Understanding ALFAM2 digestate predictions

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To try to understand combined DM and pH effects that drive differences in emission from digestate vs. raw slurry.

Prep

```
rm(list = ls())
library(ALFAM2)
library(ggplot2)
library(dplyr)
source('../../functions/rounddf.R')
```

Parameters

Get, set pars

```
load('../../parameters/parf.RData')
pars <- parf
pars['man.ph.r1'] <- 0.66
pars['man.ph.r3'] <- 0.24
```

View pars

```
signif(pars, 3)
```

```
##        man.ph.r1        man.ph.r3             int.f0             int.r1
##          0.66000          0.24000           -0.61400           -1.09000
##           int.r2           int.r3       app.mthd.os.f0     app.rate.nos.f0
##         -1.12000          -2.79000           -1.86000           -0.00957
```

```
##         man.dm.f0       app.mthd.bc.r1            man.dm.r1            air.temp.r1
##           0.39200              0.83800             -0.11200                0.08270
##          wind.2m.r1           air.temp.r3        app.mthd.os.r3           rain.rate.r2
##           0.14700              0.00893             -0.25900                0.43100
##         rain.cum.r3     man.source.pig.f0       app.mthd.ts.r1 bsth.cereal.hght.r1
##          -0.01200             -0.48800             -0.50500               -0.01100
##     ts.grass.hght.r1     ts.cereal.hght.r1          country.NL.f0          country.CH.f0
##           0.01440             -0.22700              0.82700                0.07390
```

DM and pH

```
signif(pars, 3)[grepl('\\.dm\\.', names(pars))]
```

```
## man.dm.f0 man.dm.r1
##     0.392    -0.112
```

```
signif(pars, 3)[grepl('\\.ph\\.', names(pars))]
```

```
## man.ph.r1 man.ph.r3
##      0.66      0.24
```

Note that these are different from the defaults. These new values are based on the EF work.

Defaults:

```
pars = c(int.f0           = -0.7364889,
         int.r1           = -1.1785848,
         int.r2           = -0.9543731,
         int.r3           = -2.9012937,
         app.mthd.os.f0   = -1.1717859,
         app.rate.f0      = -0.0134681,
         man.dm.f0        =  0.407466,
         incorp.deep.f4   = -3.6477259,
         incorp.shallow.f4 = -0.4121023,
         app.mthd.bc.r1   =  0.6283396,
         man.dm.r1        = -0.075822,
         air.temp.r1      =  0.0492777,
         wind.2m.r1       =  0.0486651,
         man.ph.r1        =  0.5327231,
         air.temp.r3      =  0.0152419,
         incorp.deep.r3   = -0.3838862,
         app.mthd.os.r3   = -0.122883,
```

```
          man.ph.r3         =  0.2663616,
          rain.rate.r2      =  0.4327281,
          rain.cum.r3       = -0.0300936),
```

Input data

Input data, from the acidification report.

```
dat <- data.frame(ct = 168, animal = c('pig', 'cattle', 'mixed', 'digestate', 'digestate DM', 'digestate pH'),
                  man.source.pig = c(TRUE, rep(FALSE, 5)),
                  man.dm = c(3.5, 7.5, 5.5, 7.8, 7.8, 5.5),
                  man.ph = c(7.1, 7.0, 7.1, 8.1, 7.1, 8.1),
                  TAN.app = 100)
dat$id <- 1:nrow(dat)
dat.input <- dat
```

Run model

```
pred <- ALFAM2mod(dat, pars = pars, group = 'id')
```

```
## Warning in ALFAM2mod(dat, pars = pars, group = "id"): Running with 9 parameters. Dropped 15 with no match.
## These secondary parameters have been dropped: app.mthd.os.f0, app.rate.nos.f0, app.mthd.bc.r1, air.temp.r1, wind.2m.r1, air.temp.r3, ap
dat <- merge(dat, pred, by = c('id', 'ct'))
dat <- rounddf(dat, digits = 3, func = signif)
```
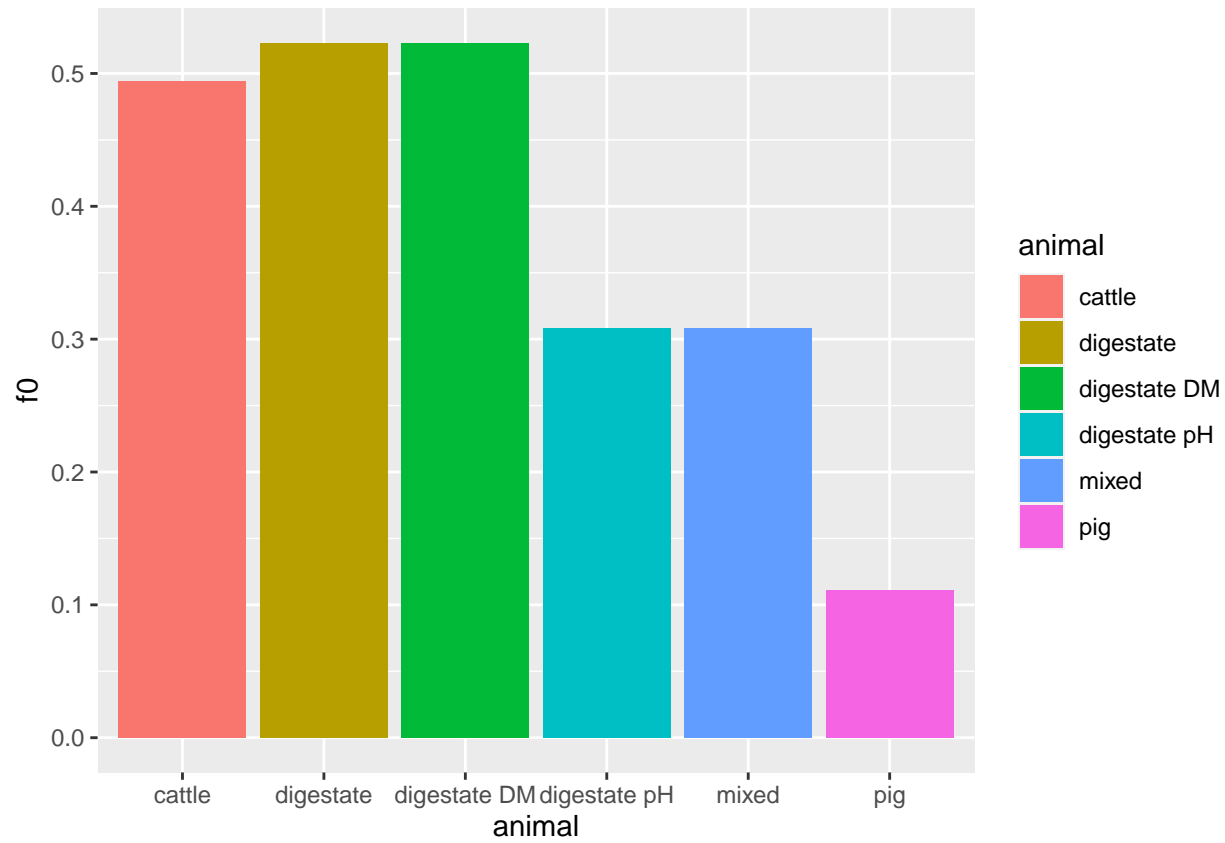
Output

Parameter values.

```
rounddf(dat[, c(3, 9:12)], func = signif, digits = 2)
```
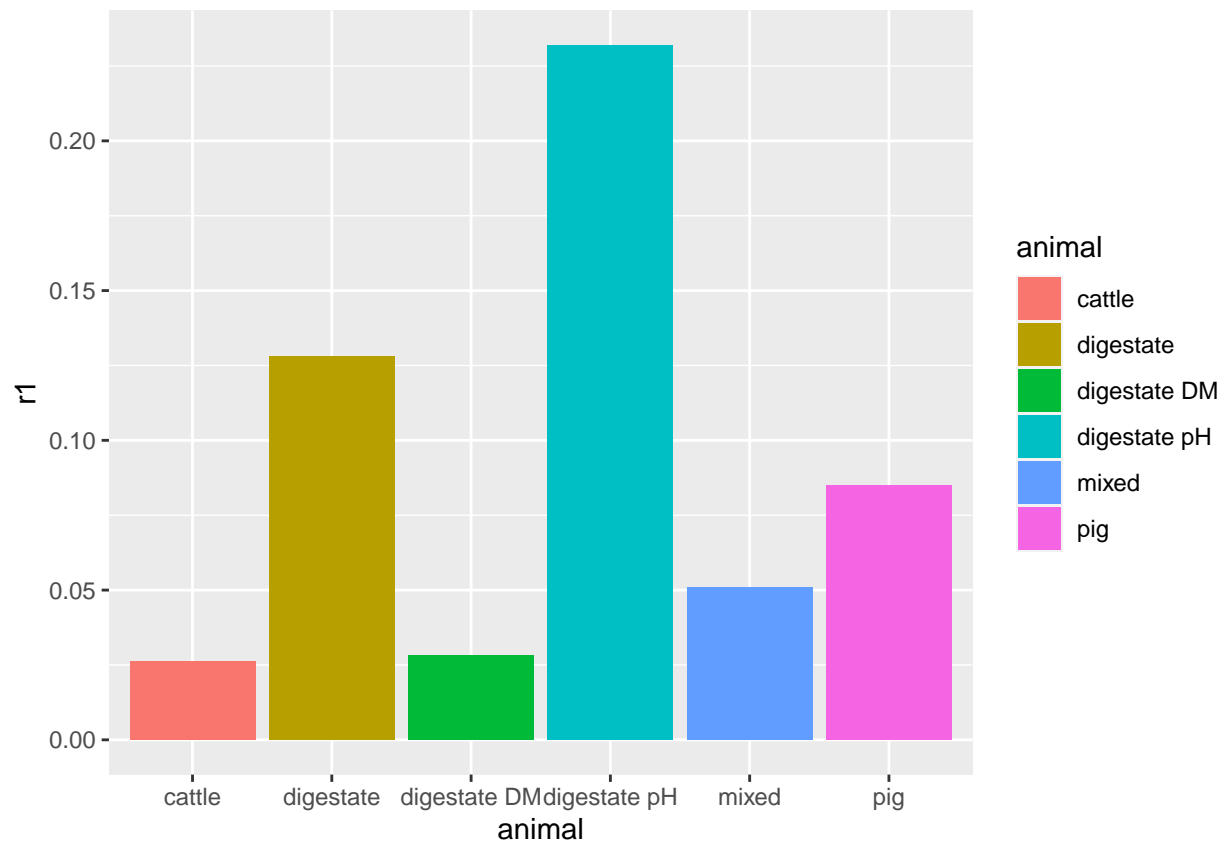
```
##          animal   f0    r1    r2     r3
## 1           pig 0.11 0.085 0.076 0.0013
## 2        cattle 0.49 0.026 0.076 0.0012
## 3         mixed 0.31 0.051 0.076 0.0013
```

```
## 4      digestate 0.52 0.130 0.076 0.0023
## 5 digestate DM 0.52 0.028 0.076 0.0013
## 6 digestate pH 0.31 0.230 0.076 0.0023
```
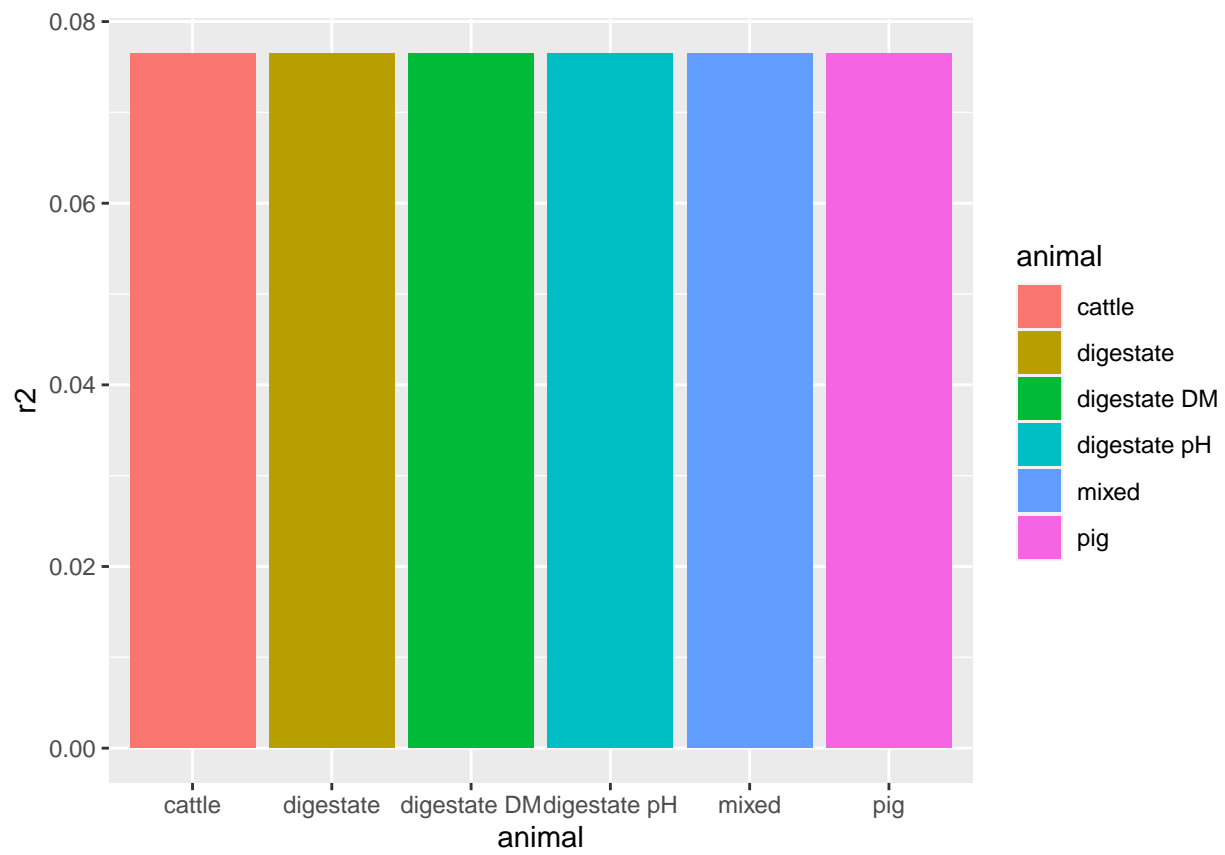
```
ggplot(dat, aes(animal, f0, fill = animal)) +
  geom_col()
```
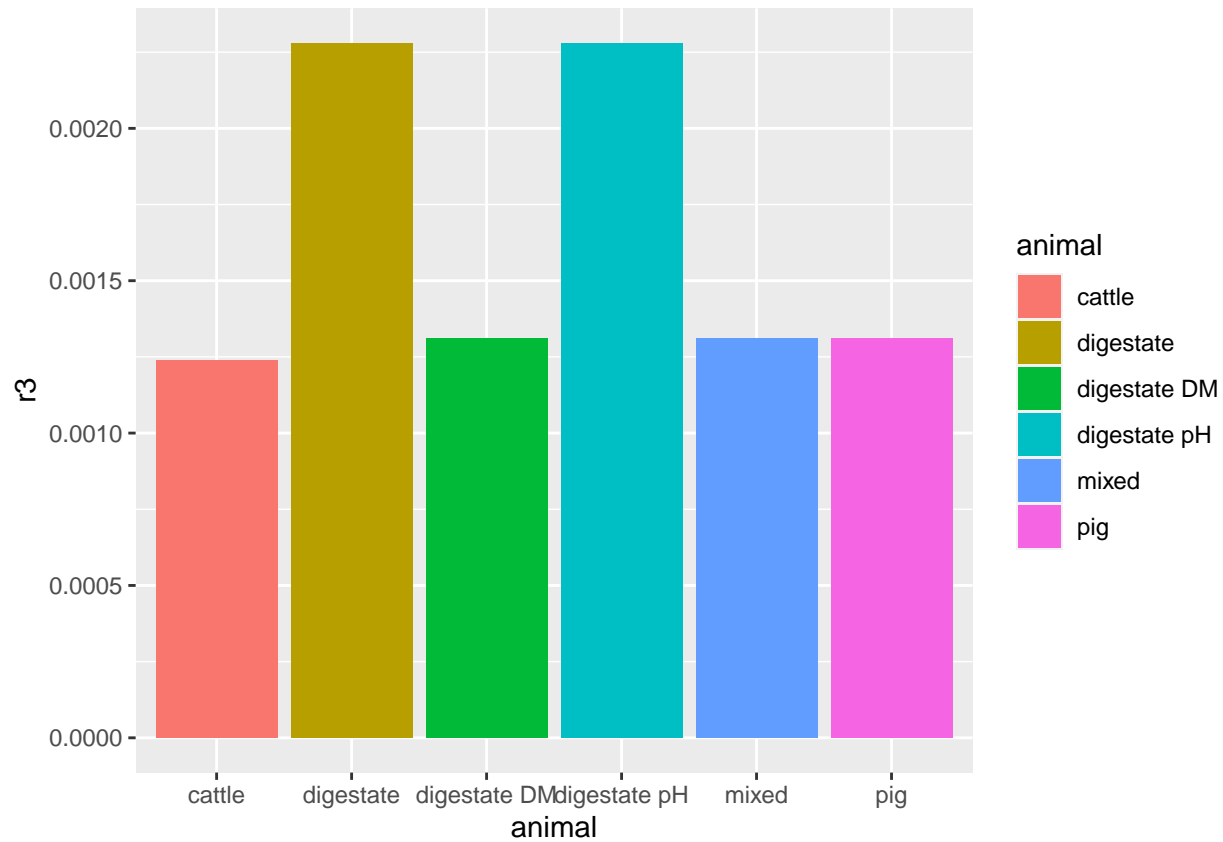


```
ggplot(dat, aes(animal, r1, fill = animal)) +
  geom_col()
```

```
ggplot(dat, aes(animal, r2, fill = animal)) +
  geom_col()
```

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```
ggplot(dat, aes(animal, r3, fill = animal)) +
  geom_col()
```
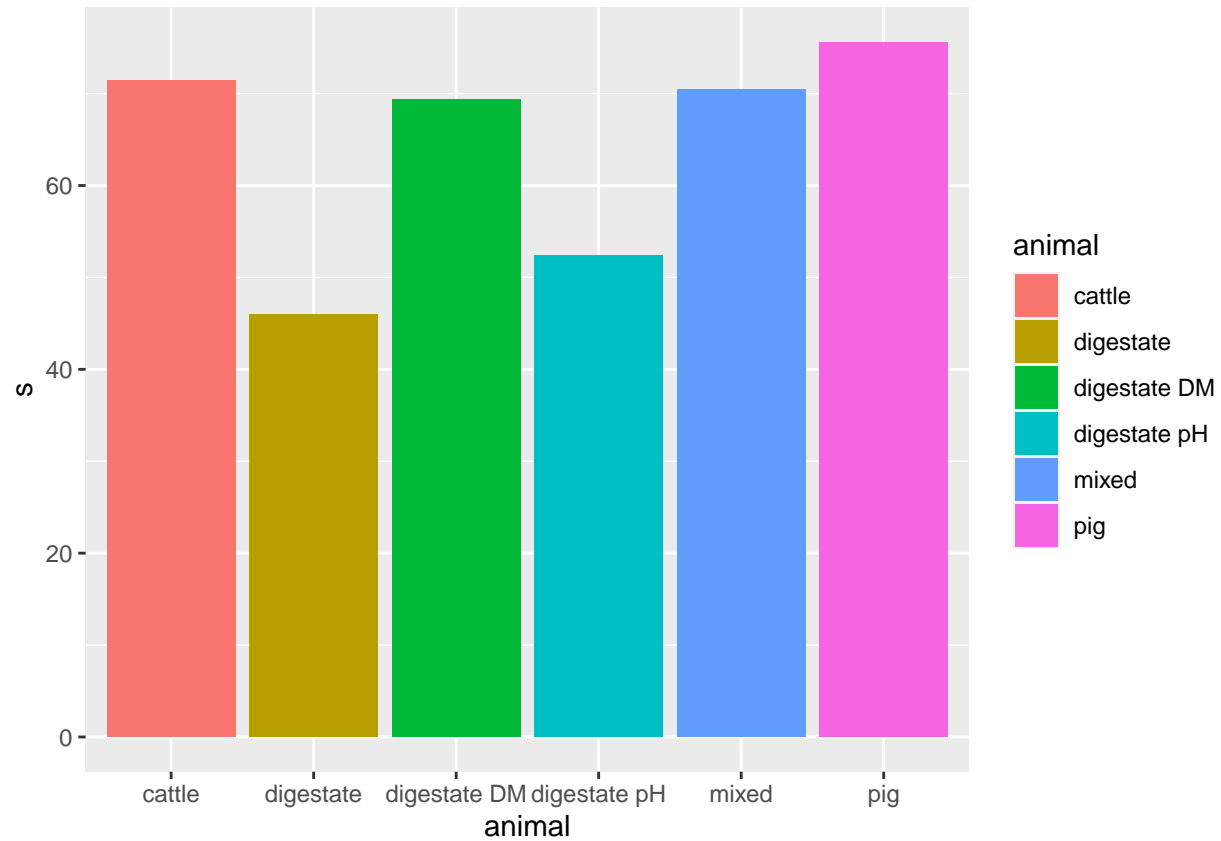
Emission and pools.

f = fast pool, s = slow, e = cumulative emission (% applied TAN here). All fast TAN is lost by 168 h, so r3 becomes important.

```r
rounddf(dat[, c(3, 14, 15, 17)], func = signif, digits = 2)
```
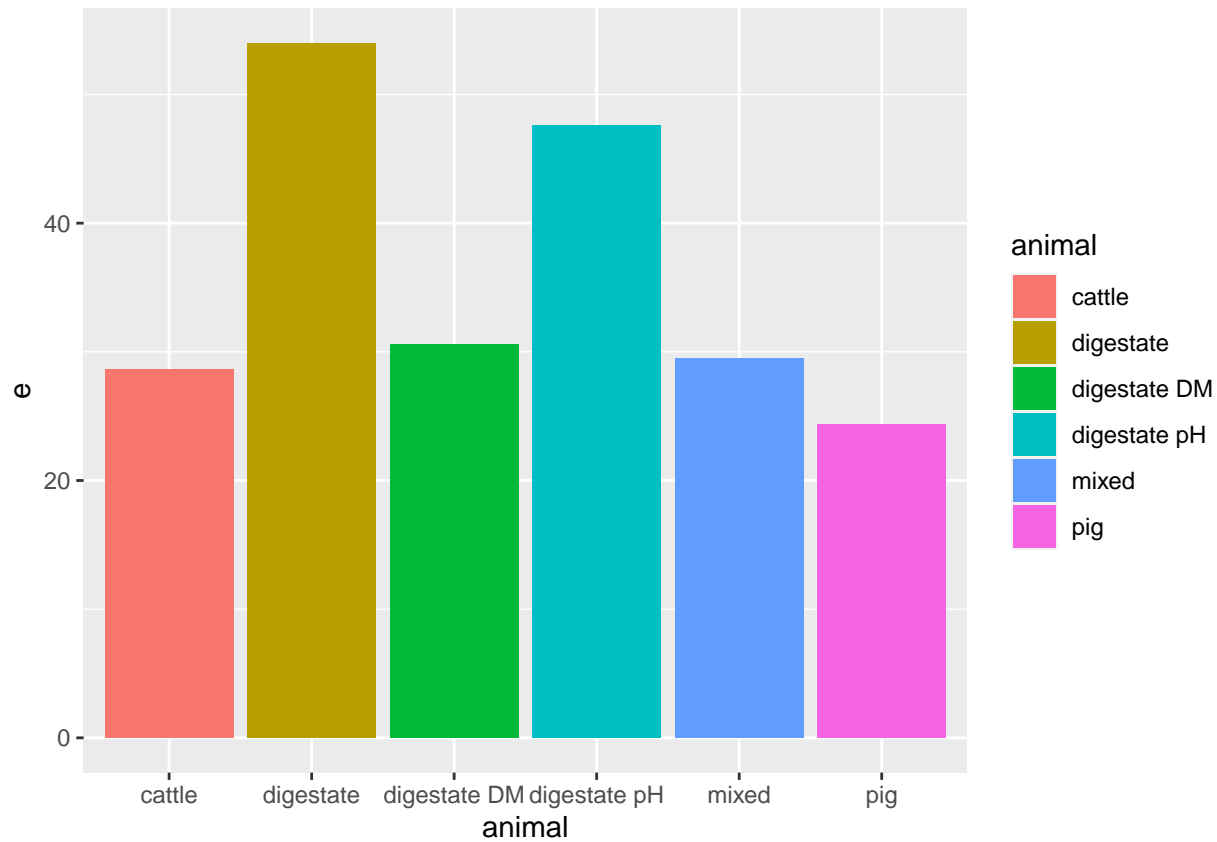
```
##           animal       f  s  e
## 1            pig 1.8e-11 76 24
## 2         cattle 1.6e-06 71 29
## 3          mixed 1.6e-08 70 30
## 4      digestate 5.9e-14 46 54
## 5 digestate DM 1.2e-06 69 31
```

```
## 6 digestate pH 9.2e-22 52 48
```

```
ggplot(dat, aes(animal, s, fill = animal)) +
  geom_col()
```



```
ggplot(dat, aes(animal, e, fill = animal)) +
  geom_col()
```

Initial partitioning (f0) is not as influential as might be expected, because there is a fast -> slow transfer over time (through r2). This makes the shape of the emission curve important; cases with low emission rates will still tend to have lower emission. This is why digestate DM alone doesn't have a large effect, and why the combination of DM and pH (digestate), in contrast, has a big effect.

Detailed curves

Generate curves.

Input data

```
dat2 <- dat.input[rep(1:6, each = 169), ]
dat2$ct <- rep(0:168, 6)
dat2$rain.rate <- 0.09
dat2$rain.cum <- dat2$ct * dat2$rain.rate - 0.5 * dat2$rain.rate
```

Run model

```
pred2 <- ALFAM2mod(dat2, pars = pars, group = 'id')
```

```
## Warning in ALFAM2mod(dat2, pars = pars, group = "id"): Running with 11 parameters. Dropped 13 with no match.
## These secondary parameters have been dropped: app.mthd.os.f0, app.rate.nos.f0, app.mthd.bc.r1, air.temp.r1, wind.2m.r1, air.temp.r3, a
```
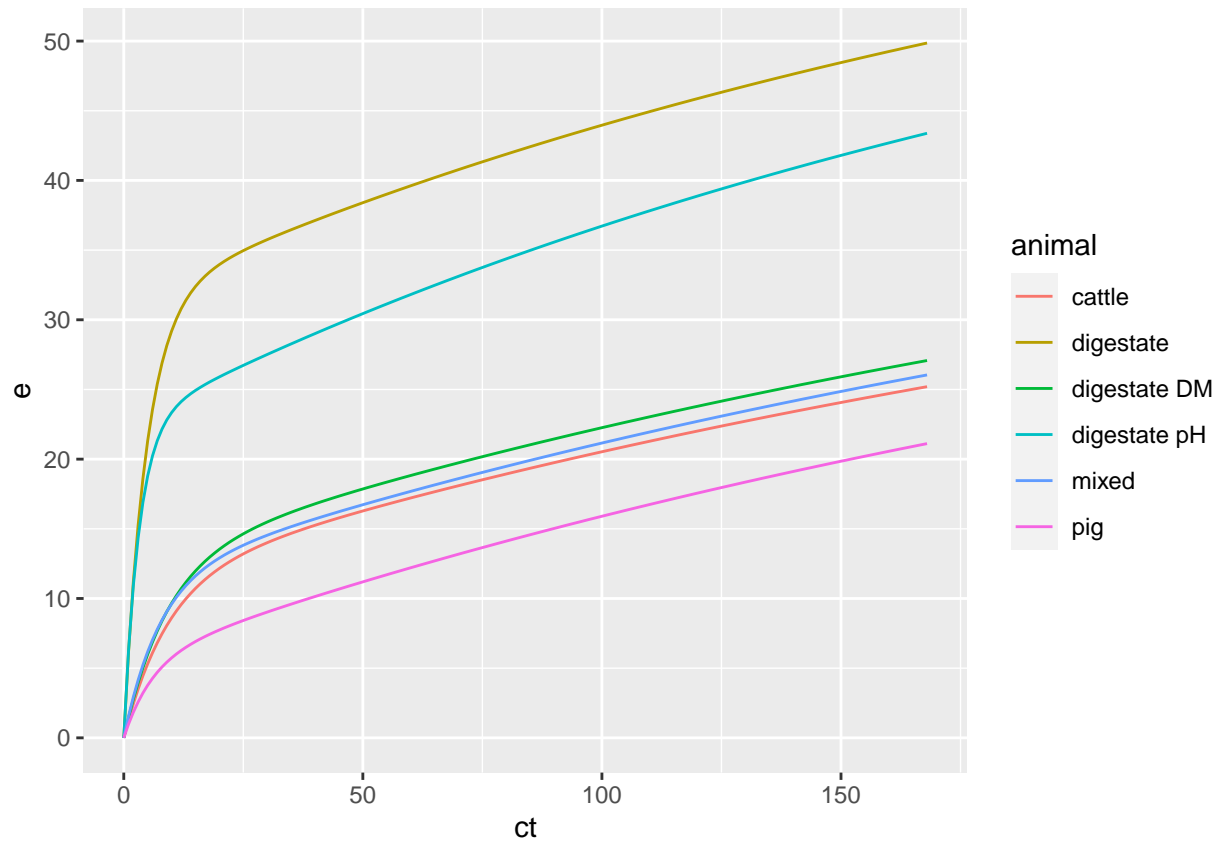
```
dat2 <- merge(dat2, pred2, by = c('id', 'ct'))
```
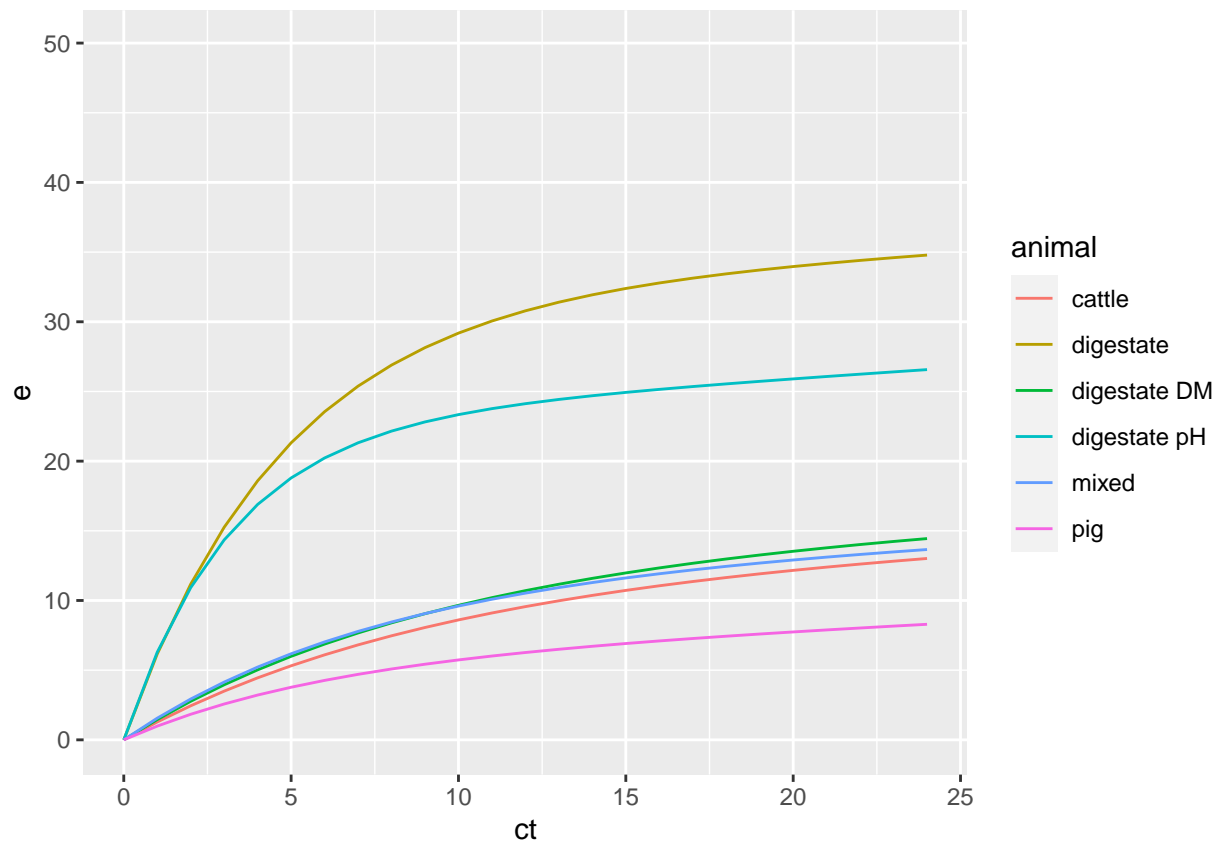
Output

Plot. Cumulative emission.

```
ggplot(dat2, aes(ct, e, colour = animal)) +
  geom_line()
```

```
ggplot(dat2, aes(ct, e, colour = animal)) +
  geom_line() +
  xlim(0, 24)
```
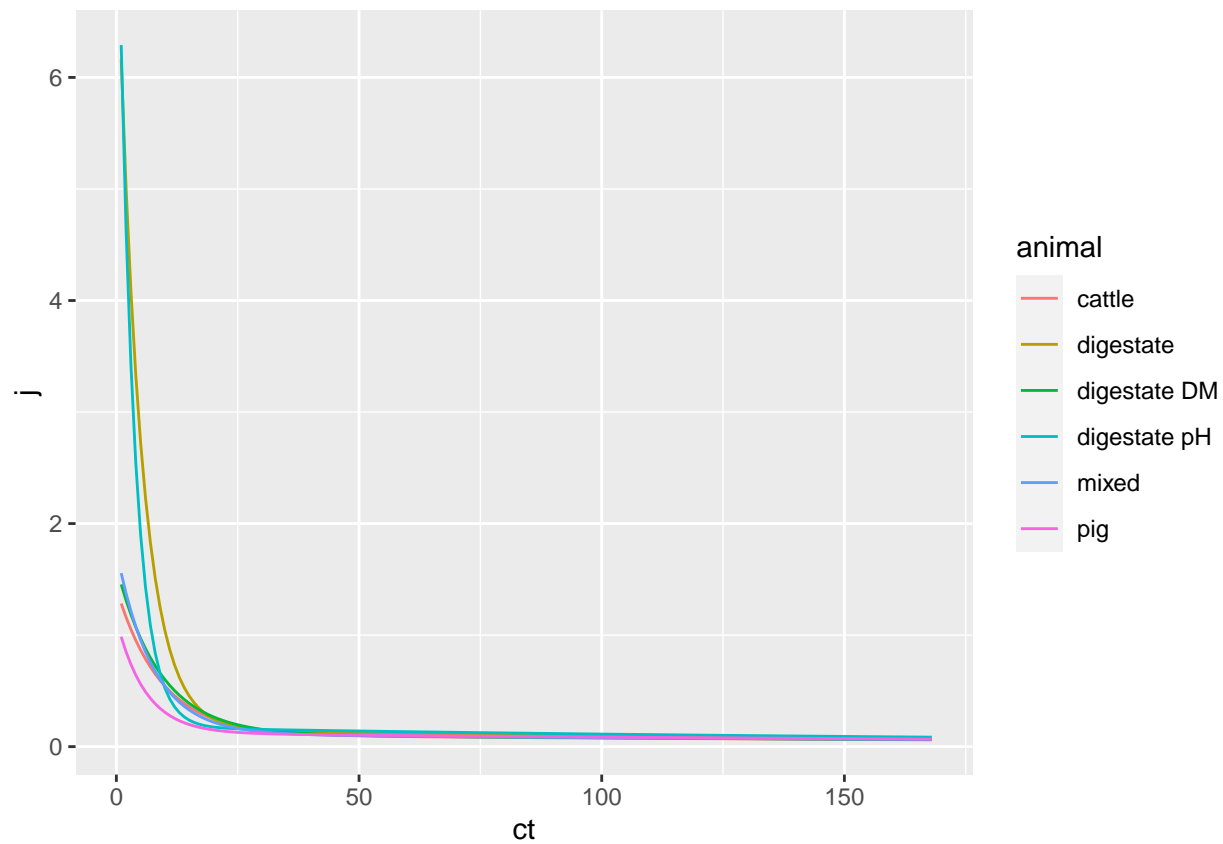
```
## Warning: Removed 864 row(s) containing missing values (geom_path).
```

Emission rate.

```
ggplot(dat2, aes(ct, j, colour = animal)) +
  geom_line()
```

Warning: Removed 6 row(s) containing missing values (geom_path).

```
ggplot(dat2, aes(ct, j, colour = animal)) +
  geom_line() +
  xlim(0, 24)
```

Warning: Removed 870 row(s) containing missing values (geom_path).

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