

Short vs. long

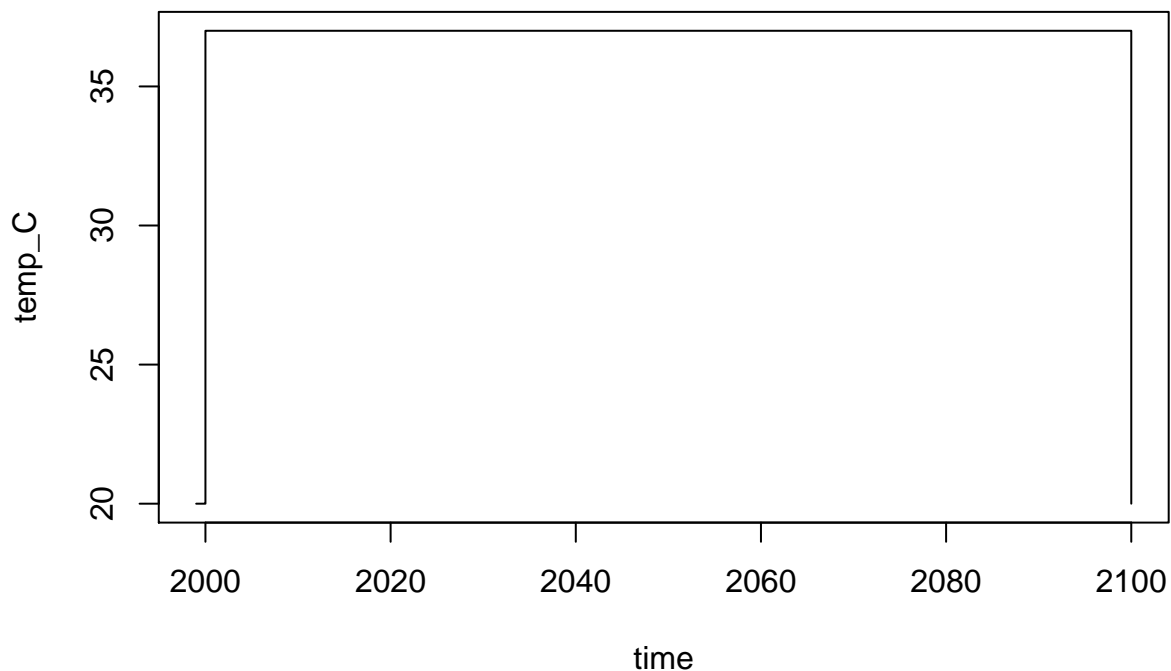
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```
library(ABM)
```

Psychro and meso temps

```
temp_dat <- data.frame(time = 2000 + c(-1, 0, 100),  
                        temp_C = c(20, 37, 20))  
plot(temp_C ~ time, data = temp_dat, type = 's')
```



```
grp_pars1 <- list(grps = c('m1', 'm3', 'p1', 'p2', 'sr1'),  
                  yield = c(default = 0.04, sr1 = 0.065),  
                  xa_fresh = c(default = 0.001, sr1 = 0.001),  
                  xa_init = c(m1 = 0.01, m3 = 0.01, p1 = 0.01, p2 = 0.01, sr1 = 0.01),  
                  decay_rate = c(m1 = 0.02, m3 = 0.02, p1 = 0.02, p2 = 0.02, sr1 = 0.02),  
                  ks_coefficient = c(m1 = 0.5, m3 = 1.0, p1 = 1.0, p2 = 1.0, sr1 = 0.4),  
                  resid_enrich = c(m1 = 0.0, m3 = 0.0, p1 = 0.0, p2 = 0.0, sr1 = 0.0),  
                  qhat_opt = c(m1 = 8, m3 = 5.75, p1 = 2.77, p2 = 0.72, sr1 = 8.3),  
                  T_opt = c(m1 = 313, m3 = 303, p1 = 293, p2 = 283, sr1 = 313),  
                  T_min = c(m1 = 295.31, m3 = 285.31, p1 = 275.31, p2 = 265.31, sr1 = 273),  
                  T_max = c(m1 = 320.67, m3 = 310.67, p1 = 300.67, p2 = 290.67, sr1 = 320.67),  
                  ki_NH3_min = c(m1 = 0.01, m3 = 0.015, p1 = 0.015, p2 = 0.015, sr1 = 0.015),
```

```

ki_NH3_max = c(m1 = 0.10, m3 = 0.131, p1 = 0.131, p2 = 0.131, sr1 = 0.131),
ki_NH4_min = c(m1 = 1.70, m3 = 2.714, p1 = 2.714, p2 = 2.714, sr1 = 2.714),
ki_NH4_max = c(m1 = 3.10, m3 = 4.764, p1 = 4.764, p2 = 4.764, sr1 = 4.764),
pH_upr = c(m1 = 8.0, m3 = 8.0, p1 = 8.0, p2 = 8.0, sr1 = 8.0),
pH_lwr = c(m1 = 6.5, m3 = 6.5, p1 = 6.5, p2 = 6.5, sr1 = 6.0))

```

Single group

```

grp_pars2 <- list(grps = c('m1', 'sr1'),
  yield = c(default = 0.04, sr1 = 0.065),
  xa_fresh = c(default = 0.001, sr1 = 0.001),
  xa_init = c(m1 = 0.01, sr1 = 0.01),
  decay_rate = c(m1 = 0.02, sr1 = 0.02),
  ks_coefficient = c(m1 = 1.0, sr1 = 0.4),
  resid_enrich = c(m1 = 0.0, sr1 = 0.0),
  qhat_opt = c(m1 = 5.75, sr1 = 8.3),
  T_opt = c(m1 = 310, sr1 = 313),
  T_min = c(m1 = 292, sr1 = 273),
  T_max = c(m1 = 317, sr1 = 320.67),
  ki_NH3_min = c(m1 = 0.015, sr1 = 0.015),
  ki_NH3_max = c(m1 = 0.131, sr1 = 0.131),
  ki_NH4_min = c(m1 = 2.714, sr1 = 2.714),
  ki_NH4_max = c(m1 = 4.764, sr1 = 4.764),
  pH_upr = c(m1 = 8.0, sr1 = 8.0),
  pH_lwr = c(m1 = 6.5, sr1 = 6.0))

```

Single but broad group

```

grp_pars3 <- list(grps = c('m1', 'sr1'),
  yield = c(default = 0.04, sr1 = 0.065),
  xa_fresh = c(default = 0.001, sr1 = 0.001),
  xa_init = c(m1 = 0.01, sr1 = 0.01),
  decay_rate = c(m1 = 0.02, sr1 = 0.02),
  ks_coefficient = c(m1 = 1.0, sr1 = 0.4),
  resid_enrich = c(m1 = 0.0, sr1 = 0.0),
  qhat_opt = c(m1 = 5.75, sr1 = 8.3),
  T_opt = c(m1 = 310, sr1 = 313),
  T_min = c(m1 = 265, sr1 = 273),
  T_max = c(m1 = 321, sr1 = 320.67),
  ki_NH3_min = c(m1 = 0.015, sr1 = 0.015),
  ki_NH3_max = c(m1 = 0.131, sr1 = 0.131),
  ki_NH4_min = c(m1 = 2.714, sr1 = 2.714),
  ki_NH4_max = c(m1 = 4.764, sr1 = 4.764),
  pH_upr = c(m1 = 8.0, sr1 = 8.0),
  pH_lwr = c(m1 = 6.5, sr1 = 6.0))

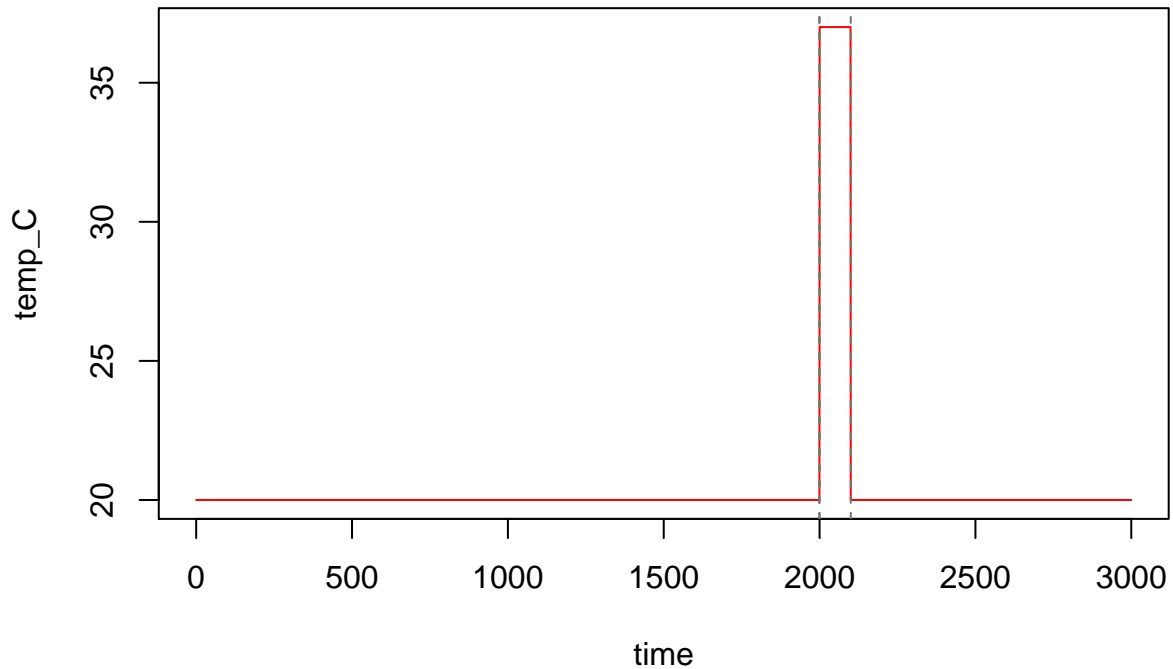
```

```

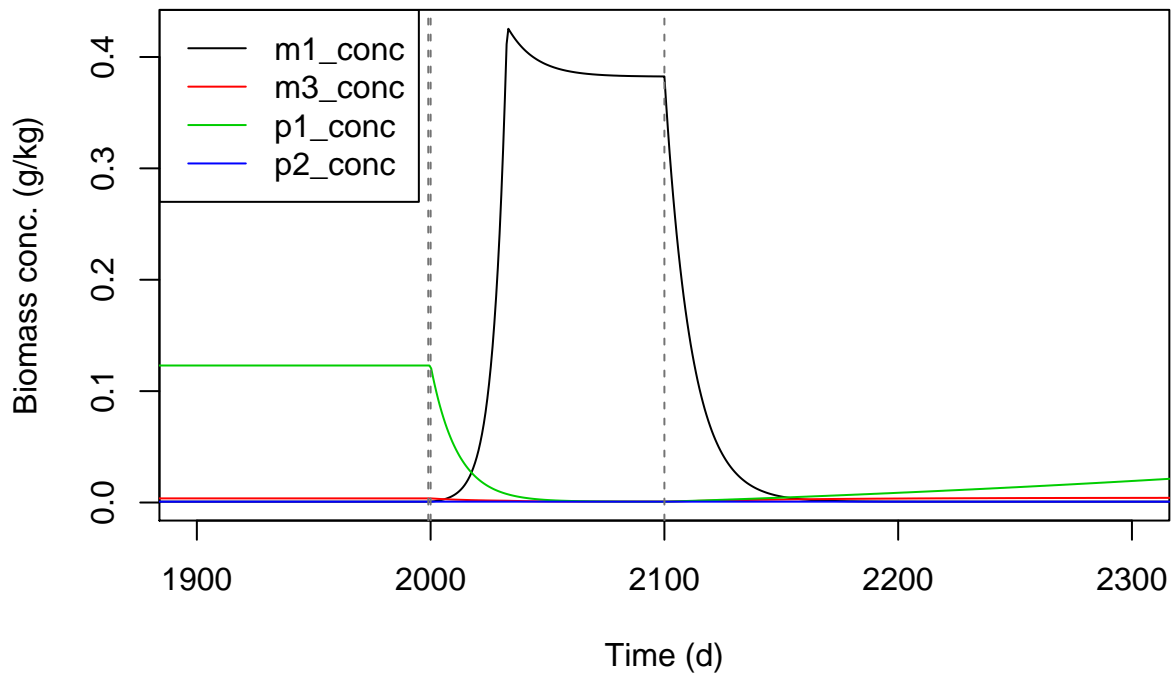
out1 <- abm(3000, 1,
  grp_pars = grp_pars1,
  add_pars = list(temp_C = temp_dat, resid_frac = 0.95,
    max_slurry_mass = 1,
    slurry_mass = 0.95 * 1, slurry_prod_rate = 1/15,
    conc_fresh.Sp = 50, conc_fresh.COD = 60, conc_fresh.VFA = 4,
    area = 0),
  approx_method_temp = 'constant')

```

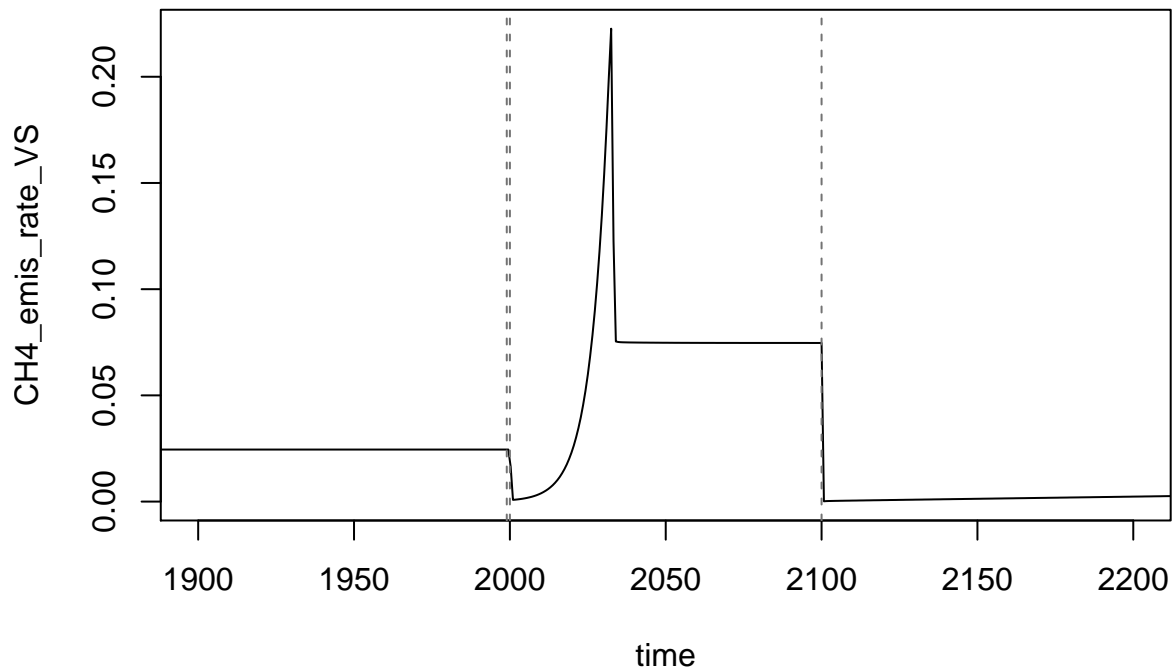
```
plot(temp_C ~ time, type = 'l', col = 'red', data = out1)
abline(v = temp_dat$time, lty = 2, col = 'gray45')
```



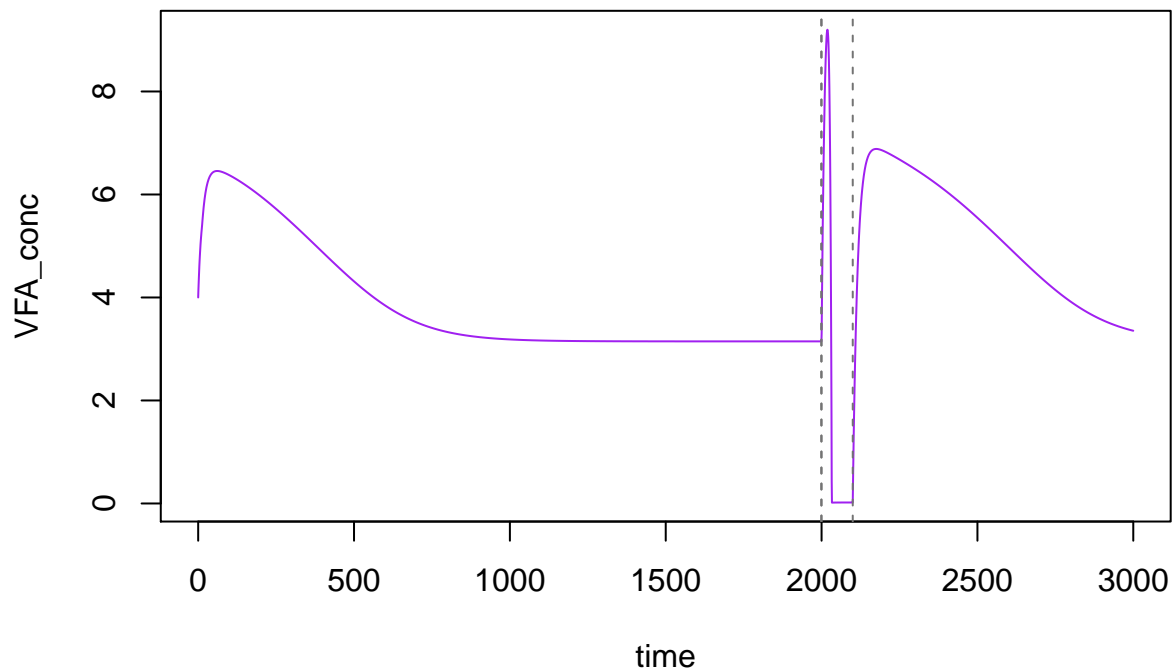
```
matplot(out1$time, out1[, nn <- c('m1_conc', 'm3_conc', 'p1_conc', 'p2_conc')],
        type = 'l', lty = 1, xlab = 'Time (d)', ylab = 'Biomass conc. (g/kg)',
        xlim = c(1900, 2300))
legend('topleft', nn, col = 1:5, lty = 1)
abline(v = temp_dat$time, lty = 2, col = 'gray45')
```



```
plot(CH4_emis_rate_VS ~ time, data = out1, type = 'l', xlim = c(1900, 2200))
abline(v = temp_dat$time, lty = 2, col = 'gray45')
```



```
plot(VFA_conc ~ time, type = 'l', col = 'purple', data = out1)
abline(v = temp_dat$time, lty = 2, col = 'gray45')
```



Now single mesophilic group

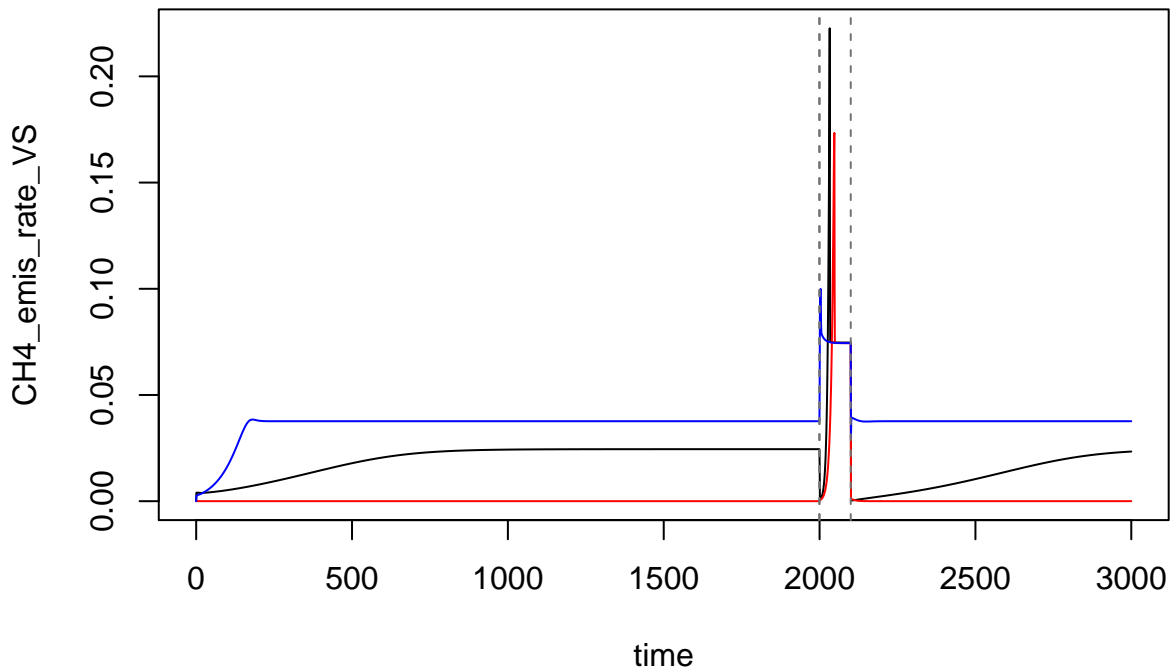
```
out2 <- abm(3000, 1,
  grp_pars = grp_pars2,
  add_pars = list(temp_C = temp_dat, resid_frac = 0.95,
    max_slurry_mass = 1,
    slurry_mass = 0.95 * 1, slurry_prod_rate = 1/15,
    conc_fresh.Sp = 50, conc_fresh.COD = 60, conc_fresh.VFA = 4,
    area = 0),
```

```
approx_method_temp = 'constant')
```

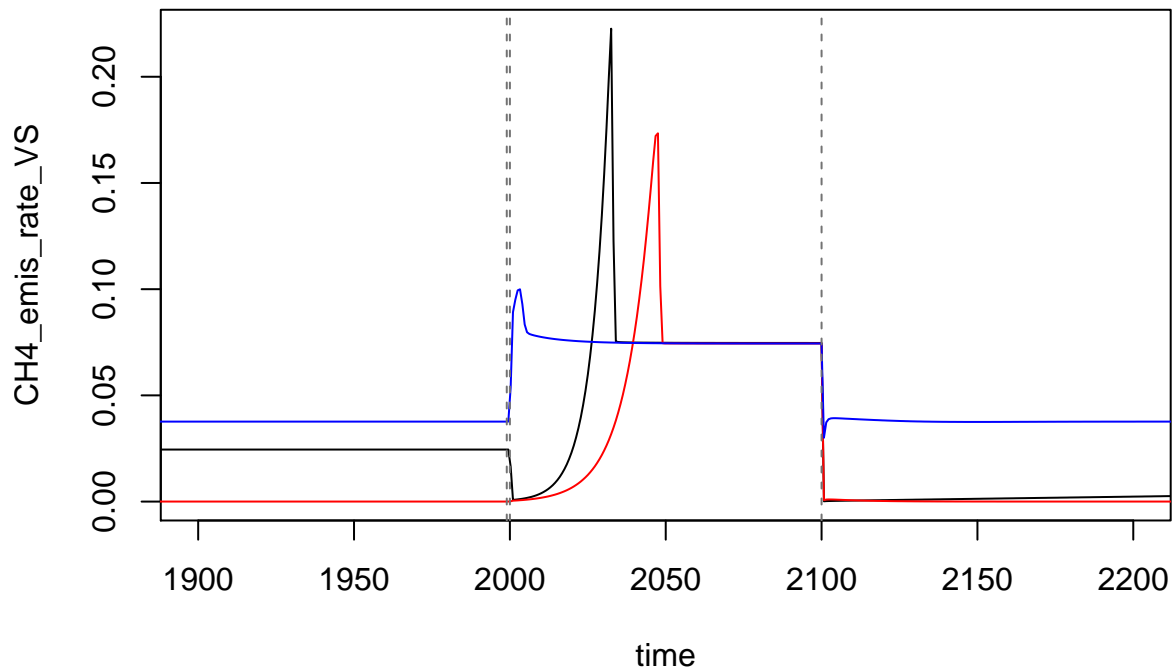
One very broad group.

```
out3 <- abm(3000, 1,
  grp_pars = grp_pars3,
  add_pars = list(temp_C = temp_dat, resid_frac = 0.95,
    max_slurry_mass = 1,
    slurry_mass = 0.95 * 1, slurry_prod_rate = 1/15,
    conc_fresh.Sp = 50, conc_fresh.COD = 60, conc_fresh.VFA = 4,
    area = 0),
  approx_method_temp = 'constant')
```

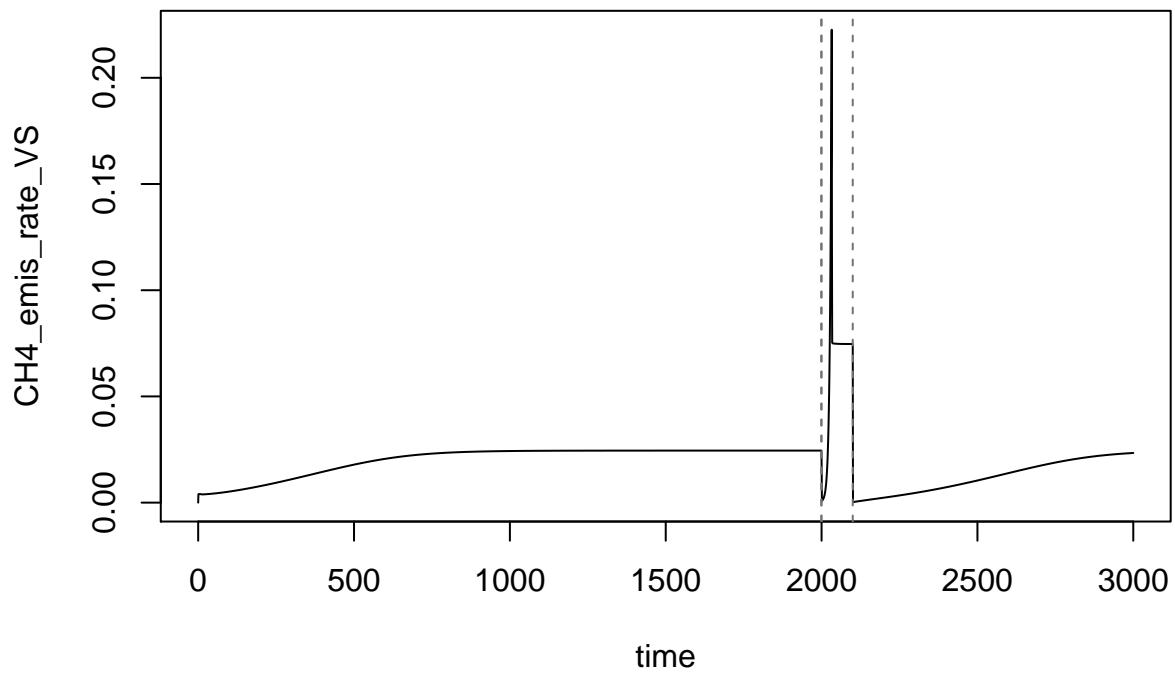
```
plot(CH4_emis_rate_VS ~ time, data = out1, type = 'l')
lines(CH4_emis_rate_VS ~ time, data = out2, type = 'l', col = 'red')
lines(CH4_emis_rate_VS ~ time, data = out3, type = 'l', col = 'blue')
abline(v = temp_dat$time, lty = 2, col = 'gray45')
```



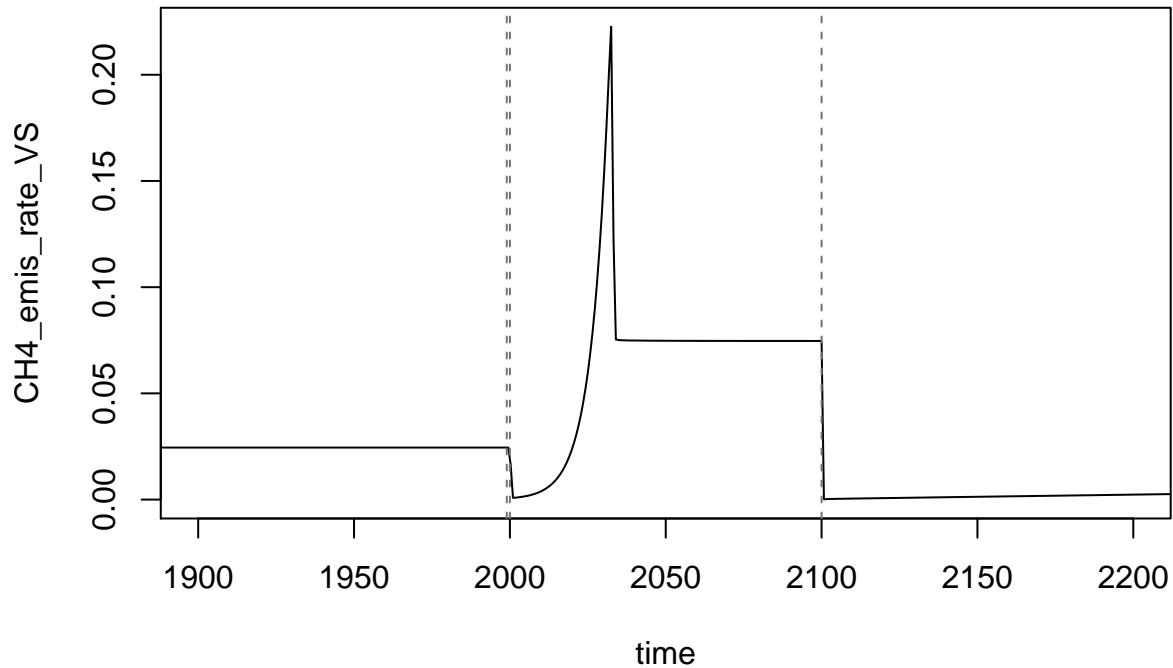
```
plot(CH4_emis_rate_VS ~ time, data = out1, type = 'l', xlim = c(1900, 2200))
lines(CH4_emis_rate_VS ~ time, data = out2, type = 'l', col = 'red')
lines(CH4_emis_rate_VS ~ time, data = out3, type = 'l', col = 'blue')
abline(v = temp_dat$time, lty = 2, col = 'gray45')
```



```
plot(CH4_emis_rate_VS ~ time, data = out1, type = 'l')
abline(v = temp_dat$time, lty = 2, col = 'gray45')
```



```
plot(CH4_emis_rate_VS ~ time, data = out1, type = 'l', xlim = c(1900, 2200))
abline(v = temp_dat$time, lty = 2, col = 'gray45')
```



Different simulation

From Soren:

1. Temperature at e.g. 50 degrees during, say, 40 days to simulate AD.
2. Transfer to e.g. 20 degrees (immediate change can be explained by heat exchange) for another 40 days.
3. Population 1 with a temperature optimum at 52? degrees, and distribution corresponding to Fig. 1c.
4. Population 2 and 3 with temperature profiles that correspond to pig and cattle slurry (1a and 1b).
5. Methane production rates of each population at 20 and 50 degrees are defined in Fig. 1

So. . . Three groups

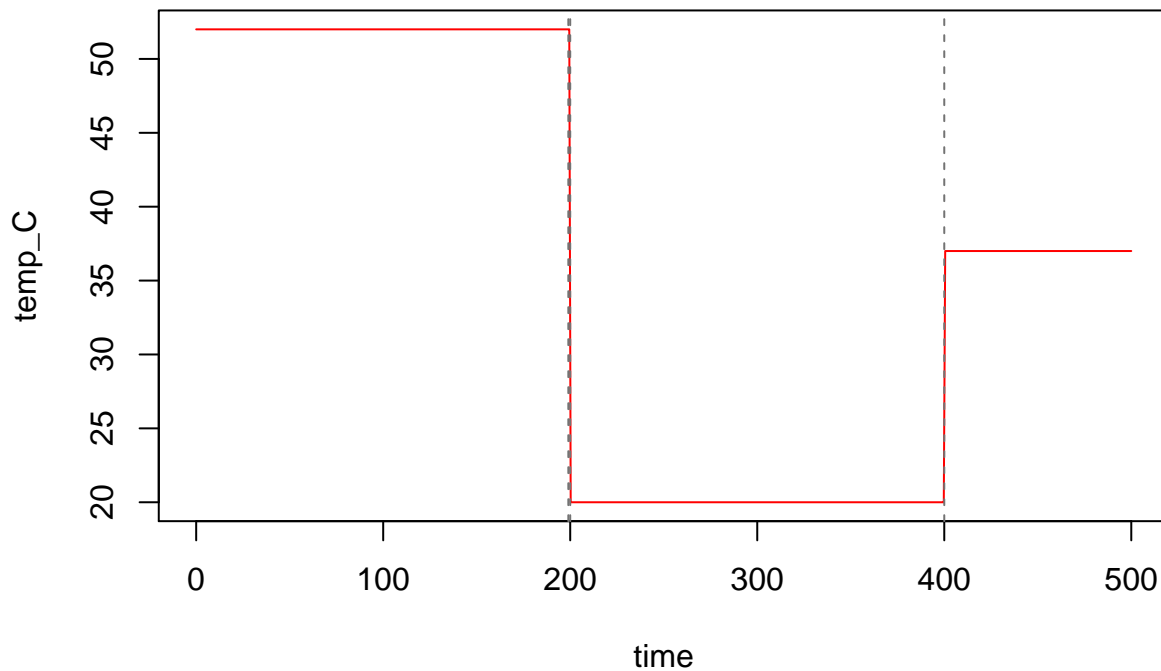
```
grp_pars4 <- list(
  grps = c('m1', 'm2', 'sr1'),
  yield = c(default = 0.04, sr1 = 0.065),
  xa_fresh = c(all = 0.001),
  xa_init = c(all = 0.01),
  decay_rate = c(all = 0.02),
  ks_coefficient = c(default = 1.0, sr1 = 0.4),
  resid_enrich = c(all = 0),
  qhat_opt = c(all = 8),
  T_opt = 273.15 + c(m1 = 35, m2 = 52, sr1 = 40),
  T_min = 273.15 + c(m1 = 5, m2 = 20, sr1 = 0),
  T_max = 273.15 + c(m1 = 50, m2 = 65, sr1 = 55),
  ki_NH3_min = c(all = 0.01),
  ki_NH3_max = c(all = 0.10),
  ki_NH4_min = c(all = 2),
  ki_NH4_max = c(all = 3),
  pH_upr = c(all = 8),
  pH_lwr = c(all = 6.5))
```

```
temp_dat <- data.frame(time = 200 + c(-1, 0, 200),
  temp_C = c(52, 20, 37))
```

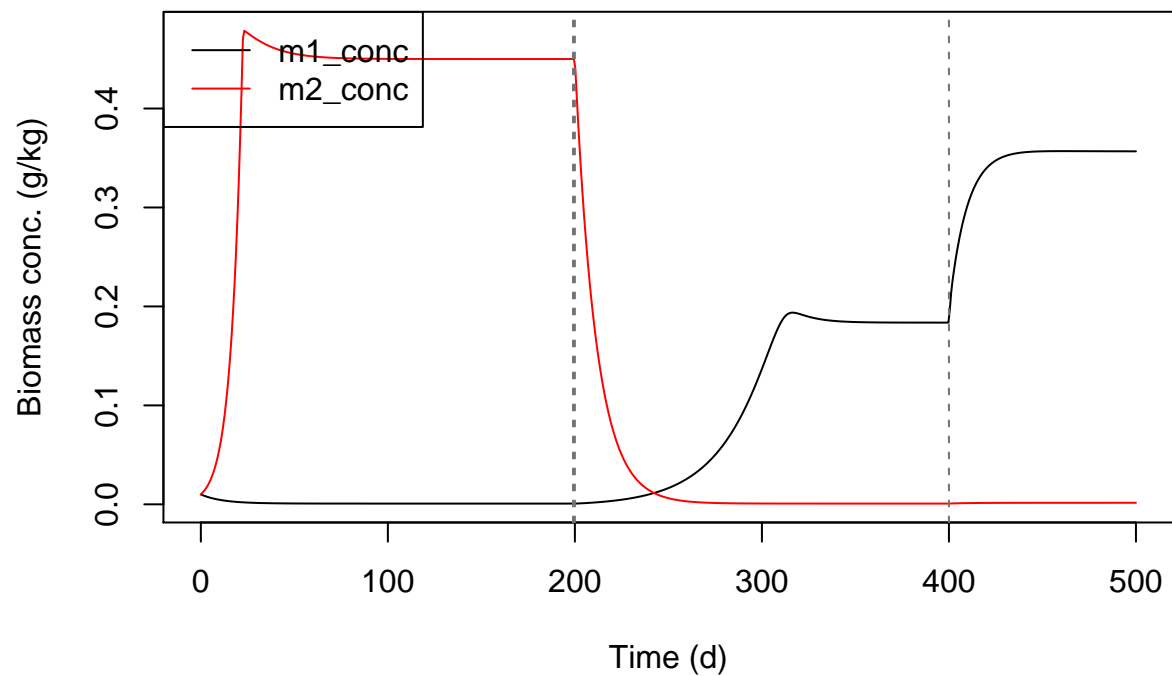
Hydrolysis optimum is increased to 52C.

```
out4 <- abm(500, 1,
  grp_pars = grp_pars4,
  add_pars = list(temp_C = temp_dat, resid_frac = 0.95,
    max_slurry_mass = 1,
    slurry_mass = 0.95 * 1, slurry_prod_rate = 1/15,
    conc_fresh.Sp = 50, conc_fresh.COD = 60, conc_fresh.VFA = 4,
    area = 0, alpha_T_max = 328, alpha_T_opt = 323, alpha_opt = 0.02),
  approx_method_temp = 'constant')

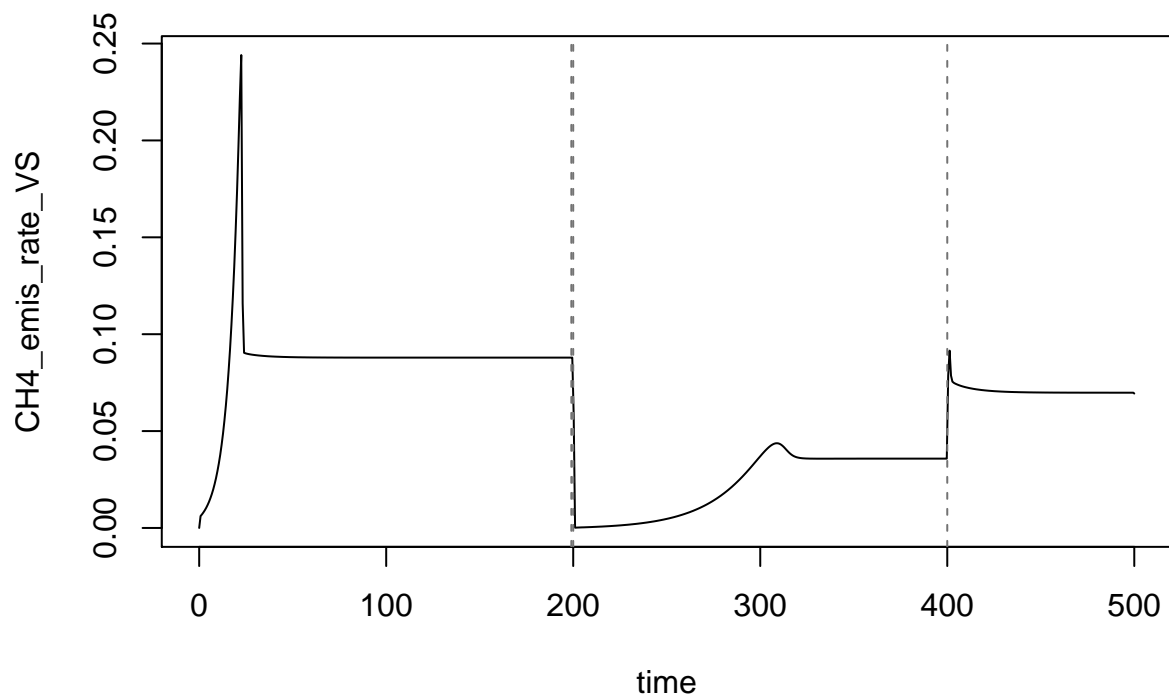
plot(temp_C ~ time, type = 'l', col = 'red', data = out4)
abline(v = temp_dat$time, lty = 2, col = 'gray45')
```



```
matplot(out4$time, out4[, nn <- c('m1_conc', 'm2_conc')],
  type = 'l', lty = 1, xlab = 'Time (d)', ylab = 'Biomass conc. (g/kg)')
legend('topleft', nn, col = 1:3, lty = 1)
abline(v = temp_dat$time, lty = 2, col = 'gray45')
```

```
plot(CH4_emis_rate_VS ~ time, data = out4, type = 'l')
abline(v = temp_dat$time, lty = 2, col = 'gray45')
```



```
plot(VFA_conc ~ time, type = 'l', col = 'purple', data = out4)
abline(v = temp_dat$time, lty = 2, col = 'gray45')
```

