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

```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 3.3.5     v purrr   0.3.4
```

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```
## v tibble  3.1.3     v dplyr   1.0.7
## v tidyr   1.1.3     v stringr 1.4.0
## v readr   2.0.0     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/uriah/Documents/1_Projects/diversity_envresp1
```

```r
library(parallel)
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

General simulation conditions

```r
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

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

## 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
```
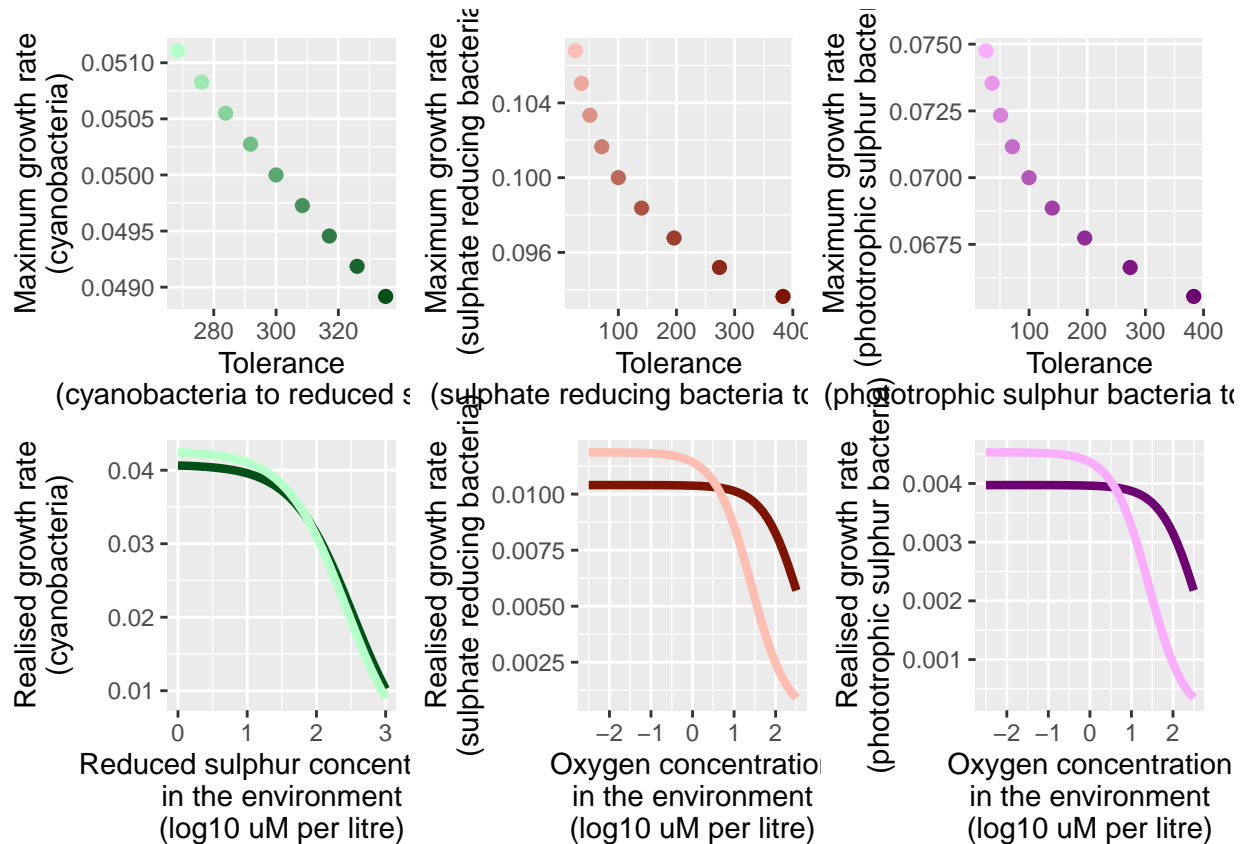
Create diversity

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

Display diversity

```
display_diversity(400)
```


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)
```
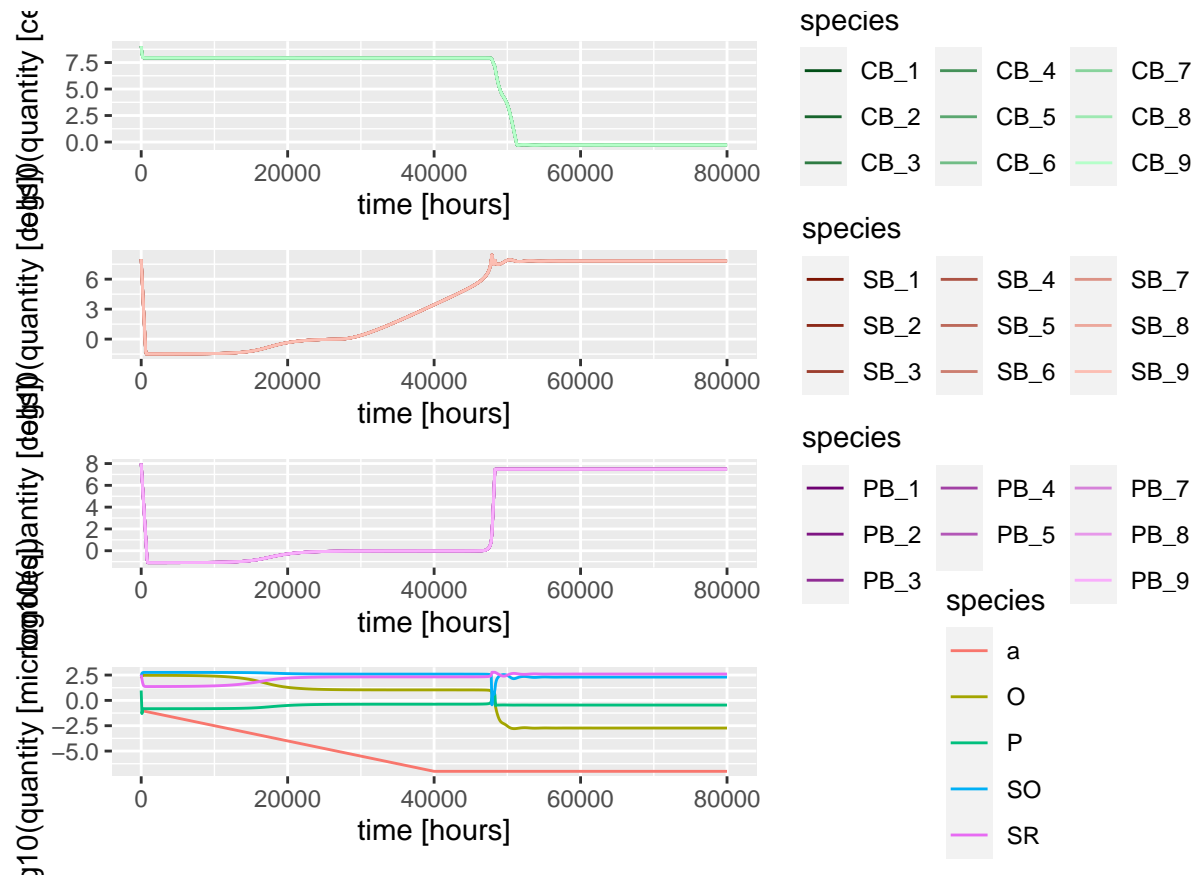


```
#ggsave(here("simulations/expt2/figures/switching_novar.pdf"), width = 10)
```

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"))
```

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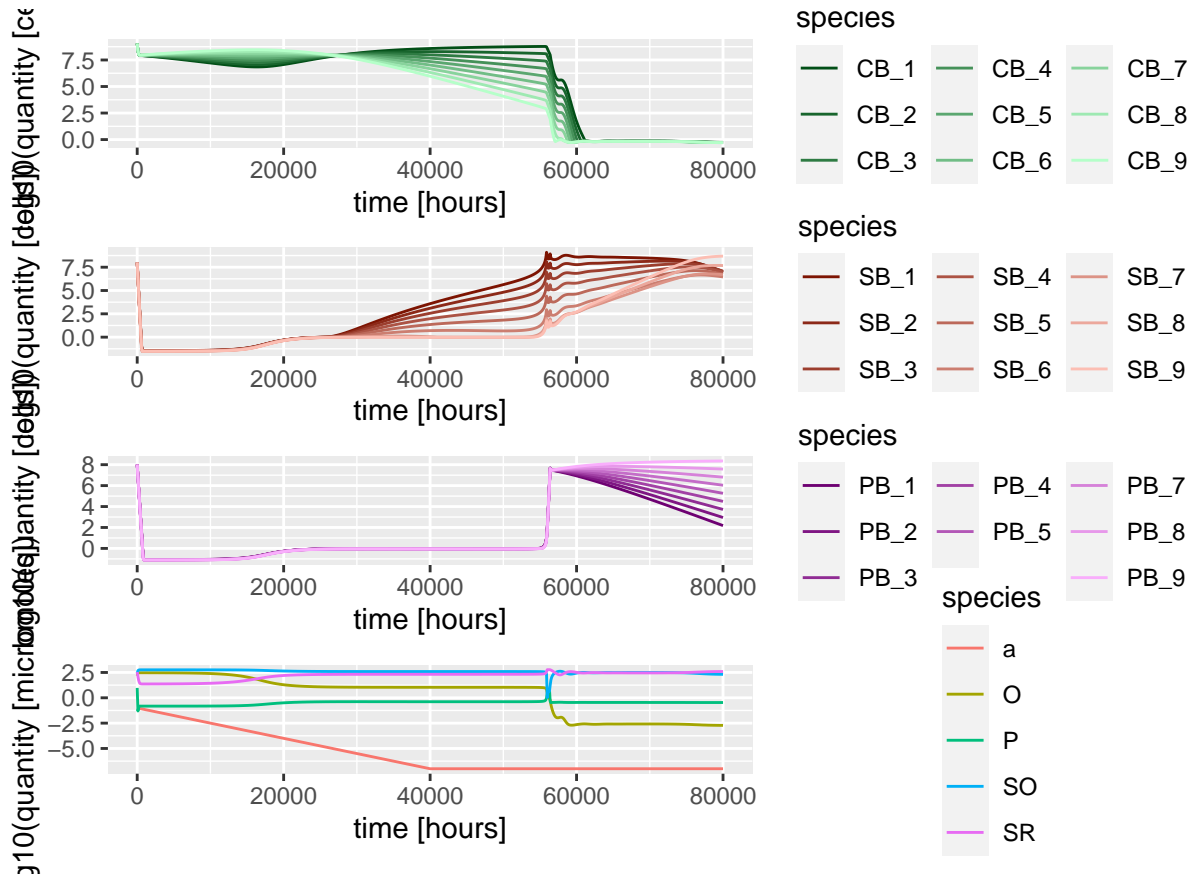


```
#ggsave(here("simulationsexpt2/figures/switching_highvar.pdf"), width = 10)
```

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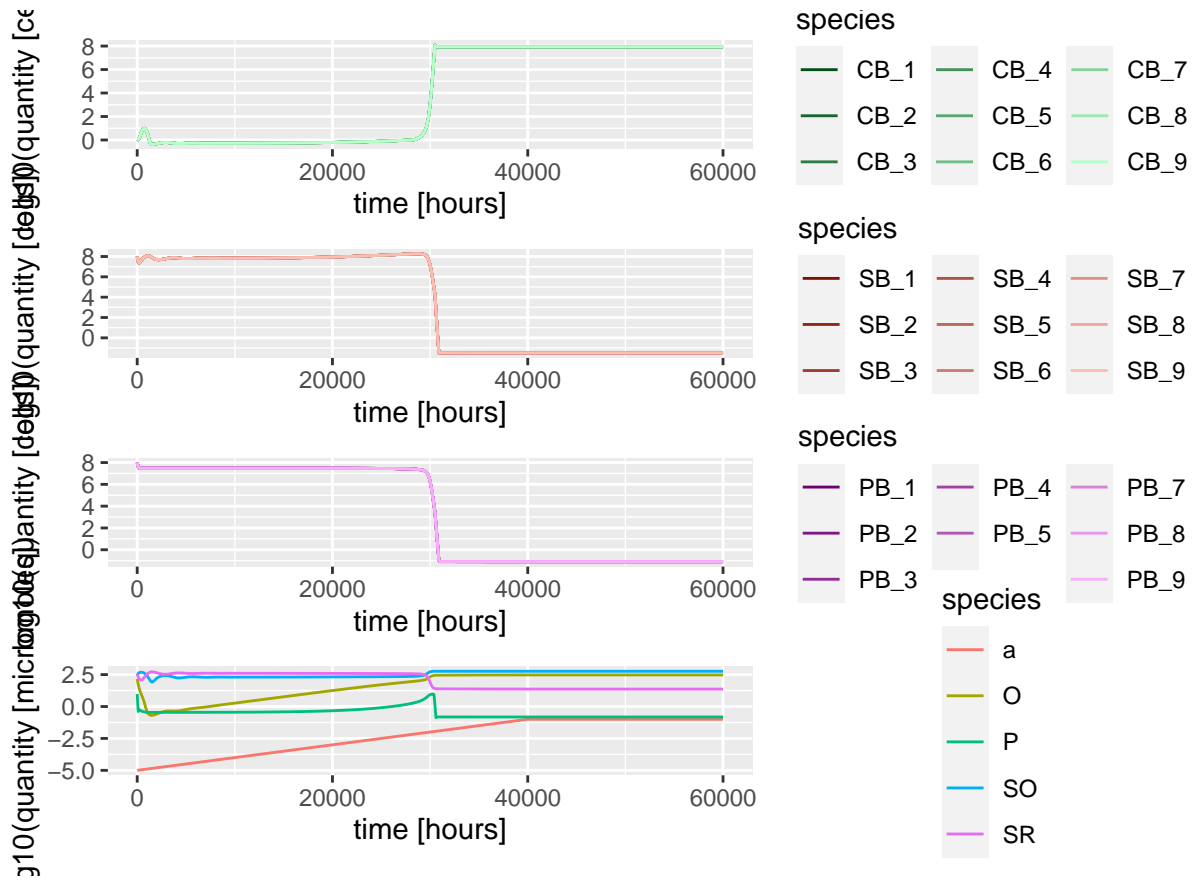
```
#ggsave(here("simulations/expt2/figures/switching_novar.pdf"), width = 10)
```

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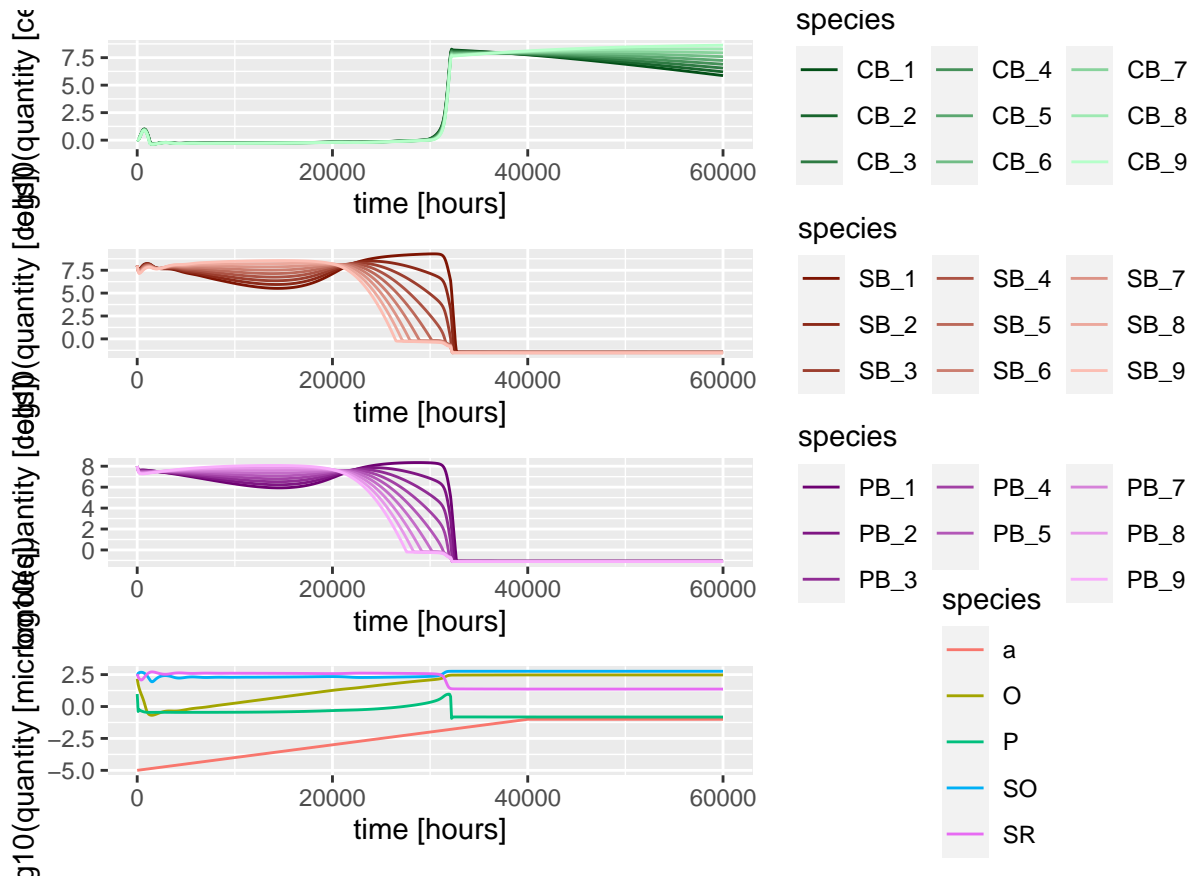
```
#ggsave(here("simulationsexpt2/figures/switching_highvar.pdf"), width = 10)
```

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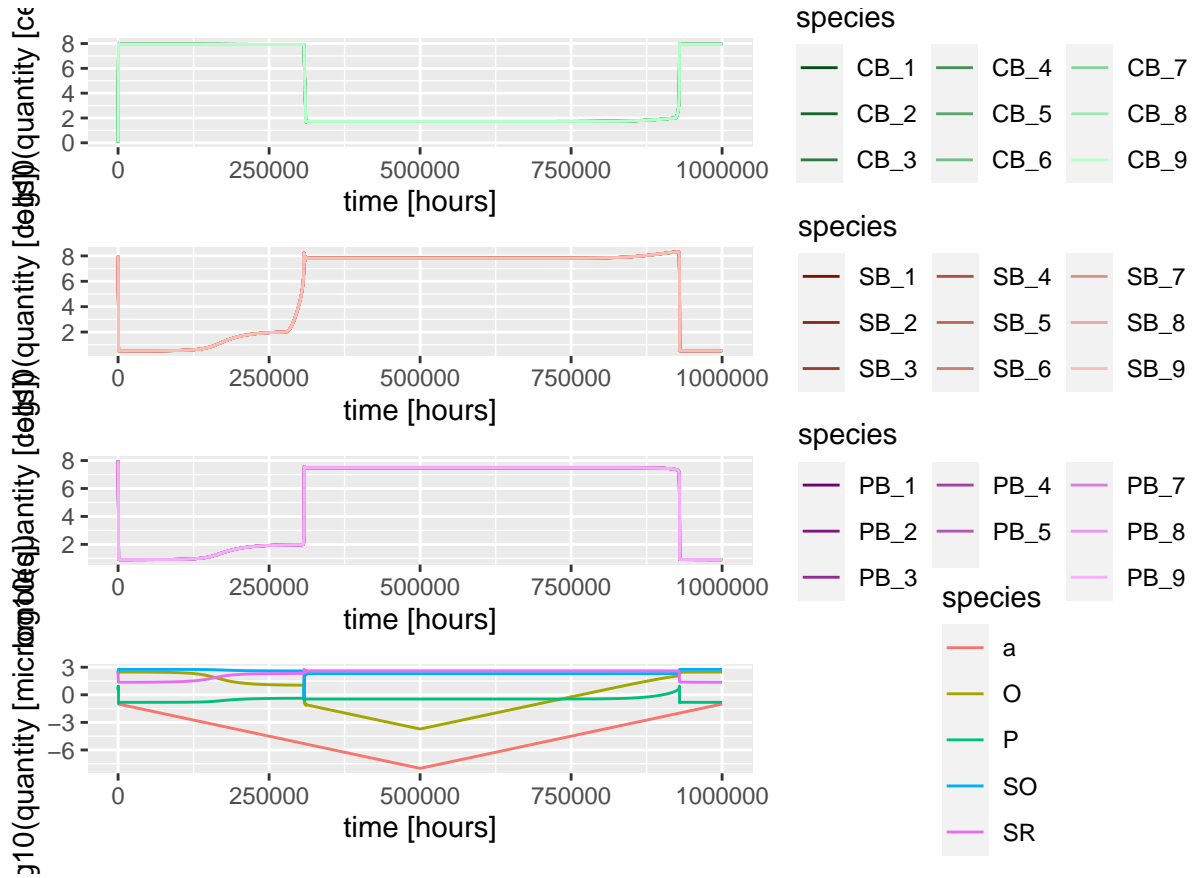
```
#ggsave(here("simulations/expt2/figures/switching_novar.pdf"), width = 10)
```

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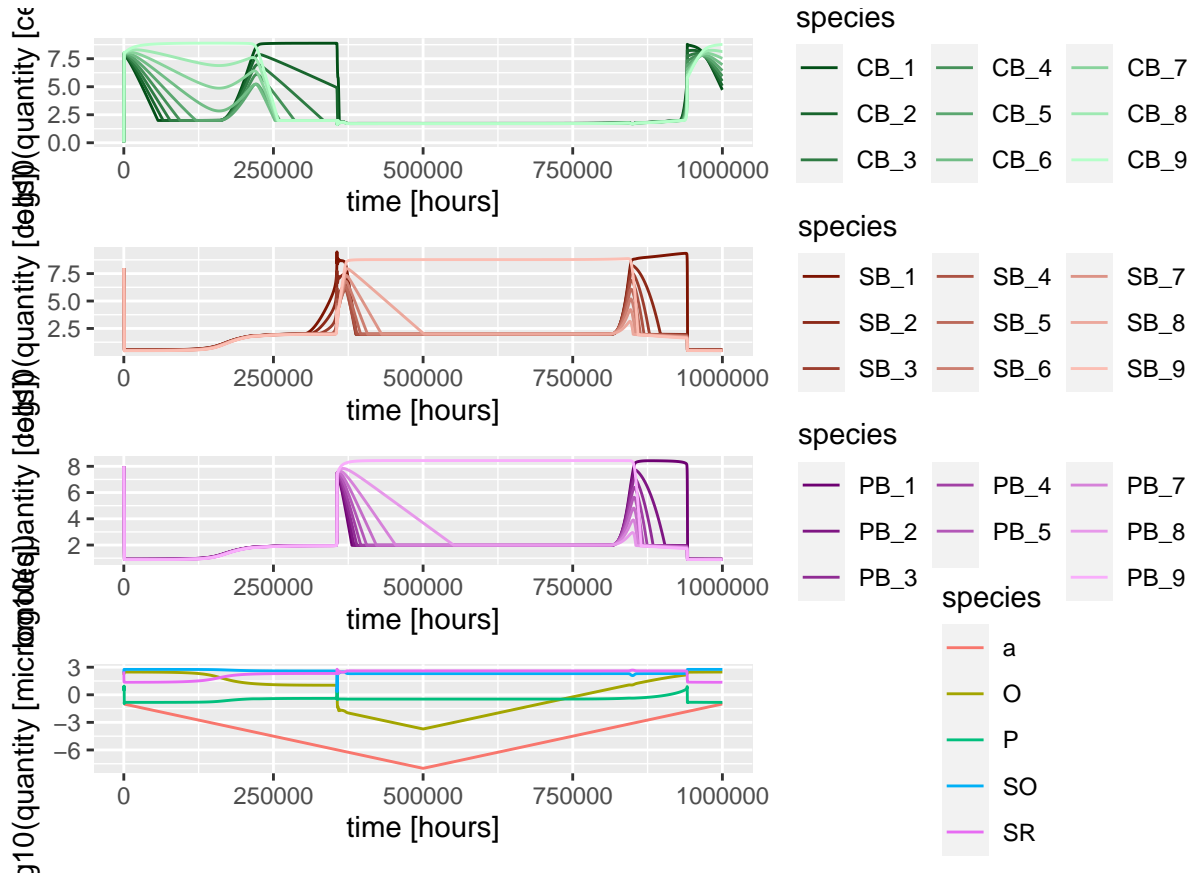
```
#ggsave(here("simulationsexpt2/figures/switching_highvar.pdf"), width = 10)
```

Visualise

```
visualise_temporal_env_eco()
```

Stable state finding

Finding

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

```
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_Os <- 10^seq(-7, -0.5, 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
```

```r
ss_expt <- expand.grid(N_CB = initial_CBs,
                       N_PB = initial_PBs,
                       N_SB = initial_SBs,
                       a_O = a_Os)
```

Run stable state finding

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

```r
var_expt <- run_ss_var_experiment()
saveRDS(var_expt, here("experiments/experiment 1/data/ss_data_1e6_x2x6_factorial.RDS"))
```

Process the stable state data

Bring in various stable state datasets

```r
## 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)
```

```r
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"))


## sim length 1'000'000, 20 SBPBgrad, 2xCB variation, 6xSBPB variation
var_expt5 <- readRDS(here("experiments/experiment 1/data/ss_data_1e6_x2x6_factorial.RDS")) %>%
  mutate(sim_length = 1000000)
stab_data5 <- var_expt5 %>%
  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_data5 <- unnest(stab_data5, cols = c(stability_measures))
saveRDS(stab_data5, here("experiments/experiment 1/data/stab_data_1e6_x2x6_factorial.RDS"))
```

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

```r
## 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
```
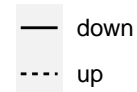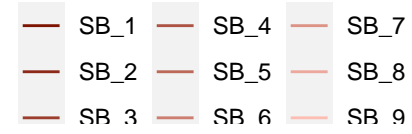
CB_gmax_var = 0 CB_h_var =0
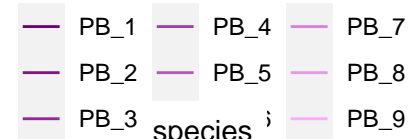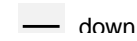SB_gmax_var = 0 SB_h_var =0
PB_gmax_var = 0 PB_h_var =0
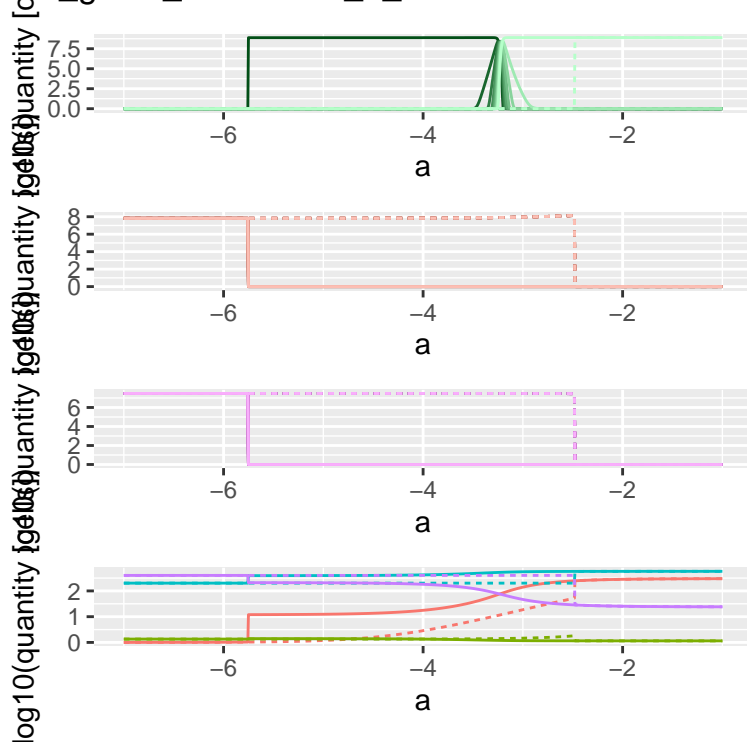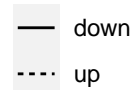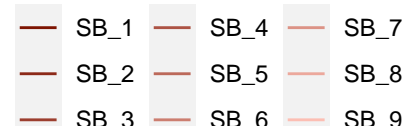

direction
——— down
------ up

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
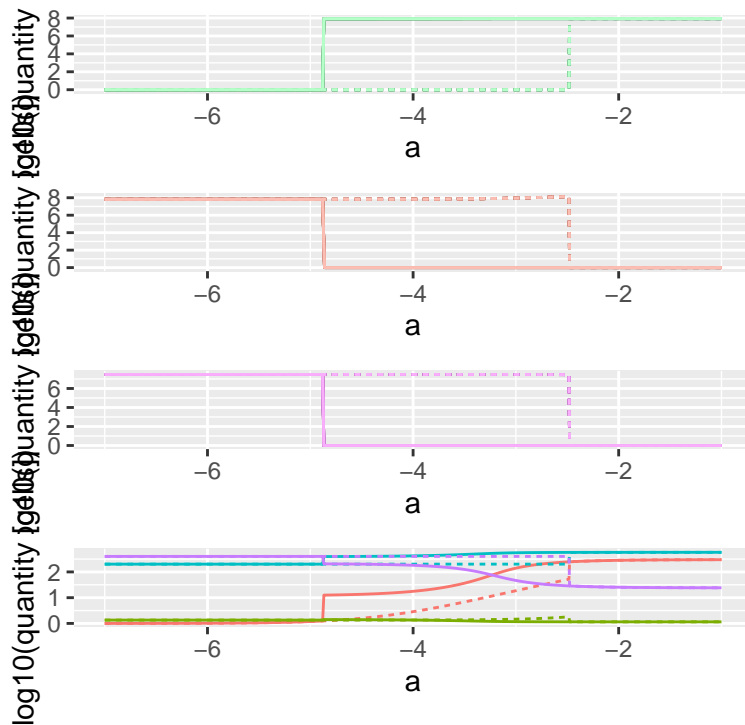
direction
——— down

direction
down

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

```
p2  <- plot_ss_result1_v2(var_expt,
              result_index = max_diversty_all,
              filename_prefix = NULL,
              save_image_file = FALSE)
p2
```

CB_gmax_var = 0.015789474 CB_h_var =−0.08
SB_gmax_var = 0.015789474 SB_h_var =−0.323
PB_gmax_var = 0.015789474 PB_h_var =−0.323
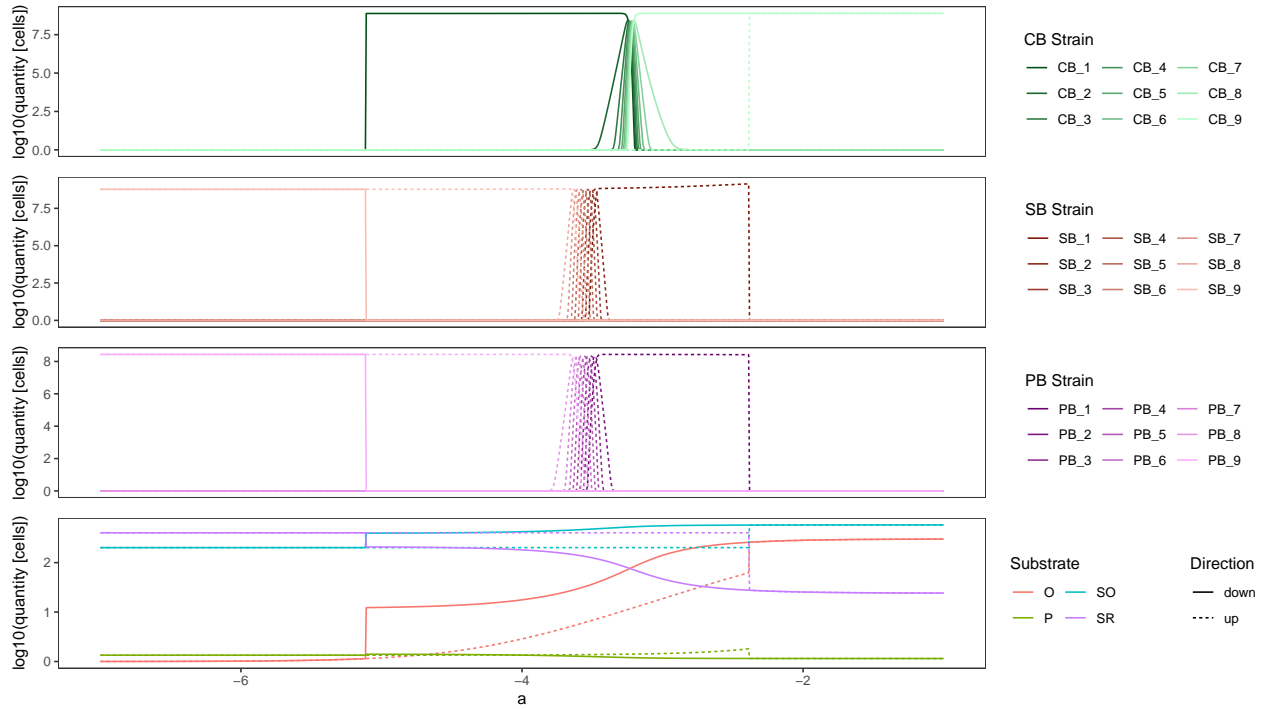

```r
p3  <- plot_ss_result1(var_expt,
            result_index = max_only_CB_diversity,
            filename_prefix = NULL,
            save_image_file = FALSE)
p3
```

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CB_gmax_var = 0.015789474 CB_h_var =−0.08
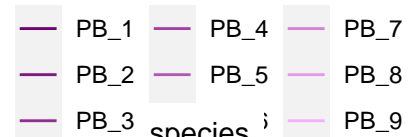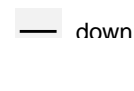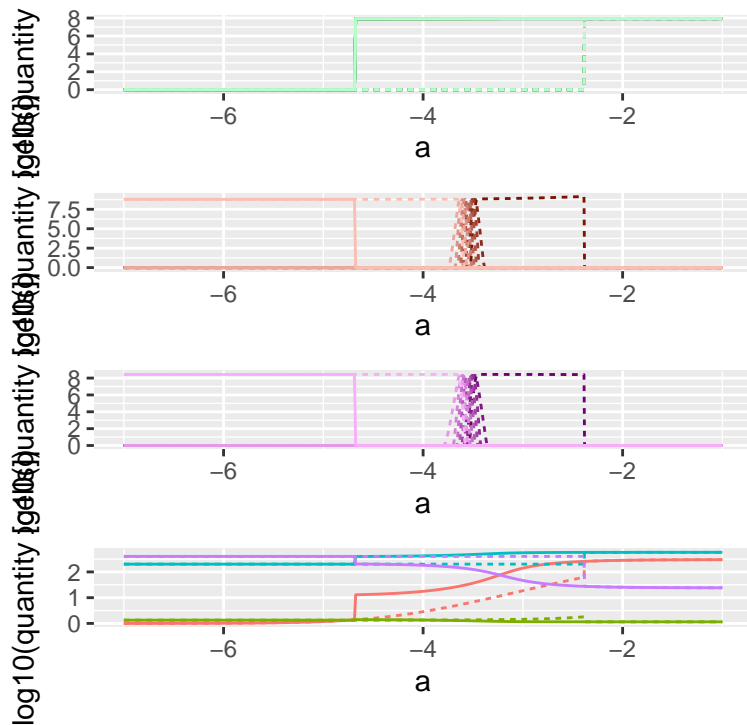SB_gmax_var = 0 SB_h_var =0
PB_gmax_var = 0 PB_h_var =0

```
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 = 0.015789474 SB_h_var =−0.323
PB_gmax_var = 0.015789474 PB_h_var =−0.323
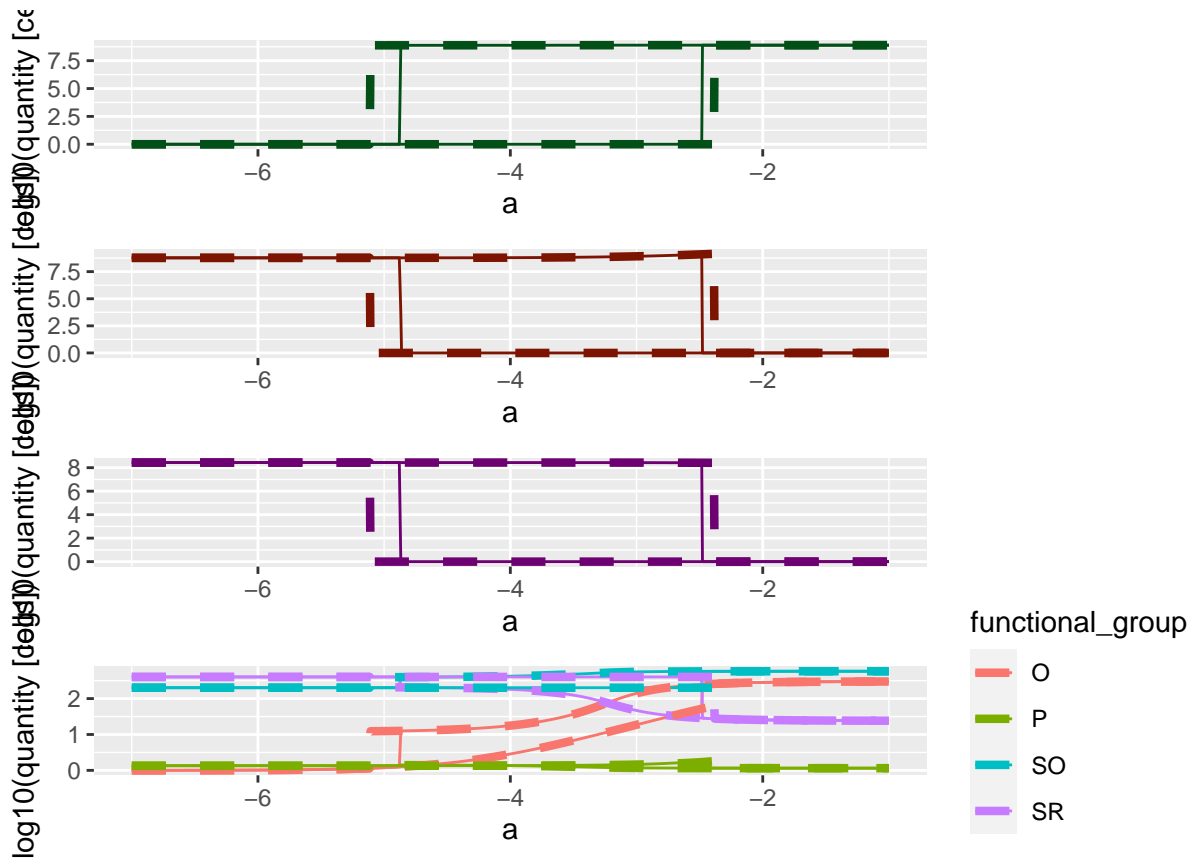
```
p_overlay1 <- plot_ss_result2(var_expt[no_diversity,]$ss_res[[1]],
                              var_expt[max_diversty_all,]$ss_res[[1]],
                              xlims = c(-7, -1))
```

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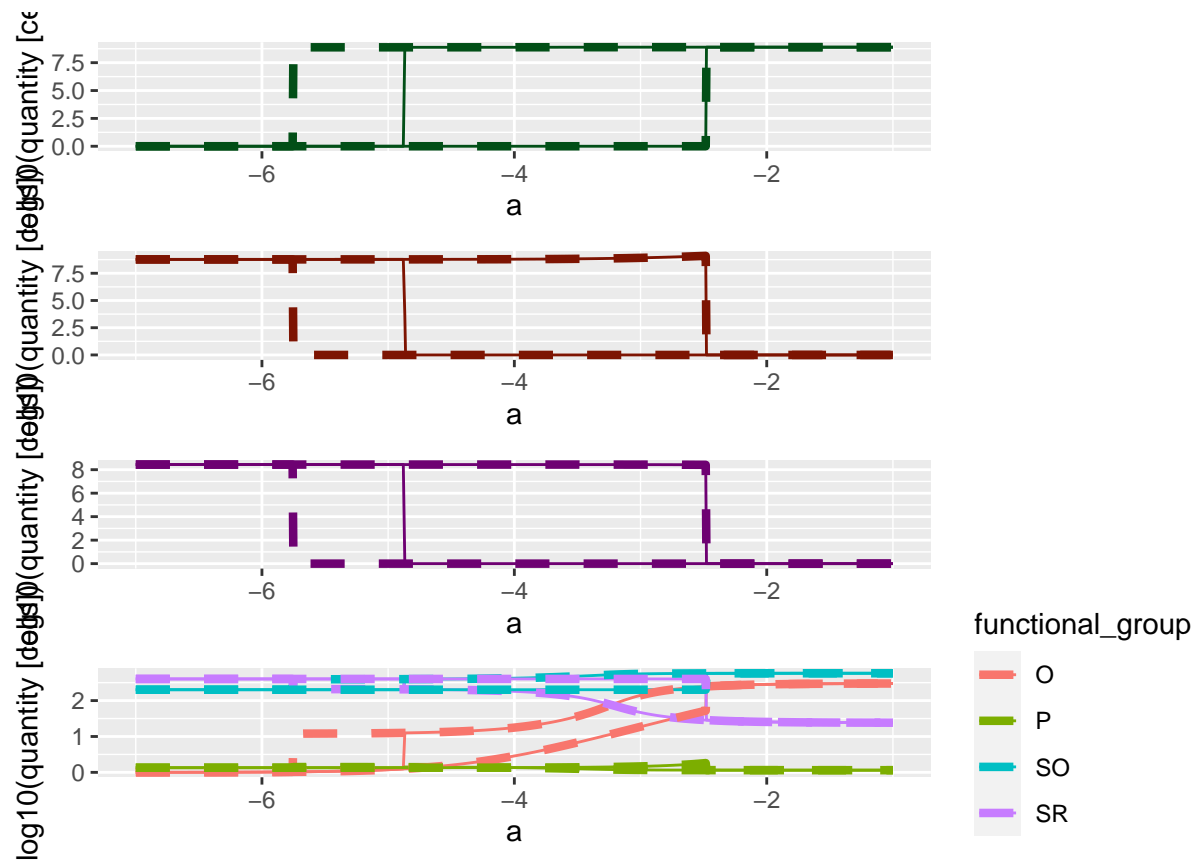
```
p_overlay2 <- plot_ss_result2(var_expt[no_diversity,]$ss_res[[1]],
                              var_expt[max_only_CB_diversity,]$ss_res[[1]],
                              xlims = c(-7, -1))
```

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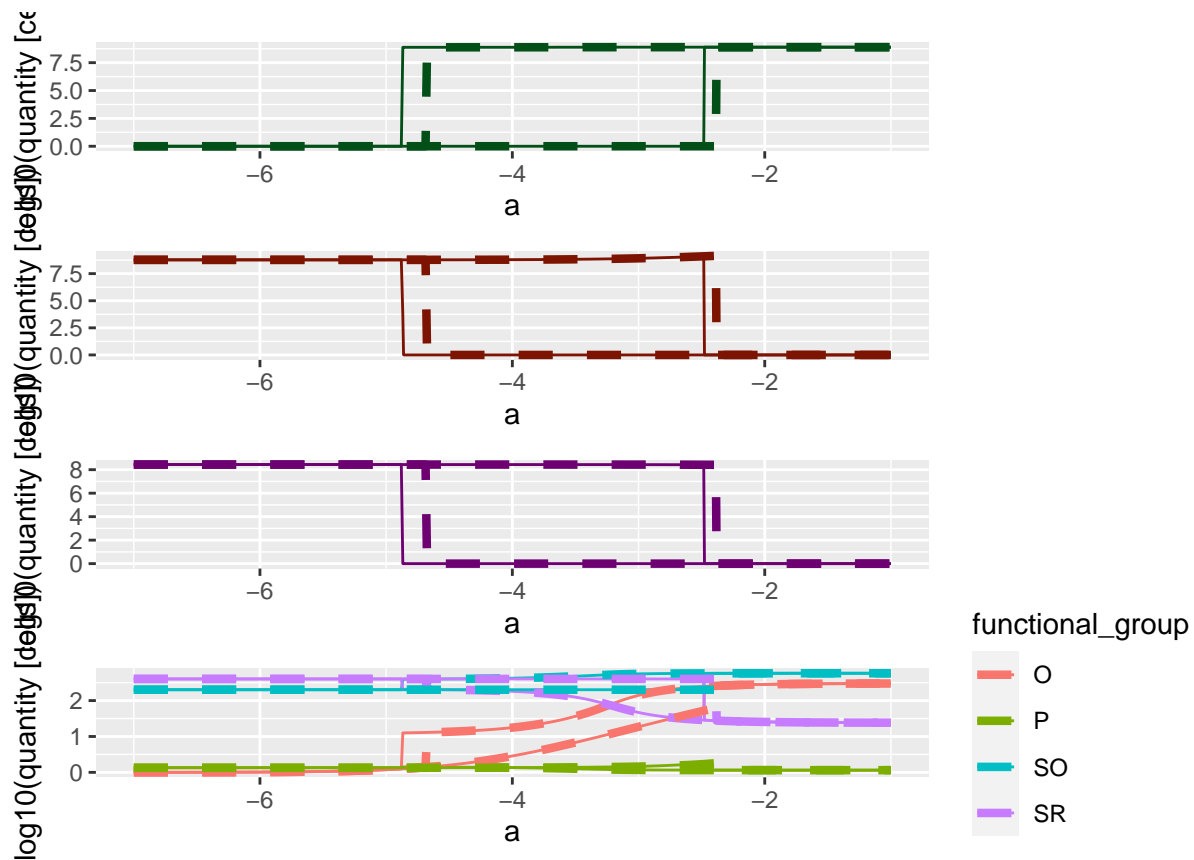
```
#ss_result3 <- var_expt[max_only_SBPB_diversity,]$ss_res[[1]]
```

Look at stability measures

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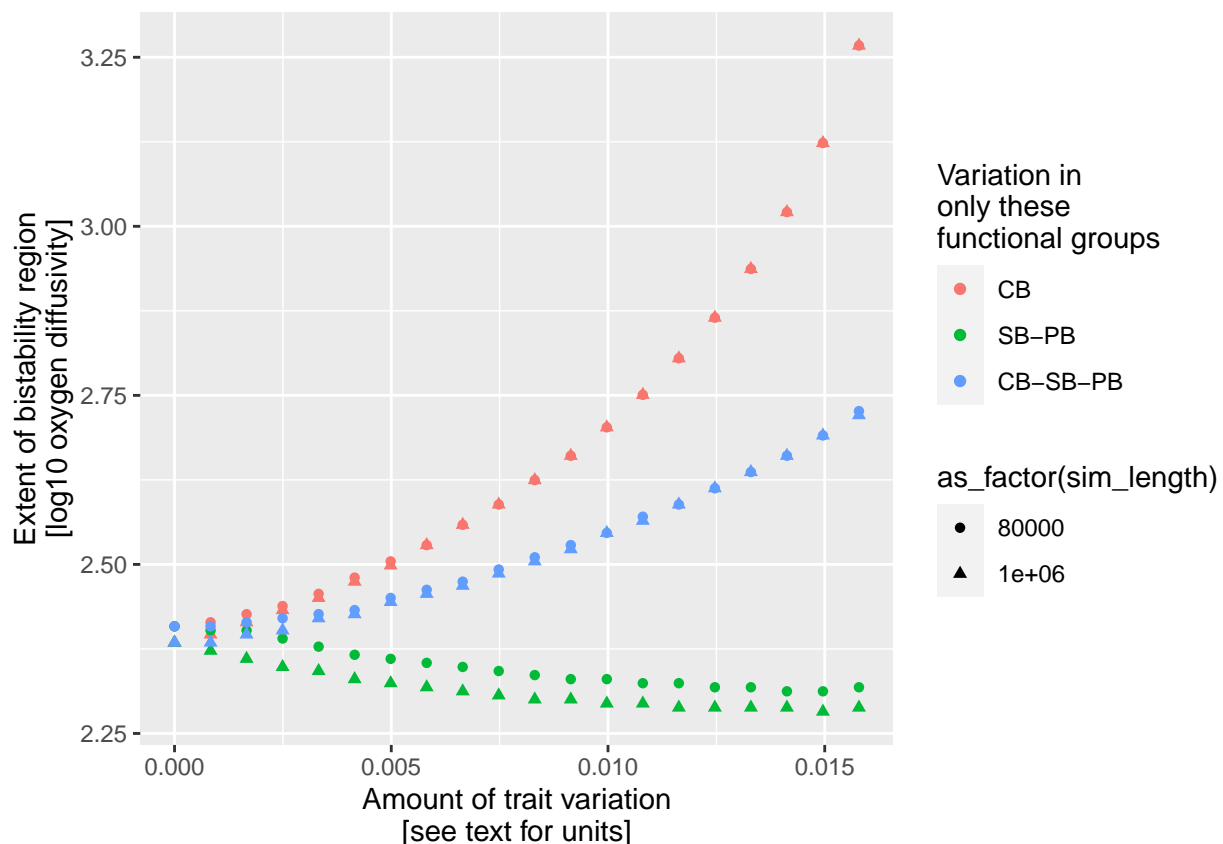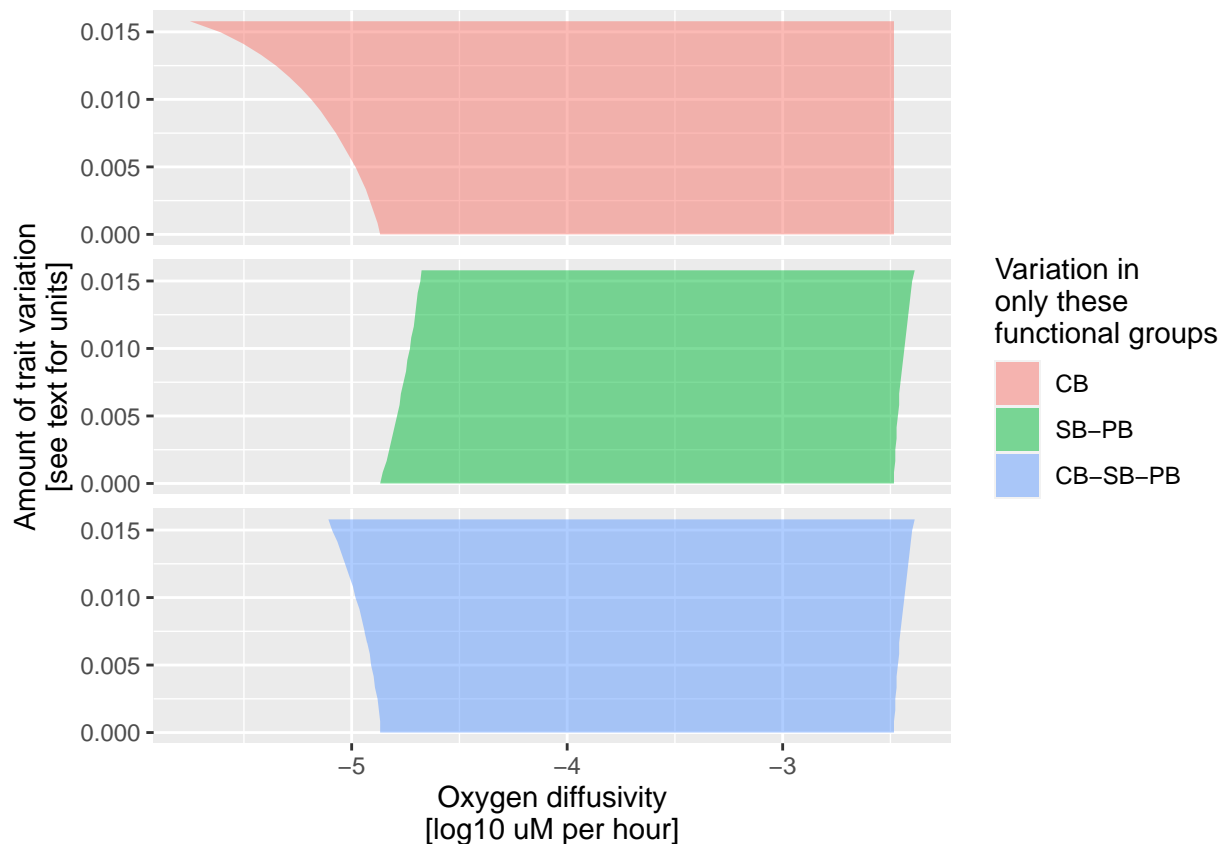
```
##ggsave("manuscript/figures/extent_of_bistab1.pdf", height = 4)

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()
)
```
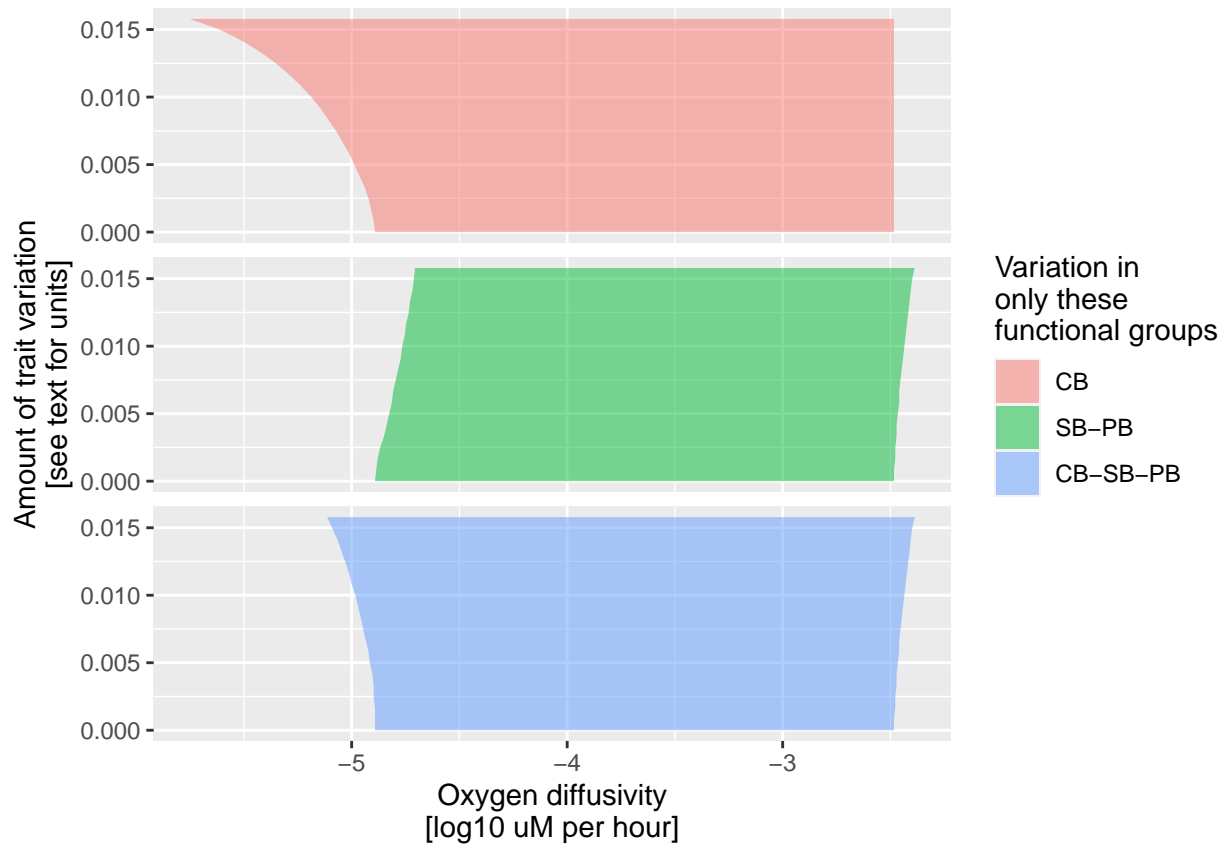


```
##ggsave("manuscript/figures/extent_of_bistab2.pdf", height = 4)
stab_data1 <- readRDS(here("experiments/experiment 1/data/stab_data_1000000_20factorial.RDS"))
stab_data_x <- readRDS(here("experiments/experiment 1/data/stab_data_1e6_noCB_5xSBPB_.RDS"))
stab_data_plus <- bind_rows(stab_data1, stab_data_x)
stab_data_plus %>%
  filter(Species == "O",
         sim_length == 1e6) %>%
  ggplot(aes(x = CB_var_gmax_s, y = SB_var_gmax_s, fill = hyst_range, col = hyst_range)) +
  geom_point(size = 3)
```
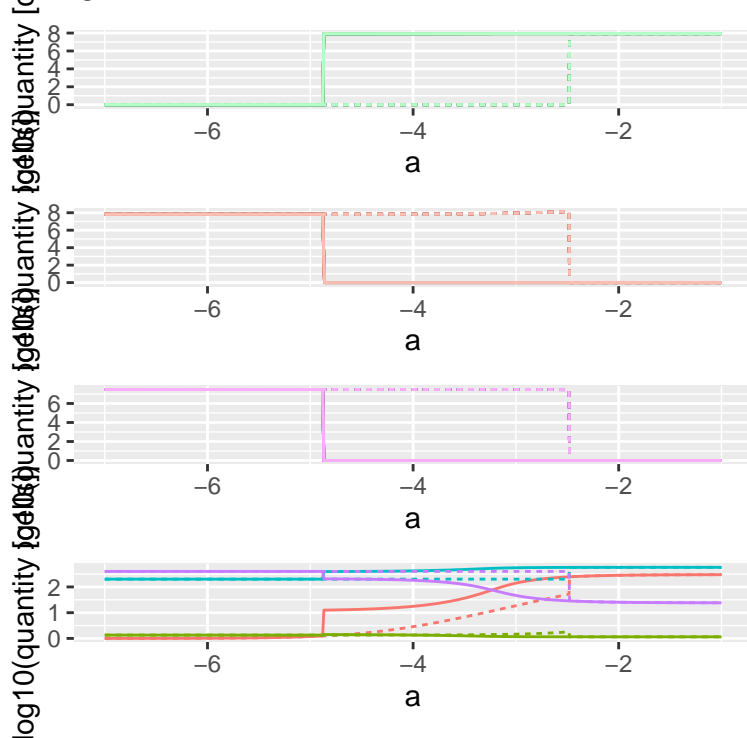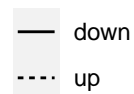
21
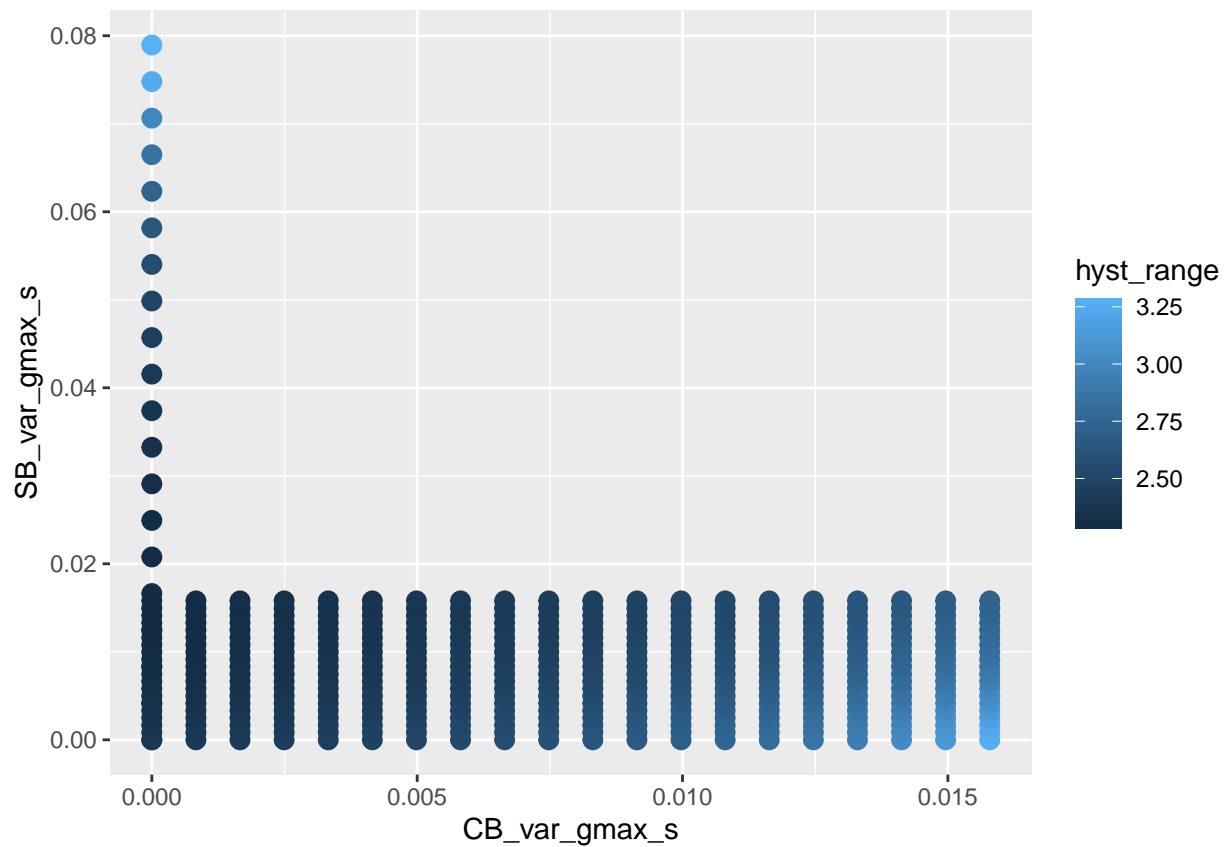
Extra SBPB diversity

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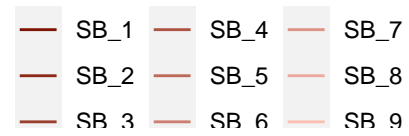
CB_gmax_var = 0 CB_h_var =0
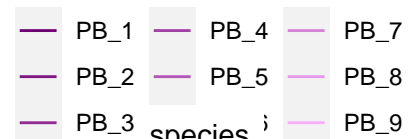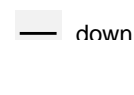SB_gmax_var = 0 SB_h_var =0
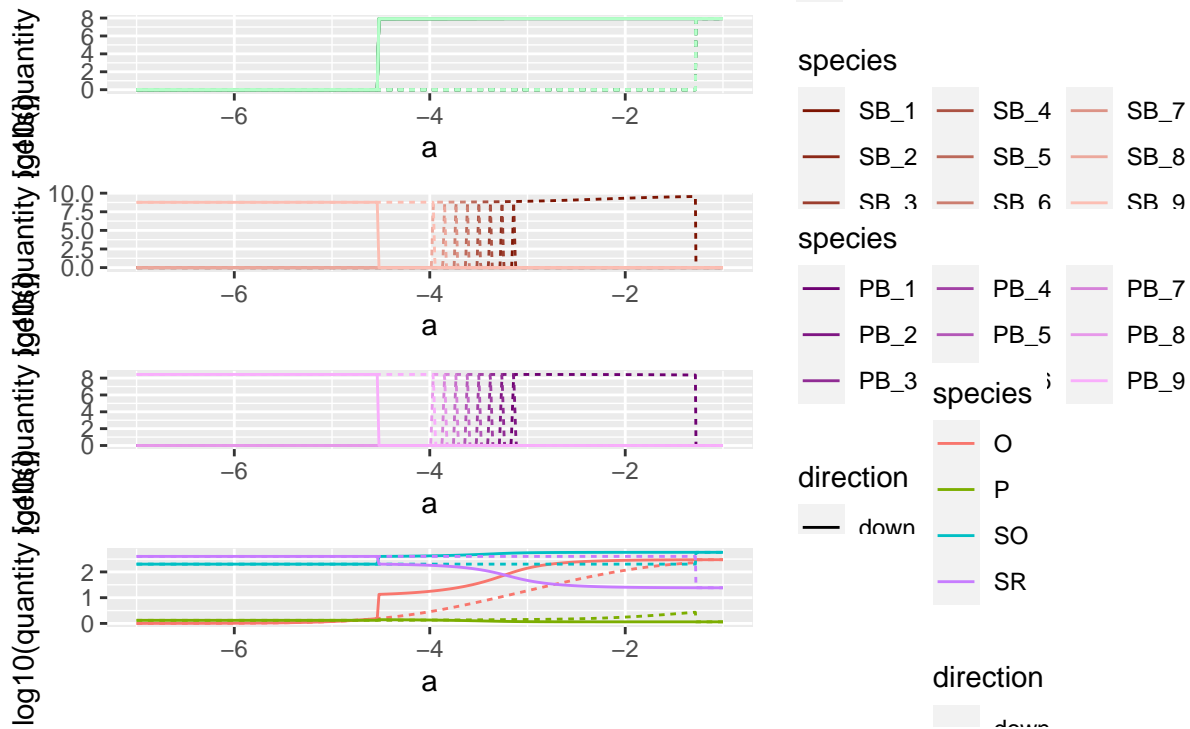PB_gmax_var = 0 PB_h_var =0

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

CB_gmax_var = 0 CB_h_var =0
SB_gmax_var = 0.0747922452631579 SB_h_var =−1.53
PB_gmax_var = 0.0747922452631579 PB_h_var =−1.53

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_6	— PB_9

species
— O
— P
— SO
— SR

direction
— down

direction
down

```
p_overlay1 <- plot_ss_result2(var_expt_x[1,]$ss_res[[1]],
                              var_expt_x[19,]$ss_res[[1]],
                              xlims = c(-7, -1))
```
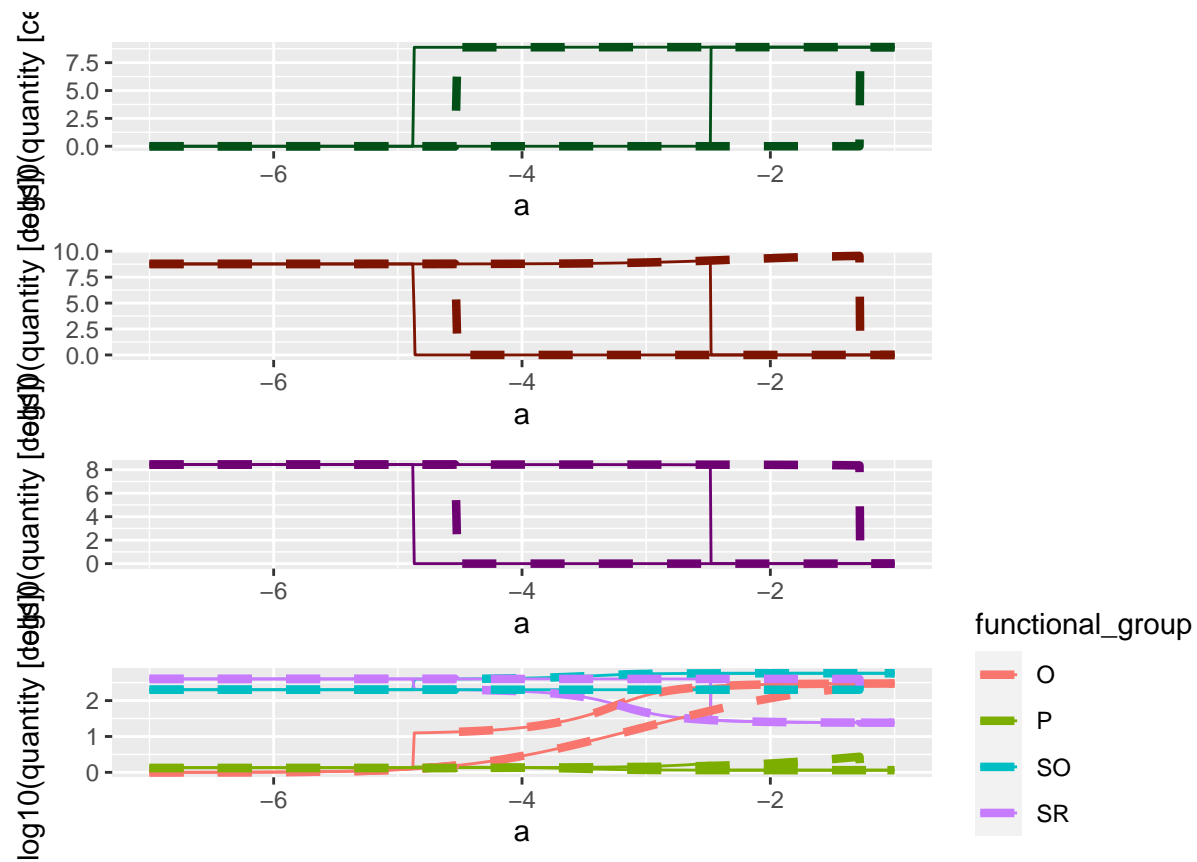
```
## `summarise()` has grouped output by 'a', 'direction', 'var_type'. You can override using the `.groups
## `summarise()` has grouped output by 'a', 'direction', 'var_type'. You can override using the `.groups
```

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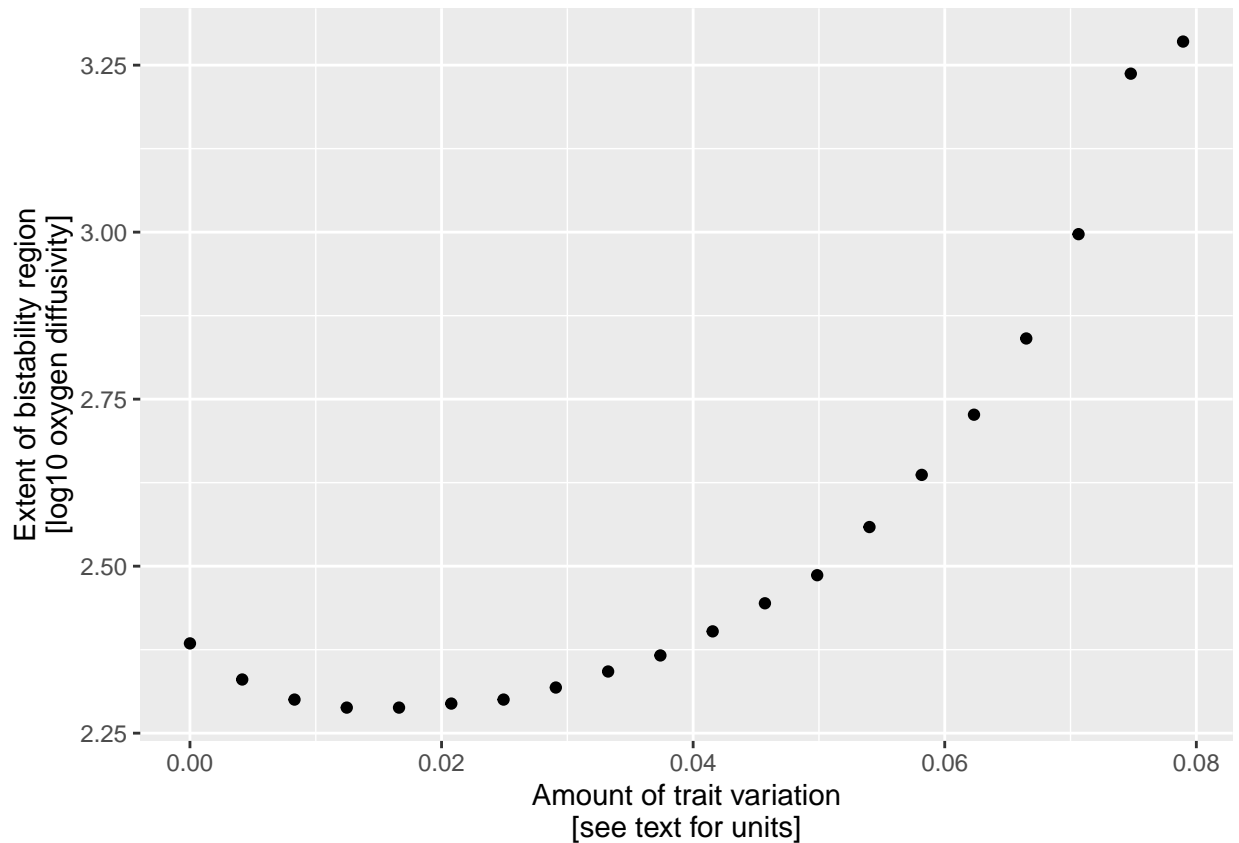
```
##ggsave("manuscript/figures/extent_of_bistab1.pdf", height = 4)

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()
  )
```
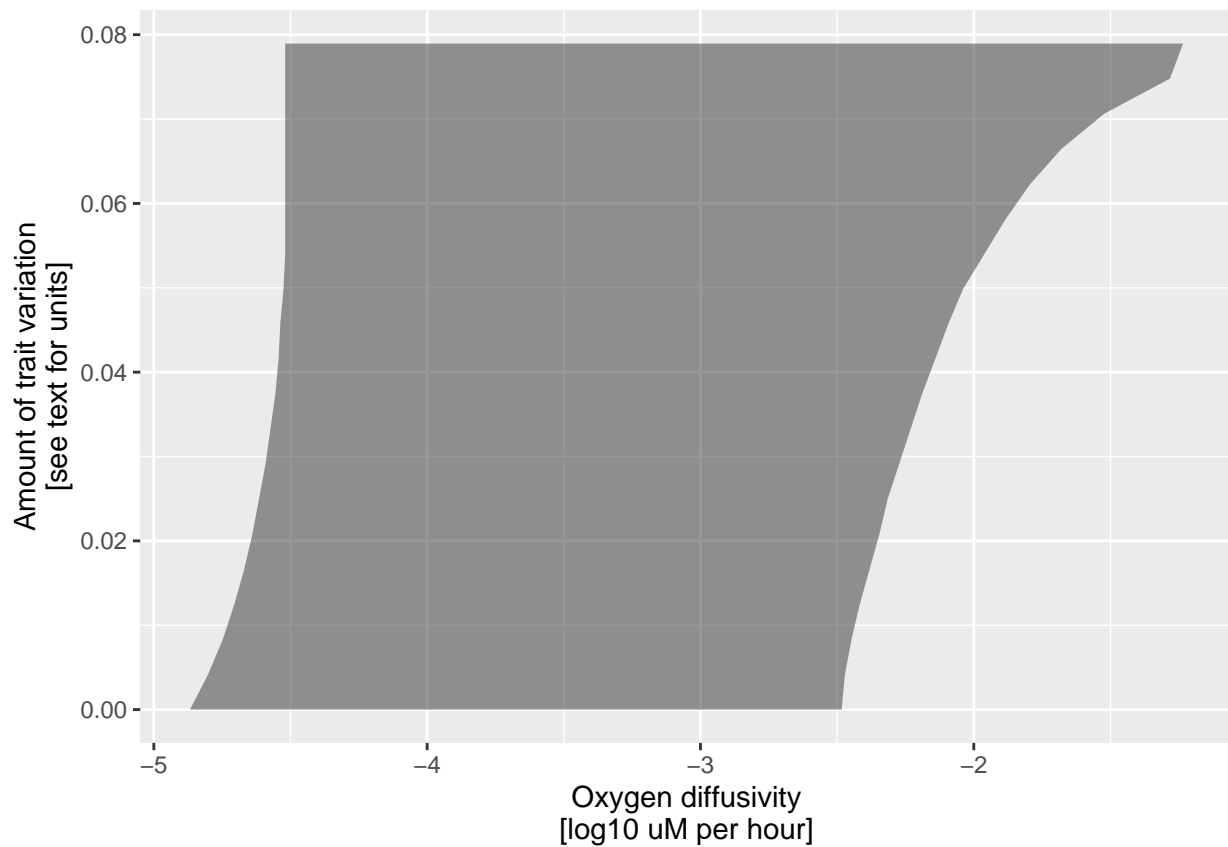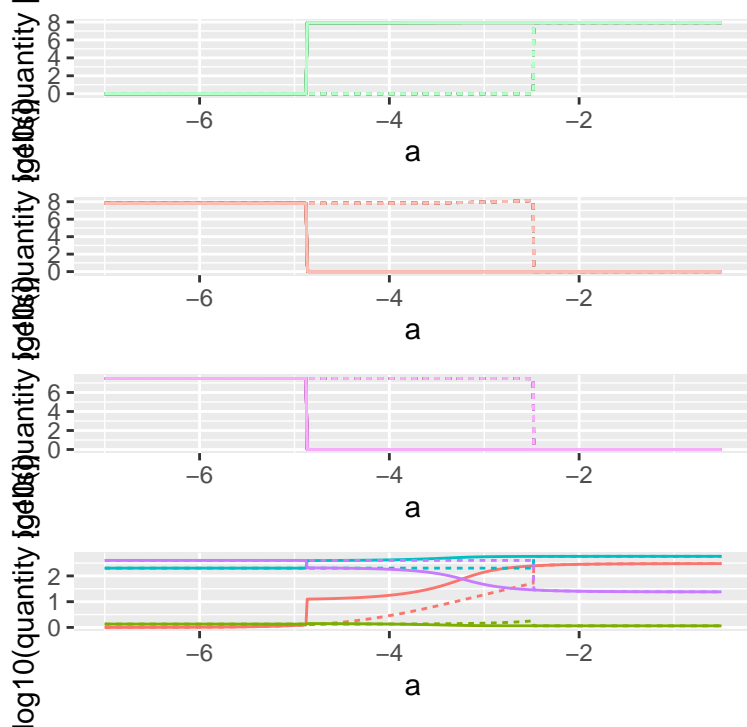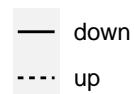
2x CB, 6xSBPB diversity

```
var_expt <- readRDS(here("experiments/experiment 1/data/ss_data_1e6_x2x6_factorial.RDS"))
stab_data <- readRDS(here("experiments/experiment 1/data/stab_data_1e6_x2x6_factorial.RDS"))

p1  <- plot_ss_result1(var_expt,
             result_index = 1,
             filename_prefix = NULL,
             save_image_file = FALSE)
p1
```
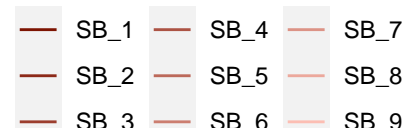
CB_gmax_var = 0 CB_h_var =0
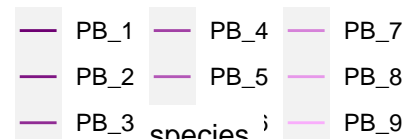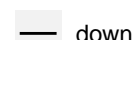SB_gmax_var = 0 SB_h_var =0
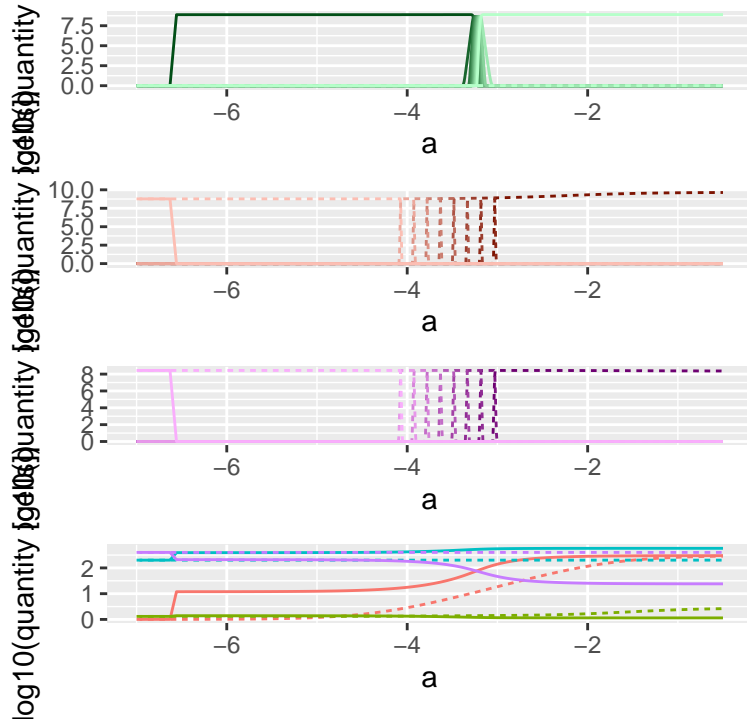PB_gmax_var = 0 PB_h_var =0


```
p1  <- plot_ss_result1(var_expt,
              result_index = 400,
              filename_prefix = NULL,
              save_image_file = FALSE)
p1
```

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

```
p_overlay1 <- plot_ss_result2(var_expt[1,]$ss_res[[1]],
                              var_expt[400,]$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 154 row(s) containing missing values (geom_path).

Warning: Removed 154 row(s) containing missing values (geom_path).

Warning: Removed 154 row(s) containing missing values (geom_path).

Warning: Removed 154 row(s) containing missing values (geom_path).

Warning: Removed 154 row(s) containing missing values (geom_path).

Warning: Removed 154 row(s) containing missing values (geom_path).

Warning: Removed 616 row(s) containing missing values (geom_path).

Warning: Removed 616 row(s) containing missing values (geom_path).
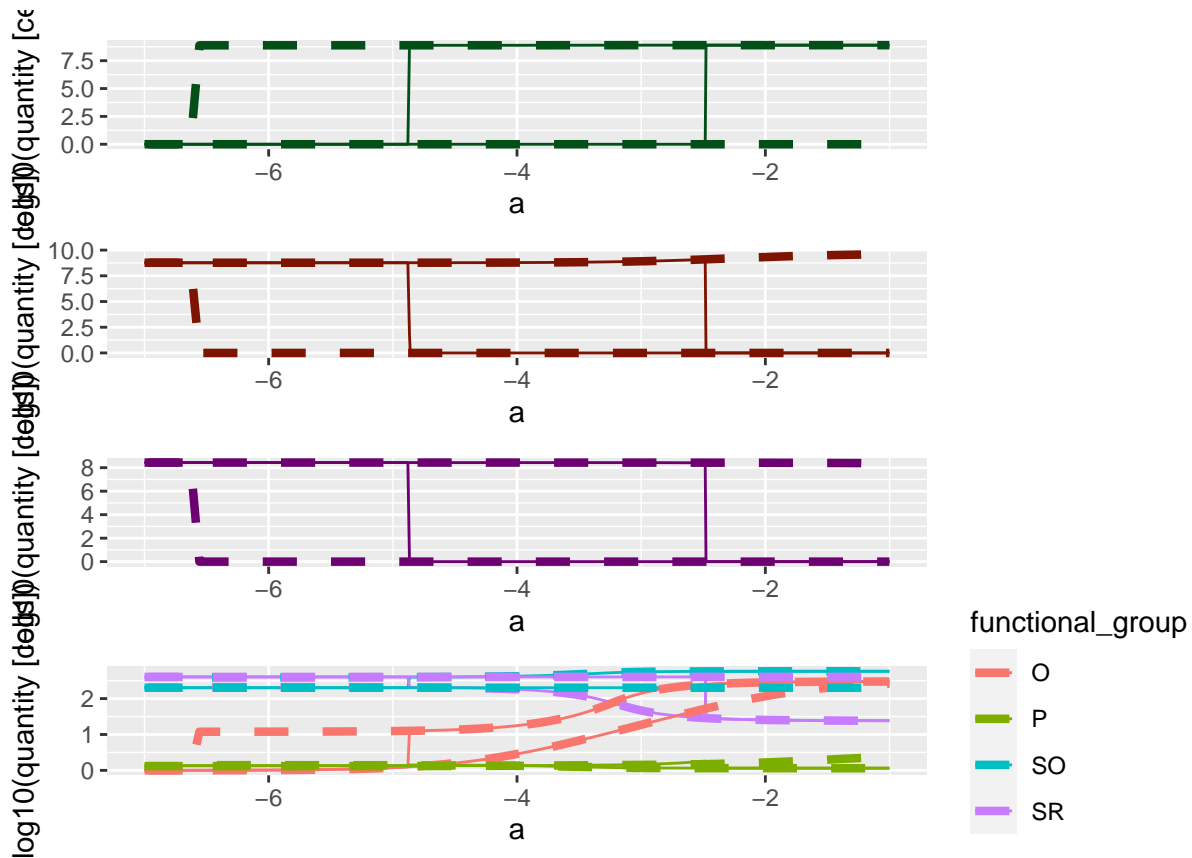
```
CB_vars <- unique(stab_data$CB_var_gmax_s)
SB_vars <- unique(stab_data$SB_var_gmax_s)

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 = 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()
)
```



```
##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, col = hyst_range)) +
  geom_point(size = 3)
```
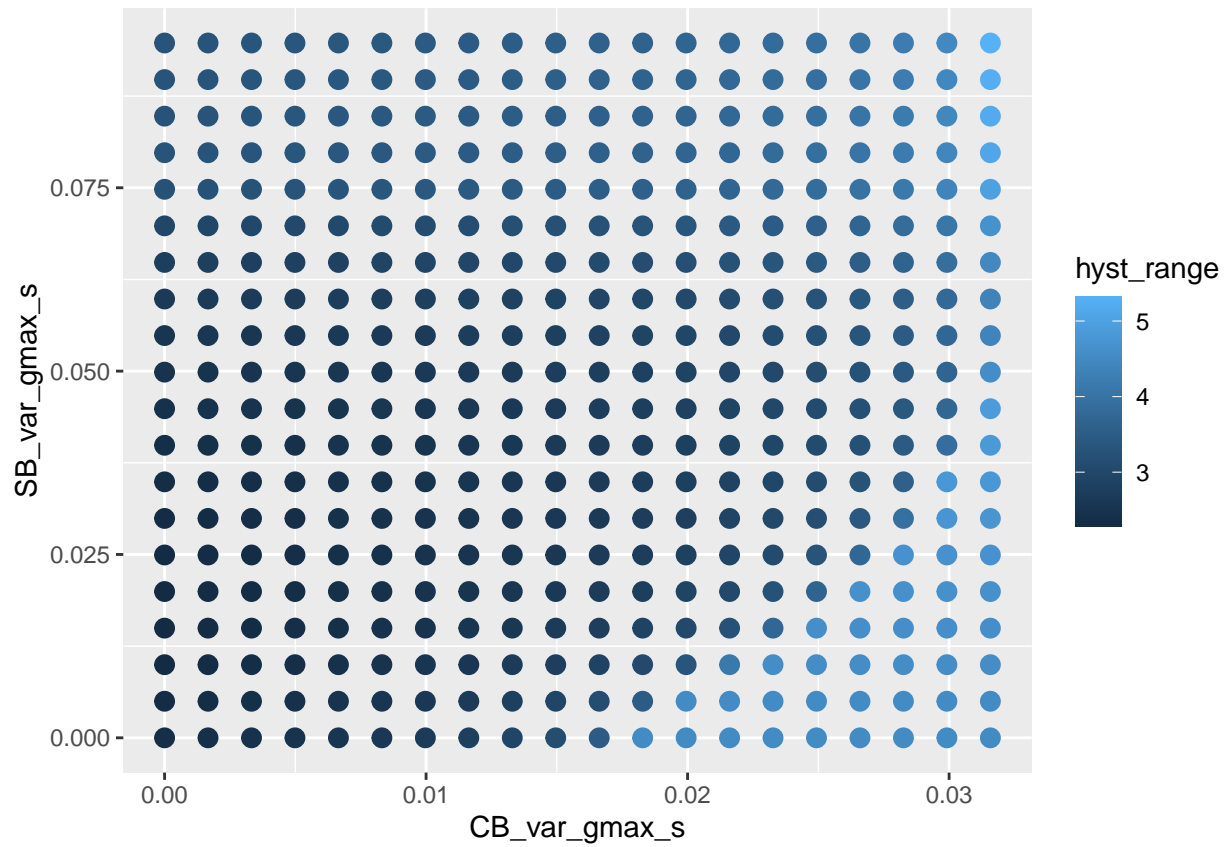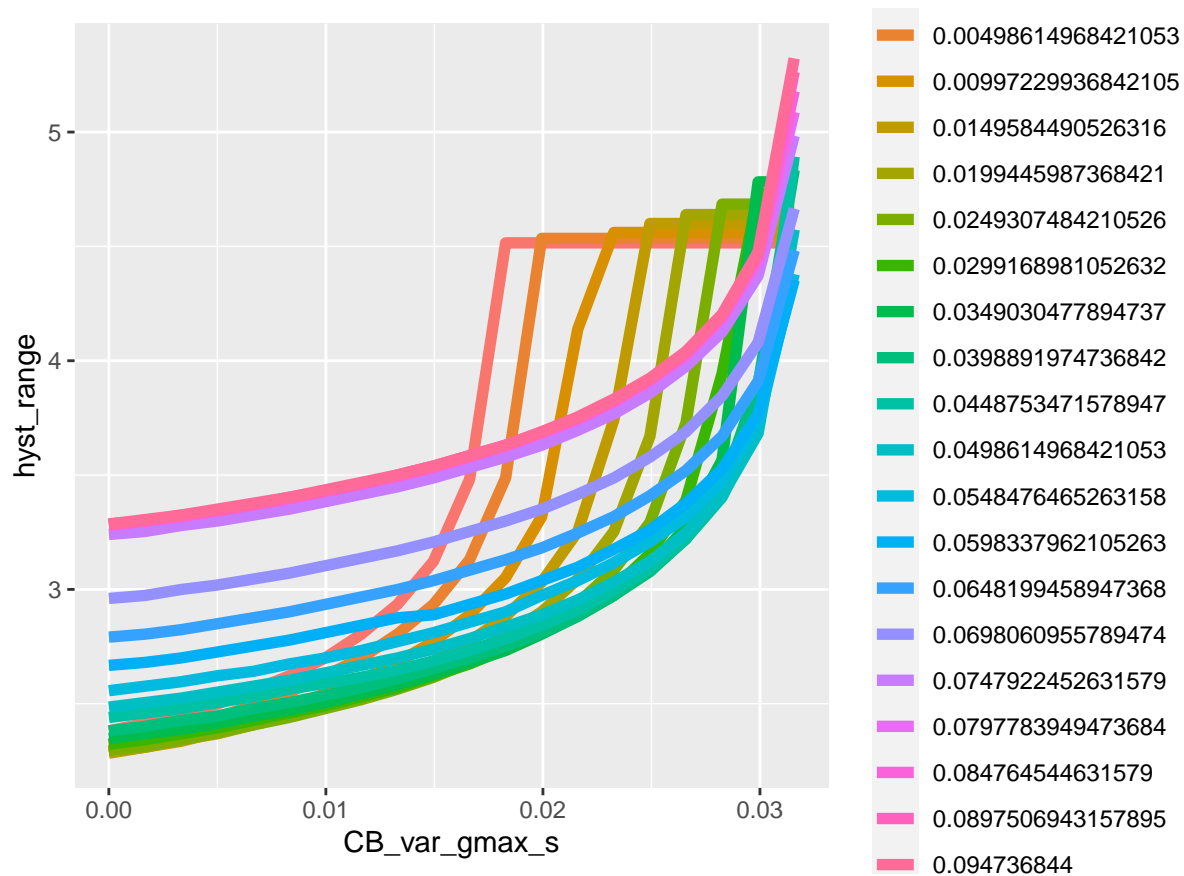
```
##ggsave("manuscript/figures/extent_of_bistab2.pdf", height = 4)

stab_data %>%
  filter(Species == "O",
         sim_length == 1e6) %>%
  ggplot(aes(x = CB_var_gmax_s, y = hyst_range, 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

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
```

CB_gmax_var = 0.015789474 CB_h_var =−0.08
SB_gmax_var = 0.015789474 SB_h_var =−0.323
PB_gmax_var = 0.015789474 PB_h_var =−0.323
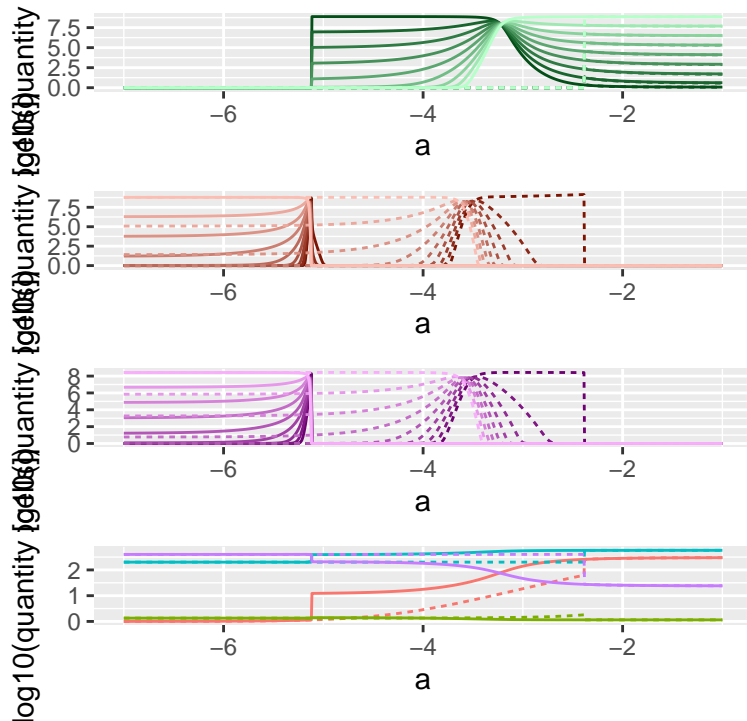

```
p1_long  <- plot_ss_result1(var_expt1,
              result_index = max_diversty_all,
              filename_prefix = NULL,
              save_image_file = FALSE)
p1_long
```

CB_gmax_var = 0.015789474 CB_h_var =−0.08
SB_gmax_var = 0.015789474 SB_h_var =−0.323
PB_gmax_var = 0.015789474 PB_h_var =−0.323
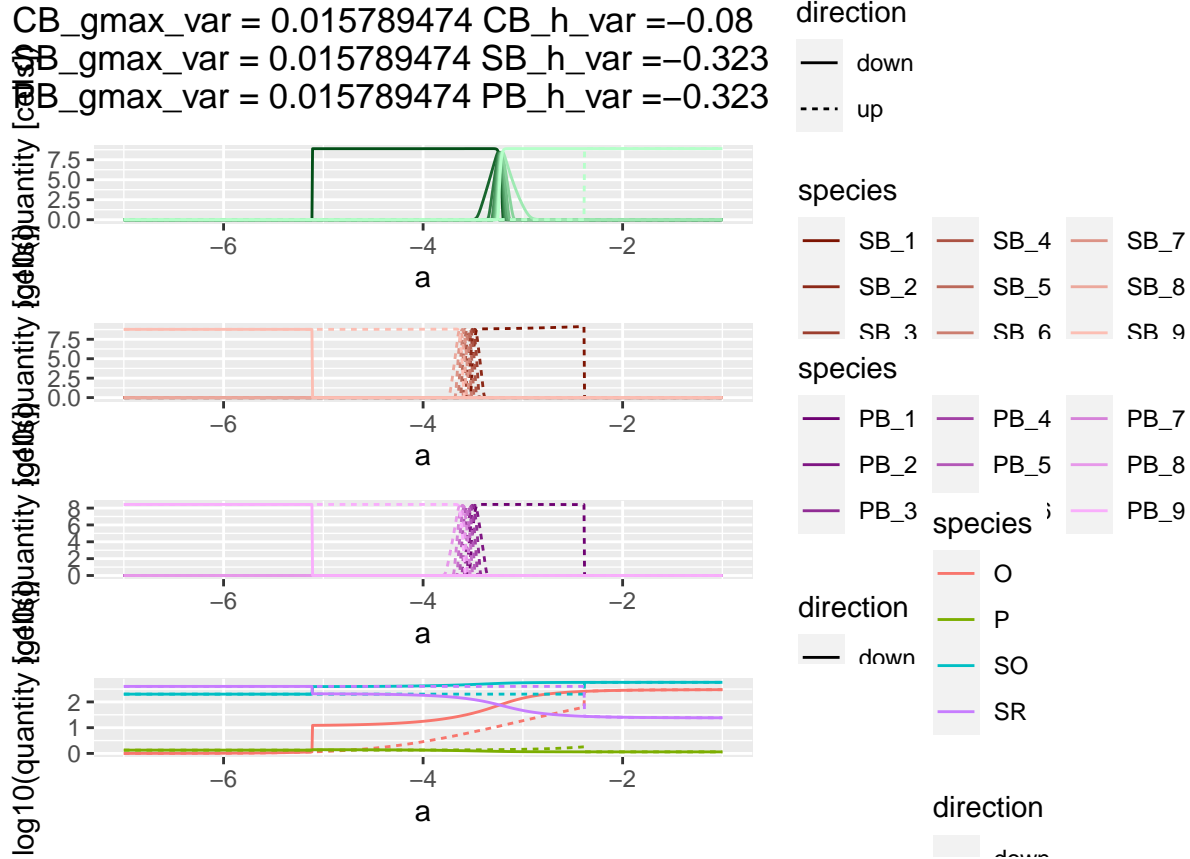
Analysis with least and most tolerant Sulfur Bacteria

```
#########################################
###### Setup copy-pasted from above

num_CB_strains <- 9
num_SB_strains <- 9
num_PB_strains <- 9

## multiplier of SBPB variation
CB_var_multiplier <- 1
SBPB_var_multiplier <- 1

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

var_expt <- create_diversity_factorial()

## rows of interest
```

```r
var_expt_levels <- var_expt[,1:6]
no_diversity <- which(rowSums(abs(var_expt_levels))==0)
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)

## Overwriting average values with most and least tolerant values (tolerance and respective growth)

most_tolerant_PB <- var_expt[max_only_SBPB_diversity,]$pars[[1]]$PB
least_tolerant_PB <- most_tolerant_PB[which.min(most_tolerant_PB$h_0_PB),]
most_tolerant_PB <- most_tolerant_PB[which.max(most_tolerant_PB$h_0_PB),]

most_tolerant_SB <- var_expt[max_only_SBPB_diversity,]$pars[[1]]$SB
least_tolerant_SB <- most_tolerant_SB[which.min(most_tolerant_SB$h_0_SB),]
most_tolerant_SB <- most_tolerant_SB[which.max(most_tolerant_SB$h_0_SB),]

var_expt_most_tolerant_SBPB <- var_expt[no_diversity, ]
var_expt_most_tolerant_SBPB$pars[[1]]$PB[1:9] <- most_tolerant_PB
var_expt_most_tolerant_SBPB$pars[[1]]$SB[1:9] <- most_tolerant_SB
var_expt_most_tolerant_SBPB$pars[[1]]$PB$strain_name <- paste0("PB_",1:9)
var_expt_most_tolerant_SBPB$pars[[1]]$SB$strain_name <- paste0("SB_",1:9)

var_expt_least_tolerant_SBPB <- var_expt[no_diversity, ]
var_expt_least_tolerant_SBPB$pars[[1]]$PB[1:9] <- least_tolerant_PB
var_expt_least_tolerant_SBPB$pars[[1]]$SB[1:9] <- least_tolerant_SB
var_expt_least_tolerant_SBPB$pars[[1]]$PB$strain_name <- paste0("PB_",1:9)
var_expt_least_tolerant_SBPB$pars[[1]]$SB$strain_name <- paste0("SB_",1:9)
## number of cores usable
options(mc.cores = detectCores()-1)

## setup copy-pasted from above
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_Os <- 10^seq(-7, -0.5, 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_Os)

## Here the simulations with least and most tolerantsulfur bacteria are run.
var_expt <- var_expt_least_tolerant_SBPB
var_expt_least_tolerant_SBPB <- run_ss_var_experiment()
saveRDS(var_expt_least_tolerant_SBPB, here("experiments/experiment 1/data/ss_data_1e6_x1x1_factorial_SB
```
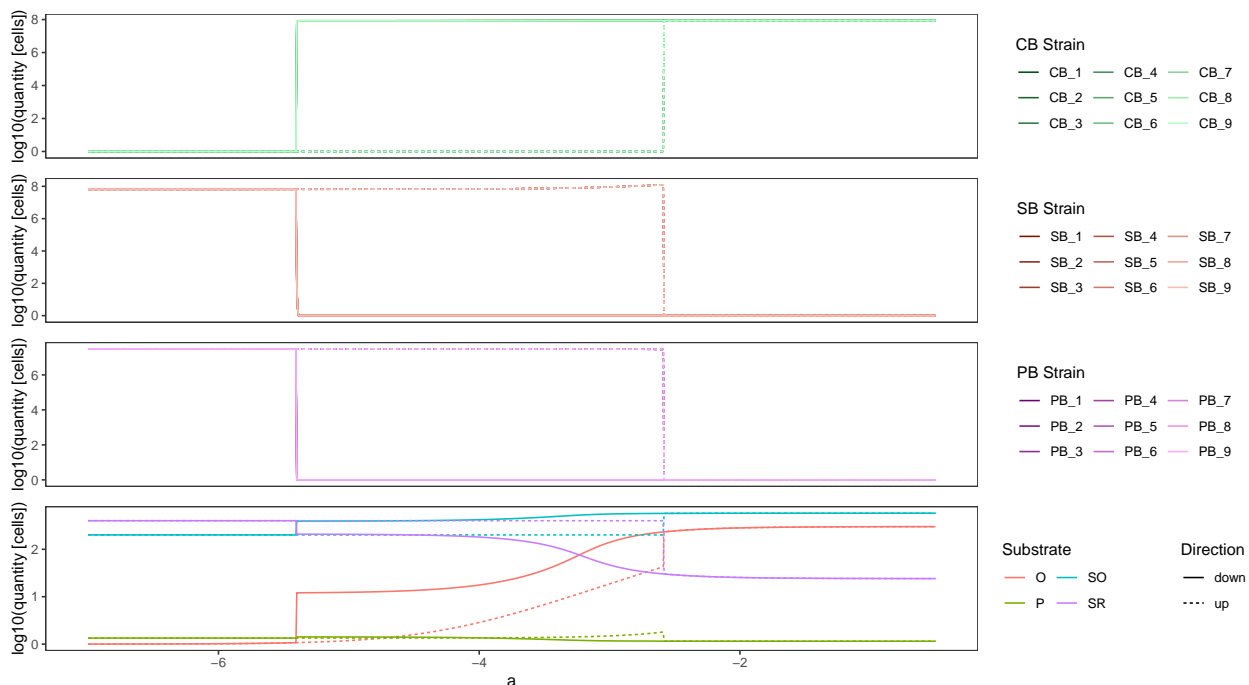
```
var_expt <- var_expt_most_tolerant_SBPB
var_expt_most_tolerant_SBPB <- run_ss_var_experiment()
saveRDS(var_expt_most_tolerant_SBPB, here("experiments/experiment 1/data/ss_data_1e6_x1x1_factorial_SBPI

var_expt_least_tolerant_SBPB <- readRDS(here("experiments/experiment 1/data/ss_data_1e6_x1x1_factorial_S
var_expt_most_tolerant_SBPB <- readRDS(here("experiments/experiment 1/data/ss_data_1e6_x1x1_factorial_SI

plot_ss_result1_v2(var_expt_least_tolerant_SBPB,
                   result_index = 1,
                   filename_prefix = NULL,
                   save_image_file = FALSE) +
  plot_annotation(caption = 'Least tolerant SB and PB strains + average CB strain')
```
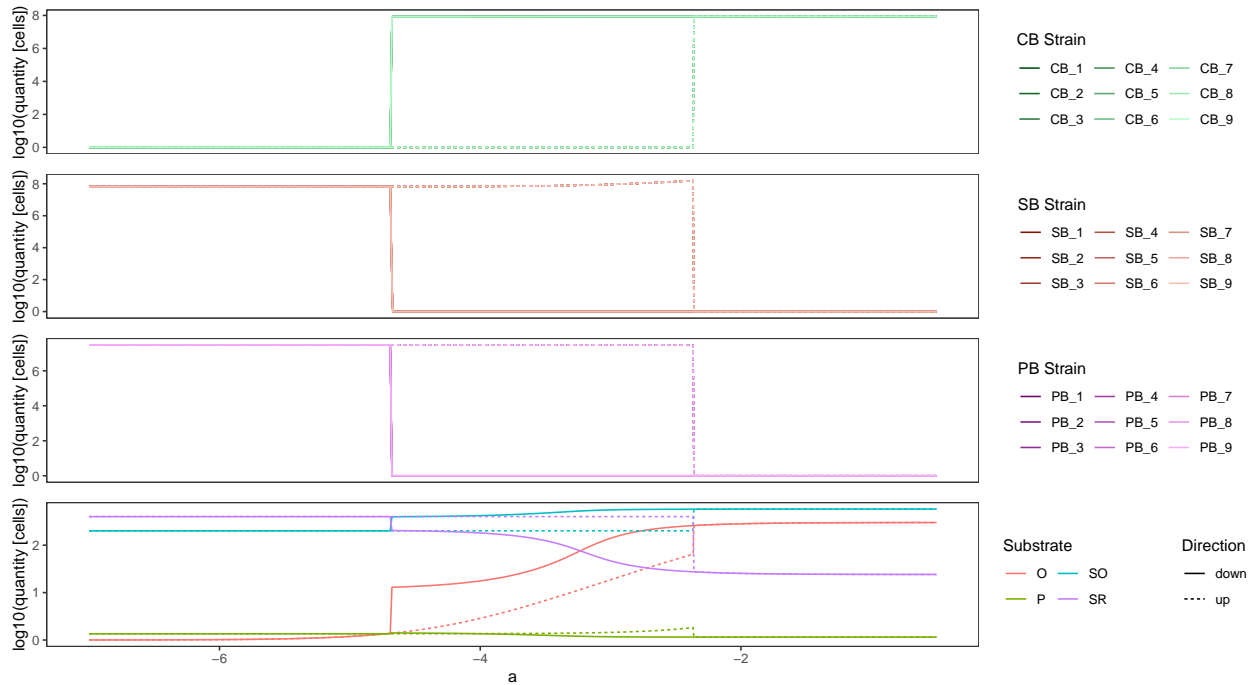

Least tolerant SB and PB strains + average CB strain

```
plot_ss_result1_v2(var_expt_most_tolerant_SBPB,
                   result_index = 1,
                   filename_prefix = NULL,
                   save_image_file = FALSE)+
  plot_annotation(caption = 'Most tolerant SB and PB strains + average CB strain')
```

CB_gmax_var = 0 CB_h_var =0
SB_gmax_var = 0 SB_h_var =0
PB_gmax_var = 0 PB_h_var =0
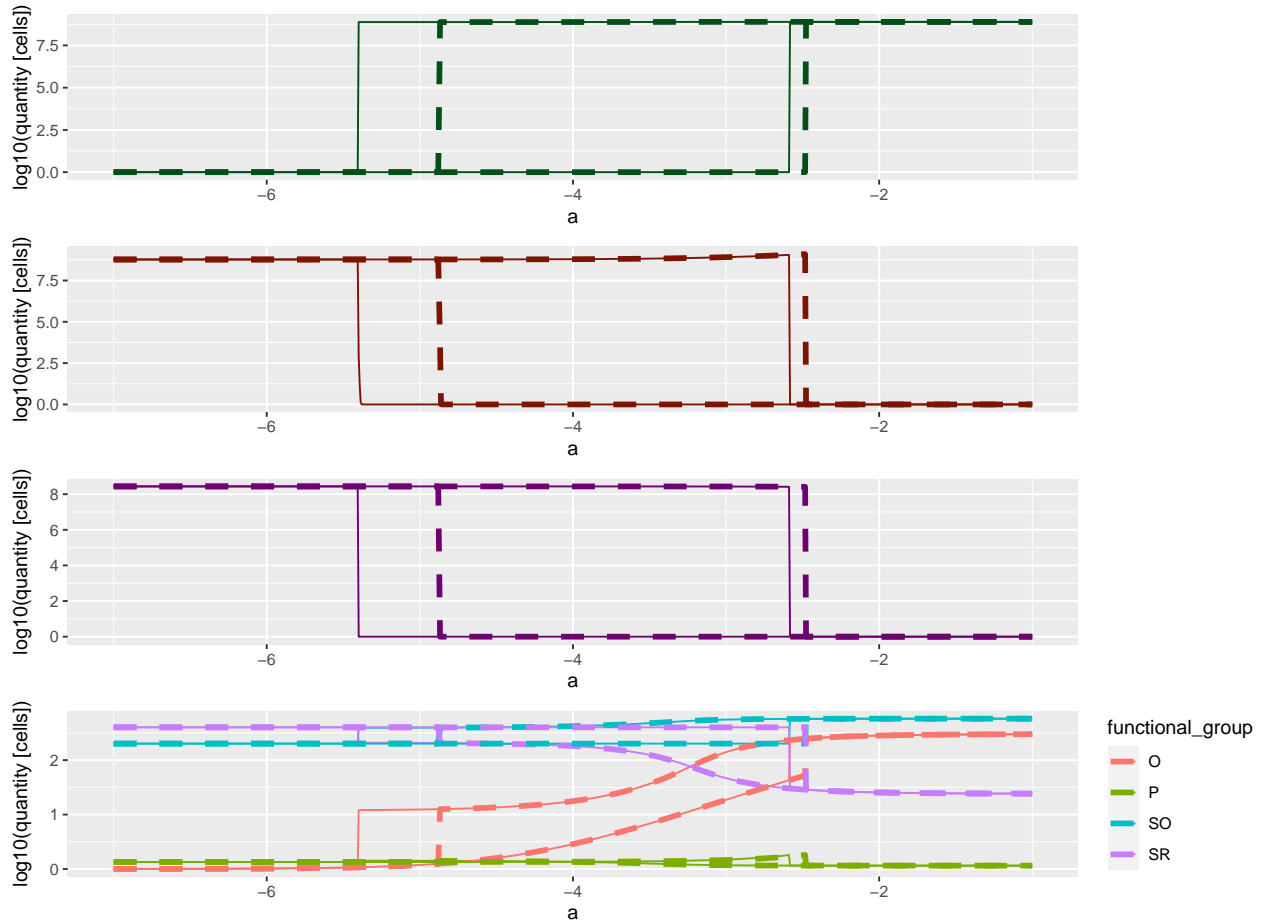
Most tolerant SB and PB strains + average CB strain

```
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_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)

plot_ss_result2(var_expt_least_tolerant_SBPB$ss_res[[1]],
                var_expt[no_diversity,]$ss_res[[1]],
                xlims = c(-7, -1))+
  plot_annotation(title = 'Sims with LEAST tolerant SB and PB strains + average CB strain (solid line)\i
```

Sims with LEAST tolerant SB and PB strains + average CB strain (solid line)
Versus
Sims with no diversity (average values) (dashed line)


```
plot_ss_result2(var_expt_least_tolerant_SBPB$ss_res[[1]],
                var_expt[max_only_SBPB_diversity,]$ss_res[[1]],
                xlims = c(-7, -1))+
  plot_annotation(title = 'Sims with LEAST tolerant SB and PB strains + average CB strain (solid line)\
```

Sims with LEAST tolerant SB and PB strains + average CB strain (solid line)
Versus
Sims with diversity in SBPB, no diversity (average value) in CB (dashed line)


```
plot_ss_result2(var_expt_most_tolerant_SBPB$ss_res[[1]],
                var_expt[no_diversity,]$ss_res[[1]],
                xlims = c(-7, -1))+
    plot_annotation(title = 'Sims with MOST tolerant SB and PB strains + average CB strain (solid line)\n'
```

Sims with MOST tolerant SB and PB strains + average CB strain (solid line)
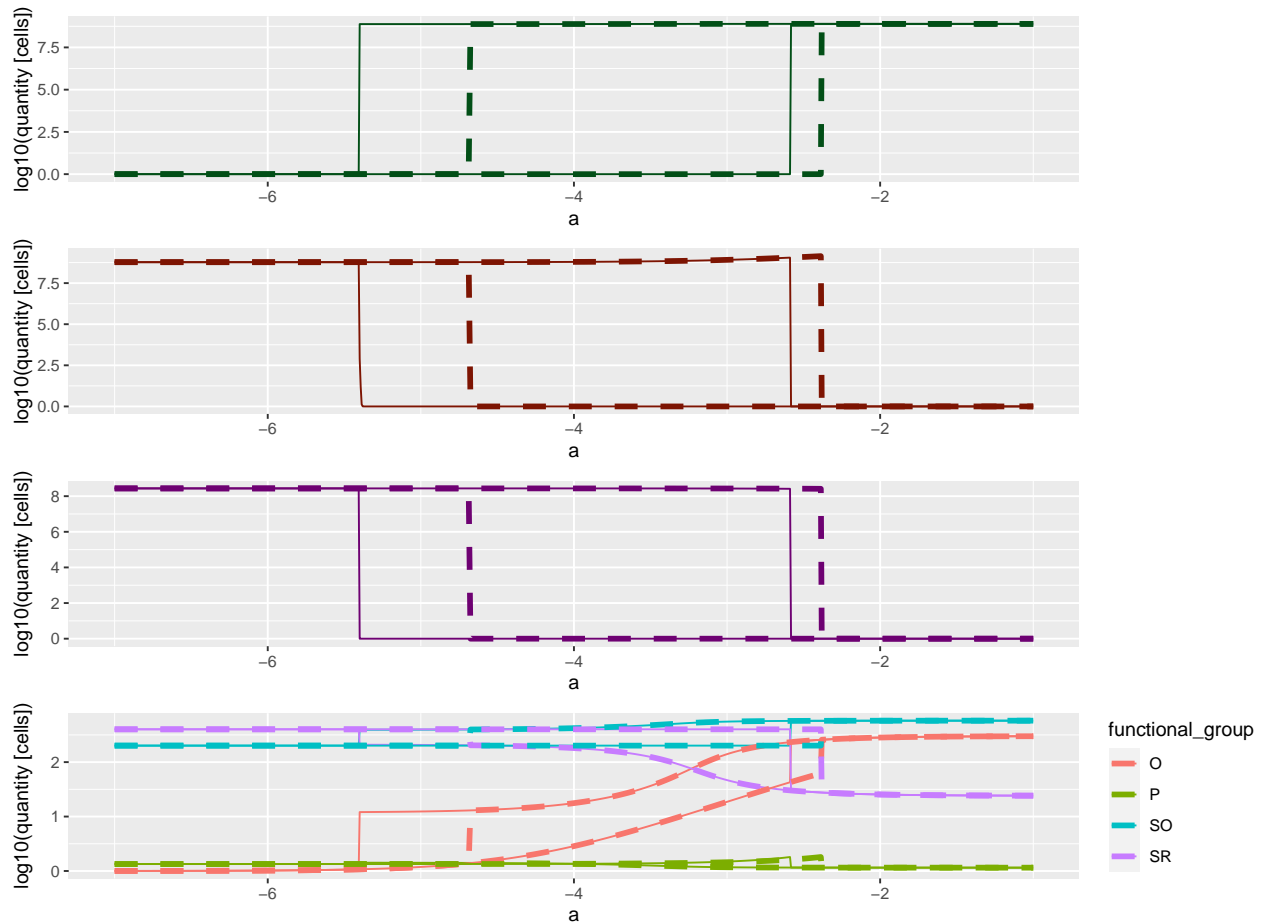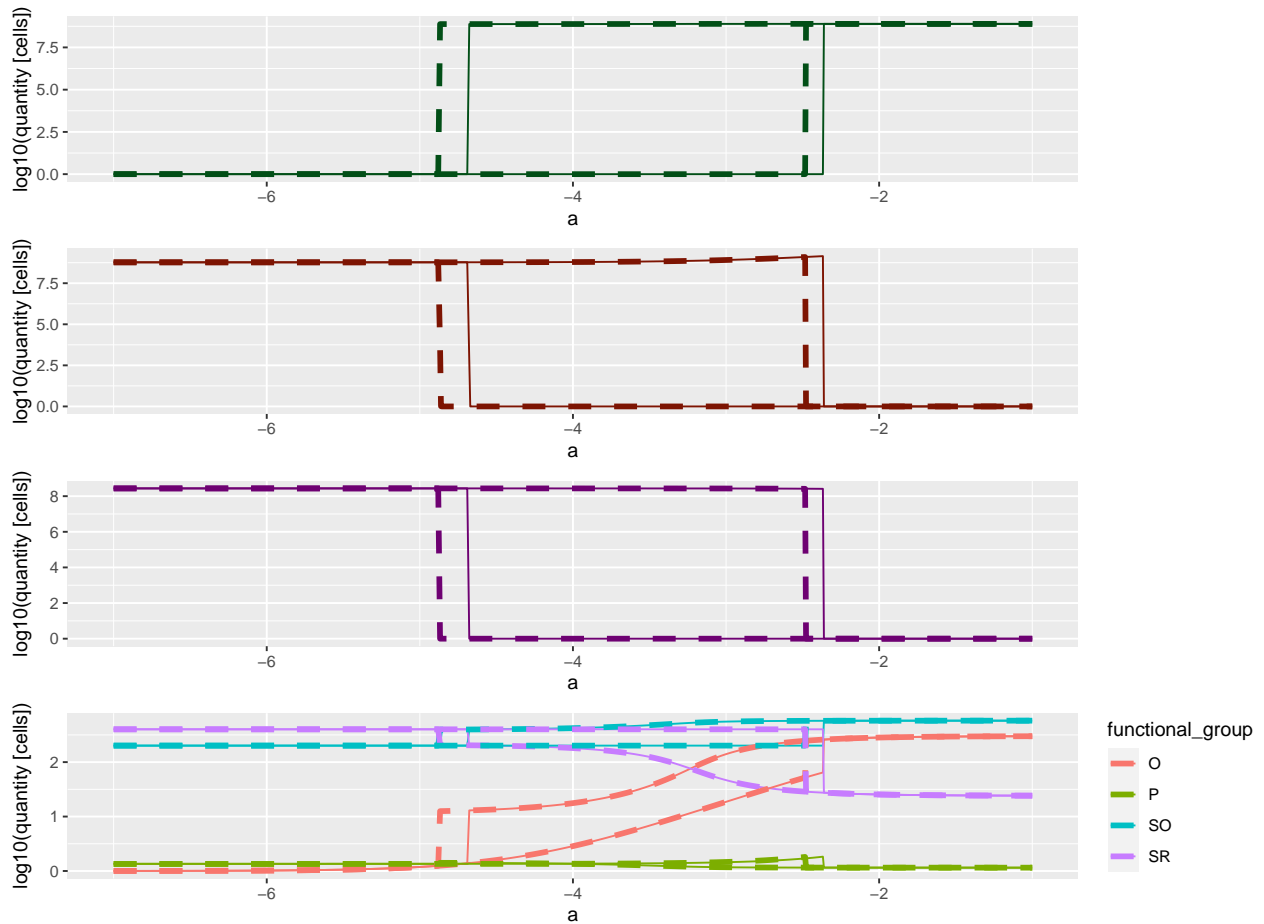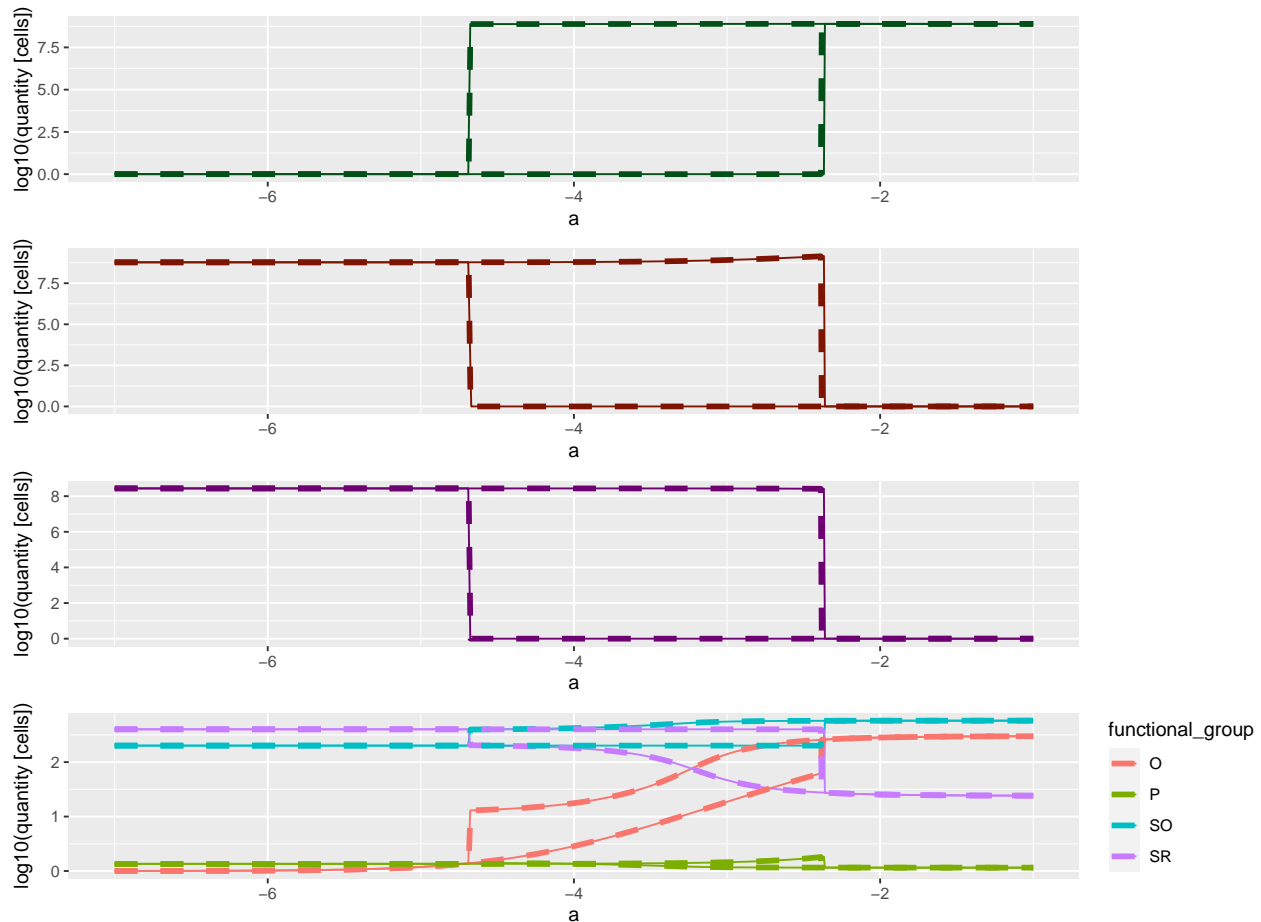Versus
Sims with no diversity (average values) (dashed line)


```
plot_ss_result2(var_expt_most_tolerant_SBPB$ss_res[[1]],
                var_expt[max_only_SBPB_diversity,]$ss_res[[1]],
                xlims = c(-7, -1))+
  plot_annotation(title = 'Sims with MOST tolerant SB and PB strains + average CB strain (solid line)\n'
```

Sims with MOST tolerant SB and PB strains + average CB strain (solid line)
Versus
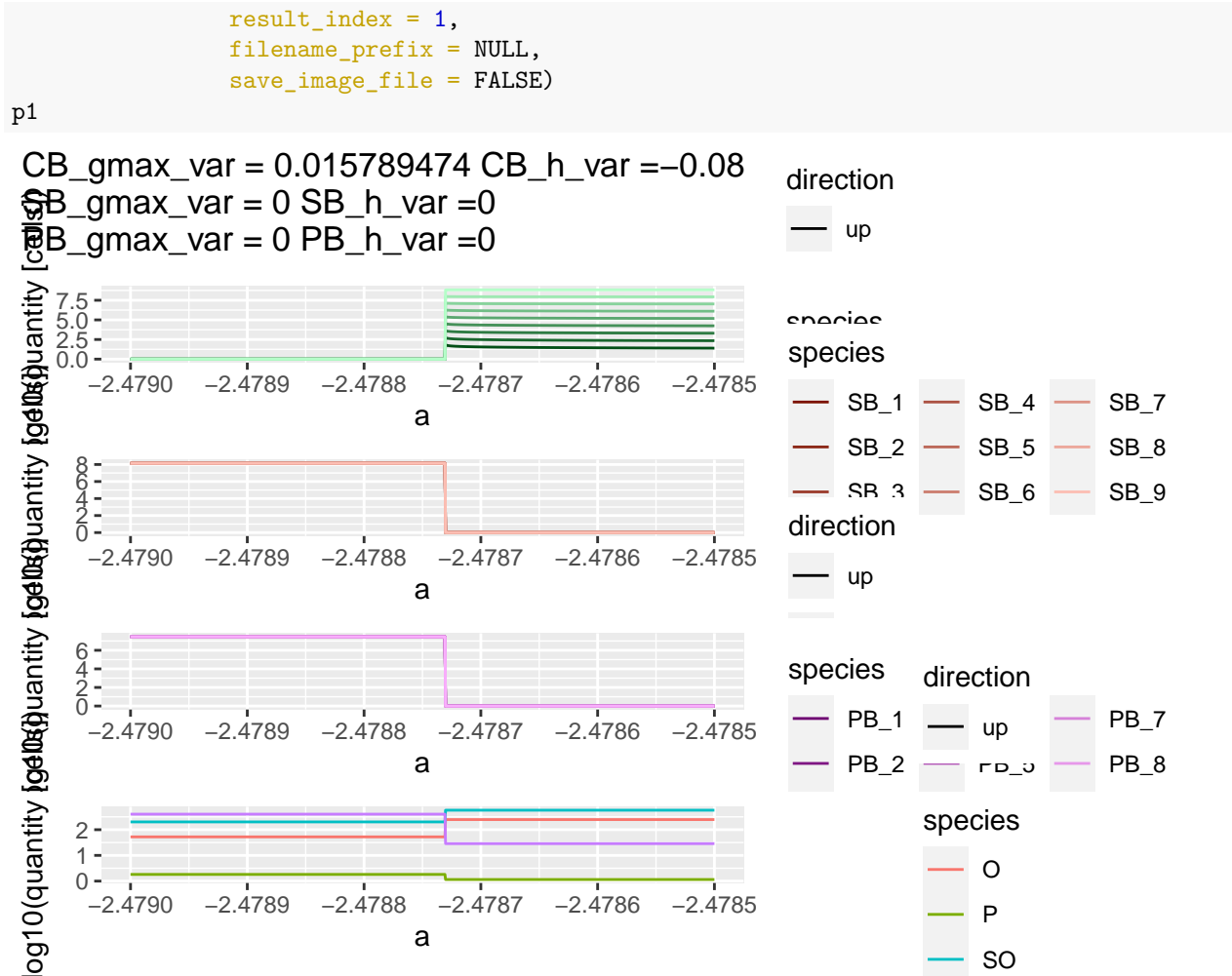Sims with diversity in SBPB, no diversity (average value) in CB (dashed line)

Zoom in on SS

```r
a_Os <- 10^seq(-2.479, -2.4785, length=grid_num_a) ## sequence of a_0 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,]
```

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

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

```r
p1  <- plot_ss_result1(zoom,
```

```
            result_index = 1,
            filename_prefix = NULL,
            save_image_file = FALSE)
p1
```


CB_gmax_var = 0.015789474 CB_h_var =−0.08
SB_gmax_var = 0 SB_h_var =0
PB_gmax_var = 0 PB_h_var =0

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_O

ss_expt_master <- ss_expt
ss_expt <- ss_expt_master[abs(ss_expt_master$a_O - 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]]
```

```r
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_0s[354]) ## very slowly goes anoxic
#log10_a <- log10(a_0s[356]) ## very very very  slowly goes anoxic
#log10_a <- log10(a_0s[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
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)
```
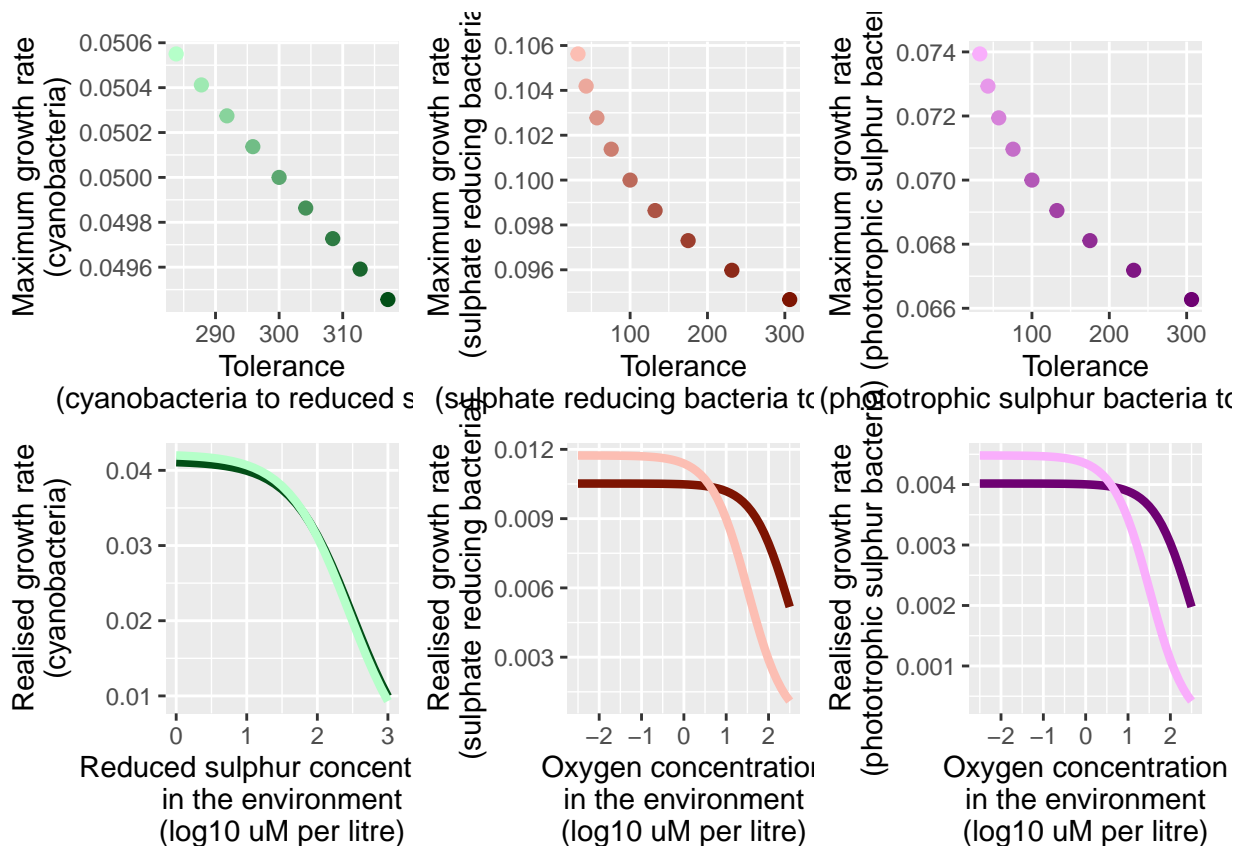
Understand about relative and absolute variation in traits


```
## [1] 0.03266455

## [1] 0.01063672

## [1] 0.004061293
```

With the CB diversity multiplier set at 1 and the SB/PB multiplier set at 5 the range of realised growth rates of CB is 0.0326645, range of SB is 0.0106367, and range of PB is 0.0040613.