

Experiment 1

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Setup

R

```
rm(list = ls())

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

microxanox_release <- "0.2.1"

#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(
#   "UZH-PEG/microxanox",
#   ref = microxanox_release,
#   # auth_token = "ENTER YOUR TOKEN or PROVED AS ENVIRONMENT VARIABLE",
#   build_vignettes = FALSE,
#   force = TRUE,
#   upgrade = FALSE
# )

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)
```

Version of microxanox package used: 0.2

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
CB_h_div <- -0.08
SB_gmax_div <- 0.015789474
SB_h_div <- -0.323
PB_gmax_div <- 0.015789474
PB_h_div <- -0.323

num_div_treatment_levels <- 20
```

Create diversity

```
var_expt <- create_diversity()

var_expt[["pars"]][[20]]$CB
```

##	strain_name	g_max_CB	k_CB_P	h_SR_CB	y_P_CB	Pr_CB	m_CB	i_CB
## 1	CB_1	0.04945576	0.2	317.1054	1.67e+08	6e-09	0.02	0
## 2	CB_2	0.04959126	0.2	312.7397	1.67e+08	6e-09	0.02	0
## 3	CB_3	0.04972714	0.2	308.4341	1.67e+08	6e-09	0.02	0
## 4	CB_4	0.04986338	0.2	304.1878	1.67e+08	6e-09	0.02	0
## 5	CB_5	0.05000000	0.2	300.0000	1.67e+08	6e-09	0.02	0
## 6	CB_6	0.05013699	0.2	295.8698	1.67e+08	6e-09	0.02	0
## 7	CB_7	0.05027436	0.2	291.7965	1.67e+08	6e-09	0.02	0
## 8	CB_8	0.05041211	0.2	287.7792	1.67e+08	6e-09	0.02	0
## 9	CB_9	0.05055023	0.2	283.8173	1.67e+08	6e-09	0.02	0

```
var_expt[["pars"]][[20]]$SB
```

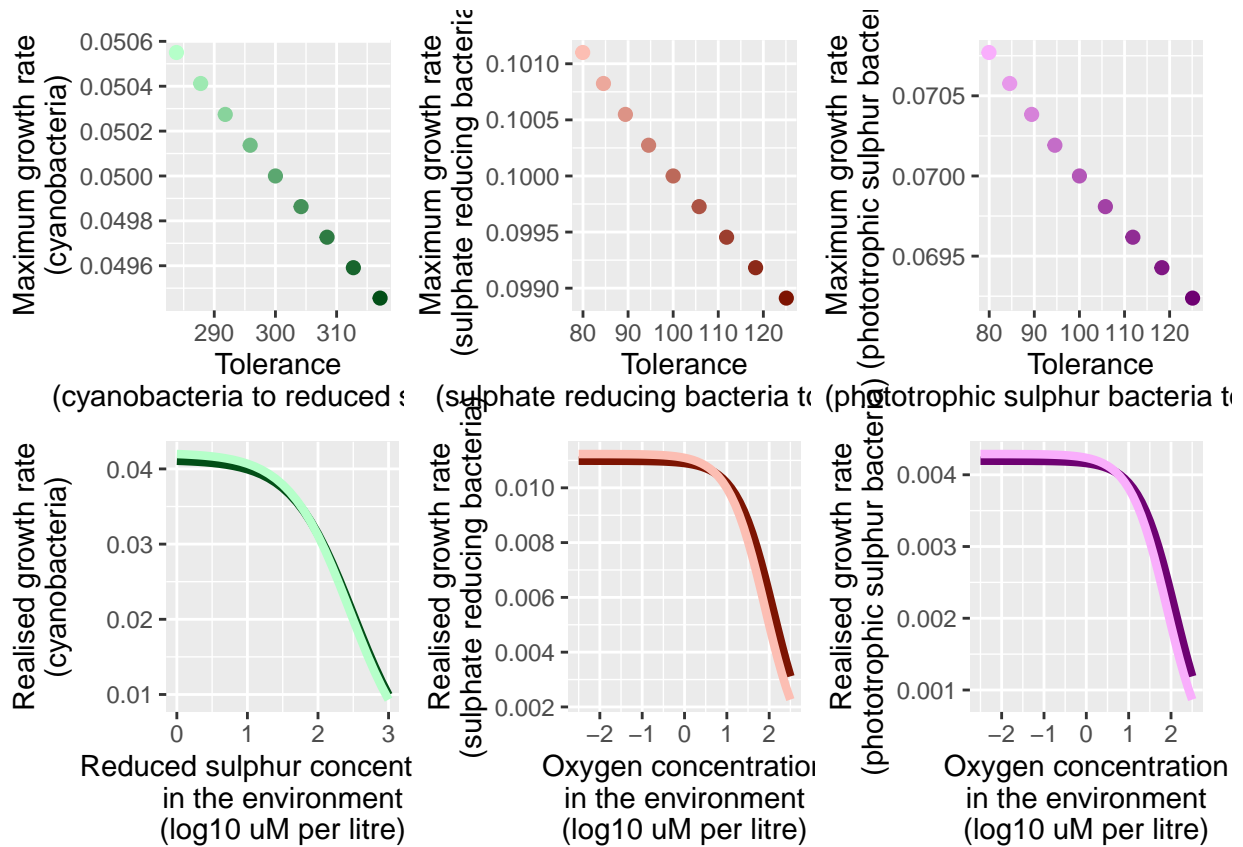
##	strain_name	g_max_SB	k_SB_SO	k_SB_P	h_O_SB	y_SO_SB	y_P_SB	m_SB	i_SB
## 1	SB_1	0.09891152	5	0.5	125.09291	33300000	1.67e+08	0.04	0
## 2	SB_2	0.09918253	5	0.5	118.28360	33300000	1.67e+08	0.04	0
## 3	SB_3	0.09945427	5	0.5	111.84494	33300000	1.67e+08	0.04	0
## 4	SB_4	0.09972676	5	0.5	105.75677	33300000	1.67e+08	0.04	0
## 5	SB_5	0.10000000	5	0.5	100.00000	33300000	1.67e+08	0.04	0
## 6	SB_6	0.10027399	5	0.5	94.55660	33300000	1.67e+08	0.04	0
## 7	SB_7	0.10054872	5	0.5	89.40950	33300000	1.67e+08	0.04	0
## 8	SB_8	0.10082421	5	0.5	84.54258	33300000	1.67e+08	0.04	0
## 9	SB_9	0.10110045	5	0.5	79.94058	33300000	1.67e+08	0.04	0

```
var_expt[["pars"]][[20]]$PB
```

##	strain_name	g_max_PB	k_PB_SR	k_PB_P	h_O_PB	y_SR_PB	y_P_PB	m_PB	i_PB
## 1	PB_1	0.06923807	10	0.5	125.09291	12500000	1.67e+08	0.028	0
## 2	PB_2	0.06942777	10	0.5	118.28360	12500000	1.67e+08	0.028	0
## 3	PB_3	0.06961799	10	0.5	111.84494	12500000	1.67e+08	0.028	0
## 4	PB_4	0.06980873	10	0.5	105.75677	12500000	1.67e+08	0.028	0
## 5	PB_5	0.07000000	10	0.5	100.00000	12500000	1.67e+08	0.028	0
## 6	PB_6	0.07019179	10	0.5	94.55660	12500000	1.67e+08	0.028	0
## 7	PB_7	0.07038411	10	0.5	89.40950	12500000	1.67e+08	0.028	0
## 8	PB_8	0.07057695	10	0.5	84.54258	12500000	1.67e+08	0.028	0
## 9	PB_9	0.07077032	10	0.5	79.94058	12500000	1.67e+08	0.028	0

Display diversity

```
display_diversity()
```



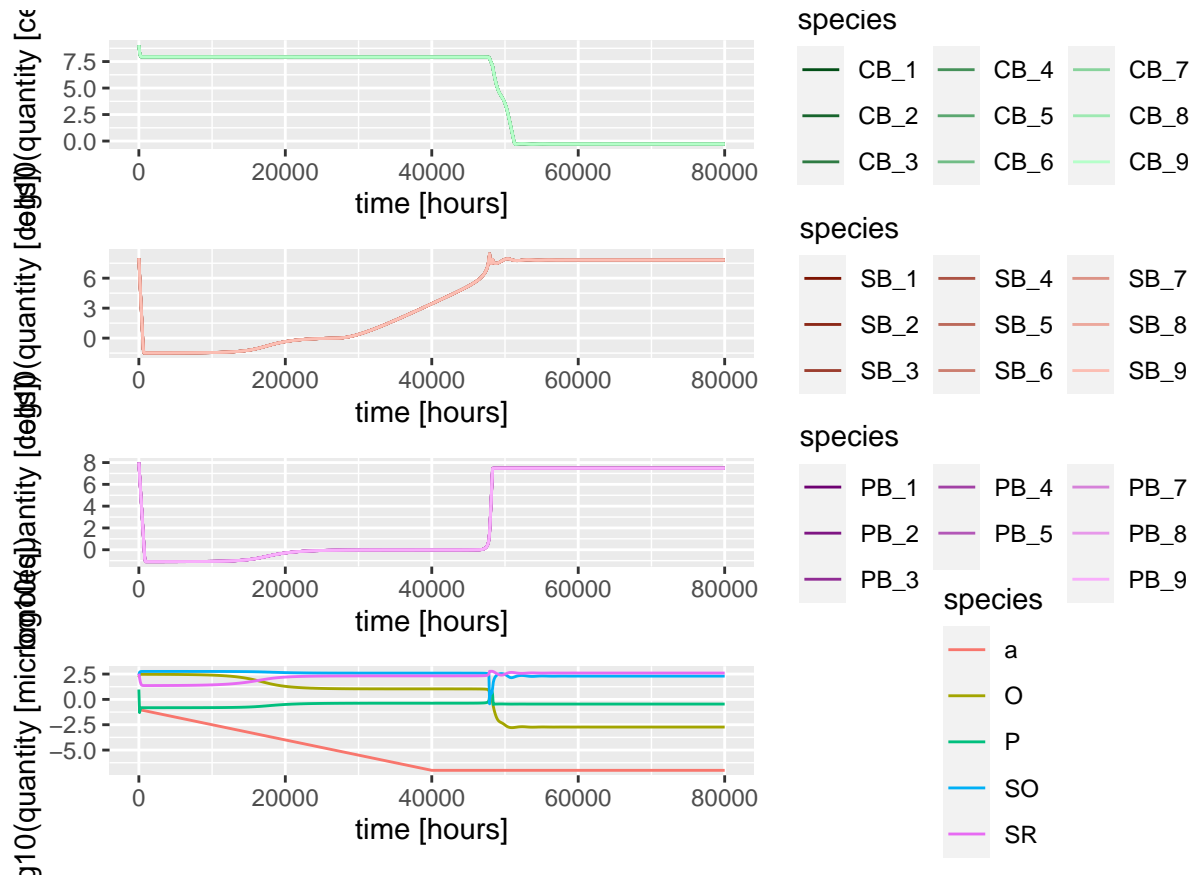
Temporal switching

Oxic to anoxic

No diversity

```
default_sim_duration <- 80000
```

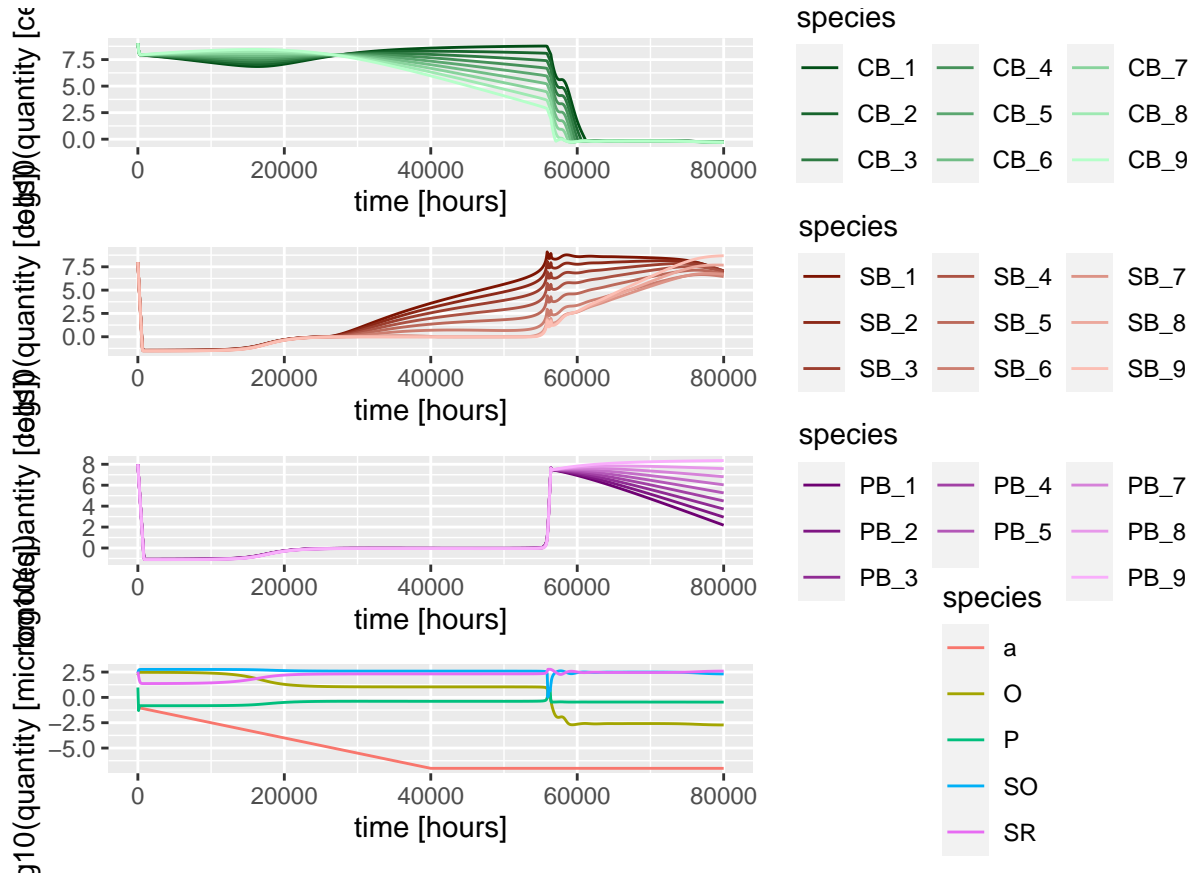
```
sim_number <- 1
default_log10a_series <- c(-1, -7, -7)
initial_state <- new_initial_state(num_CB_strains,
                                   num_PB_strains,
                                   num_SB_strains,
                                   values = "bush_ssfig3")
initial_state[grep("CB_", names(initial_state))] <- 10^10/num_CB_strains
sim_res_novar <- run_simulation(parameter_values = var_expt$pars[[sim_number]],
                               initial_state = initial_state)
plot_dynamics(sim_res_novar)
```



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

Maximum diversity

```
sim_number <- num_div_treatment_levels
sim_res_highvar <- run_simulation(parameter_values = var_expt$pars[[sim_number]],
                                initial_state = initial_state)
plot_dynamics(sim_res_highvar)
```



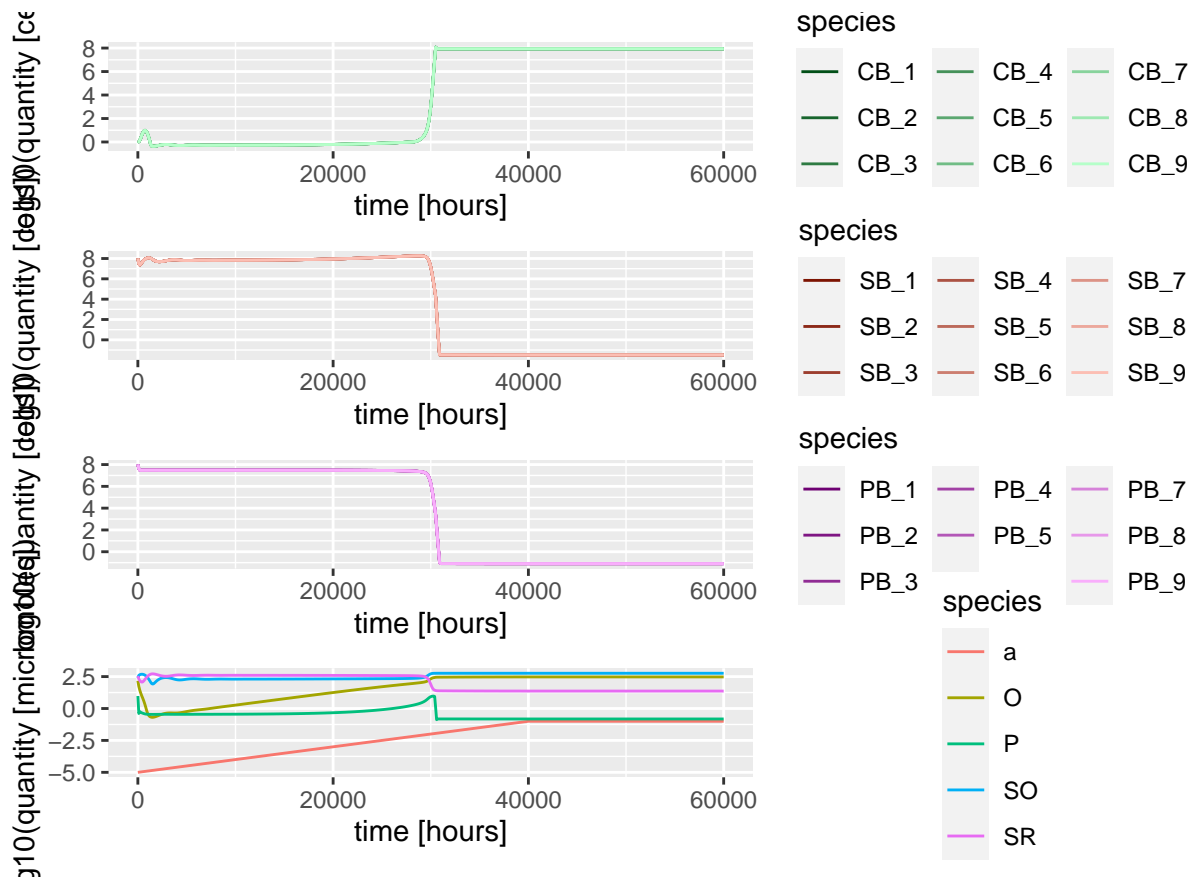
```
#ggsave(here("simulationsexpt2/figures/switching_highvar.pdf"), width = 10)
```

Anoxic to oxic

No diversity

```
default_sim_duration <- 60000
```

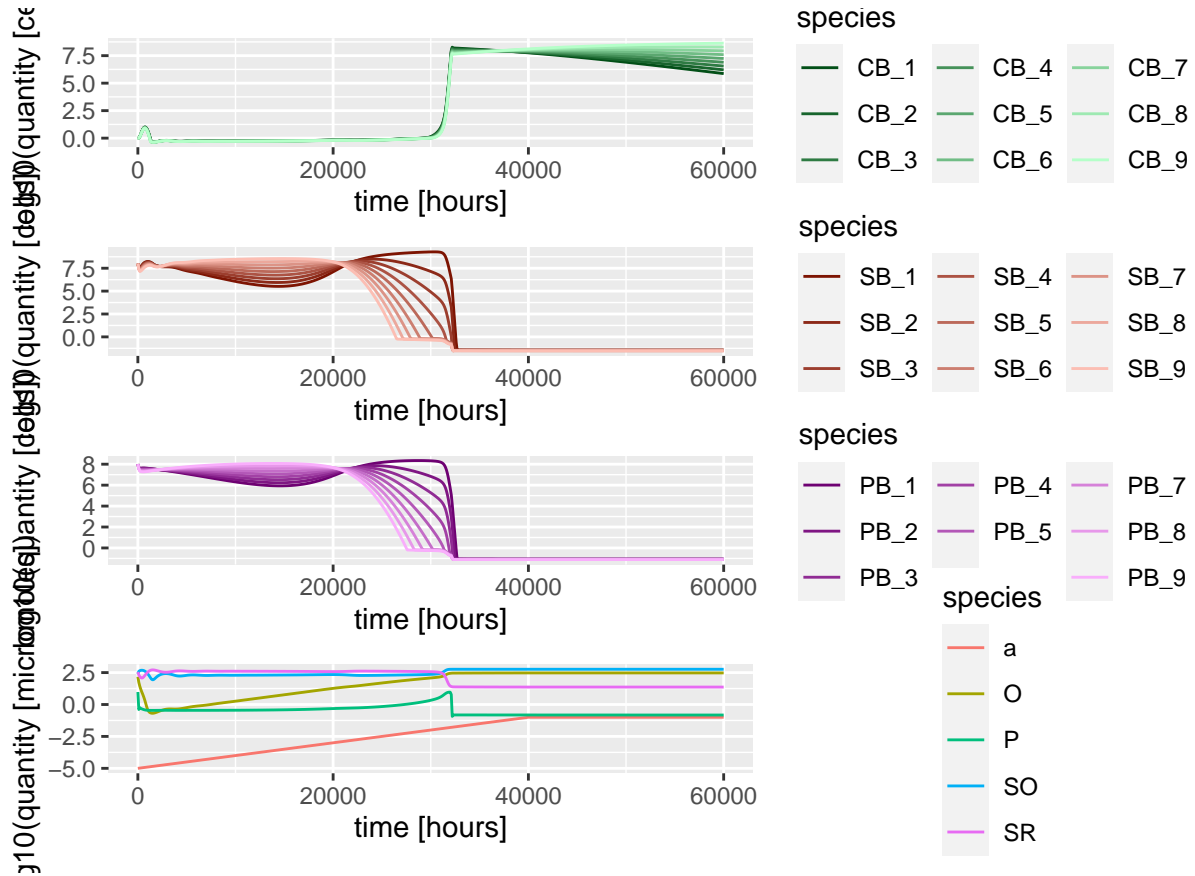
```
sim_number <- 1
default_log10a_series <- c(-5, -3, -1, -1)
initial_state <- new_initial_state(num_CB_strains,
                                   num_PB_strains,
                                   num_SB_strains,
                                   values = "bush_ssfig3")
initial_state[grepl("CB_", names(initial_state))] <- 10/num_CB_strains
sim_res_novar <- run_simulation(parameter_values = var_expt$pars[[sim_number]],
                               initial_state = initial_state)
plot_dynamics(sim_res_novar)
```



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

Maximum diversity

```
sim_number <- num_div_treatment_levels
sim_res_highvar <- run_simulation(parameter_values = var_expt$pars[[sim_number]],
                                initial_state = initial_state)
plot_dynamics(sim_res_highvar)
```



```
#ggsave(here("simulationsext2/figures/switching_highvar.pdf"), width = 10)
```

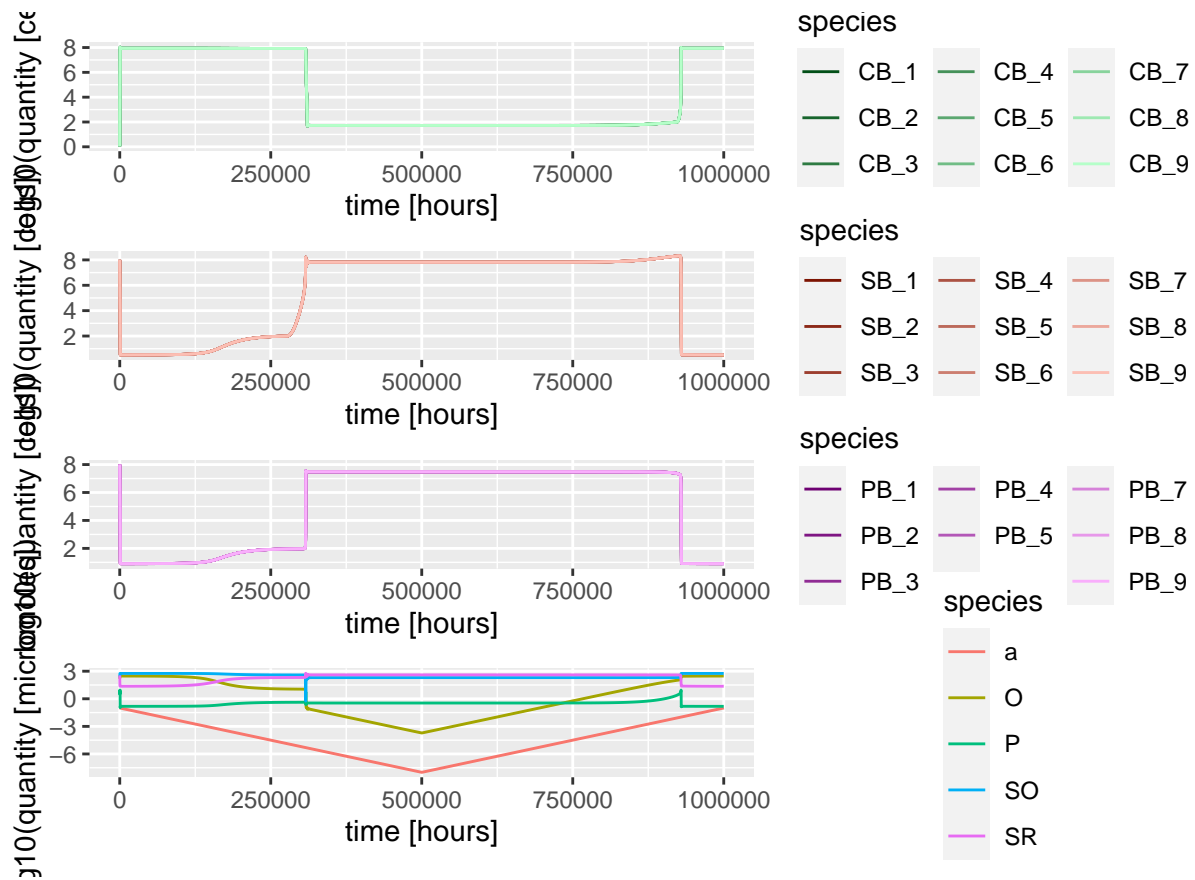
Anoxic to oxic to anoxic

No diversity

```
default_sim_duration <- 1000000
```

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

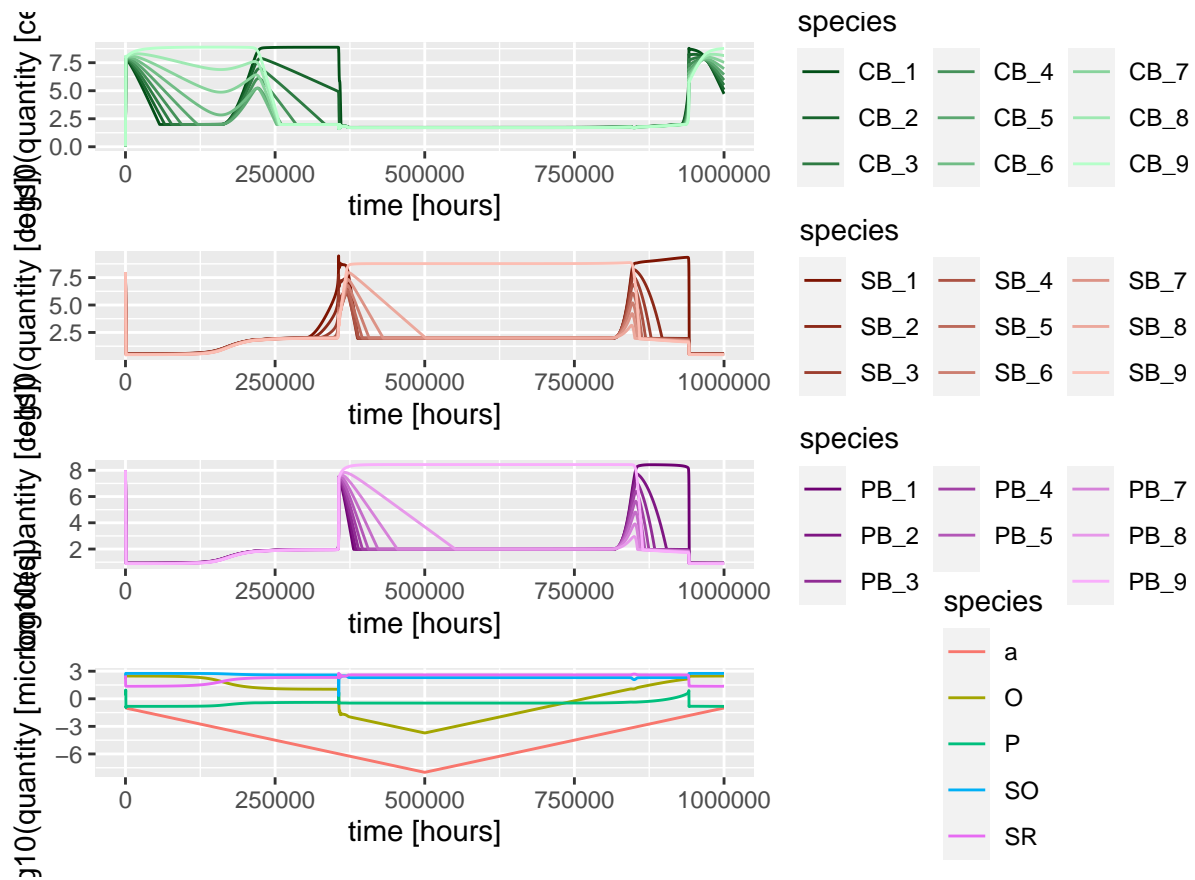
```
sim_number1 <- 1
default_log10a_series <- c(-1, -8, -1)
initial_state <- new_initial_state(num_CB_strains,
                                   num_PB_strains,
                                   num_SB_strains,
                                   values = "bush_ssfig3")
initial_state[grep("CB_", names(initial_state))] <- 10/num_CB_strains
sim_res_novar <- run_simulation(parameter_values = var_expt$pars[[sim_number1]],
                               initial_state = initial_state)
plot_dynamics(sim_res_novar)
```

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

Maximum diversity

```
sim_number2 <- num_div_treatment_levels
sim_res_highvar <- run_simulation(parameter_values = var_expt$pars[[sim_number2]],
                                initial_state = initial_state)
plot_dynamics(sim_res_highvar)
```



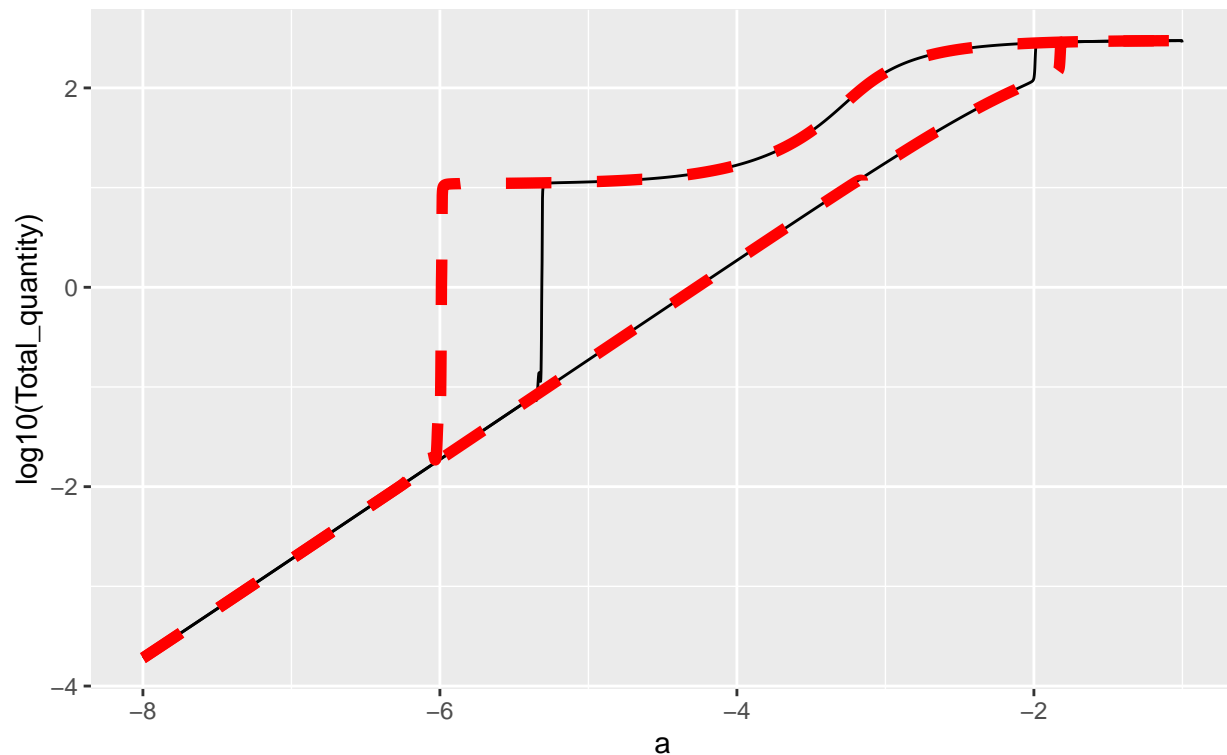
```
#ggsave(here("simulationsext2/figures/switching_highvar.pdf"), width = 10)
```

Visualise

```
visualise_temporal_env_eco()
```

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

Solid line is with no intraspecific diversity.
Dashed line is with intraspecific diversity



Stable state finding

Setup

```
options(mc.cores = 4)
```

```
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 ## 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)
```

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

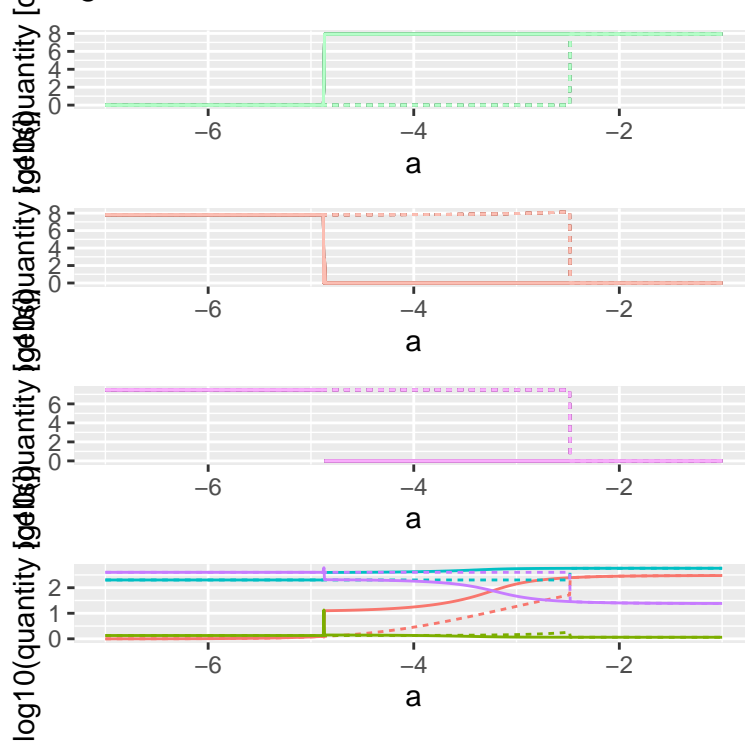
```
var_expt <- readRDS(here("experiments/experiment 1/data/ss_data.RDS"))
```

```
result_index1 <- 1
p1 <- plot_ss_result1(var_expt,
  result_index = result_index1,
  filename_prefix = NULL,
  save_image_file = FALSE)
```

```
## Warning in mask$eval_all_mutate(quo): NaNs produced
```

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
— SR_3	— SR_6	— SR_9

species

— PB_1	— PB_4	— PB_7
— PB_2	— PB_5	— PB_8
— PB_3	— PB_6	— PB_9

direction

— down
 up

species

— O
— P
— SO
— SR

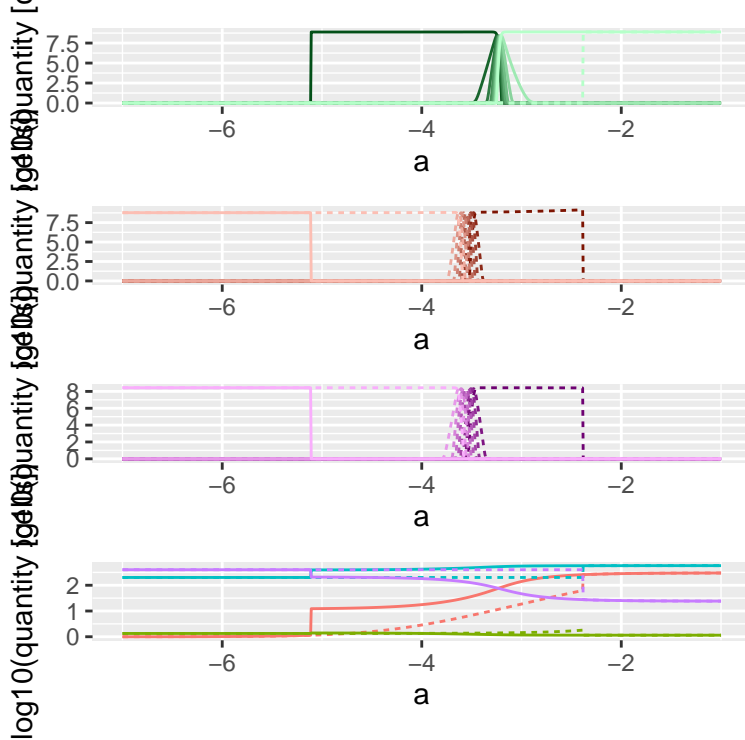
direction

— down
 up

```
result_index2 <- num_div_treatment_levels
p2 <- plot_ss_result1(var_expt,
  result_index = result_index2,
  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



direction

— down
 up

species

SB_1	SB_4	SB_7
SB_2	SB_5	SB_8
SR_3	SR_6	SR_9

species

PB_1	PB_4	PB_7
PB_2	PB_5	PB_8
PB_3		PB_9

direction

— down

species

O
P
SO
SR

direction

— down

```
p_overlay <- plot_ss_result2(var_expt[result_index1,]$ss_res[[1]],
                             var_expt[result_index2,]$ss_res[[1]],
                             xlims = c(-7, -1))
```

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

Warning in mask\$eval_all_mutate(quo): NaNs produced

Warning in mask\$eval_all_mutate(quo): NaNs produced

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

p_overlay

