Short demo of abmVar() in new simple1 version

Sasha D. Hafner

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Prep

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

```
## i Loading ABM
```

1. abmReg()

I am leaving out several elements that would only apply for `abmRegular()`.

```
mng_pars <- list(storage_depth = 4,
                 area = 100,
                 resid_enrich = 1)
```

```
sub_pars <- list(subs = c('cellulose', 'protein', 'lipids'),
                 forms = c(cellulose = 'C6H10O5', protein = 'C4 H6.1 O1.2 N',
                           lipids = 'C57 H104 O6', urea = 'CO(NH2)2'),
                 T_opt_hyd = c(default = 60),
                 T_min_hyd = c(default = 0),
                 T_max_hyd = c(default = 90),
                 hydrol_opt = c(lipids = 0.01, protein = 0.05, cellulose = 0.1),
                 sub_fresh = c(lipids = 3, protein = 20, cellulose = 35),
                 sub_init = c(lipids = 3, protein = 20, cellulose = 35))
```

```
grp_pars <- list(grps = c('m0', 'm1', 'm2'),
                 yield = c(default = 0.05),
                 xa_fresh = c(default = 0.05),
                 xa_init = c(default = 0.05),
                 dd_rate = c(default = 0.02),
                 ksv = c(default = 1),
                 qhat_opt = c(m0 = 1, m1 = 1, m2 = 2),
                 T_opt = c(m0 = 18, m1 = 18, m2 = 28),
                 T_min = c(m0 = 0, m1 = 6.41, m2 = 6.41),
                 T_max = c(m0 = 25, m1 = 25, m2 = 38))
```

```
man_pars <- list(VFA_fresh = c(CH3COOH = 2), pH = 7, dens = 1000)
chem_pars <- list(COD_conv = c(CH4 = 1/0.2507))
```

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

```
## i Loading ABM
```

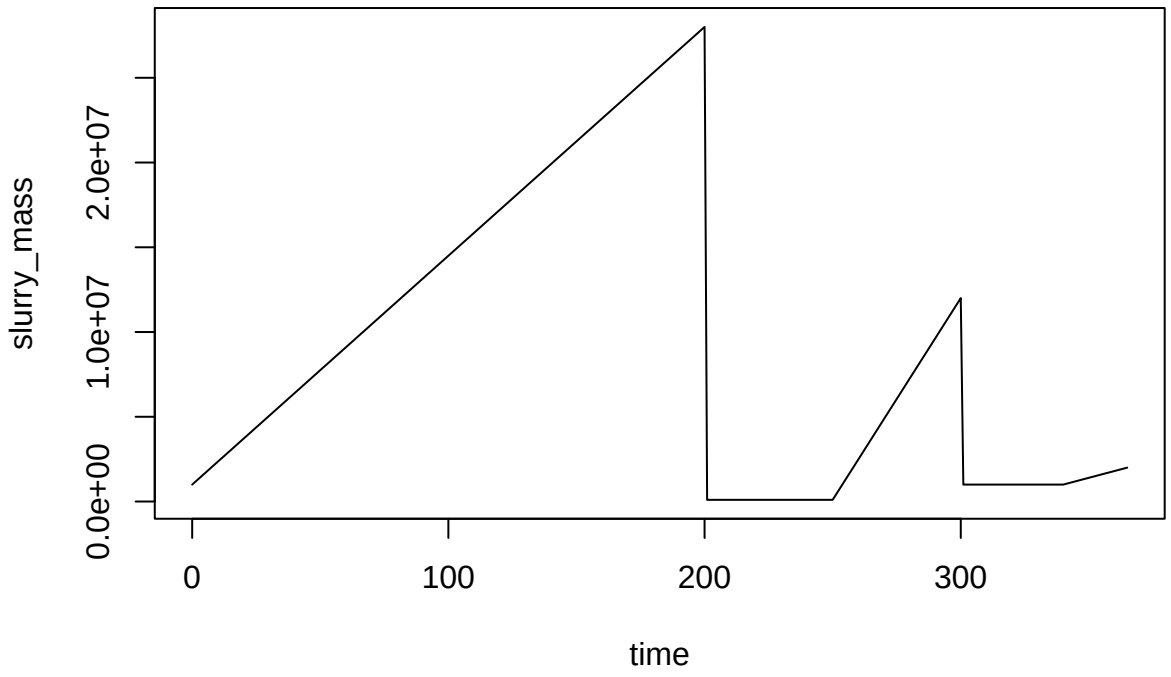
```
out1 <- abm(365,
            mng_pars = mng_pars,
            man_pars = man_pars,
            grp_pars = grp_pars,
            sub_pars = sub_pars,
            chem_pars = chem_pars,
            var_pars = var_pars,
            startup = 1)
```

```
##
## Startup run 1x -> and final run
```

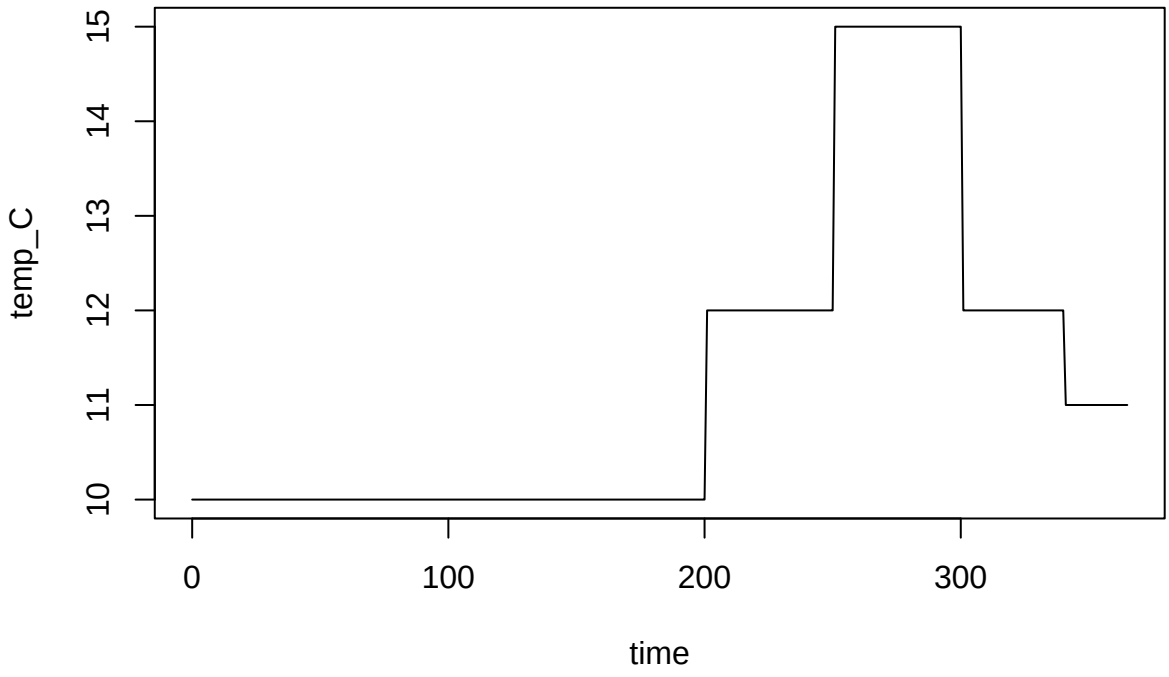
```
## Using starting conditions from `starting` argument
```

Here are some results.

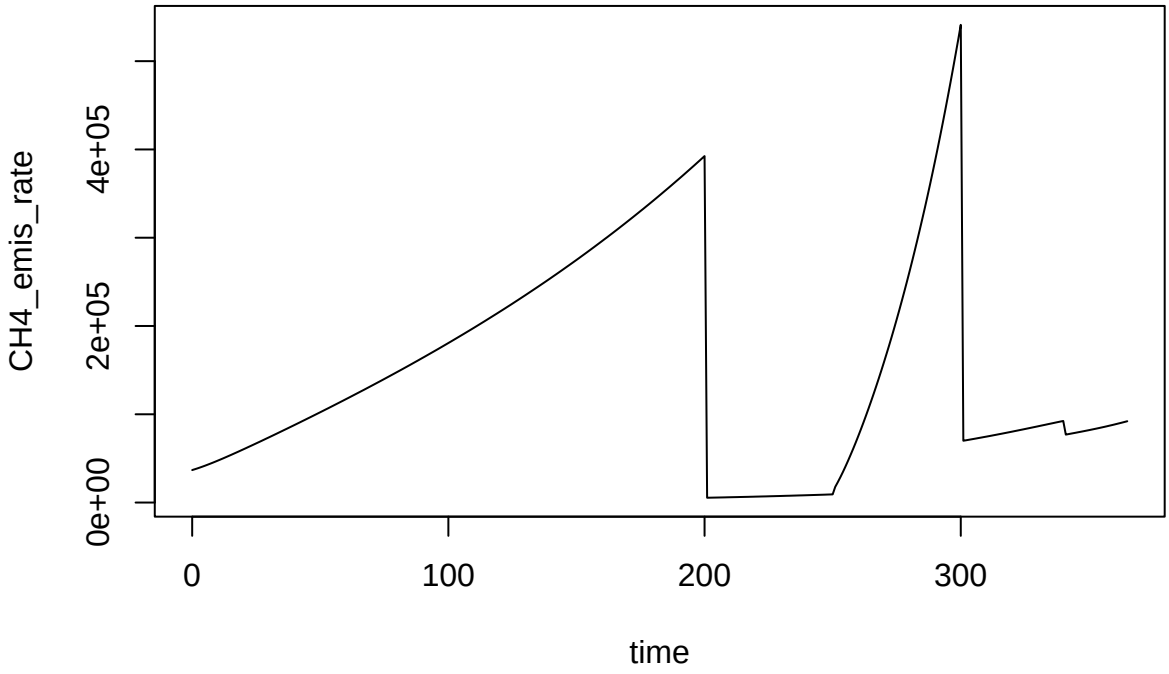
```
plot(slurry_mass ~ time, data = out1, type = 'l')
```



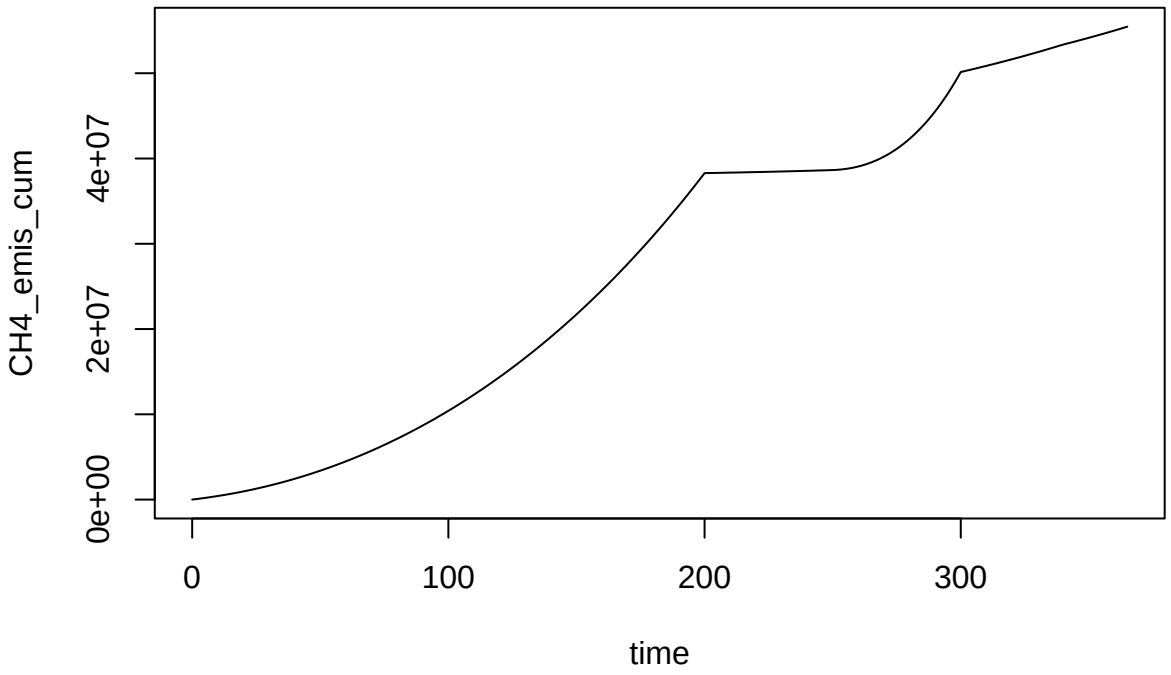

```
plot(temp_C ~ time, data = out1, type = 'l')
```



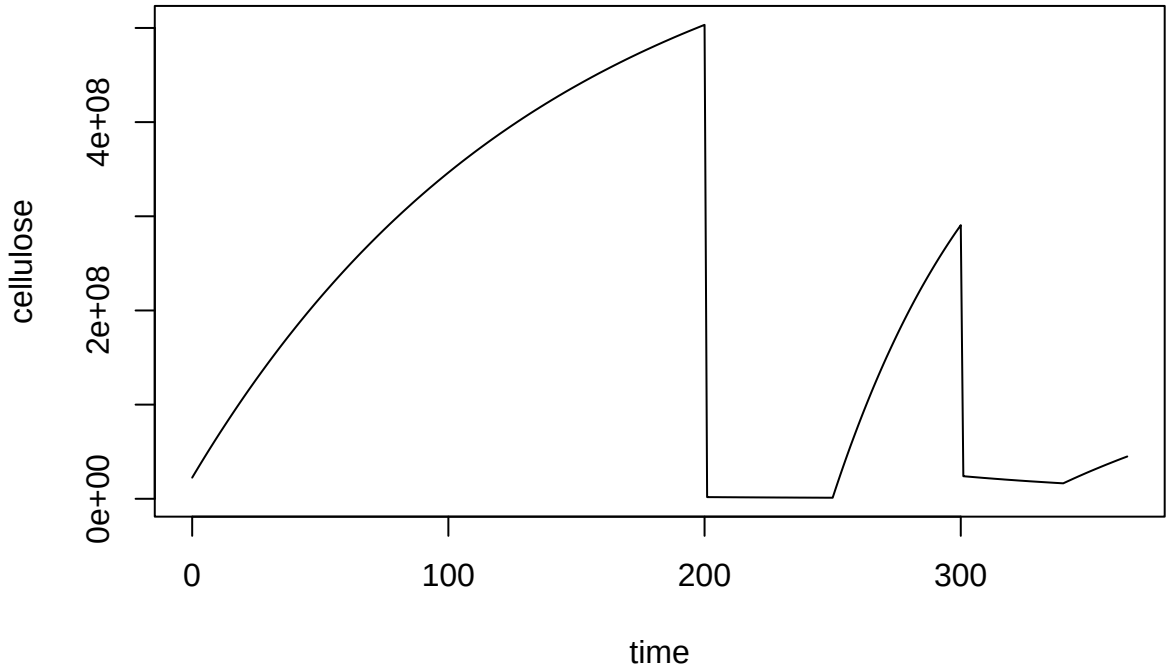

```
plot(CH4_emis_rate ~ time, data = out1, type = 'l')
```



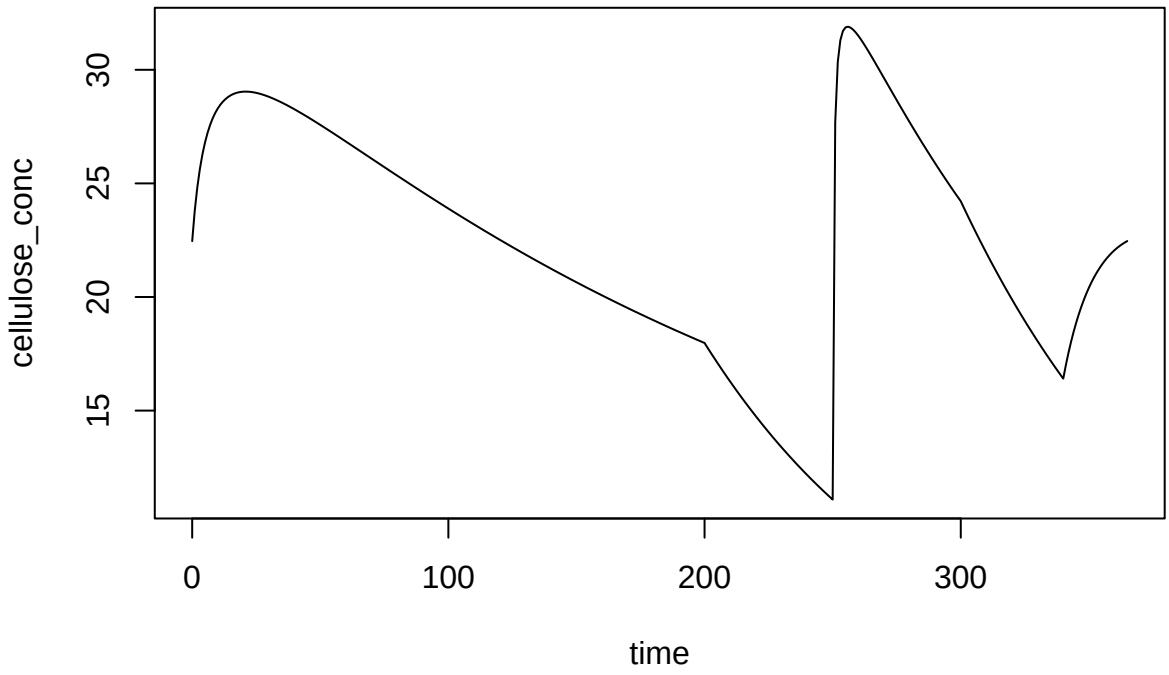

```
plot(CH4_emis_cum ~ time, data = out1, type = 'l')
```



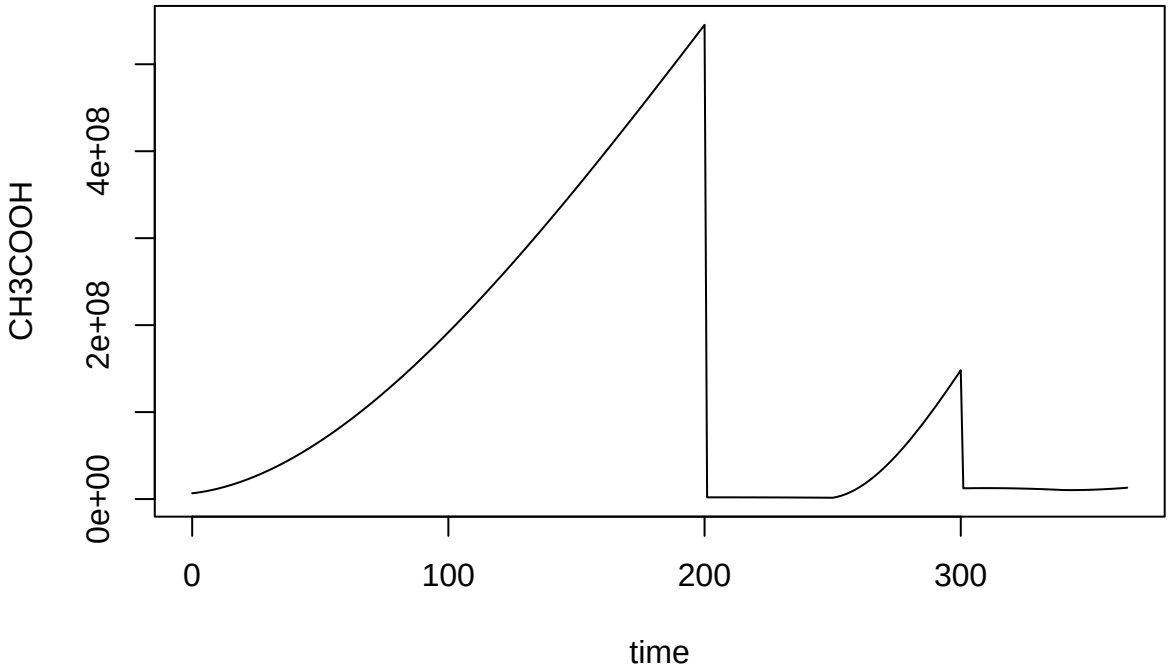

```
plot(cellulose ~ time, data = out1, type = 'l')
```



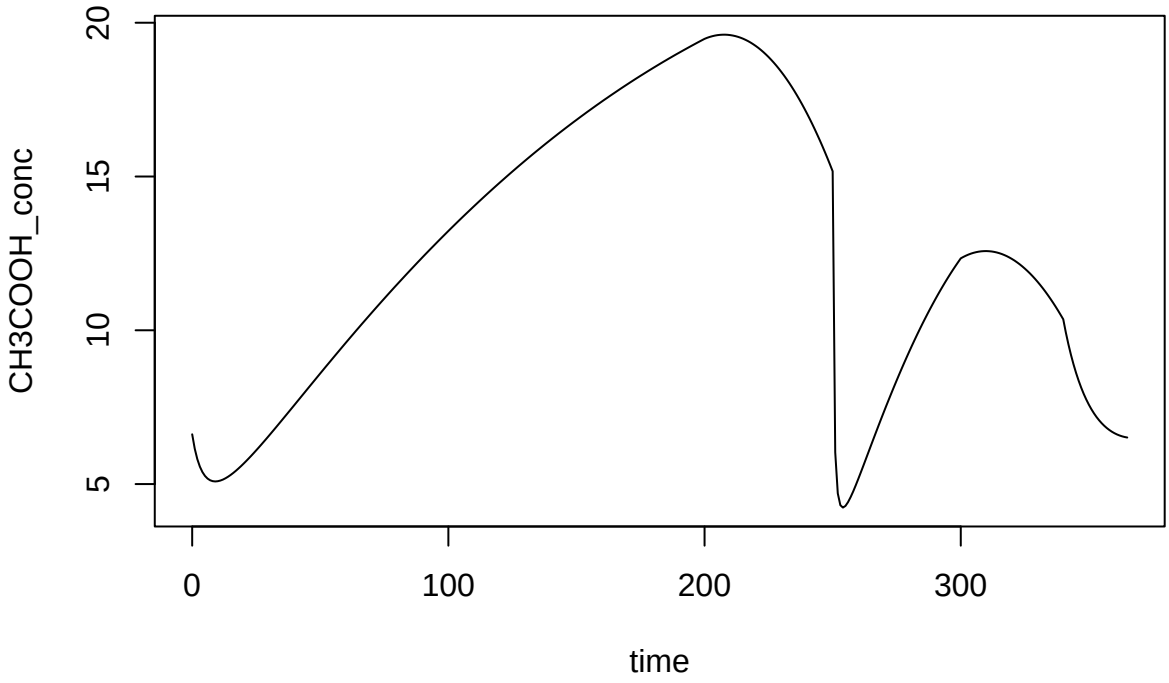

```
plot(cellulose_conc ~ time, data = out1, type = 'l')
```




```
plot(CH3COOH ~ time, data = out1, type = 'l')
```




```
plot(CH3COOH_conc ~ time, data = out1, type = 'l')
```



And methanogens.

```
line_colors <- c('red', 'blue', 'purple','orange')
matplot(out1$time, out1[, nn <- c('m0','m1','m2')]/1000,
        type = 'l', lty = c(1:length(nn)), col = line_colors, ylab = 'Microbial biomass (kg)')
legend("topright", legend = nn, lty = c(1:length(nn)), col = line_colors, lwd = 1, cex = 0.8)
```