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

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29 May, 2025 10:14

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(all = 0.05),
                 xa_fresh = c(all = 1),
                 xa_init = c(all = 0.5),
                 dd_rate = c(all = 0.1),
                 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_SO4 = 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 = 0))

man_pars <- list(conc_fresh = c(VFA = 0),
                 pH = 7, dens = 1000)
```
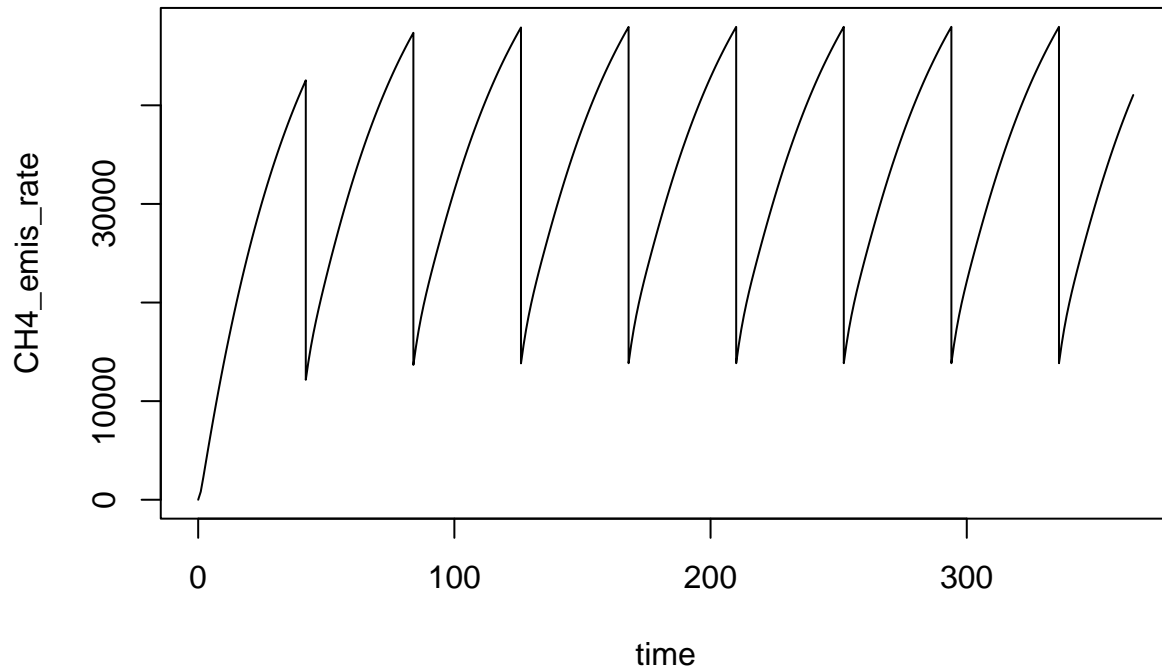
0. Single substrate
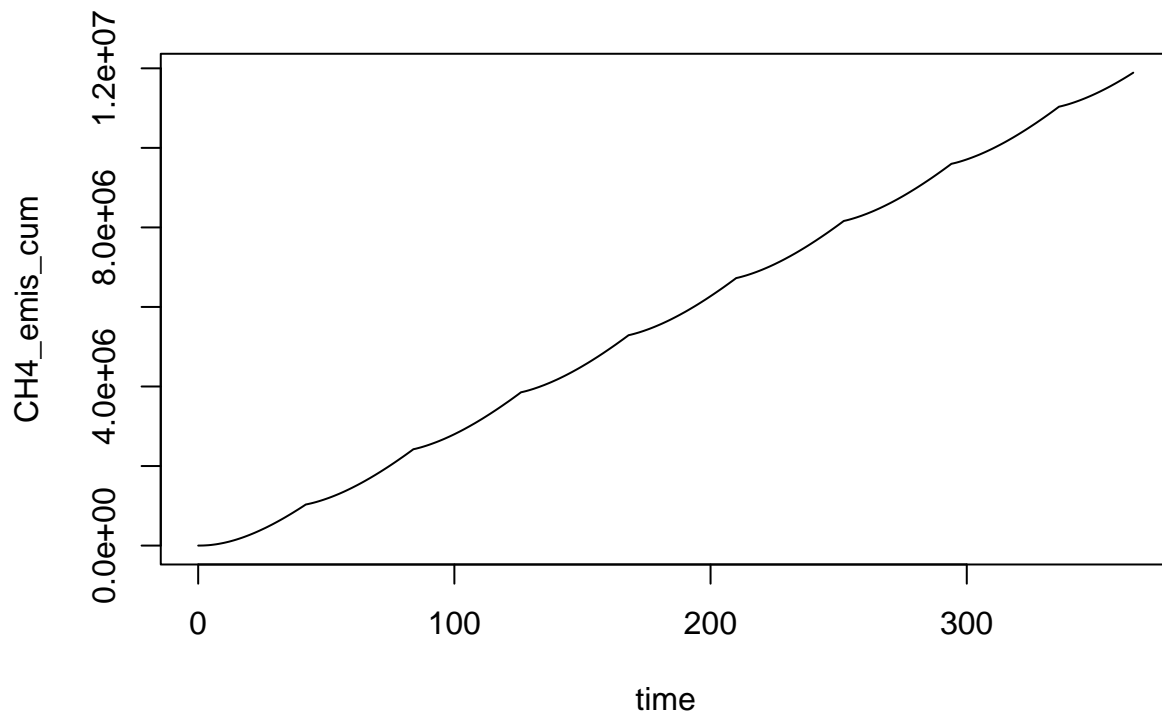
```
out0 <- abm(365,
            grp_pars = grp_pars,
            man_pars = man_pars,
            mic_pars = mic_pars,
            sub_pars = sub_pars)
```

```
## Warning in checkCOD(dat = dat, grps = pars$grps, subs = pars$subs, COD_conv =
## pars$COD_conv, : COD balance is off by 1.6%
```
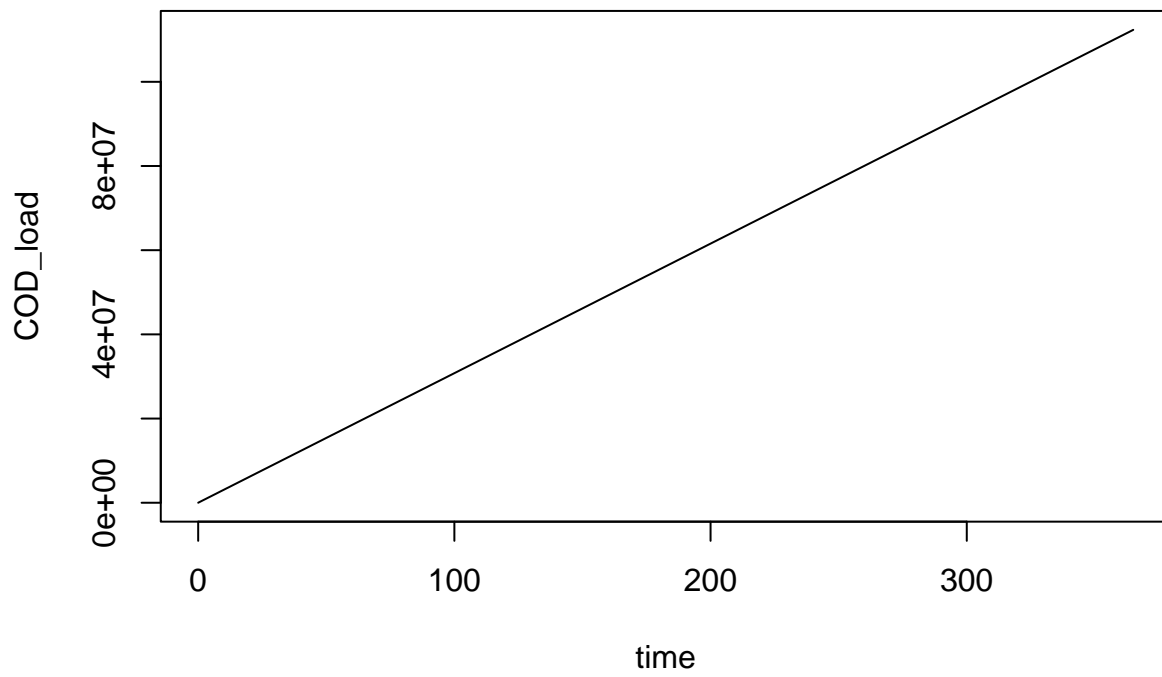
```
plot(CH4_emis_rate ~ time, data = out0, type = 'l')
```
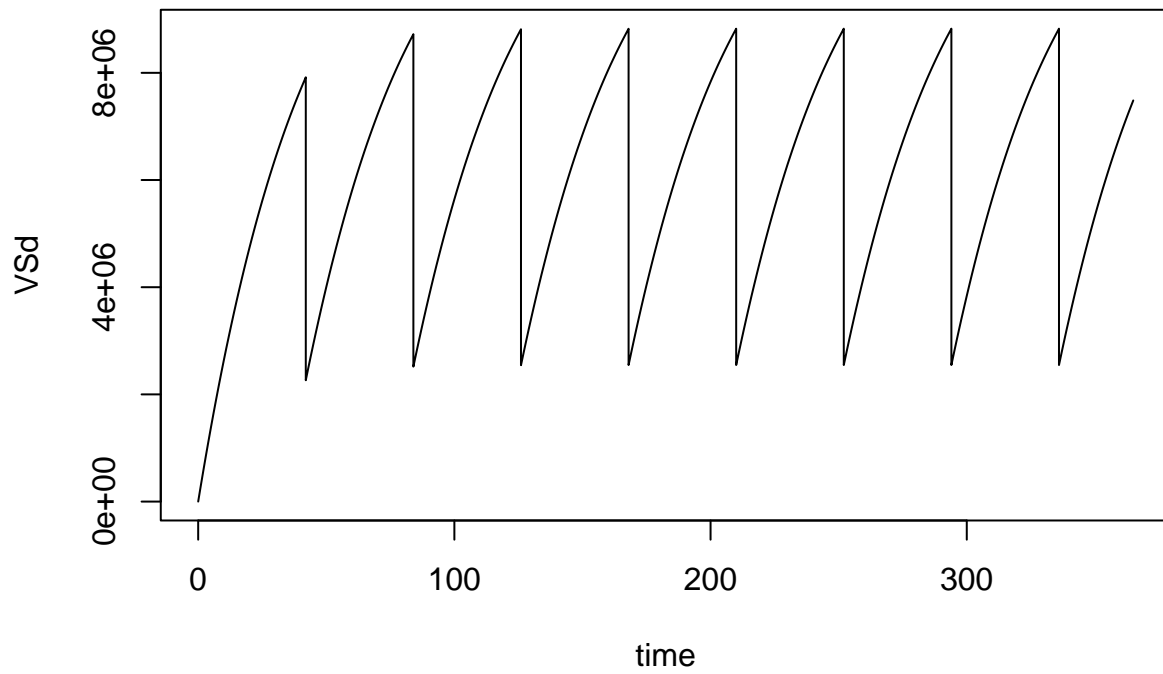

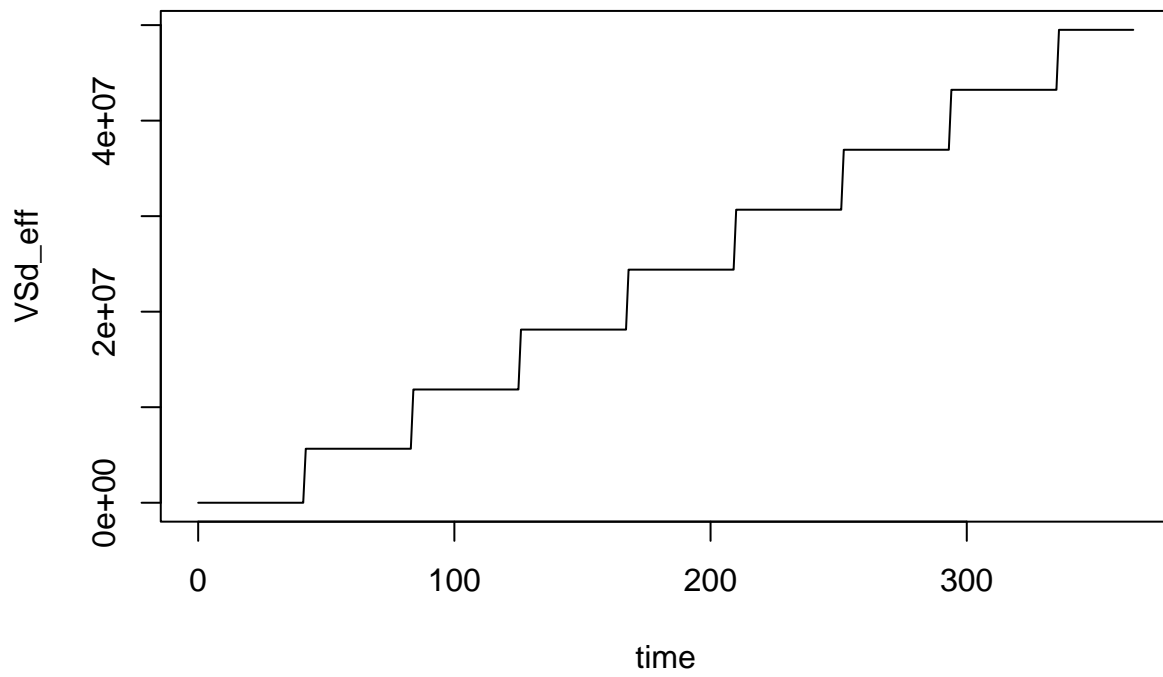```
plot(CH4_emis_cum ~ time, data = out0, type = 'l')
```

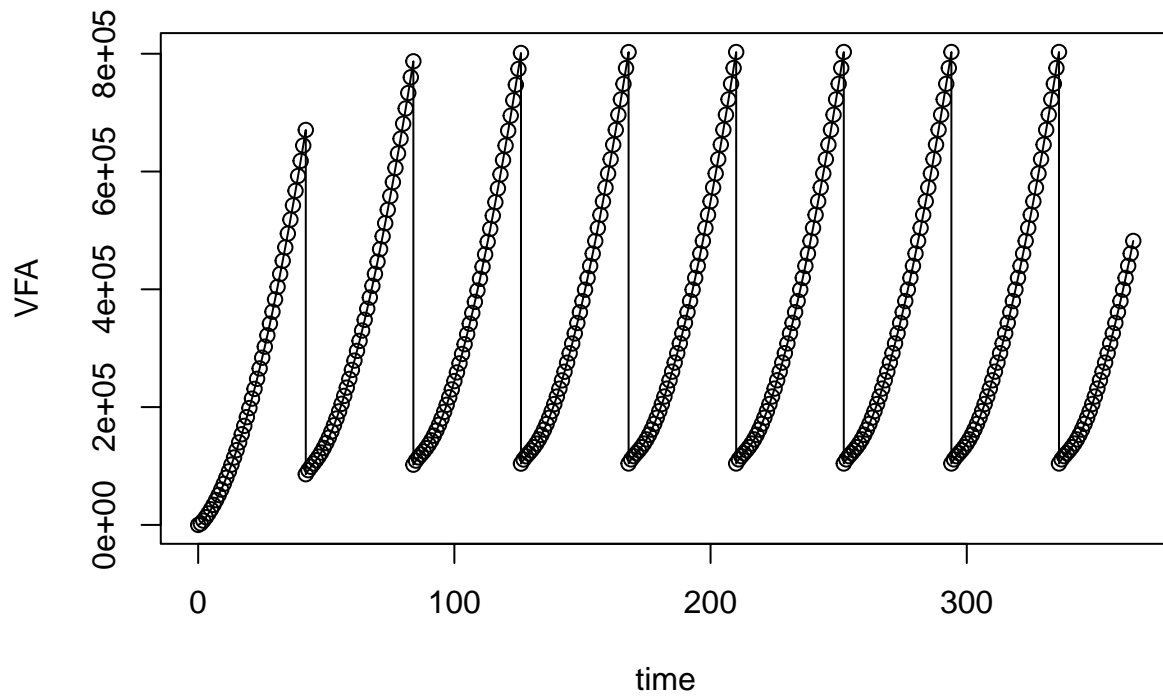```r
plot(COD_load ~ time, data = out0, type = 'l')
```



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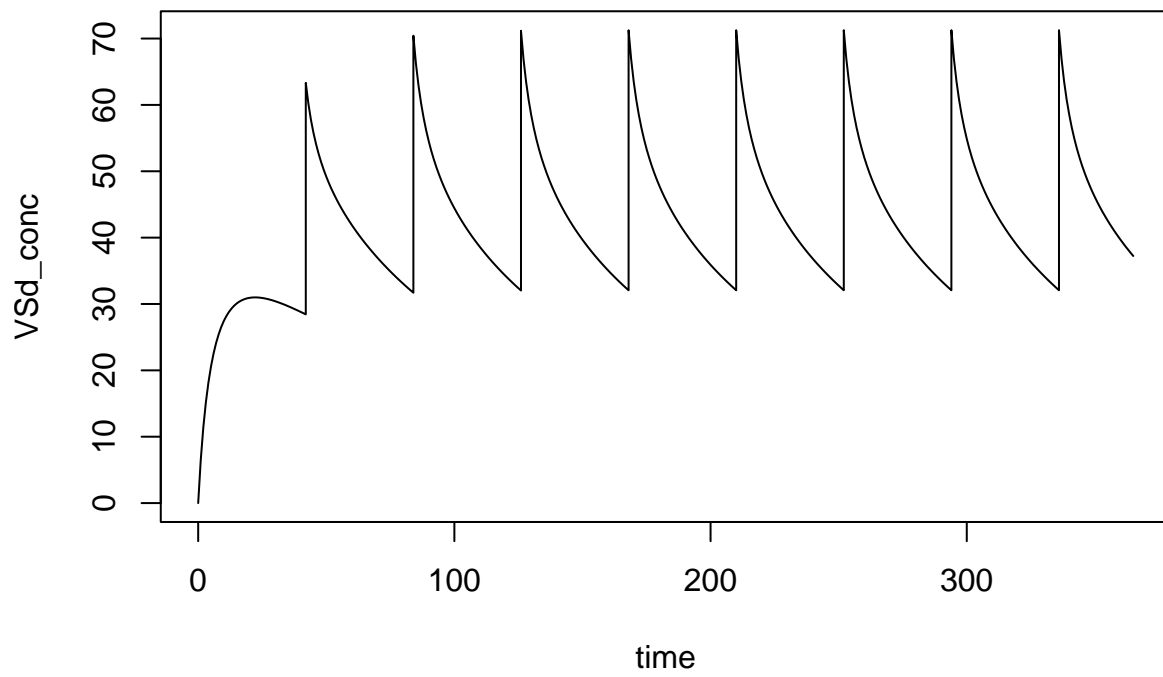
```
plot(VSd_eff ~ time, data = out0, type = 'l')
```
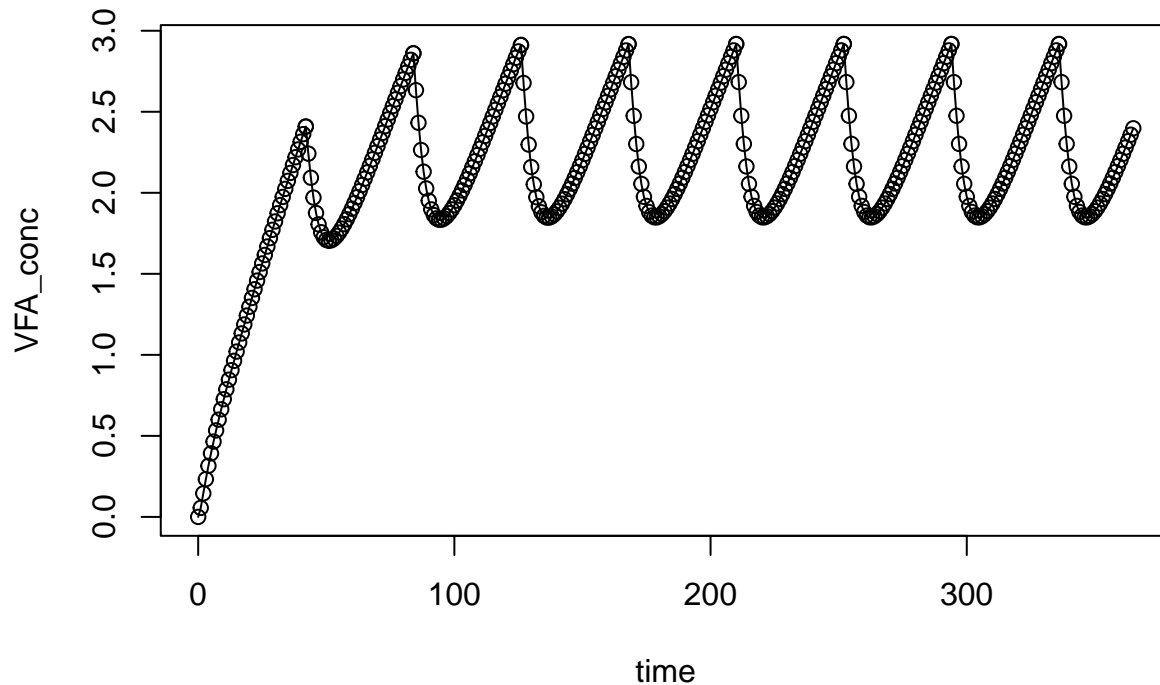


```
plot(VFA ~ time, data = out0, type = 'o')
```

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



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

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 pr
```
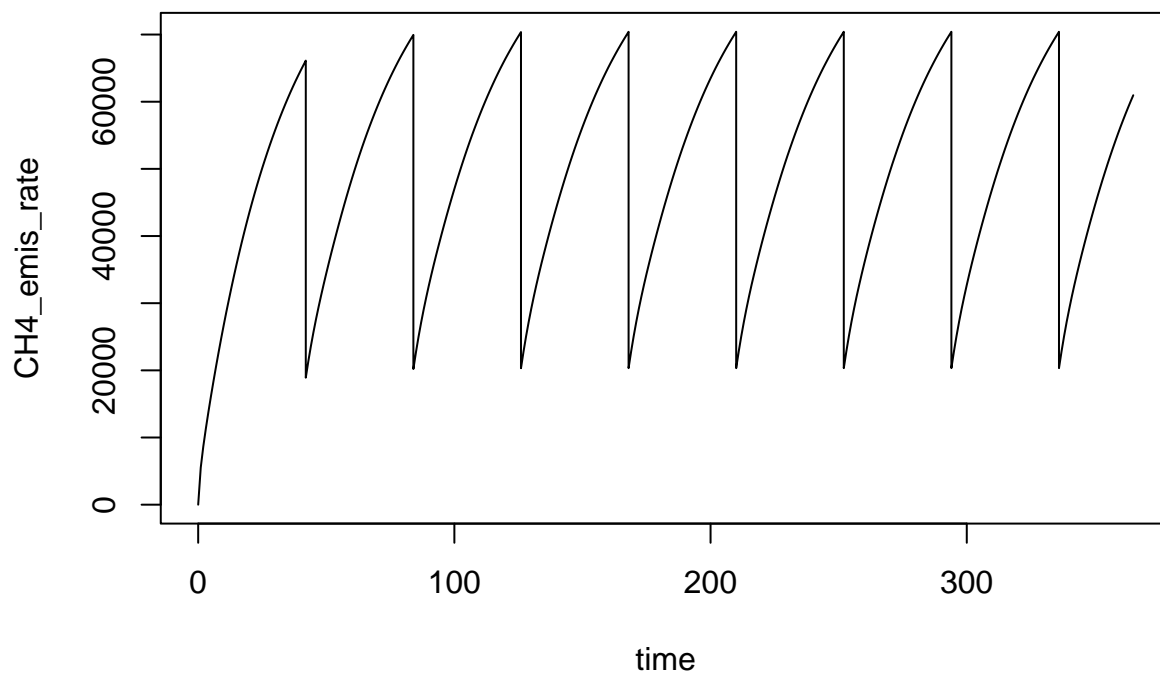
Add missing elements.

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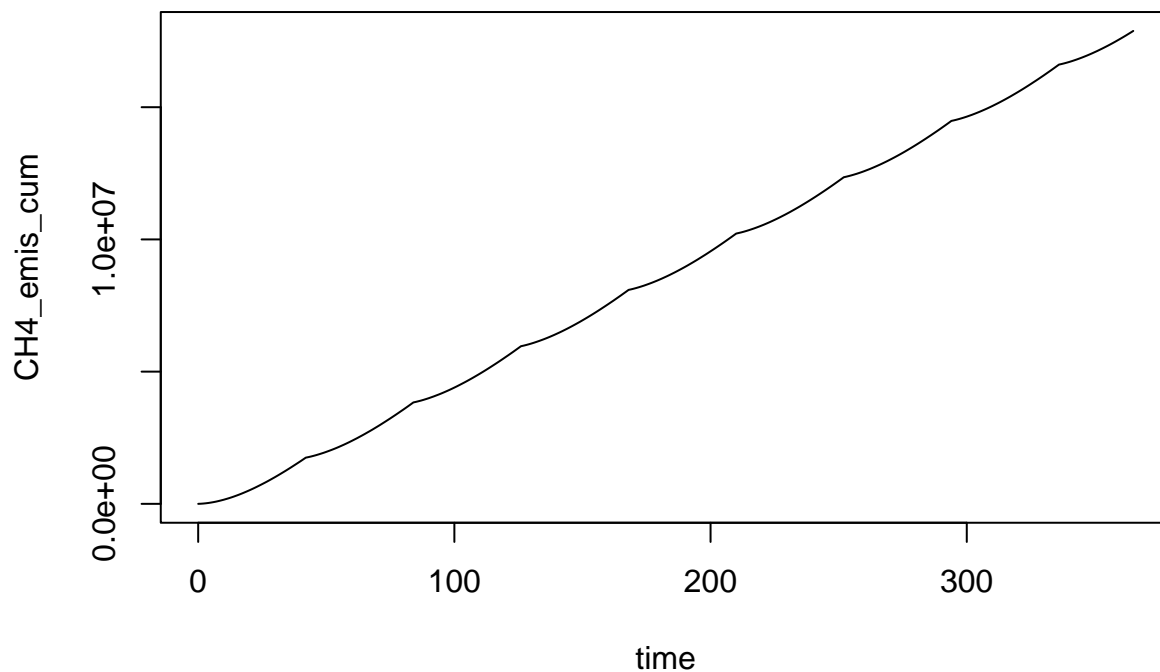
```
out1 <- abm(365,
            grp_pars = grp_pars,
            man_pars = man_pars,
```

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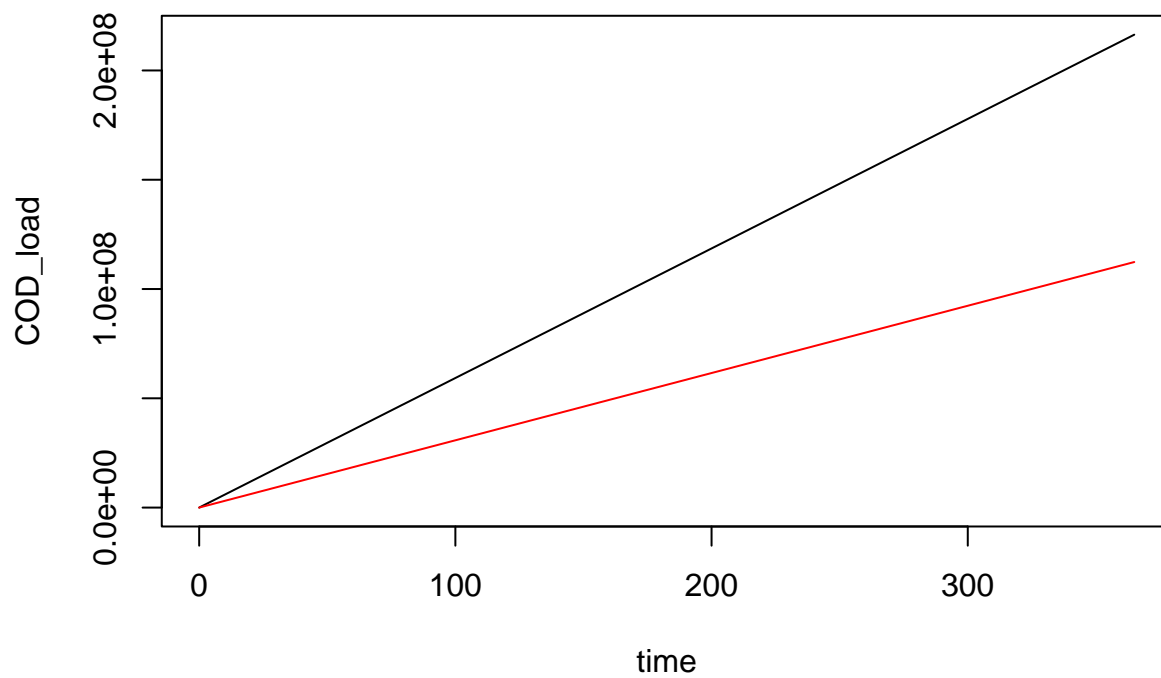
```
plot(CH4_emis_rate ~ time, data = out1, type = 'l')
```
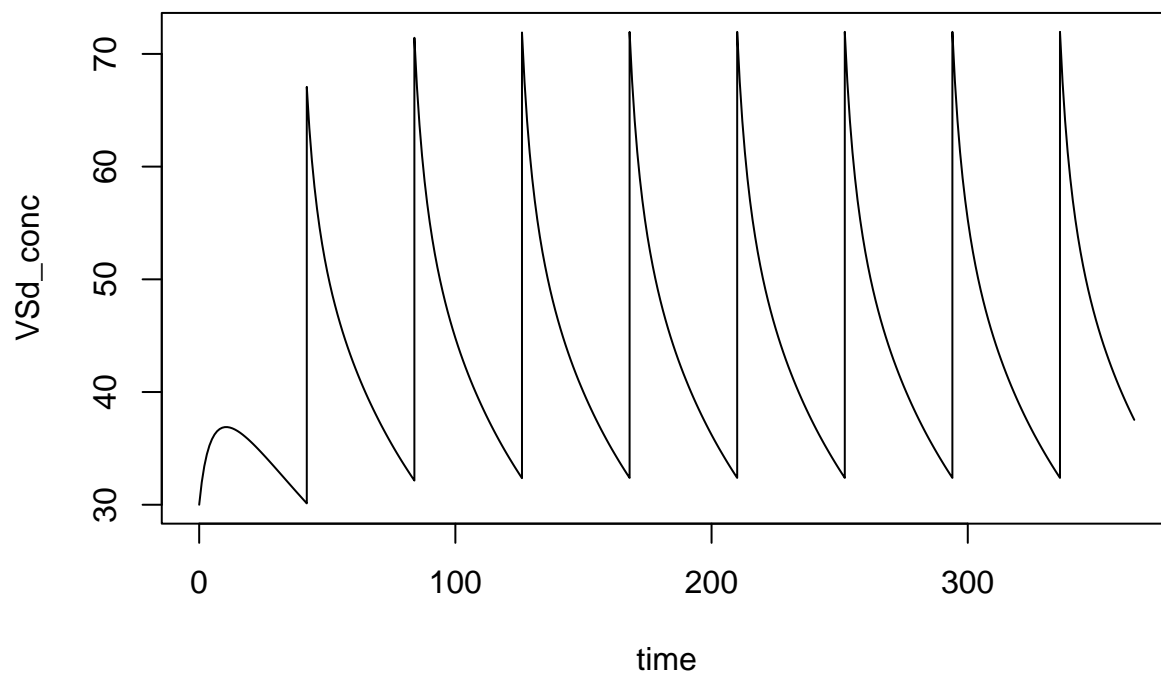


```
plot(CH4_emis_cum ~ time, data = out1, type = 'l')
```
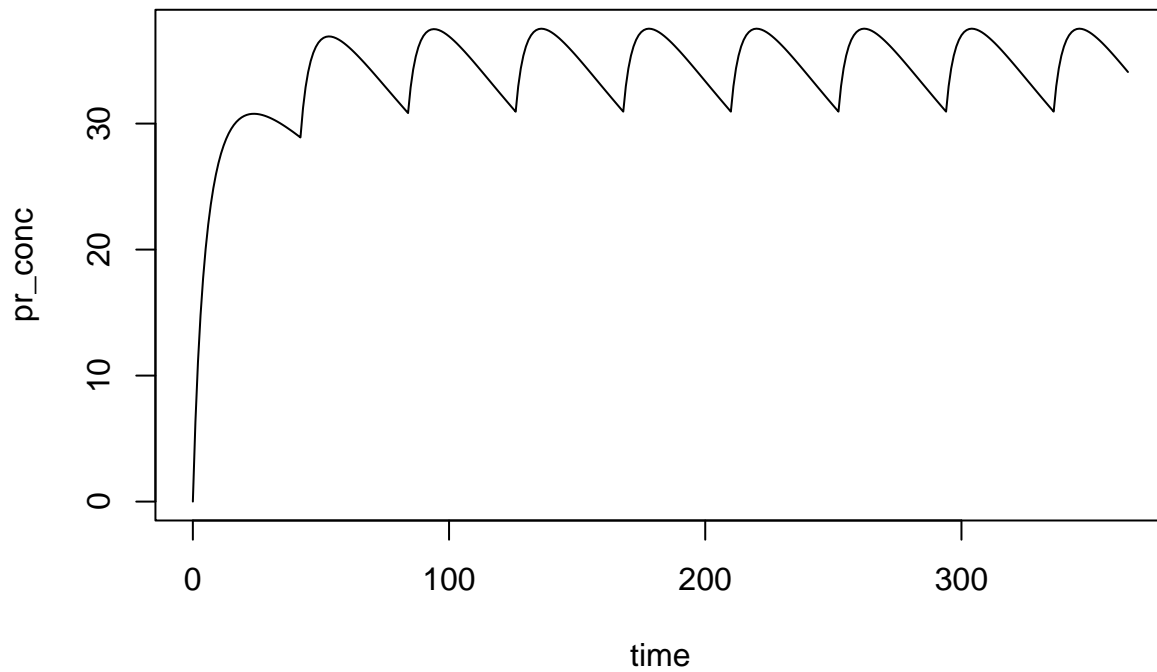


```
plot(COD_load ~ time, data = out1, type = 'l')
lines(COD_load ~ time, data = out0, col = 'red')
```
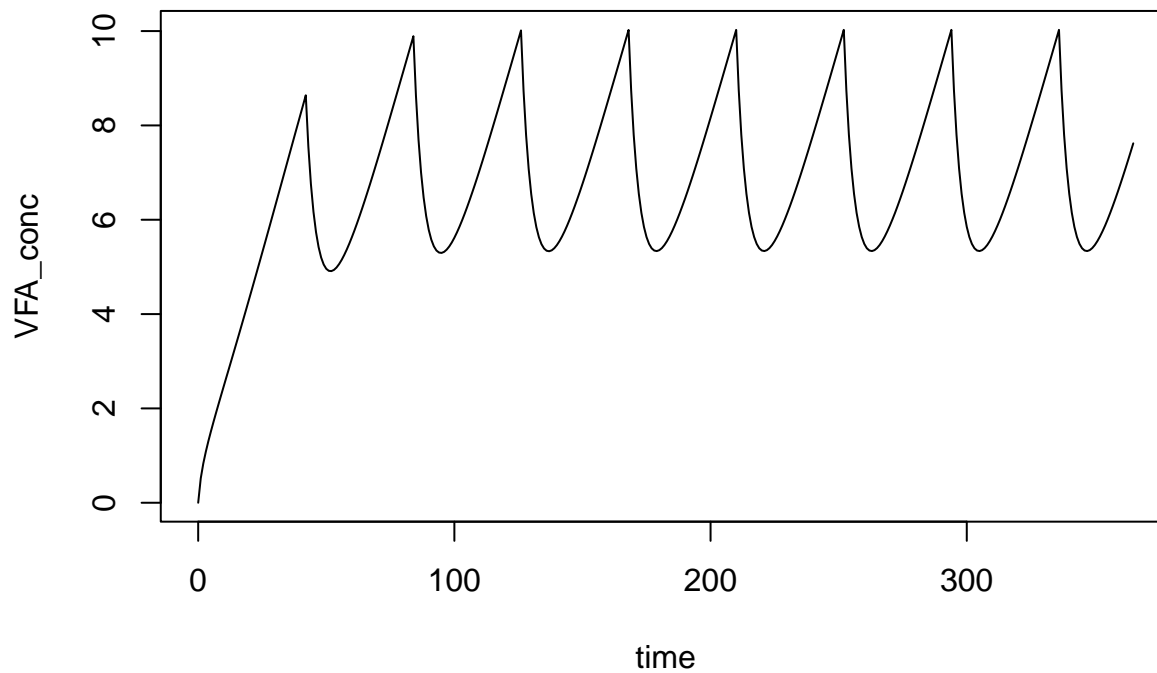
```r
plot(VSd_conc ~ time, data = out1, type = 'l')
```



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

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


2. Adjustments with `add_pars`

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

```
## i Loading ABM
```

```
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))
```

```
out2a <- abm(365,
             grp_pars = grp_pars,
             man_pars = man_pars,
             mic_pars = mic_pars,
             sub_pars = sub_pars,
             add_pars = list(sub_init.pr = 100))
```
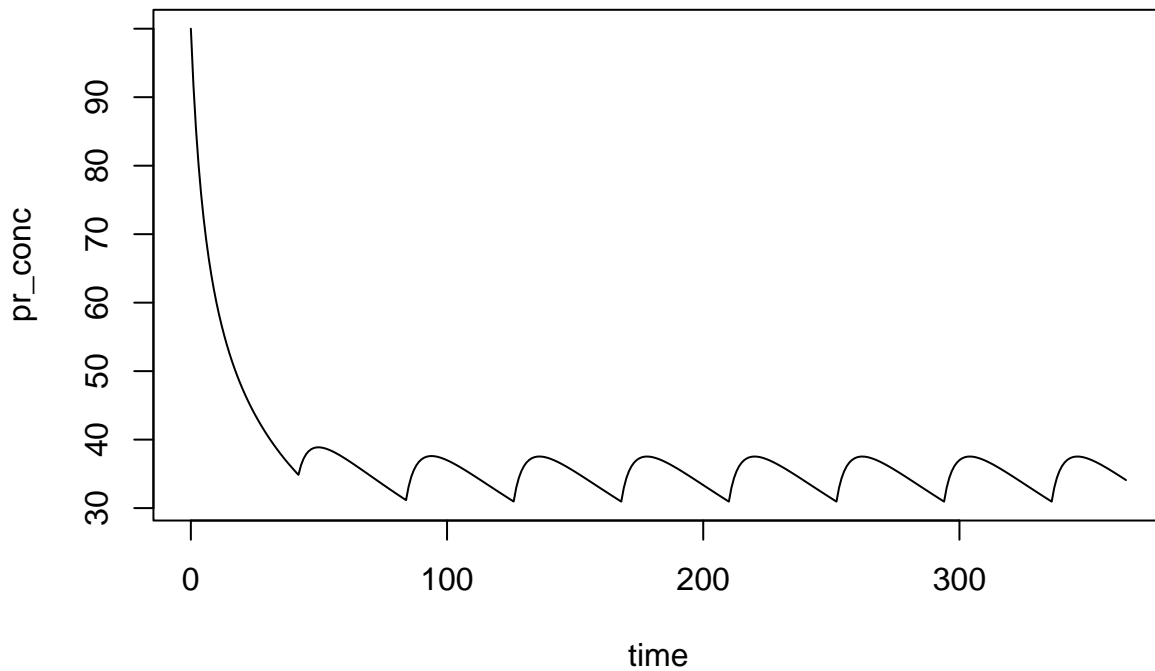
```
plot(pr_conc ~ time, data = out2a, type = 'l')
```


Will get error if `subs` has substrates not present in `sub_pars` elements.

```
out2b <- abm(365,
             grp_pars = grp_pars,
             man_pars = man_pars,
             mic_pars = mic_pars,
             sub_pars = sub_pars,
             add_pars = list(subs = c('VSd', 'pr', 'fat'), sub_init.pr = 100))
```

```
## Error in expandPars(pars = pars, elnms = pars$subs, parnms = sub_par_nms): Size-variable parameter p
```