

kableExtra.pdf

2022-10-11

Getting a nice table for parameterset

```
wait_time <- 10 # time spent at each step
num_strains <- 1 # number of strains per group
event_interval <- 10

## oxygen diffusivity equal to sulfate diffusivity means perfect symmetry
## oxygen diffusivity time series: rep(8e-2, 4), , 10 ^ c(rep(-8, 5),rep(0,5),rep(-8, 5))

log10a_series <- seq(3, -5, length = 10) # symmetry axis at -1, +- 4 units in both direction

num_CB_strains <- num_strains
num_SB_strains <- num_strains
num_PB_strains <- num_strains

sp <- new_strain_parameter(
  n_CB = num_CB_strains,
  values_CB = "symmetric",
  n_PB = num_SB_strains,
  values_PB = "symmetric",
  n_SB = num_PB_strains,
  values_SB = "symmetric",
  values_other = "symmetric",
  values_initial_state = "symmetric"
)

parameter <- new_runsim_parameter(
  dynamic_model = bushplus_dynamic_model, # look up name
  event_definition = event_definition_2,
  event_interval = event_interval,
  noise_sigma = 0,
  minimum_abundances = c(1, 0, 1), # PB stays 0
  strain_parameter = sp,
  log10a_series = log10a_series
)

names(parameter$minimum_abundances) <- c("CB", "PB", "SB")
rm(sp)
```

```
parameter$sim_duration <- wait_time * length(parameter$log10a_series)
parameter$sim_sample_interval <- wait_time # to avoid having negative ODE results
```

```
# $math format acitvation$, every \\ activates some function inside $$ only needed once -> \\mathrm{}
```

```
Parameter <- c('$\\mathrm{g}_{\\max}$',
  '$\\mathrm{k}_{B,P}$',
  '$\\mathrm{h}_{B,S}$',
  '$\\mathrm{y}^B_{P}$',
  '$\\mathrm{p}_B$',
  '$\\mathrm{m}_B$',
  '$\\mathrm{a}_{SR}$',
  '$\\mathrm{a}_P$',
  '$\\mathrm{S}_b$',
  '$\\mathrm{P}_b$',
  '$\\mathrm{c}$')
```

```
Meaning <- c("Maximum specific growth rate of CB and SB",
  "Half-saturation constant of CB and SB on phosphorus",
  "Half-inhibition constant of CB/SB on reduced sulfur/oxygen",
  "Yield of CB and SB on phosphorus",
  "Production of oxygen/reduced sulfur per CB/SB cell", "mortality rate of CB and SB",
  "Diffusivity of reduced sulfur",
  "Diffusivity of phosphorus",
  "Background concentration substrates",
  "Background concentration of phosphorus",
  "Oxidation rate of reduced sulfur")
```

```
# todo change units
```

```
Value <- c(paste(parameter$strain_parameter$CB$g_max, "$\\mathrm{hr}^{-1}$"),
  paste(parameter$strain_parameter$CB$k_CB_P, "$\\mathrm{\\mu M}$"),
  paste(parameter$strain_parameter$CB$h_SR_CB, "$\\mathrm{\\mu M}$"),
  paste(parameter$strain_parameter$CB$y_P_CB, "cells $\\mathrm{\\mu M}^{-1}$"),
  paste(parameter$strain_parameter$CB$Pr_CB, "$\\mathrm{\\mu M cell}^{-1}$"),
  paste(parameter$strain_parameter$CB$m_CB, "$\\mathrm{hr}^{-1}$"),
  paste(parameter$strain_parameter$a_S, "$\\mathrm{hr}^{-1}$"),
  paste(parameter$strain_parameter$a_P, "$\\mathrm{hr}^{-1}$"),
  paste(parameter$strain_parameter$back_O, "$\\mathrm{\\mu M}$"),
  paste(parameter$strain_parameter$back_P, "$\\mathrm{\\mu M}$"),
  paste(parameter$strain_parameter$c, "$\\mathrm{\\mu M}^{-1} hr^{-1}$"))
```

```
frame <- data.frame(Parameter, Meaning, Value)
```

```
kable(frame, booktabs = TRUE) %>%
  kable_styling(latex_options = "scale_down") %>%
  row_spec(0, bold = TRUE, font_size = 16) %>%
  row_spec(1:11, bold = TRUE, font_size = 12, hline_after = FALSE) # %>%
```

Parameter	Meaning	Value
μ_{\max}	Maximum specific growth rate of CB and SB	0.1 hr^{-1}
$K_{B,P}$	Half-saturation constant of CB and SB on phosphorus	0.5 μM
$K_{B,S}$	Half-inhibition constant of CB/SB on reduced sulfur/oxygen	100 μM
$Y_{B,P}$	Yield of CB and SB on phosphorus	1.67e+08 cells μM^{-1}
$p_{B,S}$	Production of oxygen/reduced sulfur per CB/SB cell	3e-08 $\mu\text{M cell}^{-1}$
m_B	mortality rate of CB and SB	0.04 hr^{-1}
a_{SR}	Diffusivity of reduced sulfur	0.1 hr^{-1}
a_P	Diffusivity of phosphorus	0.1 hr^{-1}
S_b	Background concentration substrates	100 μM
P_b	Background concentration of phosphorus	10 μM
c	Oxidation rate of reduced sulfur	0.01 $\mu\text{M}^{-1} \text{hr}^{-1}$

```
# row_spec(c(1:6, 9, 10), color = "green") %>%
# row_spec(c(7:11), color = "red")
# add_footnote(c("B: Bacteria, same value for cyanobacteria and sulfur reducing bacteria", "S: Substrates"))
```