3 — PB_9

species
— O
— P
— SO
— SR

direction
— down

```
p_overlay1 <- plot_ss_result2(var_expt[no_diversity,]$ss_res[[1]],
                              var_expt[max_diversty_all,]$ss_res[[1]],
                              xlims = c(-7, -1))
```
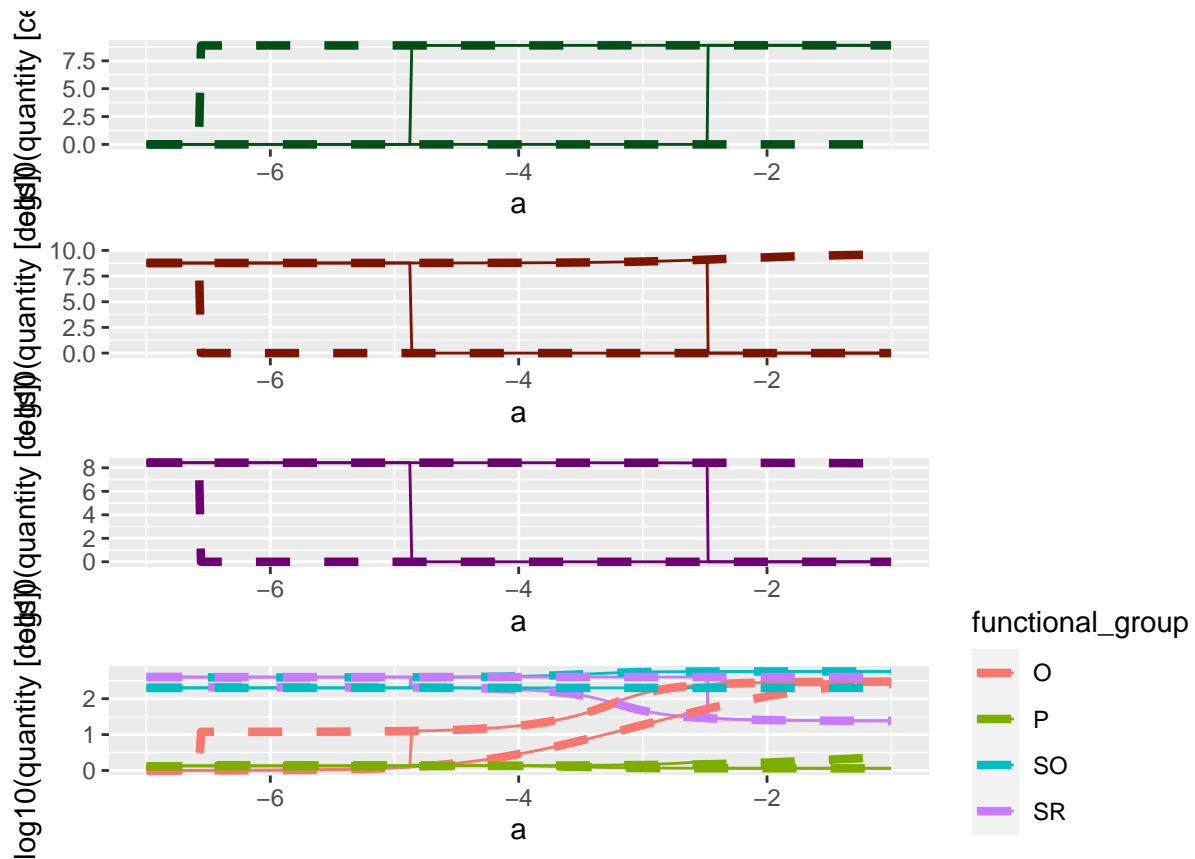
```
## 'summarise()' has grouped output by 'a', 'direction', 'var_type'. You can override using the '.groups
## 'summarise()' has grouped output by 'a', 'direction', 'var_type'. You can override using the '.groups
```

```
p_overlay1
```

```
## Warning: Removed 500 row(s) containing missing values (geom_path).
```

```
## Warning: Removed 420 row(s) containing missing values (geom_path).
```

```
## Warning: Removed 500 row(s) containing missing values (geom_path).
```

```
## Warning: Removed 420 row(s) containing missing values (geom_path).
```

```
## Warning: Removed 500 row(s) containing missing values (geom_path).
```

```
## Warning: Removed 420 row(s) containing missing values (geom_path).
```

```
## Warning: Removed 2000 row(s) containing missing values (geom_path).
```

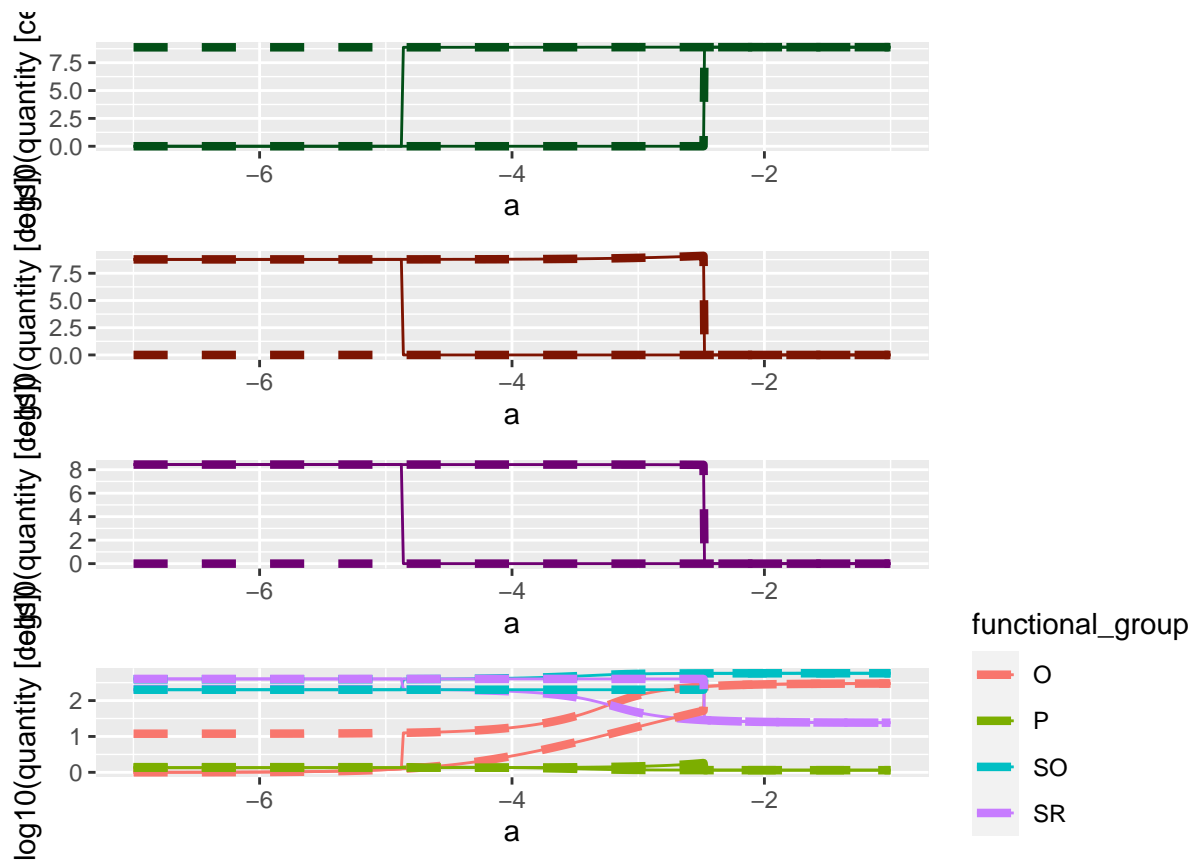## Warning: Removed 1680 row(s) containing missing values (geom_path).


```
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
```

Warning: Removed 500 row(s) containing missing values (geom_path).

Warning: Removed 500 row(s) containing missing values (geom_path).

Warning: Removed 500 row(s) containing missing values (geom_path).

Warning: Removed 500 row(s) containing missing values (geom_path).

Warning: Removed 500 row(s) containing missing values (geom_path).

Warning: Removed 500 row(s) containing missing values (geom_path).

Warning: Removed 2000 row(s) containing missing values (geom_path).

Warning: Removed 2000 row(s) containing missing values (geom_path).

18
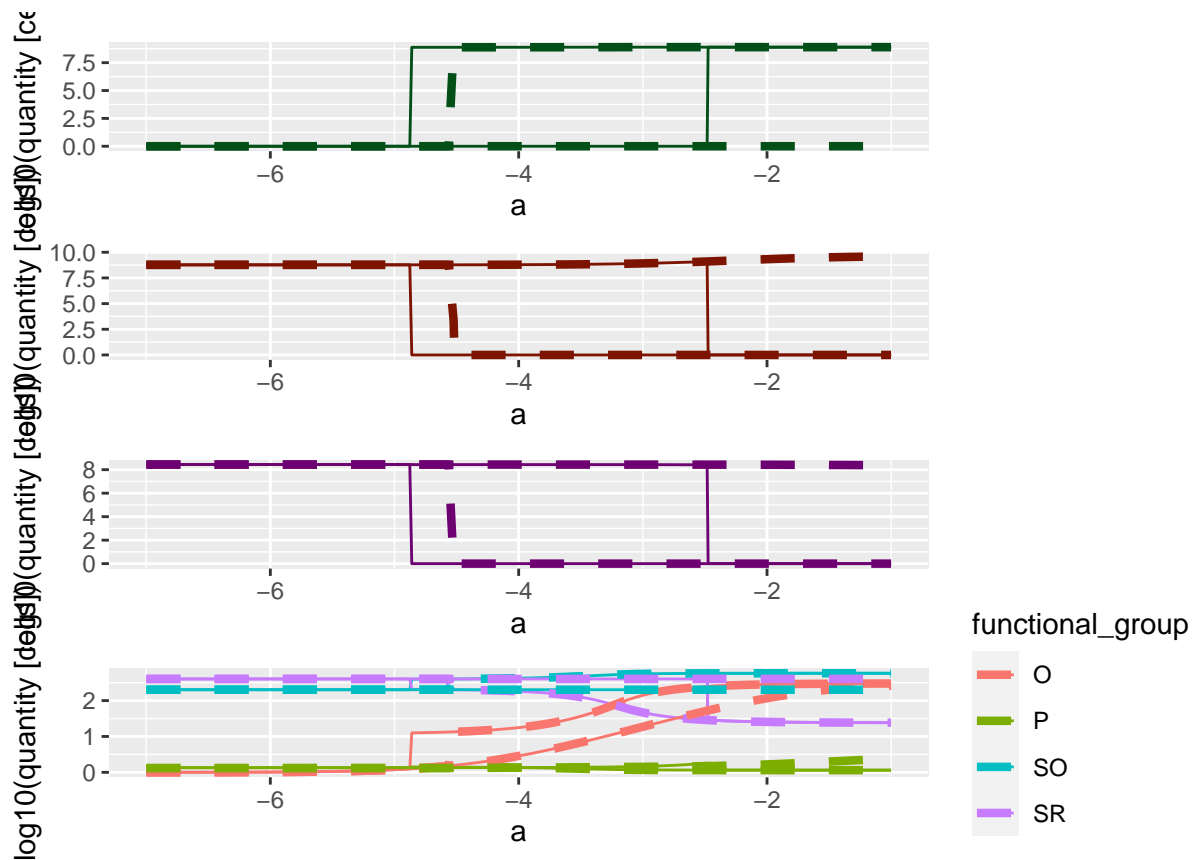
```
p_overlay3 <- plot_ss_result2(var_expt[no_diversity,]$ss_res[[1]],
                              var_expt[max_only_SBPB_diversity,]$ss_res[[1]],
                              xlims = c(-7, -1))
```

```
## '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
```

```
## Warning: Removed 500 row(s) containing missing values (geom_path).

## Warning: Removed 500 row(s) containing missing values (geom_path).

## Warning: Removed 500 row(s) containing missing values (geom_path).

## Warning: Removed 500 row(s) containing missing values (geom_path).

## Warning: Removed 500 row(s) containing missing values (geom_path).

## Warning: Removed 500 row(s) containing missing values (geom_path).

## Warning: Removed 2000 row(s) containing missing values (geom_path).

## Warning: Removed 2000 row(s) containing missing values (geom_path).
```

```
p_overlay4 <- plot_ss_result2(var_expt[no_diversity,]$ss_res[[1]],
                              var_expt[medium_diverity_varexp_row,]$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_overlay4
```

Warning: Removed 500 row(s) containing missing values (geom_path).

Warning: Removed 500 row(s) containing missing values (geom_path).

Warning: Removed 500 row(s) containing missing values (geom_path).

Warning: Removed 500 row(s) containing missing values (geom_path).

Warning: Removed 500 row(s) containing missing values (geom_path).

Warning: Removed 500 row(s) containing missing values (geom_path).

Warning: Removed 2000 row(s) containing missing values (geom_path).

## Warning: Removed 2000 row(s) containing missing values (geom_path).
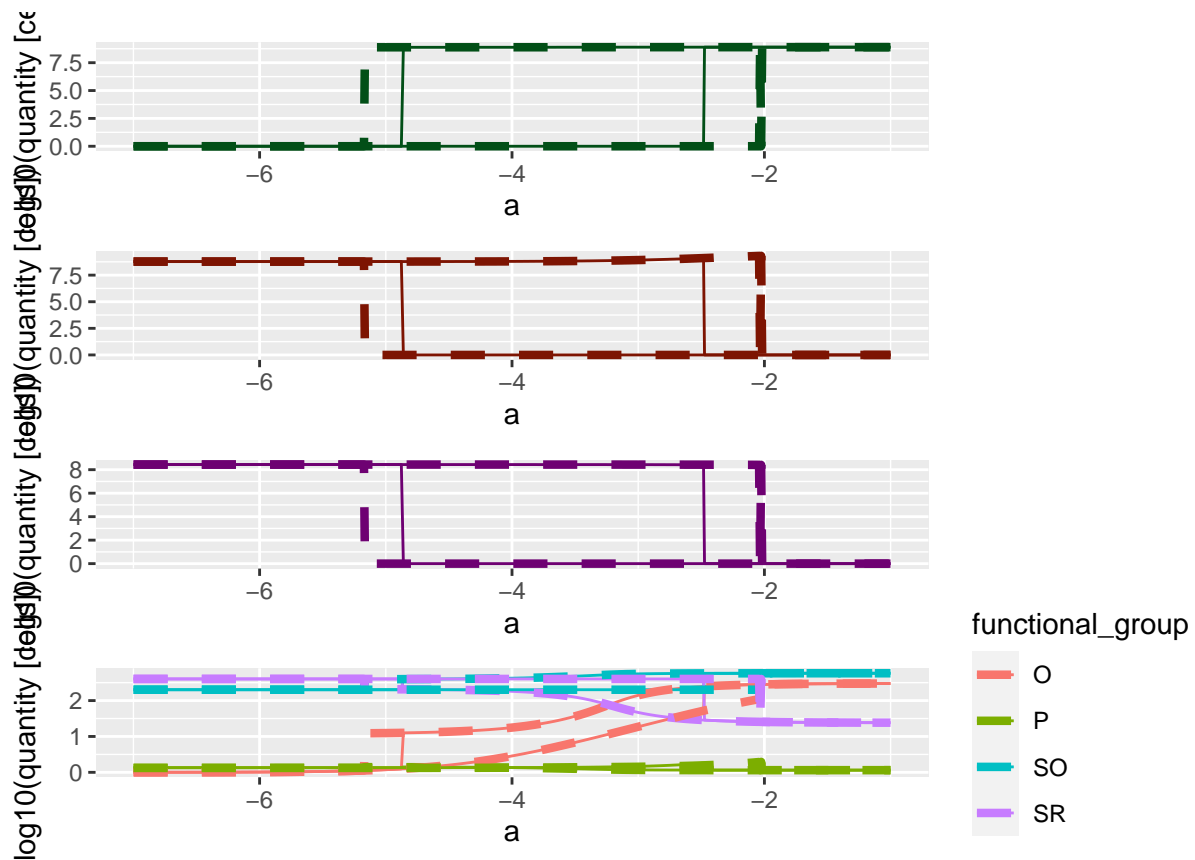
```
tempp1 <- var_expt[no_diversity,]$ss_res[[1]] %>%
  filter(initial_N_CB == 1e10,
         log10(a_O) > -4.5, log10(a_O) < -4)
tempp2 <- var_expt[max_only_SBPB_diversity,]$ss_res[[1]] %>%
  filter(initial_N_CB == 1e10,
         log10(a_O) > -4.5, log10(a_O) < -4)

ggplot() +
  geom_line(mapping = aes(x = log10(tempp1$a_O),
                          y = log10(tempp1$O))) +
  geom_line(mapping = aes(x = log10(tempp2$a_O),
                          y = log10(tempp2$O)),
            col = "blue")
```
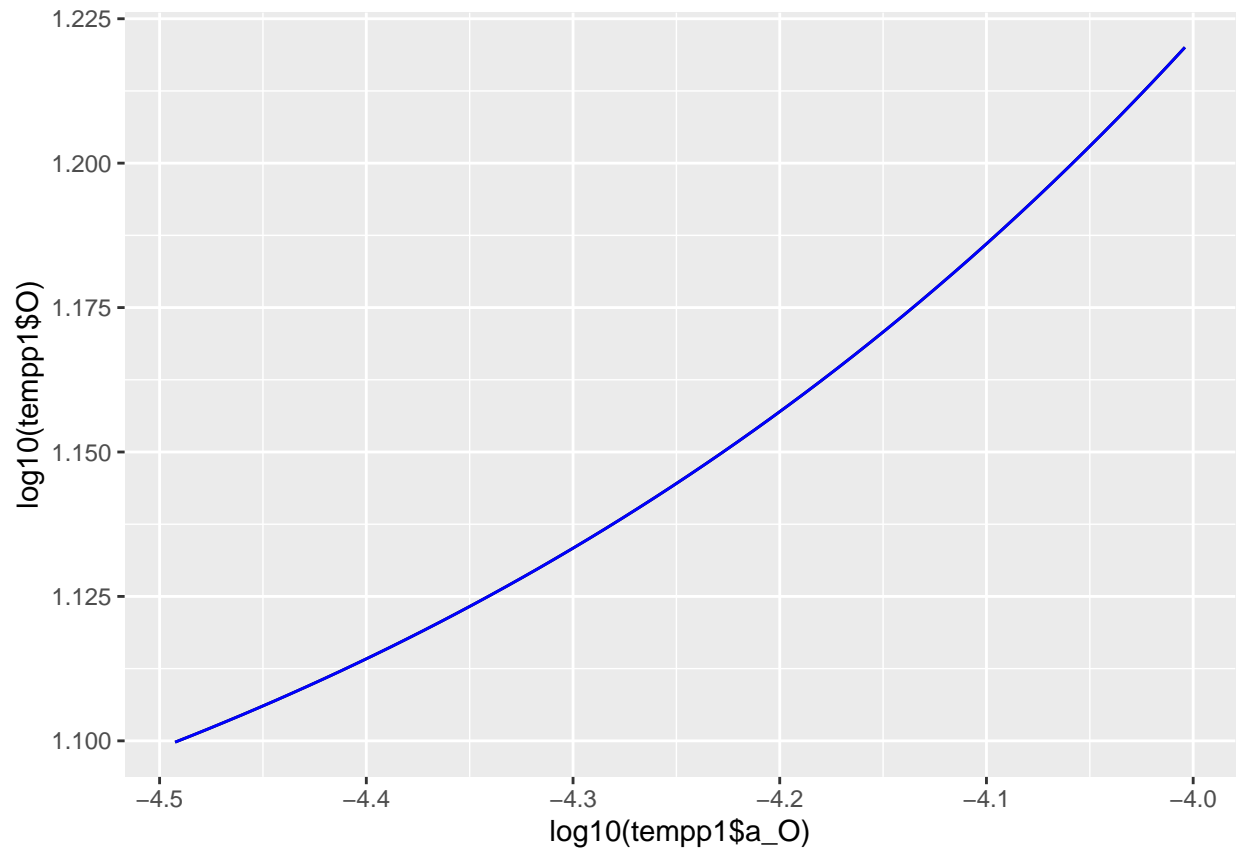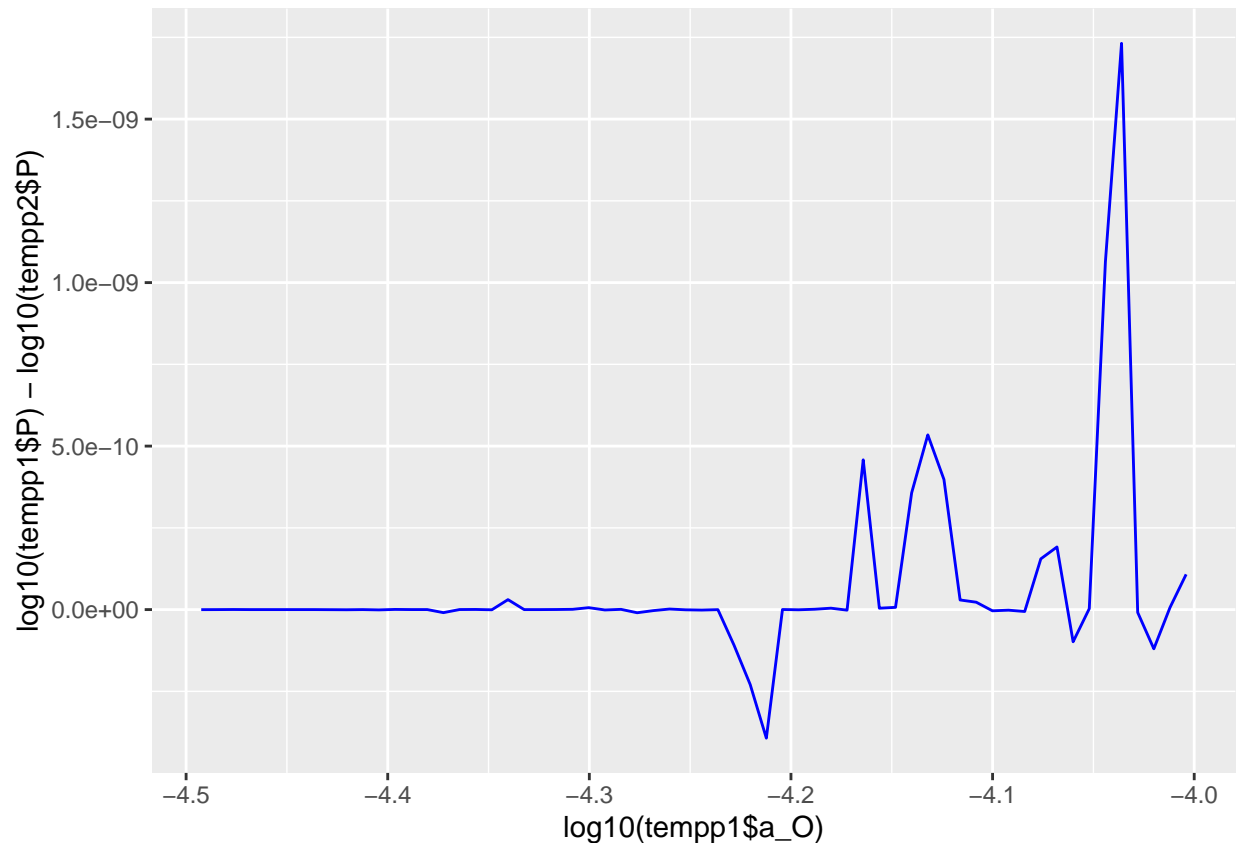
```
ggplot() +
  geom_histogram(mapping = aes(x = log10(tempp1$O) - log10(tempp2$O)),
            col = "blue")
```

`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
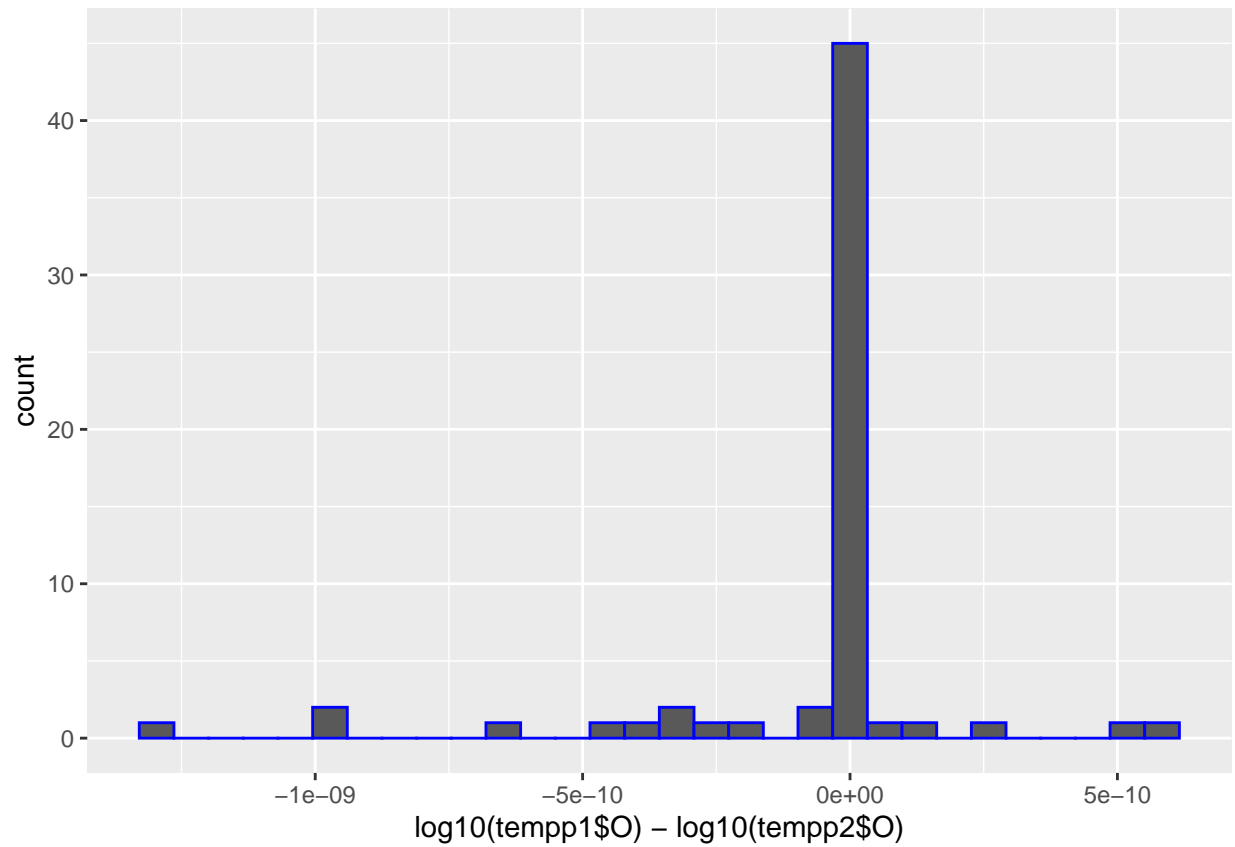
```
ggplot() +
  geom_line(mapping = aes(x = log10(tempp1$a_O),
    y = log10(tempp1$P) - log10(tempp2$P)),
            col = "blue")
```

```
CB_vars <- unique(stab_data$CB_var_gmax_s)
SB_vars <- unique(stab_data$SB_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 = sort(CB_vars),
                   SB_var_gmax_s = sort(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

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Warning: Unknown levels in 'f': CB, CB-SB-PB

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## Warning: Unknown levels in 'f': SB-PB, CB-SB-PB

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

## Warning: Unknown levels in 'f': CB, SB-PB
```

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


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

Raw

```
all_stab_results %>%
  filter(Species == "O") %>%
  ggplot(aes(x = var_gmax, y = hyst_range_raw, 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")
```
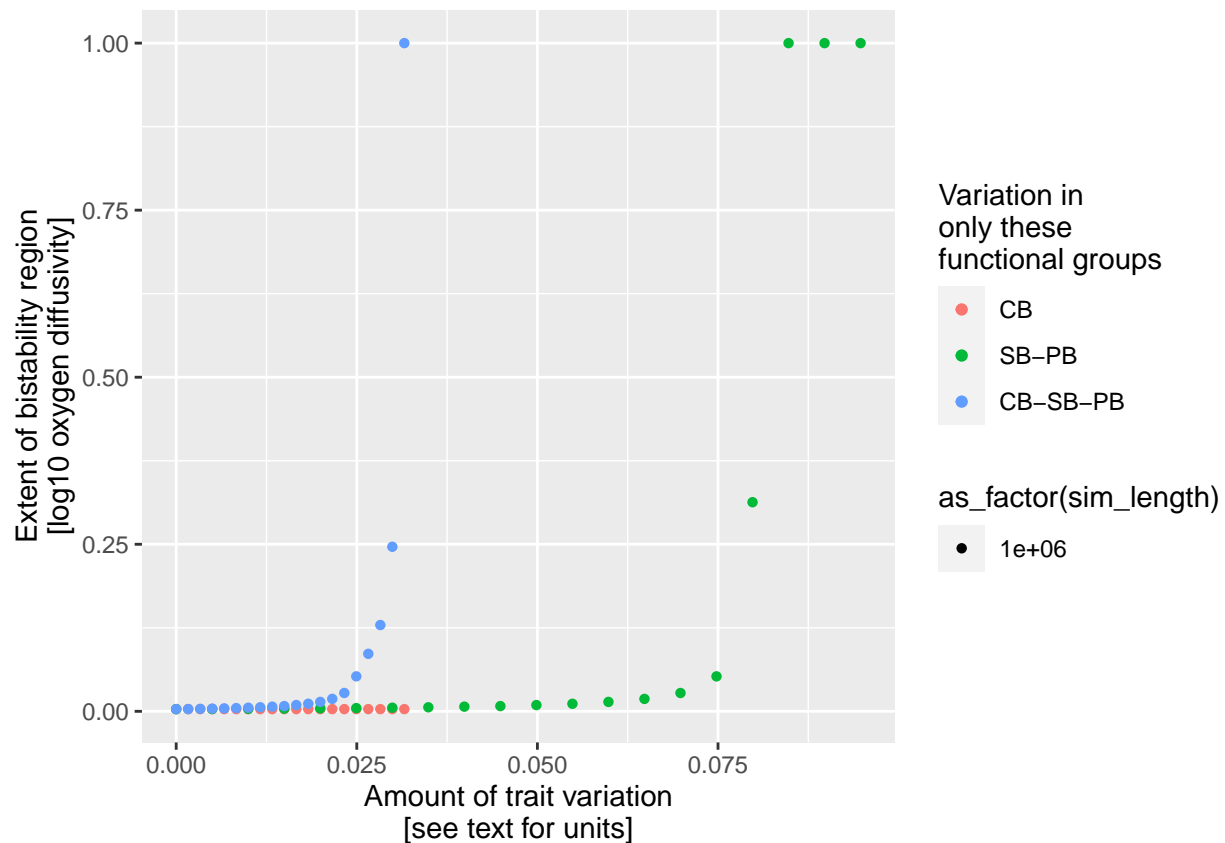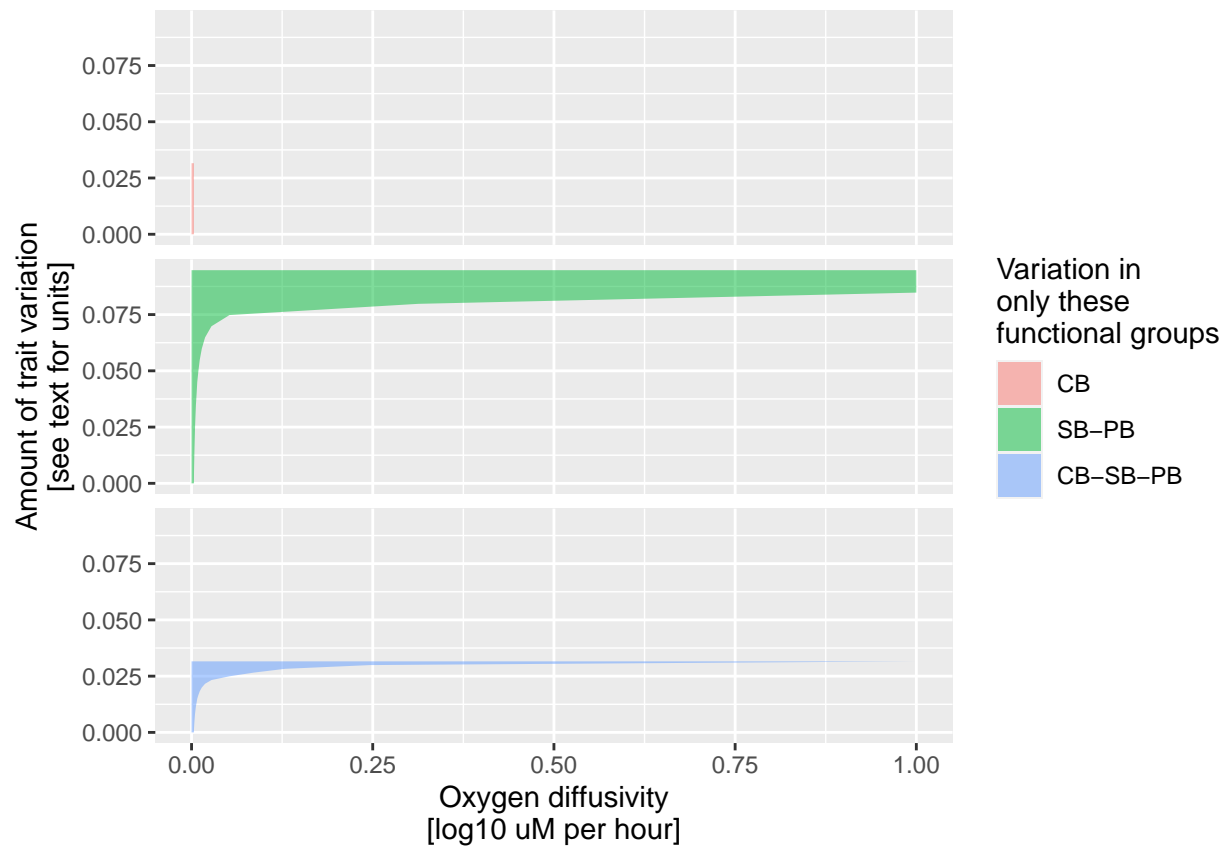


```
##ggsave("manuscript/figures/extent_of_bistab1.pdf", height = 4)

all_stab_results %>%
  #filter(var_treat == "CB") %>%
  filter(Species == "O",
         sim_length == 1e6) %>%
  ggplot(aes(x = var_gmax,
             ymin = hyst_min_raw,
             ymax = hyst_max_raw,
             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()
  )
```
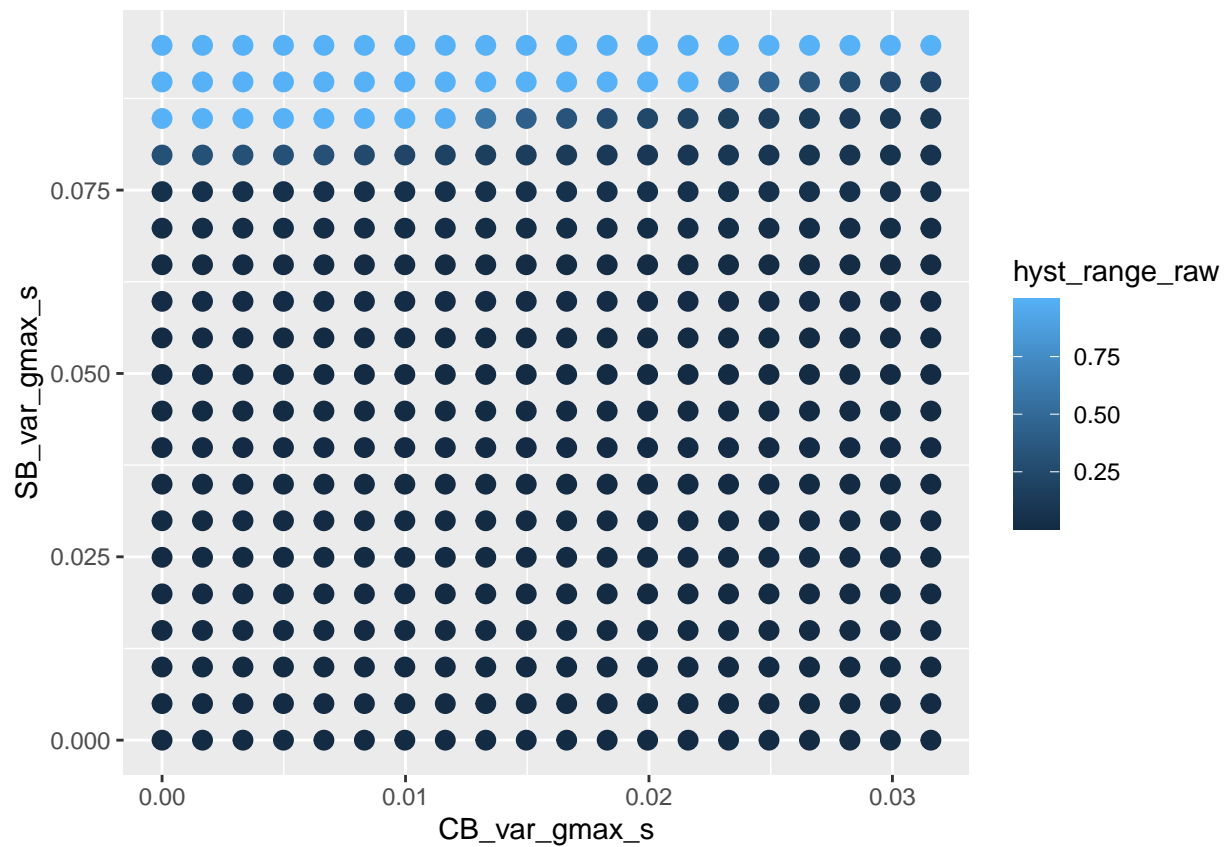


```
##ggsave("manuscript/figures/extent_of_bistab2.pdf", height = 4)
stab_data %>%
  filter(Species == "O",
         sim_length == 1e6) %>%
  ggplot(aes(x = CB_var_gmax_s, y = SB_var_gmax_s, fill = hyst_range_raw, col = hyst_range_raw)) +
  geom_point(size = 3)
```
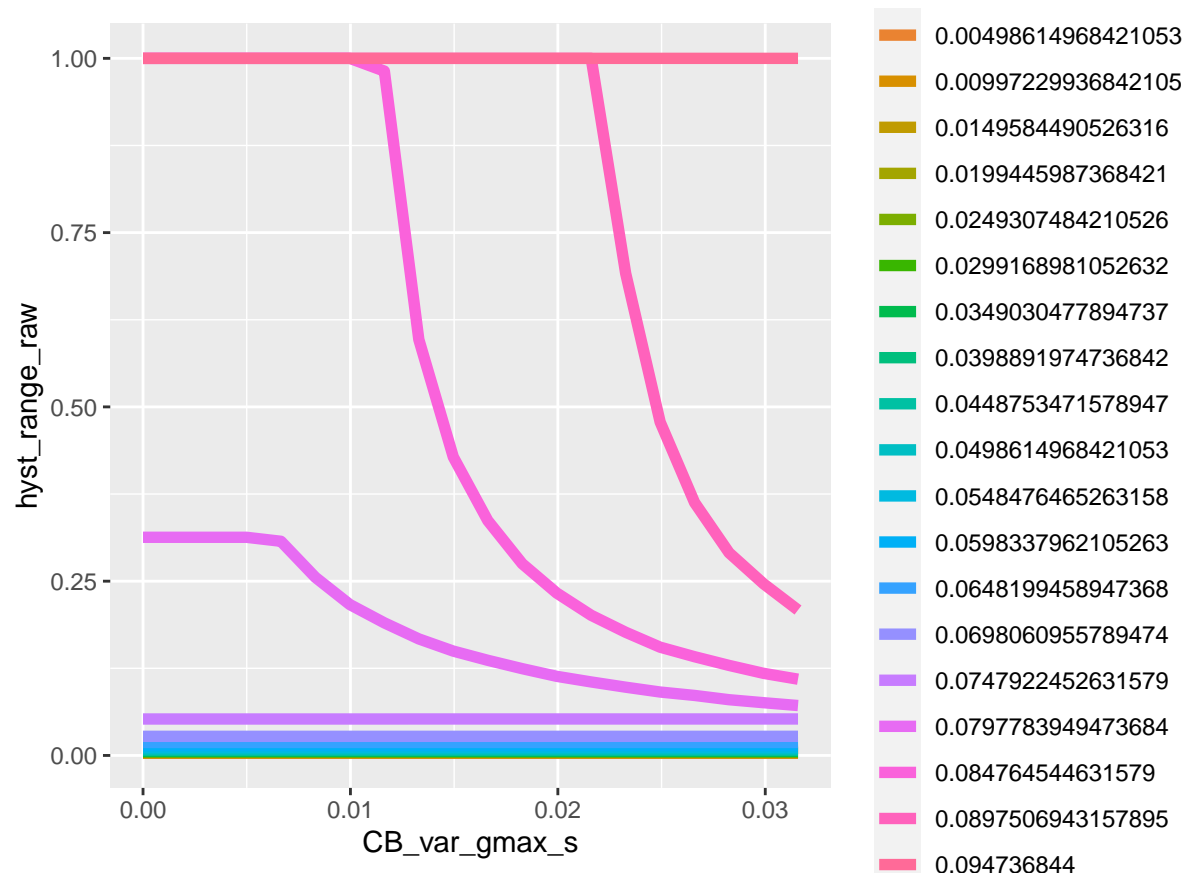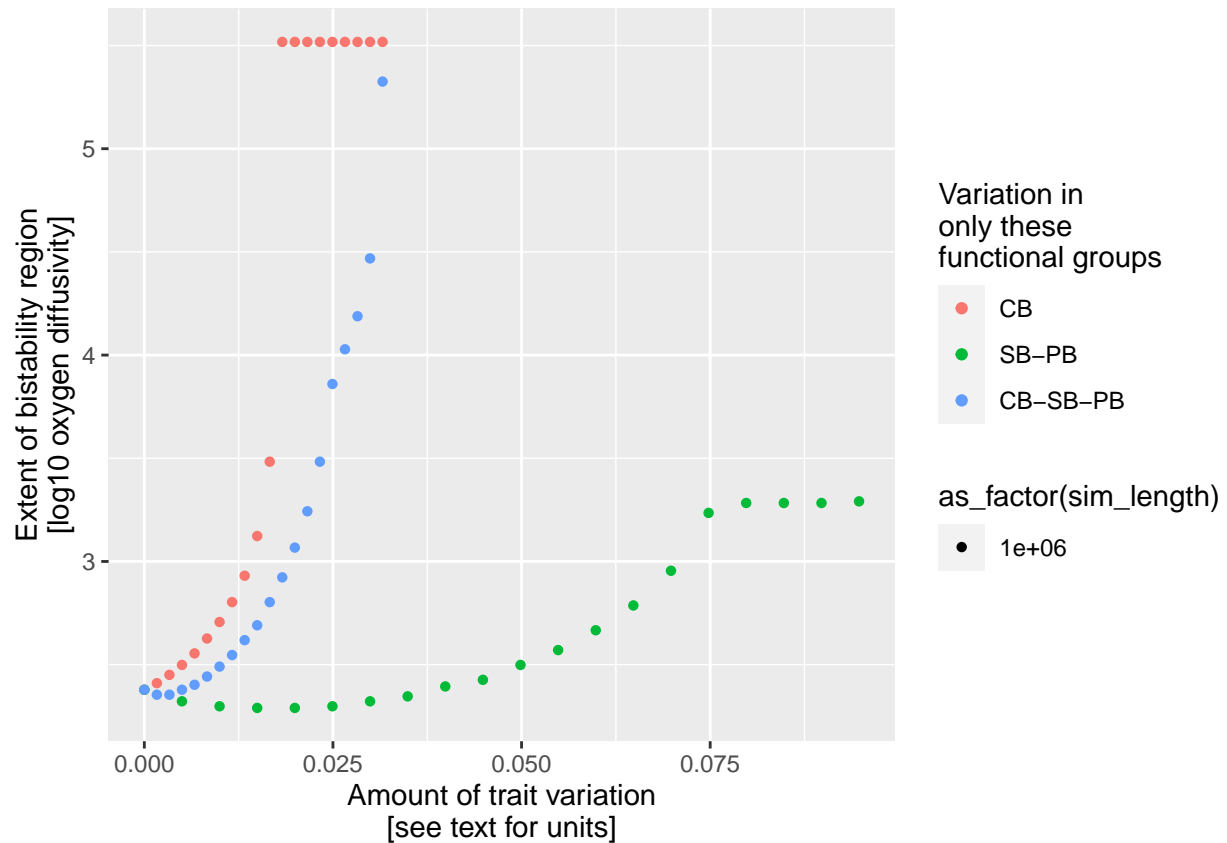
```
##ggsave("manuscript/figures/extent_of_bistab2.pdf", height = 4)

stab_data %>%
  filter(Species == "0",
         sim_length == 1e6) %>%
  ggplot(aes(x = CB_var_gmax_s, y = hyst_range_raw, col = as.factor(SB_var_gmax_s))) +
  geom_line(size = 2)
```

■	0.00498614968421053
■	0.00997229936842105
■	0.0149584490526316
■	0.0199445987368421
■	0.0249307484210526
■	0.0299168981052632
■	0.0349030477894737
■	0.0398891974736842
■	0.0448753471578947
■	0.0498614968421053
■	0.0548476465263158
■	0.0598337962105263
■	0.0648199458947368
■	0.0698060955789474
■	0.0747922452631579
■	0.0797783949473684
■	0.084764544631579
■	0.0897506943157895
■	0.094736844

Log transformed

```
all_stab_results %>%
  filter(Species == "O") %>%
  ggplot(aes(x = var_gmax, y = hyst_range_log, 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")
```
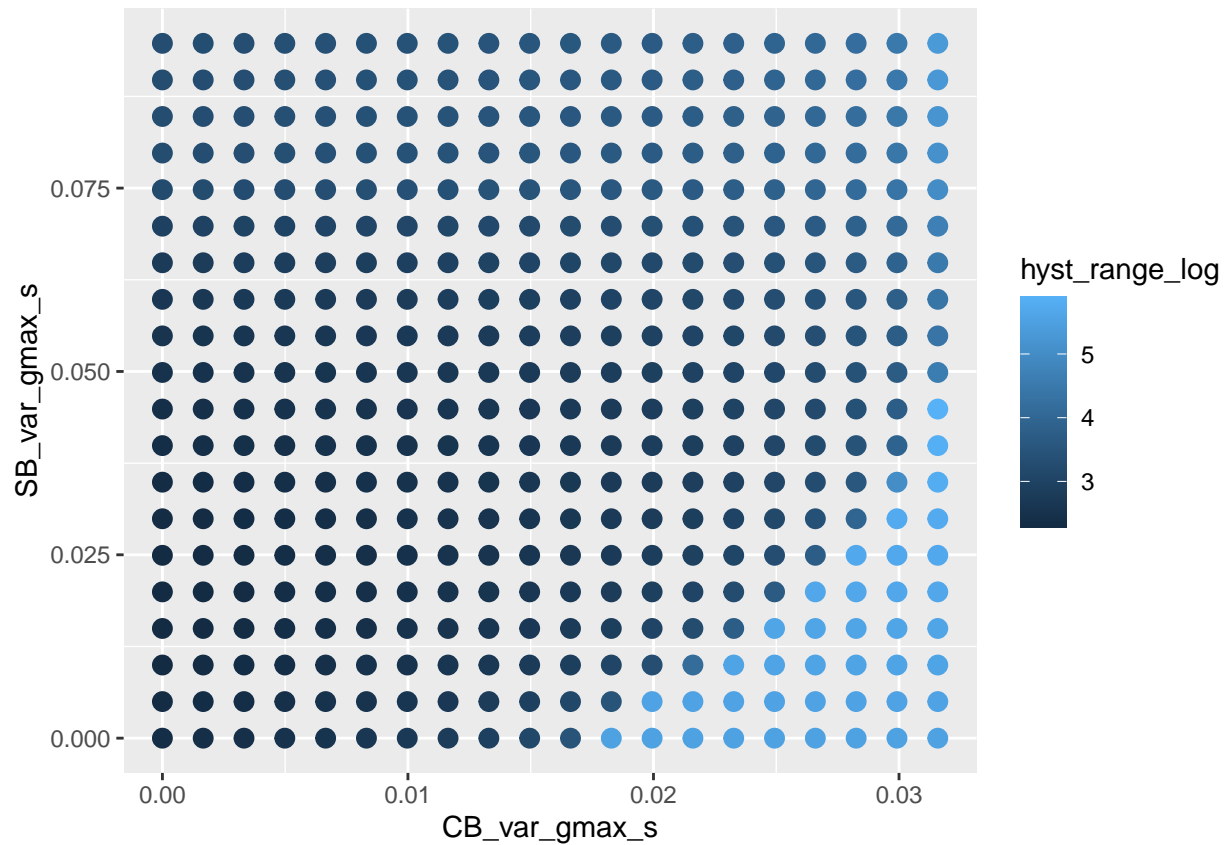
```
##ggsave("manuscript/figures/extent_of_bistab1.pdf", height = 4)

all_stab_results %>%
  #filter(var_treat == "CB") %>%
  filter(Species == "O",
         sim_length == 1e6) %>%
  ggplot(aes(x = var_gmax,
             ymin = hyst_min_log,
             ymax = hyst_max_log,
             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()
  )
```
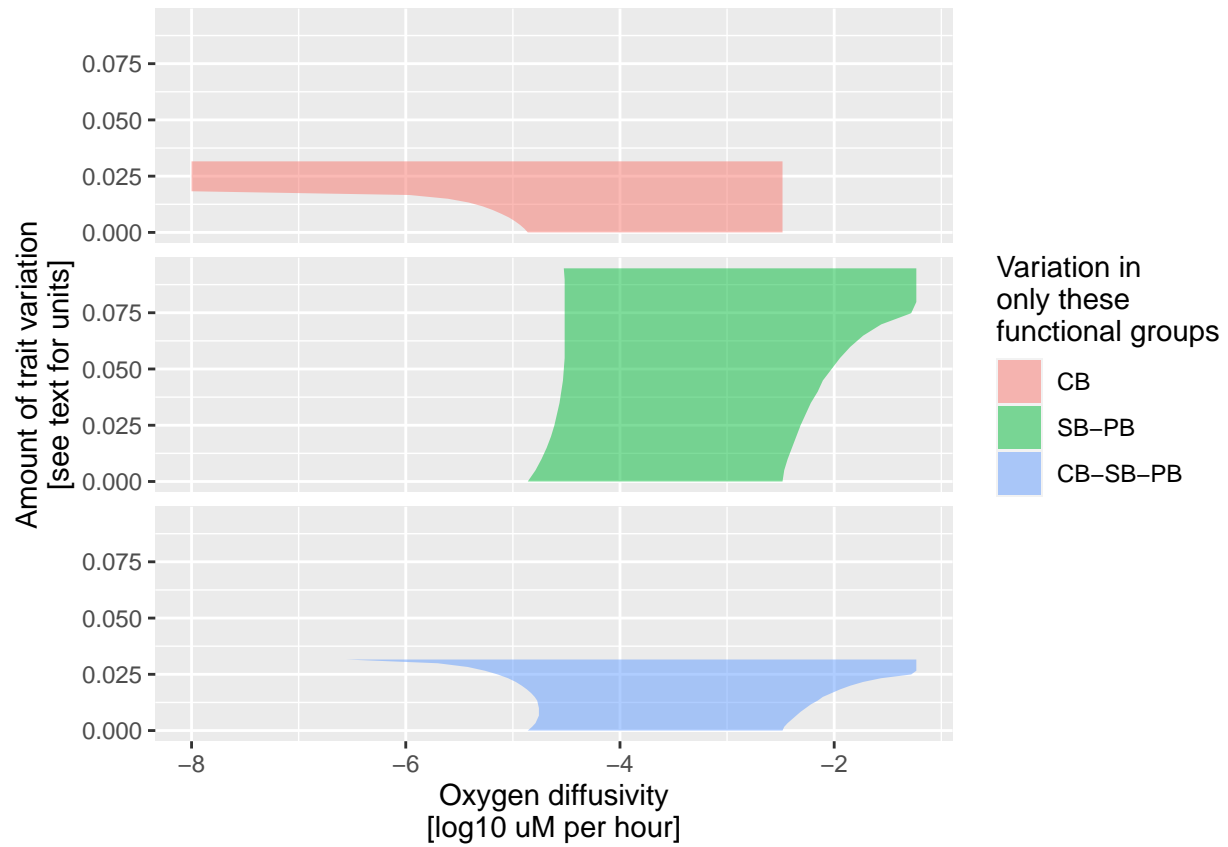
```
##ggsave("manuscript/figures/extent_of_bistab2.pdf", height = 4)
stab_data %>%
  filter(Species == "O",
         sim_length == 1e6) %>%
  ggplot(aes(x = CB_var_gmax_s, y = SB_var_gmax_s, fill = hyst_range_log, col = hyst_range_log)) +
  geom_point(size = 3)
```
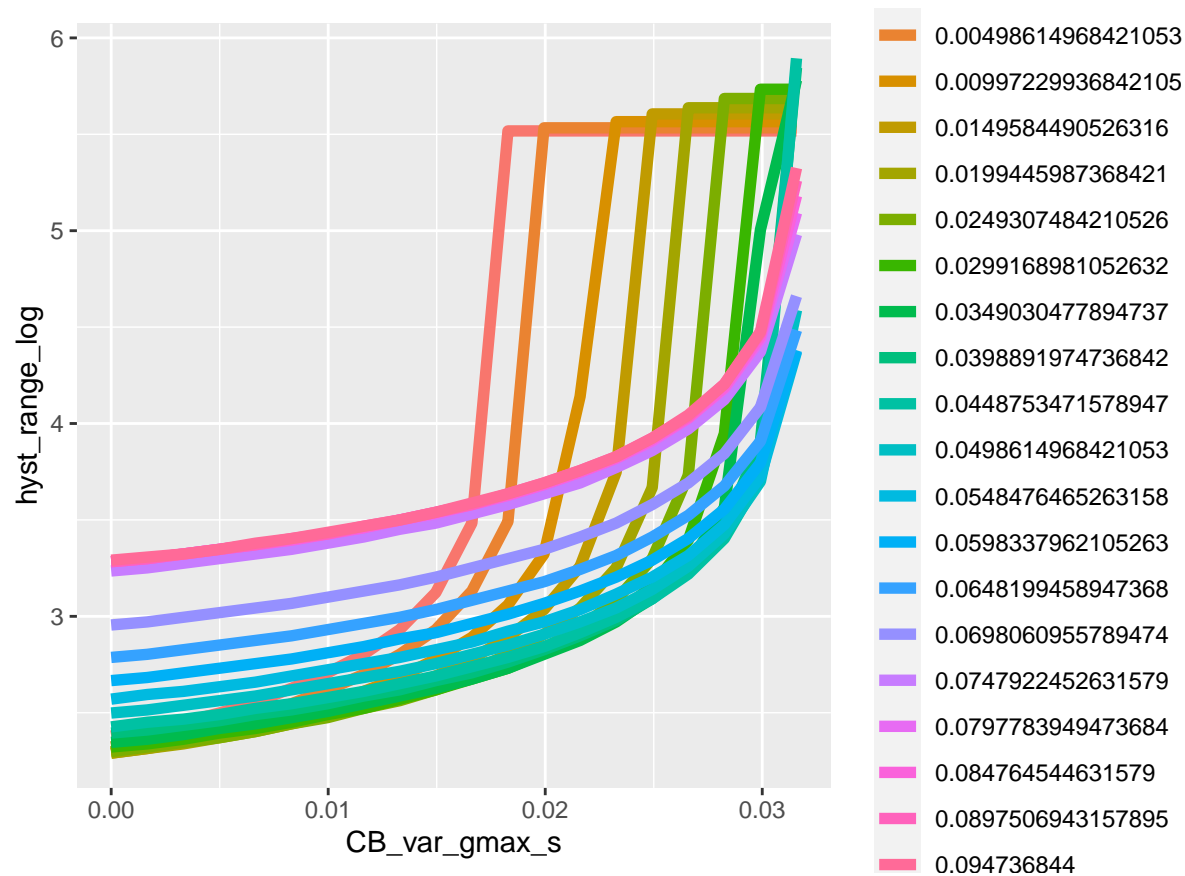
```
##ggsave("manuscript/figures/extent_of_bistab2.pdf", height = 4)

stab_data %>%
  filter(Species == "0",
         sim_length == 1e6) %>%
  ggplot(aes(x = CB_var_gmax_s, y = hyst_range_log, col = as.factor(SB_var_gmax_s))) +
  geom_line(size = 2)
```

Legend:
- 0.00498614968421053
- 0.00997229936842105
- 0.0149584490526316
- 0.0199445987368421
- 0.0249307484210526
- 0.0299168981052632
- 0.0349030477894737
- 0.0398891974736842
- 0.0448753471578947
- 0.0498614968421053
- 0.0548476465263158
- 0.0598337962105263
- 0.0648199458947368
- 0.0698060955789474
- 0.0747922452631579
- 0.0797783949473684
- 0.084764544631579
- 0.0897506943157895
- 0.094736844

Stable state finding 2

```r
rm(list = ls())
library(here)
library(tidyverse)
library(microxanox)
library(patchwork)
source(here("R/various_useful_functions.r"))


parameter = readRDS(here("experiments/9_strains/data/parameter_1e6_x2x6_factorial.RDS"))
var_expt = readRDS(here("experiments/9_strains/data/var_expt_1e6_x2x6_factorial.RDS"))

## here we choose the diversity of the system
wait_time <- 10000
parameter$log10a_series <- log10(sort(unique(parameter$ss_expt$a_0)))
#p$log10a_series <- seq(-2.5, -2, 0.025)
parameter$log10a_series <- seq(-8, 0, 0.2)

no_diverity_varexp_row <- 1
no_div_res <- get_ss_temporal_method(parameter, var_expt,
                                     no_diverity_varexp_row,
                                     wait_time)
saveRDS(no_div_res, here("experiments/9_strains/data/no_div_temporal_ss.RDS"))
```

```
medium_diverity_varexp_row <- 311
medium_div_res <- get_ss_temporal_method(parameter, var_expt,
                                         medium_diverity_varexp_row,
                                         wait_time)
saveRDS(medium_div_res, here("experiments/9_strains/data/medium_div_temporal_ss.RDS"))


no_div_res <- readRDS(here("experiments/9_strains/data/no_div_temporal_ss.RDS"))
medium_div_res <- readRDS(here("experiments/9_strains/data/medium_div_temporal_ss.RDS"))

plot_ss_result3(no_div_res)
```
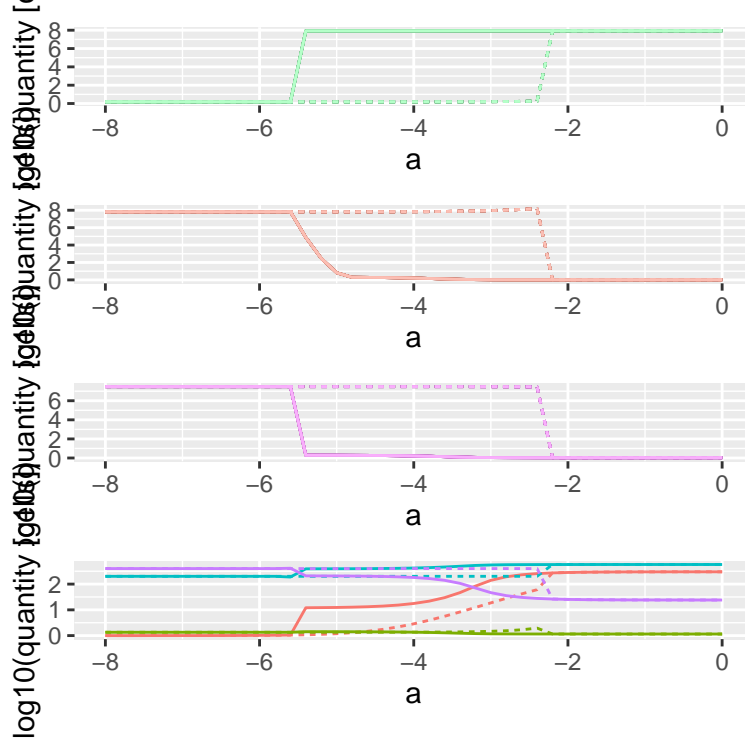


```
plot_ss_result3(medium_div_res)
```

CB_gmax_var = 0.0249307484210526 CB_h_var = 0.126315789473684
SB_gmax_var = 0.0498614968421053 SB_h_var = −1.02
PB_gmax_var = 0.0498614968421053 PB_h_var = −1.02