

Basic tests using `abm_regular()` and `abm_variable()`

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Overview

Objective is to demonstrate flexibility in substrate definitions. Particulate substrates can be entered through `sub_pars` in any number now.

Prep

```
devtools::load_all()
```

```
## i Loading ABM
```

Parameters

```
grp_pars <- list(grps = c('m0', 'm1', 'm2', 'sr1'),
  yield = c(default = 0.05, sr1 = 0.065),
  xa_fresh = c(m0 = 0.0628, m1 = 0.0628, m2 = 0.0628, sr1 = 0.0628),
  xa_init = c(all = 0.0628),
  dd_rate = c(all = 0.02),
  ks = c(default = 1.153337, sr1 = 0.461335),
  qhat_opt = c(m0 = 1, m1 = 1, m2 = 2, sr1 = 8.95),
  T_opt = c(m0 = 18, m1 = 18, m2 = 28, sr1 = 43.75),
  T_min = c(m0 = 0, m1 = 6.41, m2 = 6.41, sr1 = 0),
  T_max = c(m0 = 25, m1 = 25, m2 = 38, sr1 = 51.25))

mic_pars <- list(ks_S04 = 0.00694,
  km_urea = 0.913)

sub_pars <- list(subs = c('VSd'),
  T_opt_hyd = c(VSd = 60),
  T_min_hyd = c(all = 0),
  T_max_hyd = c(all = 90),
  hydrol_opt = c(VSd = 0.1),
  sub_fresh = c(VSd = 50),
  sub_init = c(VSd = 30))

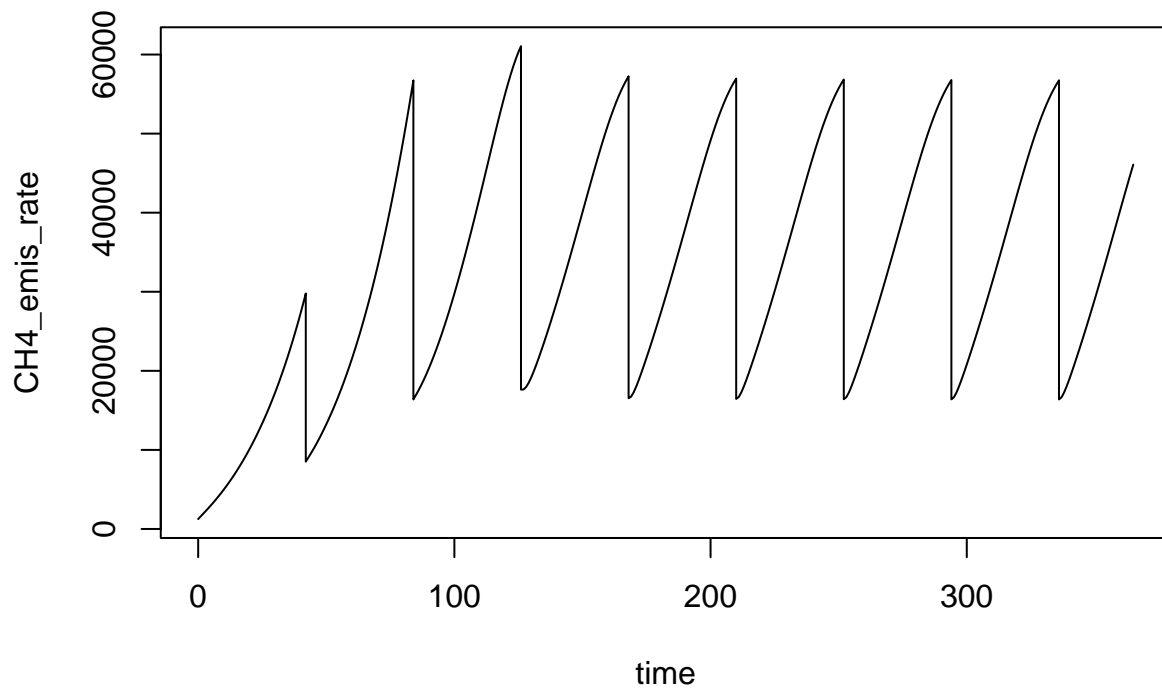
man_pars <- list(conc_fresh = c(VFA = 2),
  pH = 7, dens = 1000)
```

0. Single substrate

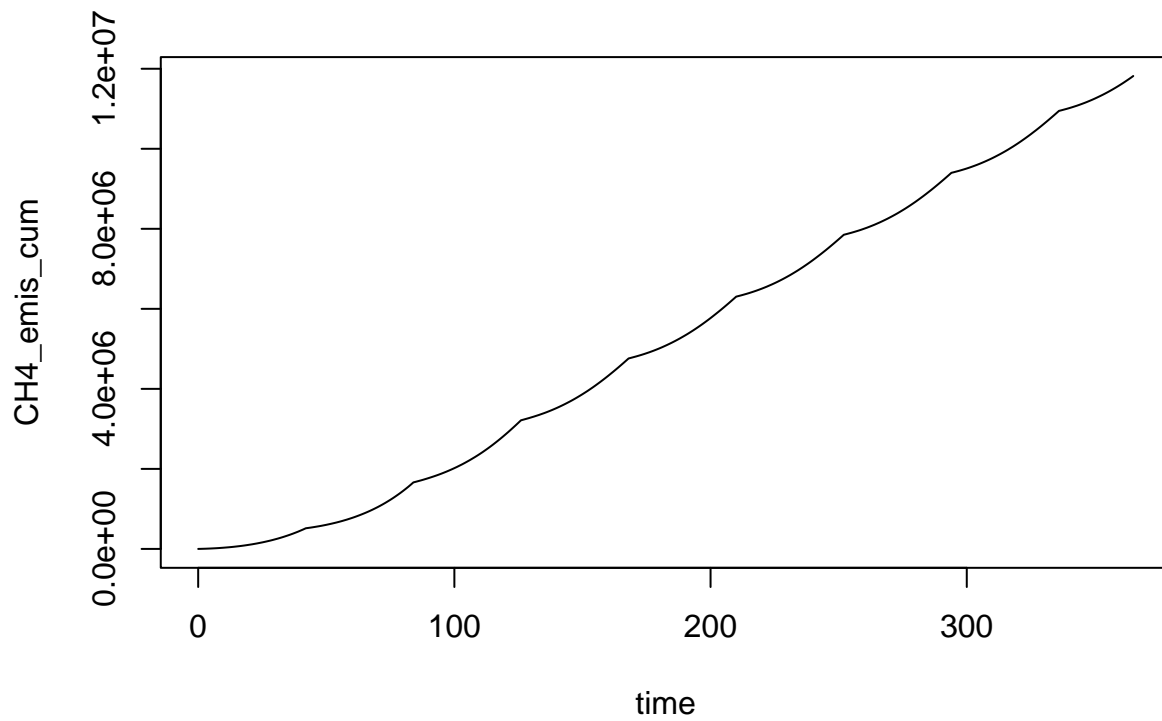
```
out0 <- abm(365,  
  grp_pars = grp_pars,  
  man_pars = man_pars,  
  mic_pars = mic_pars,  
  sub_pars = sub_pars)
```

```
## VSd  
## 333.15
```

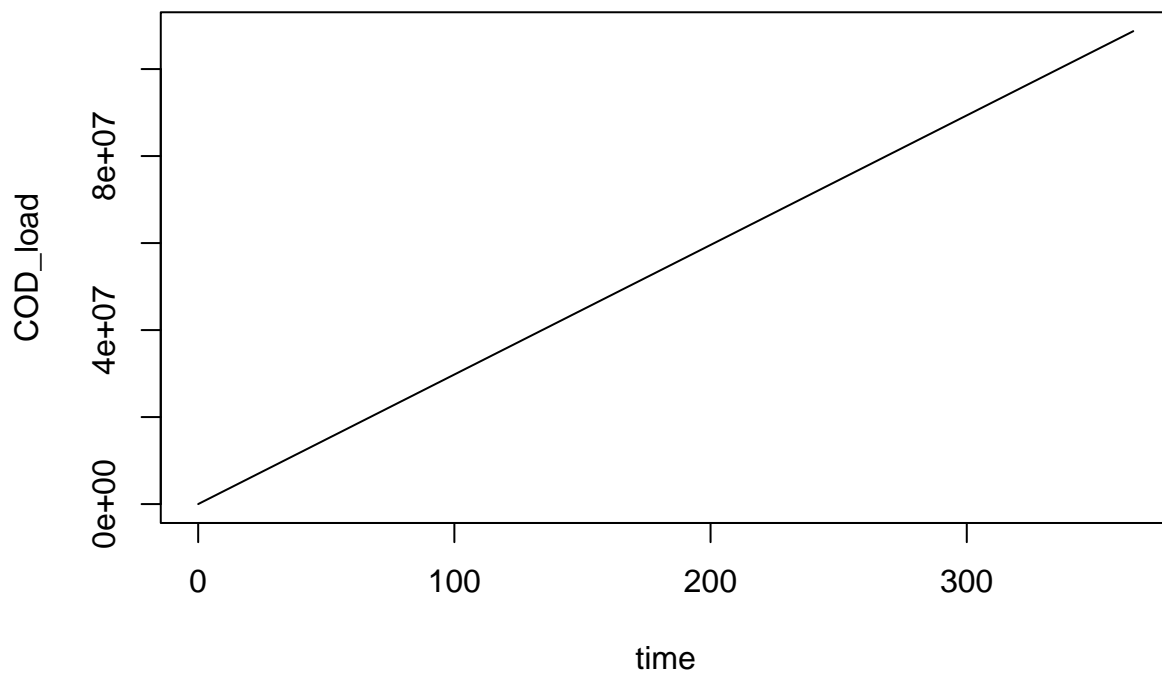
```
plot(CH4_emis_rate ~ time, data = out0, type = 'l')
```



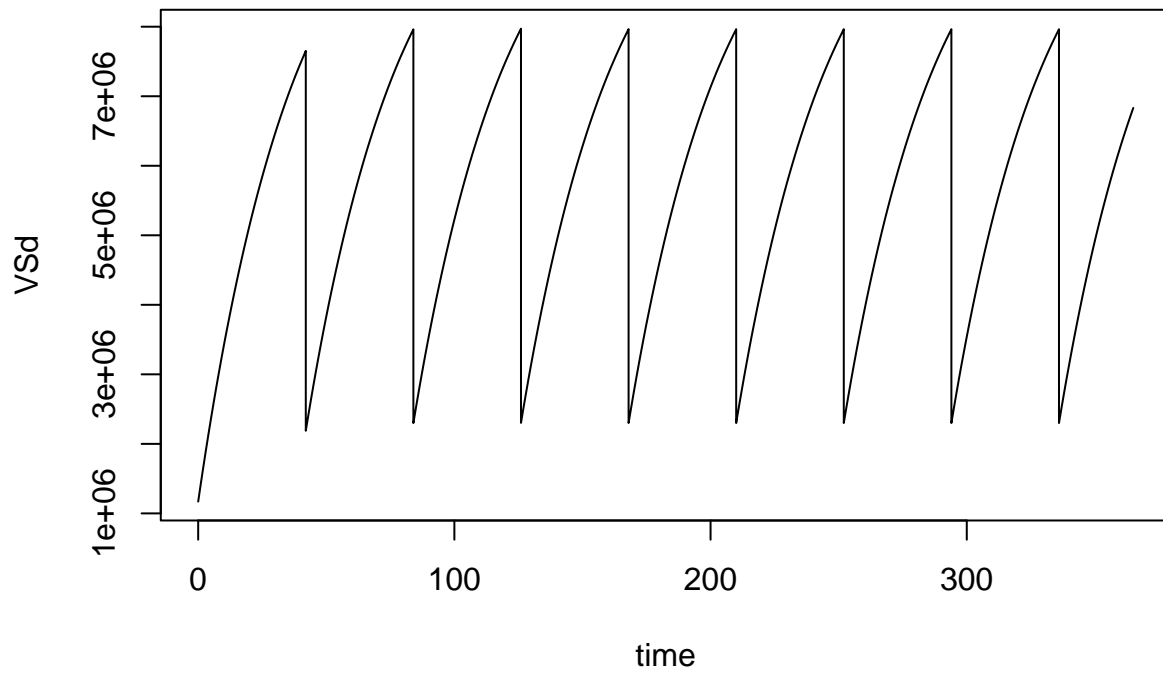
```
plot(CH4_emis_cum ~ time, data = out0, type = 'l')
```



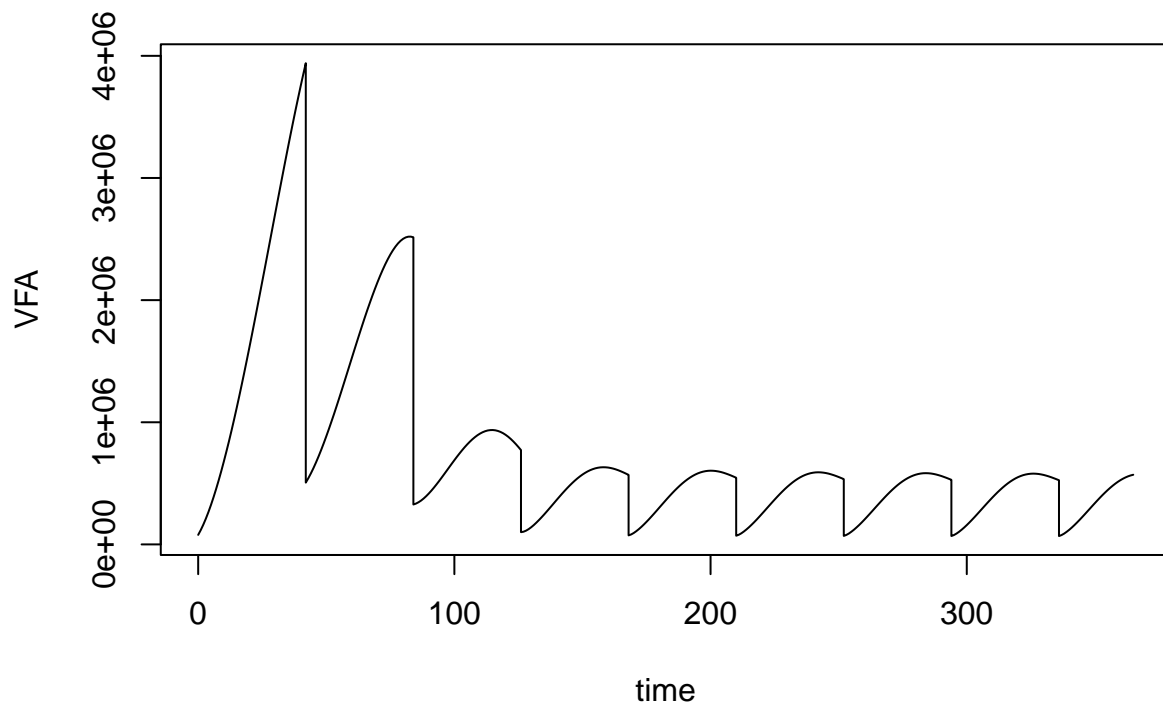
```
plot(COD_load ~ time, data = out0, type = 'l')
```



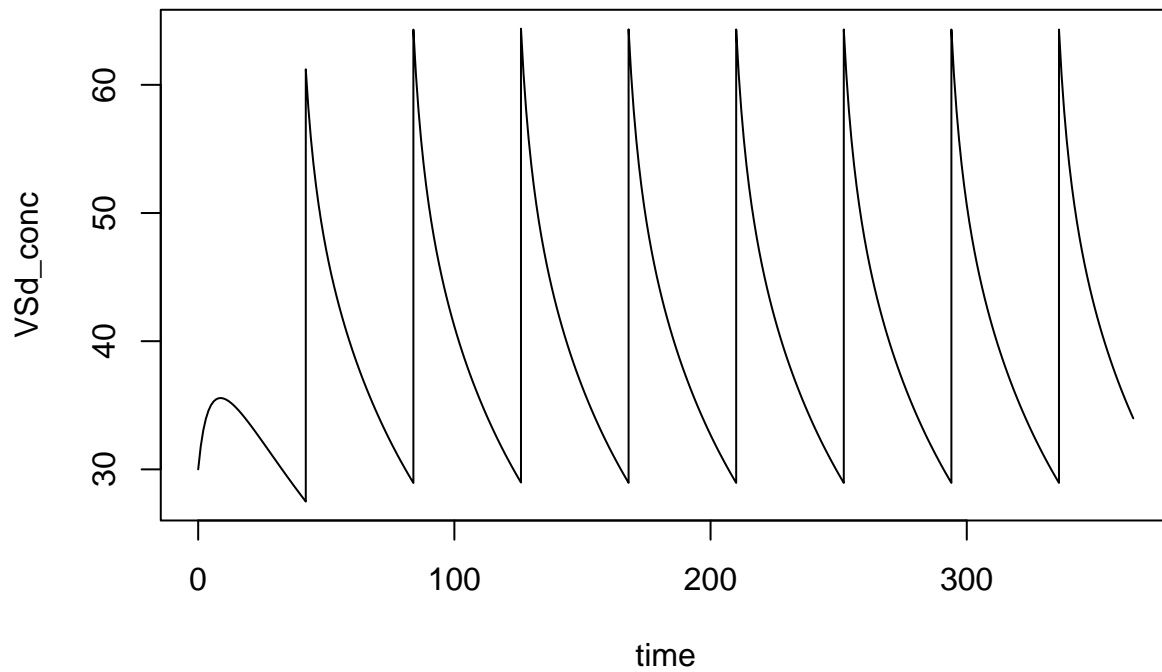
```
plot(VSd ~ time, data = out0, type = 'l')
```



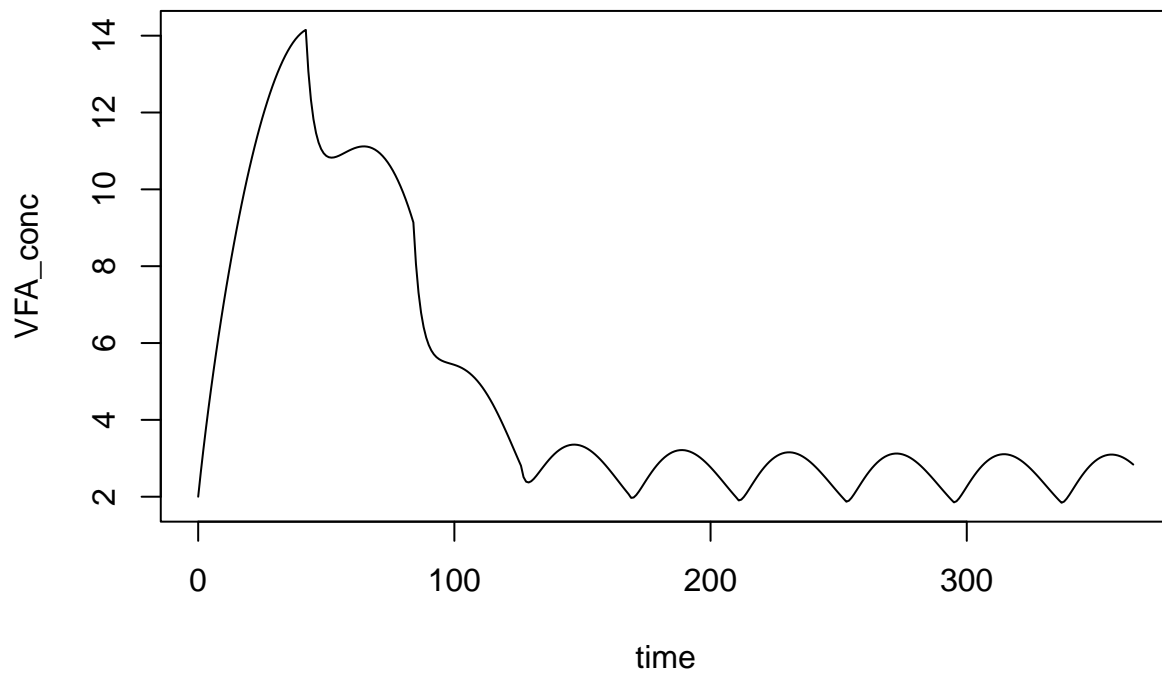
```
plot(VFA ~ time, data = out0, type = 'l')
```



```
plot(VSd_conc ~ time, data = out0, type = 'l')
```



```
plot(VFA_conc ~ time, data = out0, type = 'l')
```



1. Two substrates through sub_pars

Add pr for protein.

```
sub_pars <- list(subs = c('VSd', 'pr'),
  T_opt_hyd = c(VSd = 60),
  T_min_hyd = c(all = 0),
  T_max_hyd = c(all = 90),
  hydrol_opt = c(VSd = 0.1),
```

```
sub_fresh = c(VSd = 50),
sub_init = c(VSd = 30))
```

```
out1 <- abm(365,
  grp_pars = grp_pars,
  man_pars = man_pars,
  mic_pars = mic_pars,
  sub_pars = sub_pars)
```

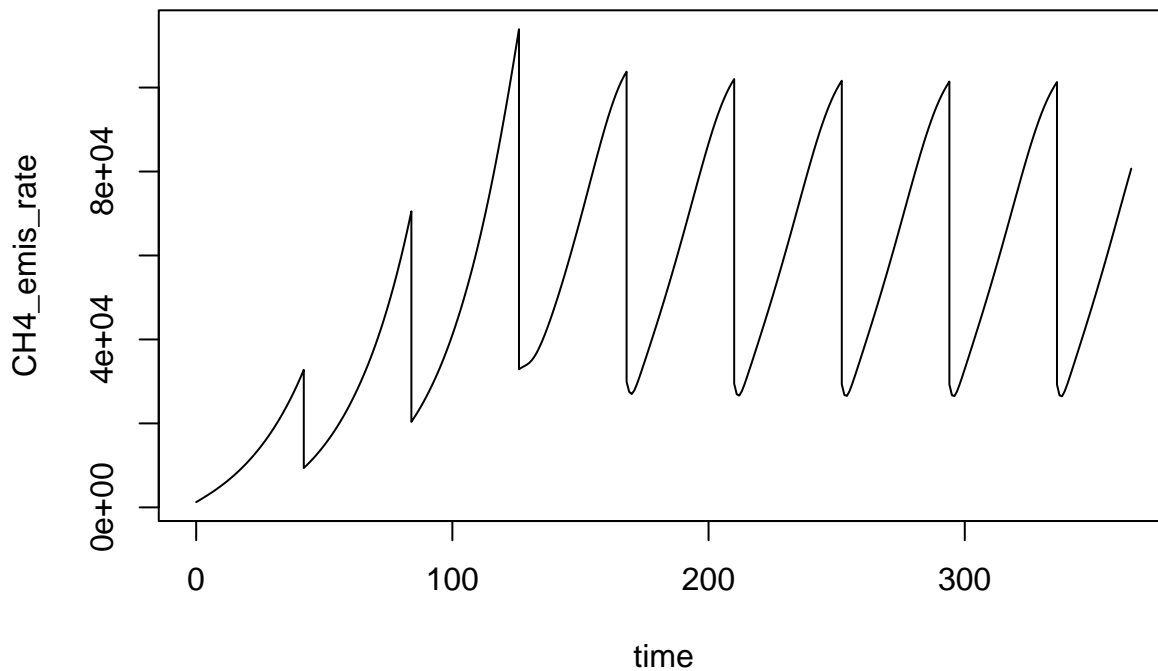
Error in expandPars(pars = pars, elnms = pars\$subs, parnms = sub_par_nms): Size-variable parameter p
Add missing elements.

```
sub_pars <- list(subs = c('VSd', 'pr'),
  T_opt_hyd = c(VSd = 60, pr = 50),
  T_min_hyd = c(all = 0),
  T_max_hyd = c(all = 90),
  hydrol_opt = c(VSd = 0.1, pr = 0.04),
  sub_fresh = c(VSd = 50, pr = 50),
  sub_init = c(VSd = 30, pr = 0))
```

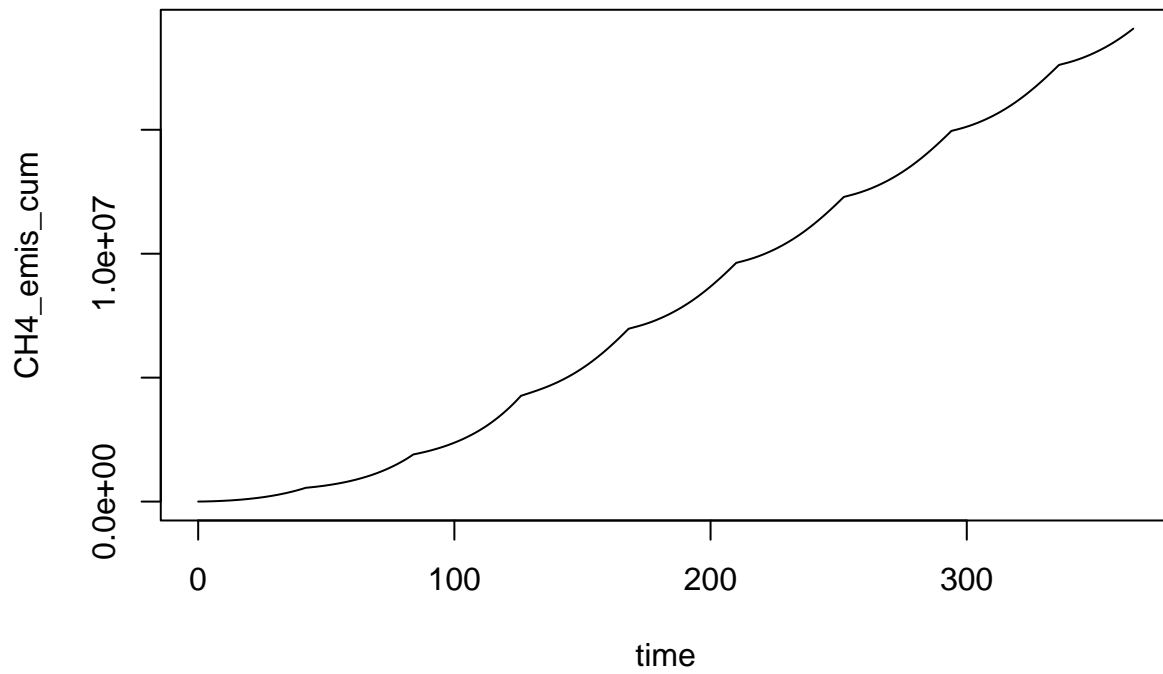
```
out1 <- abm(365,
  grp_pars = grp_pars,
  man_pars = man_pars,
  mic_pars = mic_pars,
  sub_pars = sub_pars)
```

```
## VSd pr
## 333.15 323.15
```

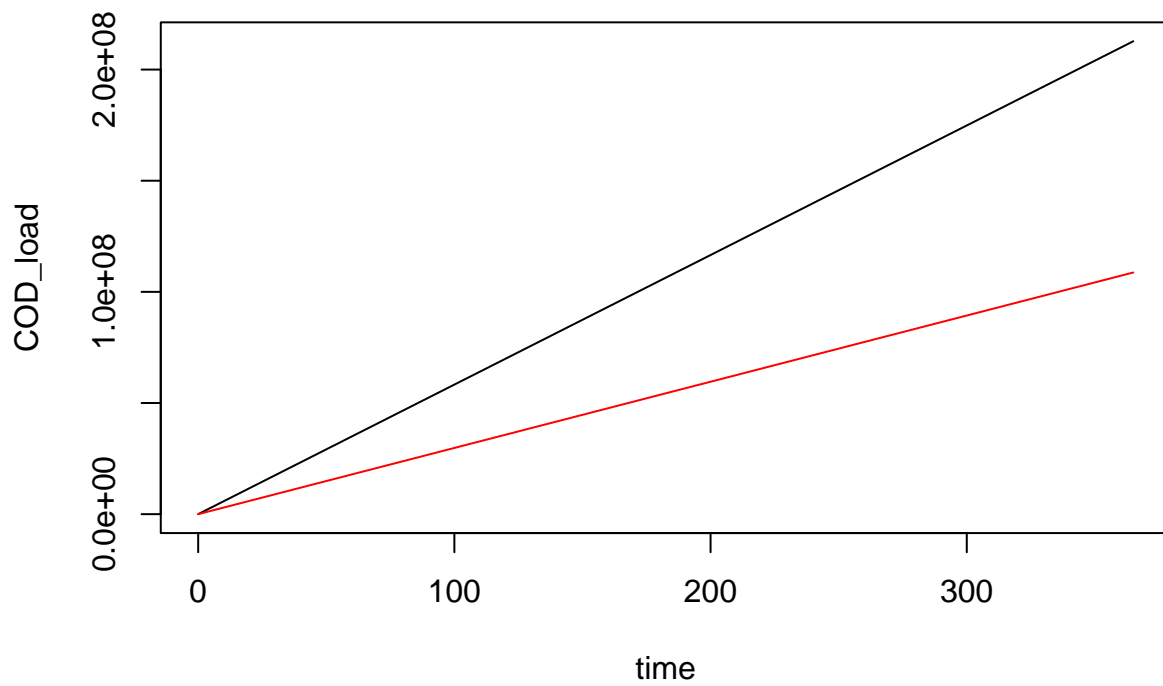
```
plot(CH4_emis_rate ~ time, data = out1, type = 'l')
```



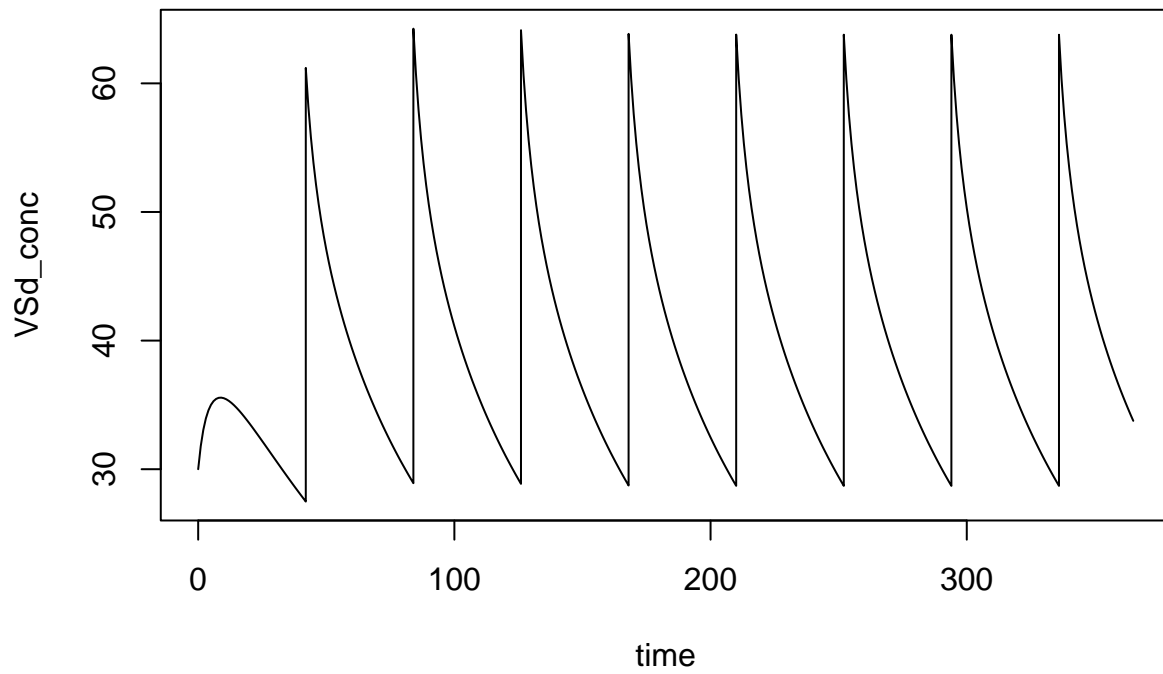
```
plot(CH4_emis_cum ~ time, data = out1, type = 'l')
```



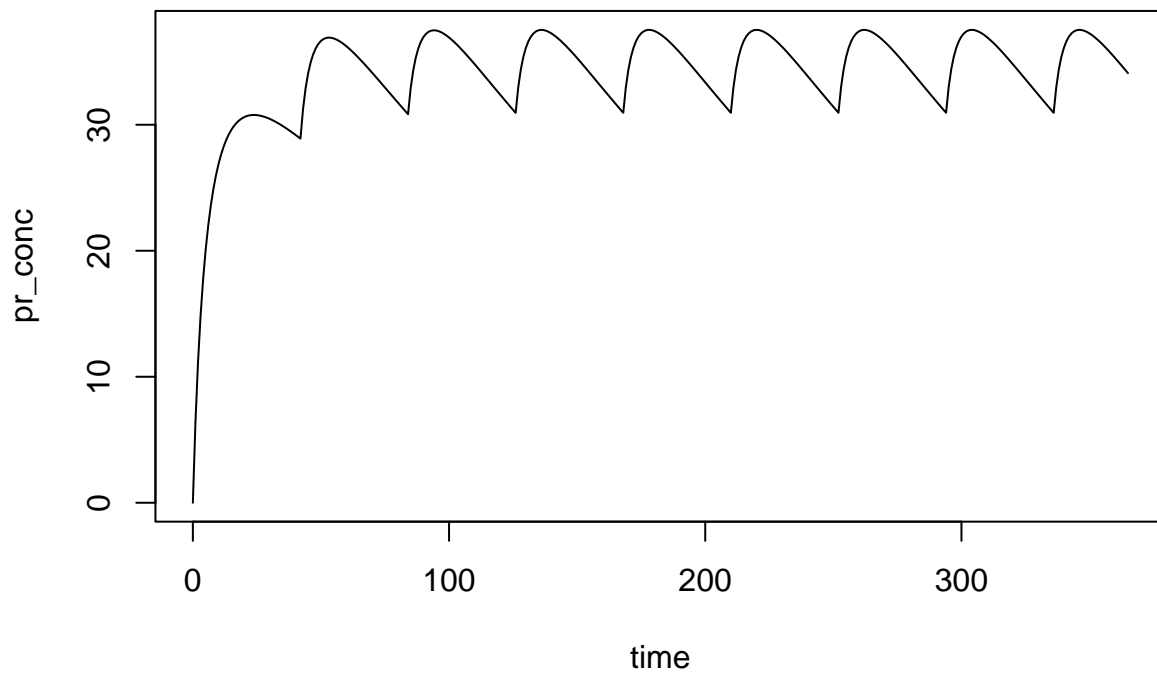
```
plot(COD_load ~ time, data = out1, type = 'l')  
lines(COD_load ~ time, data = out0, col = 'red')
```



```
plot(VSd_conc ~ time, data = out1, type = 'l')
```



```
plot(pr_conc ~ time, data = out1, type = 'l')
```



```
plot(VFA_conc ~ time, data = out1, type = 'l')
```