Stats to parse out DM and pH effects
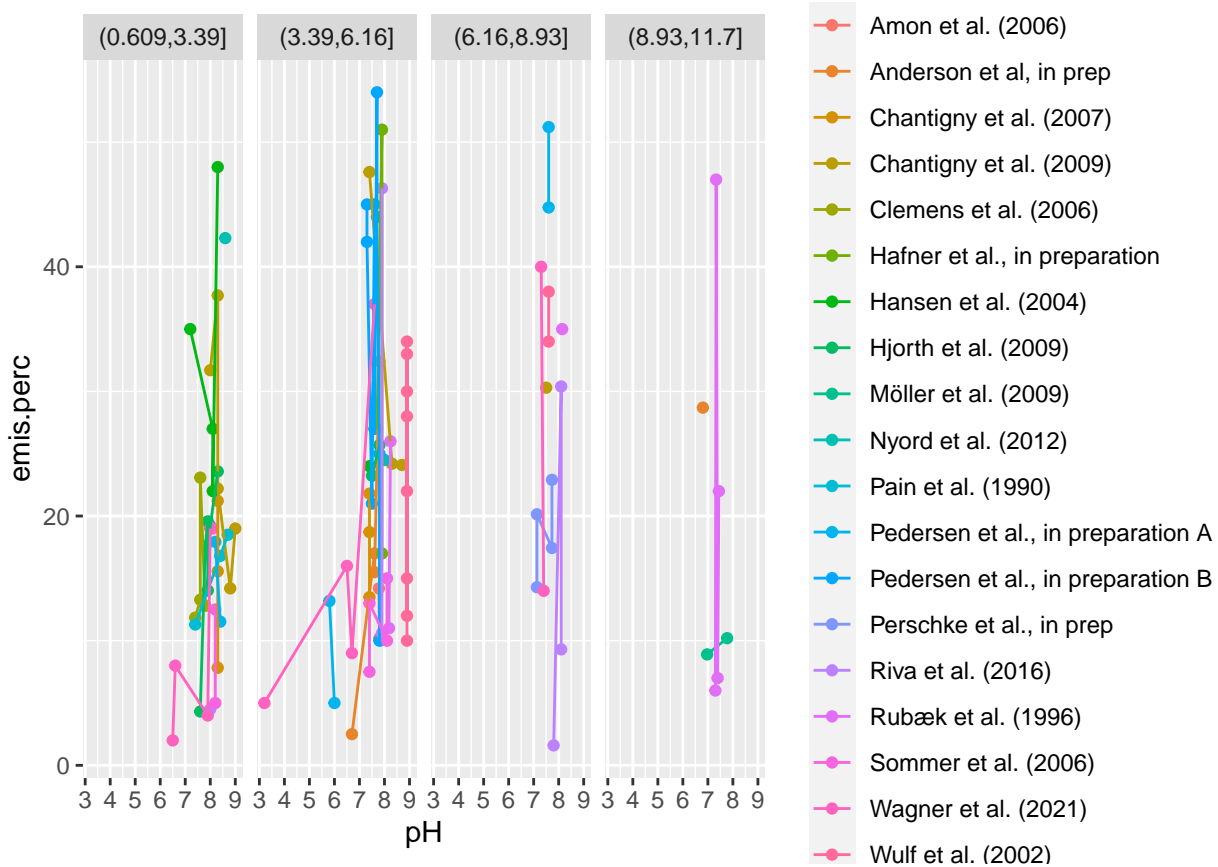
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Plots

```r
dat$DMgrp <- cut(dat$DM, 4)
dat$pHgrp <- cut(dat$pH, 4)
dd <- subset(dat, !is.na(pH) & !is.na(DM))
```
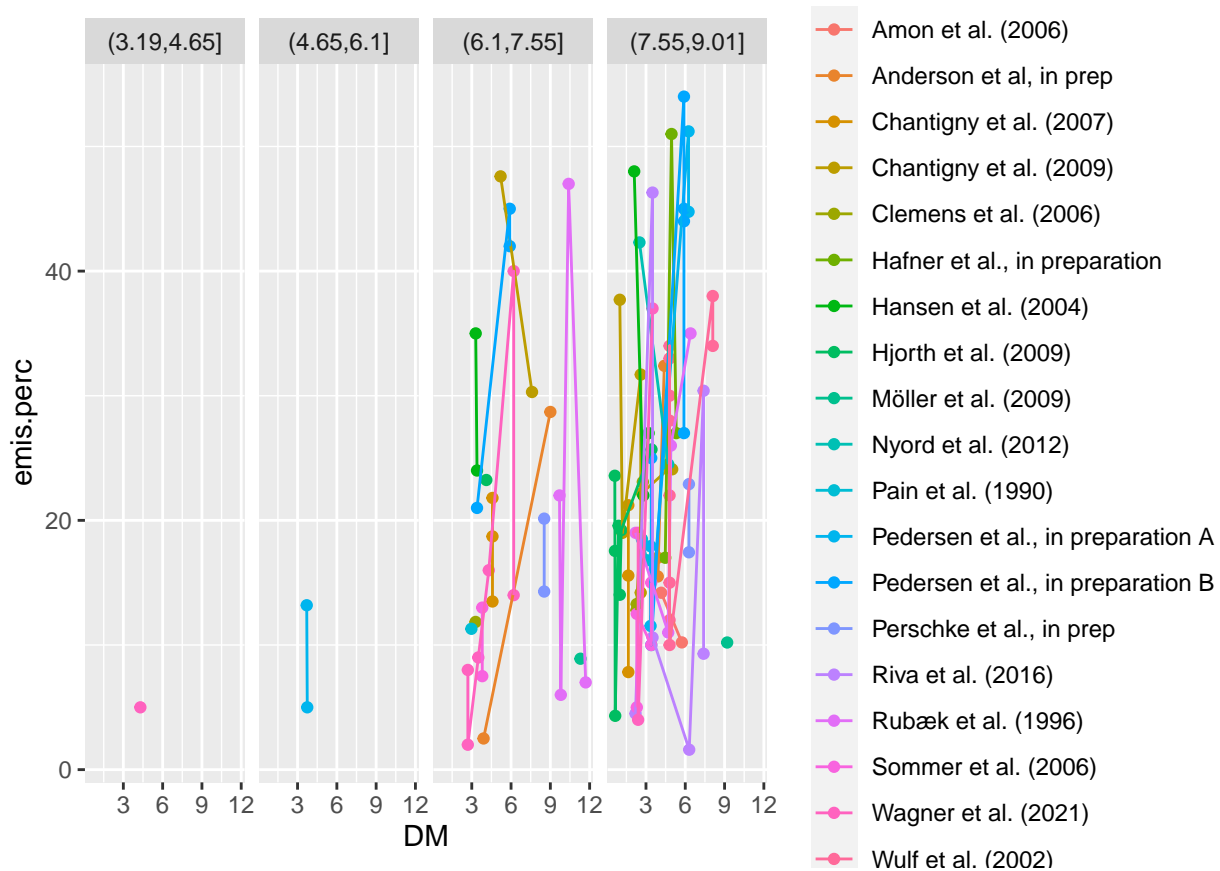
```r
ggplot(dd, aes(pH, emis.perc, colour = source)) +
  geom_point() +
  geom_line() +
  facet_wrap(~ DMgrp, ncol = 4)
```



```r
ggplot(dd, aes(DM, emis.perc, colour = source)) +
  geom_point() +
  geom_line() +
```

```
  facet_wrap(~ pHgrp, ncol = 4)
```

```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```


Not pretty but there do seem to be correlations for both DM and pH.

How did digestion change DM and pH?

```
dd <- subset(dd, !is.na(relDiff.set))
ggplot(dd, aes(DM, pH, colour = relDiff.frac, group = interaction(source, relDiff.set))) +
  geom_line(colour = 'gray85') +
  geom_point() +
  theme_bw()
```
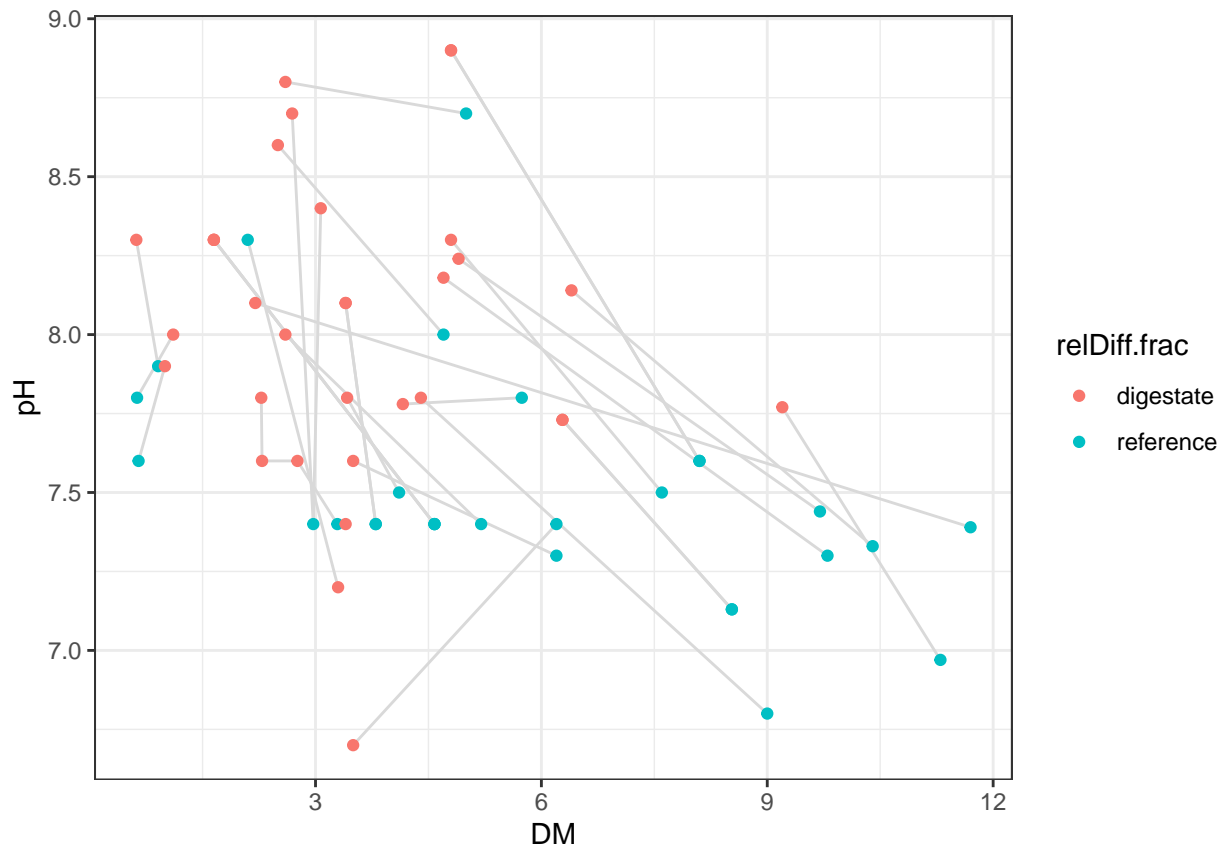
Generally increased pH and decreased DM, as expected in the absence of added high DM substrates.

Models

Summary.

```
dfsumm(dat[, c('source', 'app.meth', 'DM', 'pH', 'relDiff.frac', 'emis.perc')])
```

```
##
##   122 rows and 6 columns
##   122 unique rows
##                                  source               app.meth      DM      pH
## Class                         character              character numeric numeric
## Minimum           Amon et al. (2006)              broadcast    0.62     3.2
## Maximum           Wulf et al. (2002) trailing shoe + harrowing    11.7       9
## Mean                           <NA>                   <NA>    4.39    7.76
## Unique (excld. NA)               21                      6      71      36
## Missing values                    0                      7       2      14
## Sorted                        FALSE                  FALSE   FALSE   FALSE
##
##                   relDiff.frac emis.perc
## Class                character   numeric
## Minimum              digestate       1.6
## Maximum              reference        60
## Mean                      <NA>      22.7
## Unique (excld. NA)           2        98
## Missing values              46         0
```

```
## Sorted                      FALSE     FALSE
##
```

Overall digestion effect (not expecting much)

```
m1 <- lm(emis.perc ~ source + app.meth + relDiff.frac, data = dat)
summary.aov(m1)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)
## source       14   4828   344.9    3.98 0.000137 ***
## app.meth      2   1324   662.1    7.64 0.001252 **
## relDiff.frac  1     63    63.2    0.73 0.397011
## Residuals    51   4420    86.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 53 observations deleted due to missingness
```

```
tail(coef(m1))
```

```
##   sourceWagner et al. (2021)     sourceWulf et al. (2002)
##                    12.798830                     20.298830
## app.methopen slot injection         app.methtrailing hose
##                   -13.750000                      8.000000
##        app.methtrailing shoe        relDiff.fracreference
##                           NA                      1.933273
```

Nothing.

Separate DM and pH effects.

```
m2 <- lm(emis.perc ~ pH + DM + relDiff.frac + source + app.meth, data = dat)
summary.aov(m2)
```

```
##              Df Sum Sq Mean Sq F value  Pr(>F)
## pH            1   67.9    67.9   0.914 0.34486
## DM            1  346.3   346.3   4.661 0.03692 *
## relDiff.frac  1    1.8     1.8   0.024 0.87754
## source       12 2495.8   208.0   2.799 0.00724 **
## app.meth      1  913.2   913.2  12.289 0.00114 **
## Residuals    40 2972.6    74.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 65 observations deleted due to missingness
```

```
drop1(m2, test = 'F')
```

```
## Single term deletions
##
## Model:
## emis.perc ~ pH + DM + relDiff.frac + source + app.meth
##              Df Sum of Sq    RSS    AIC F value   Pr(>F)
## <none>                    2972.6 259.38
## pH            1      2.11 2974.7 257.43  0.0284 0.867126
## DM            1      1.59 2974.2 257.42  0.0213 0.884604
## relDiff.frac  1      2.86 2975.4 257.44  0.0385 0.845358
## source       10   2404.38 5377.0 273.17  3.2354 0.003866 **
## app.meth      1    913.25 3885.8 272.66 12.2890 0.001139 **
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
m3 <- lm(emis.perc ~ pH + DM + source + app.meth, data = dat)
summary.aov(m3)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## pH           1    463   463.0   4.694 0.033286 *
## DM           1   1312  1312.4  13.305 0.000473 ***
## source      16   4701   293.8   2.979 0.000678 ***
## app.meth     5   3023   604.6   6.130 7.55e-05 ***
## Residuals   79   7792    98.6
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 19 observations deleted due to missingness
```

```r
drop1(m3, test = 'F')
```

```
## Single term deletions
##
## Model:
## emis.perc ~ pH + DM + source + app.meth
##          Df Sum of Sq    RSS    AIC F value    Pr(>F)
## <none>                7792.1 493.59
## pH        1     529.9  8322.0 498.37  5.3722 0.0230494 *
## DM        1     981.9  8774.1 503.82  9.9554 0.0022695 **
## source   16    4917.5 12709.6 511.98  3.1160 0.0004117 ***
## app.meth  5    3023.1 10815.2 517.36  6.1300 7.548e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
cc <- coef(m3)[1:3]
cc
```

```
## (Intercept)          pH          DM
##  -25.475142    4.205796    2.109639
```

```r
confint(m3)[1:3, ]
```

```
##                   2.5 %     97.5 %
## (Intercept) -63.6388860 12.688603
## pH            0.5939860  7.817605
## DM            0.7787866  3.440491
```
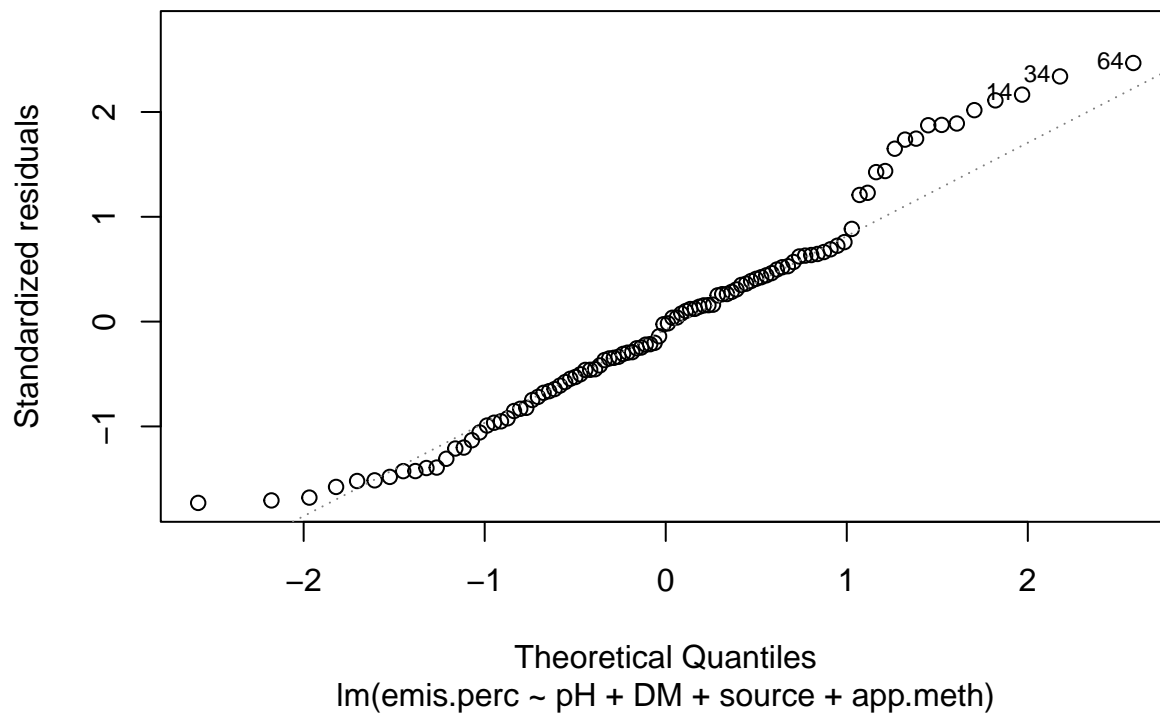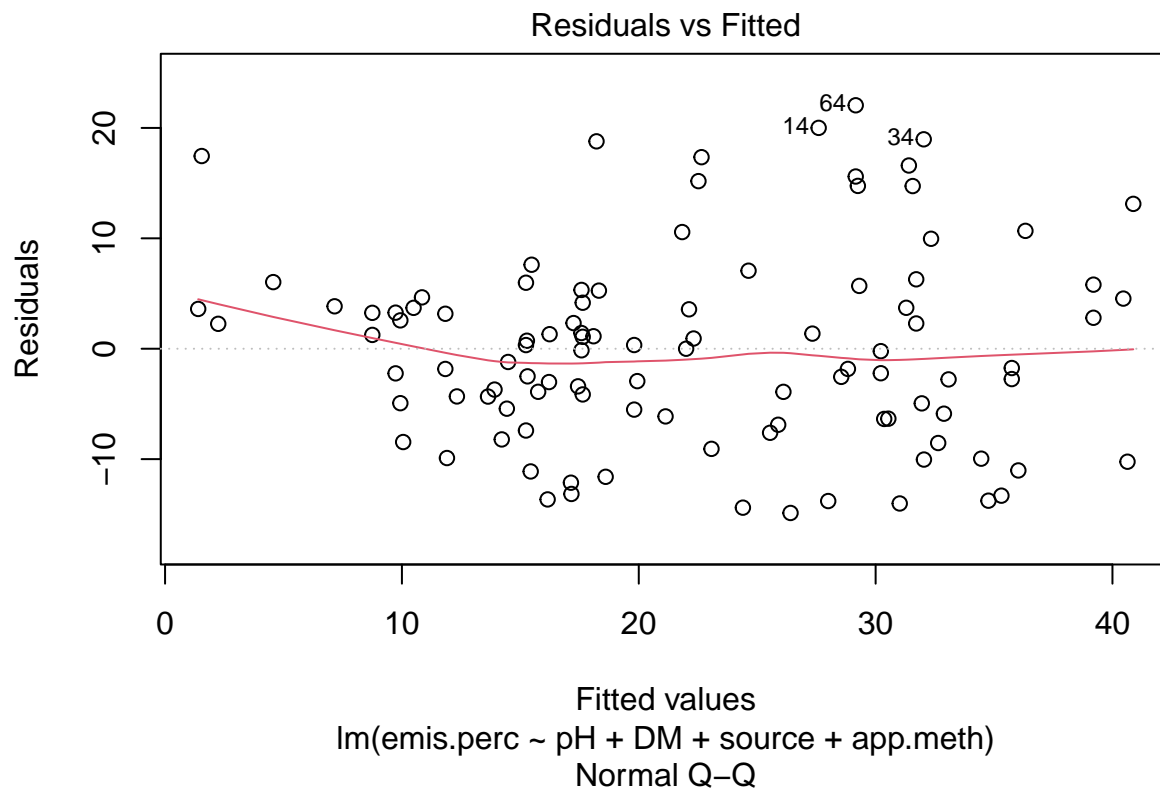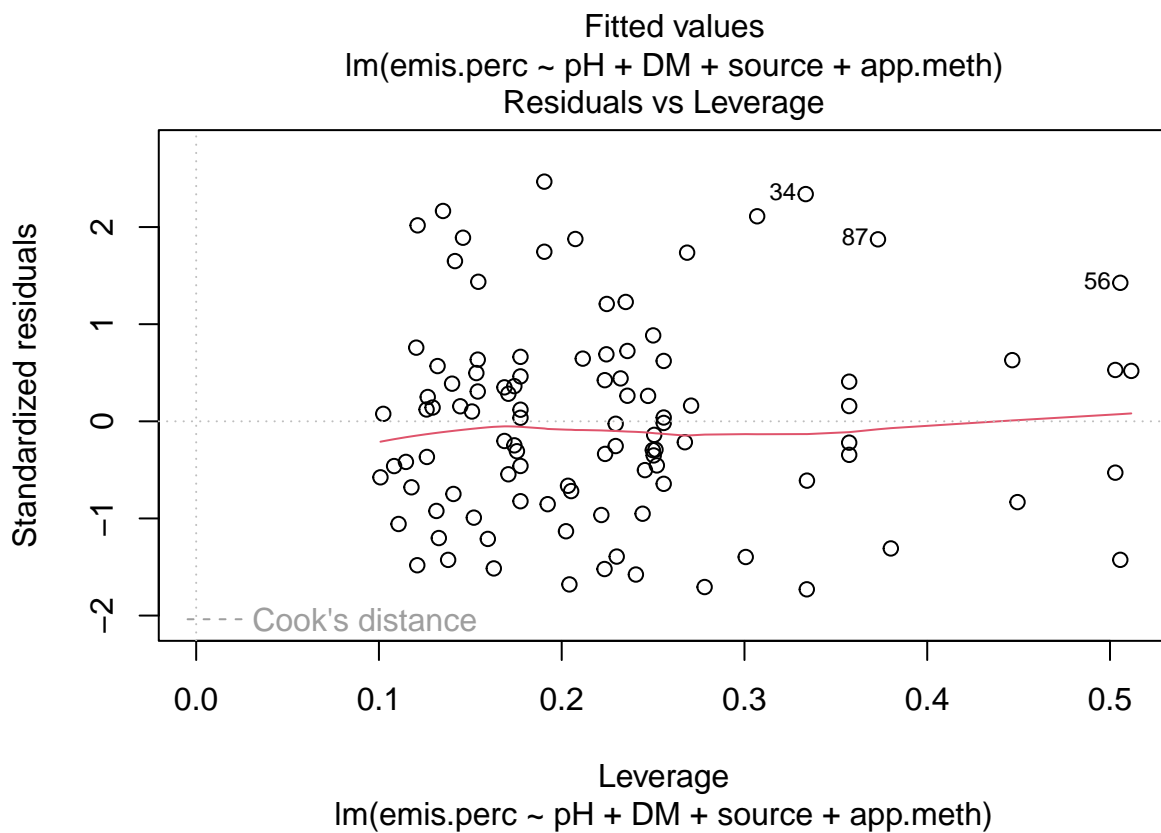
```r
cc['pH'] / cc['DM']
```
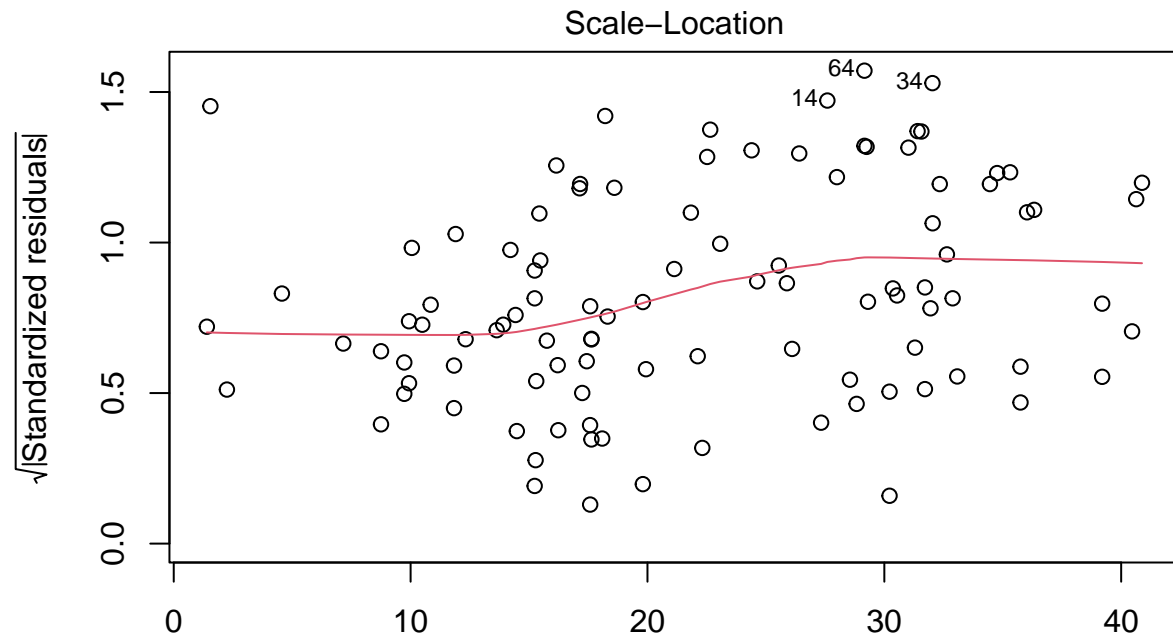
```
##       pH
## ## 1.993609
```

m3 is where it gets interesting. Clear positive effects of DM and pH, although the pH effect seems small (+4% emission (frac. of TAN) per unit pH change). Effect of pH is about 2x DM effect (1 unit pH change : 1% DM change).

```r
plot(m3, ask = FALSE)
```

```
## Warning: not plotting observations with leverage one:
##   102
```

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Residuals vs Fitted

Residuals

Fitted values
lm(emis.perc ~ pH + DM + source + app.meth)

Normal Q−Q

Standardized residuals

Theoretical Quantiles
lm(emis.perc ~ pH + DM + source + app.meth)

Scale–Location

lm(emis.perc ~ pH + DM + source + app.meth)

Residuals vs Leverage

lm(emis.perc ~ pH + DM + source + app.meth)

We might look at relative effect.

```
m4 <- lm(log10(emis.perc) ~ pH + DM + source + app.meth, data = dat)
summary.aov(m4)
```

```
##            Df Sum Sq Mean Sq F value   Pr(>F)
## pH          1  0.726  0.7257  12.252 0.000767 ***
```

```
## DM           1  0.574  0.5744    9.698 0.002570 **
## source      16  2.545  0.1591    2.686 0.001971 **
## app.meth     5  1.689  0.3377    5.702 0.000153 ***
## Residuals   79  4.679  0.0592
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 19 observations deleted due to missingness
```

```r
cc <- 100 * (10^coef(m4)[1:3] - 1)
cc
```

```
## (Intercept)          pH          DM
##   -24.47896    38.27664    11.86561
```

```r
100 * (10^confint(m4)[1:3, ] - 1)
```

```
##                   2.5 %     97.5 %
## (Intercept) -91.232586 550.52562
## pH           12.782575  69.53354
## DM            3.772978  20.58934
```
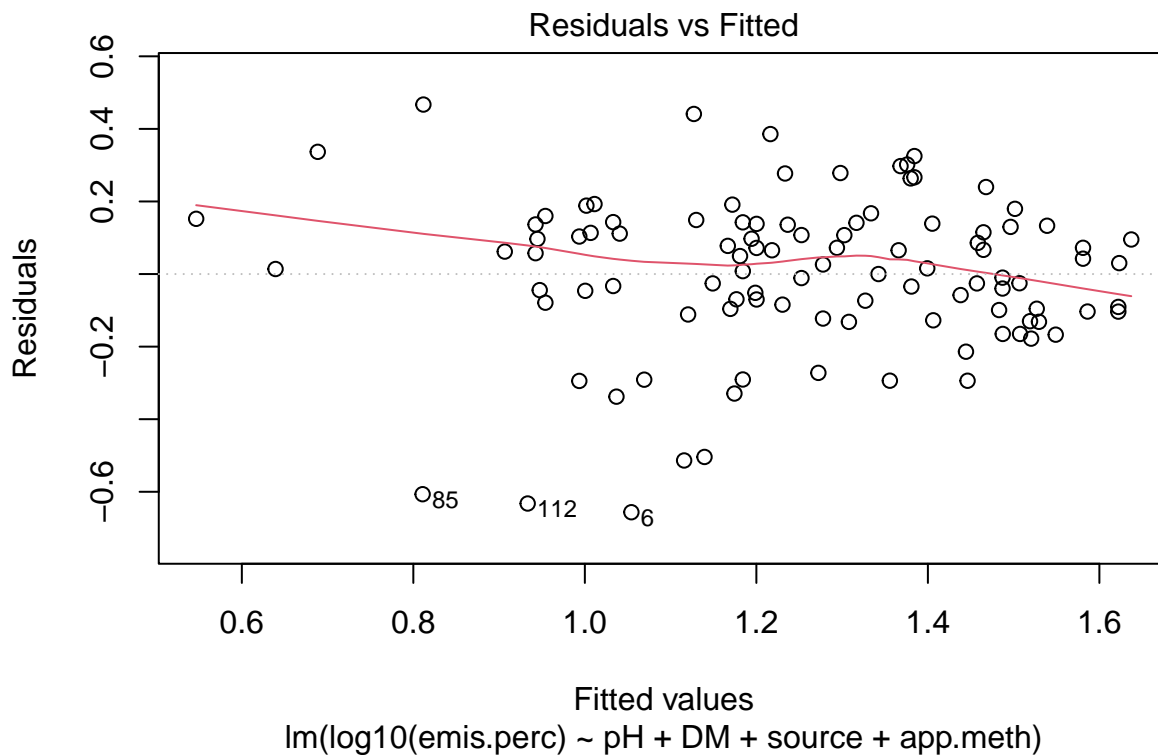
```r
cc['pH'] / cc['DM']
```

```
##        pH
## 3.225847
```
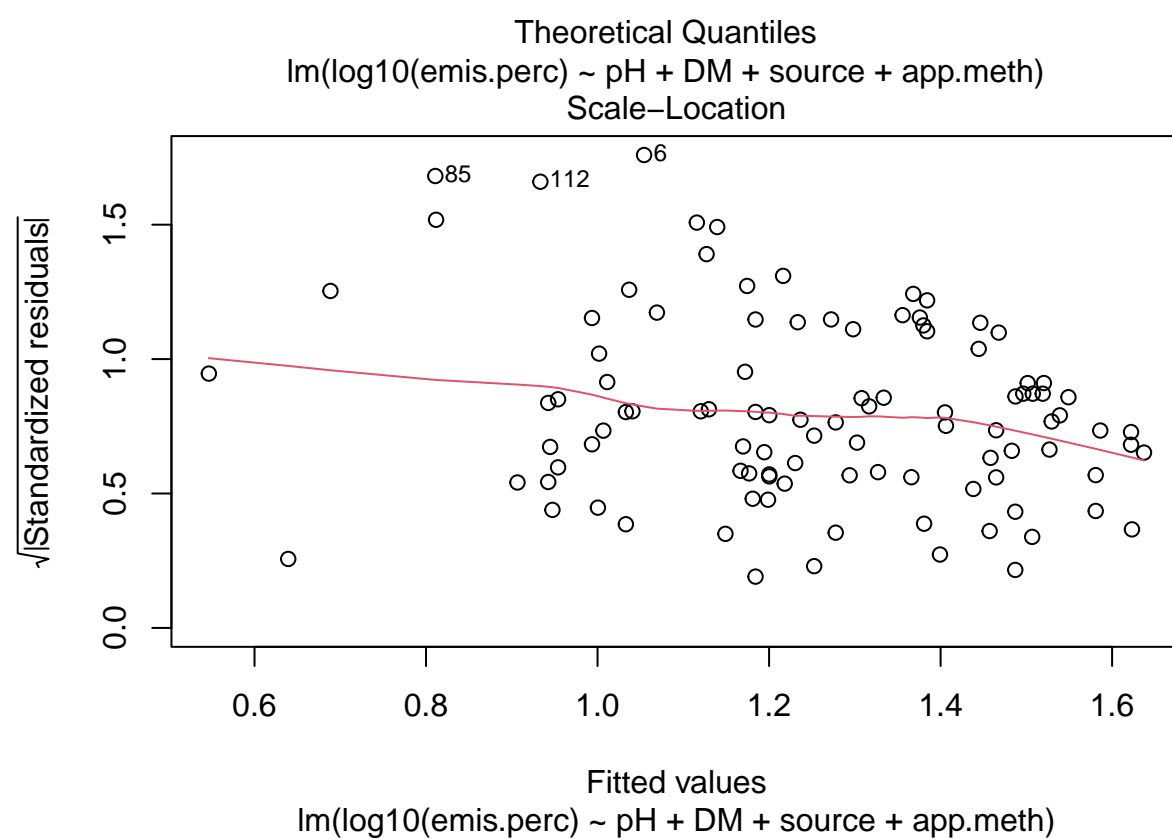
38% increase in emission with a 1 unit increase in pH, seems plausible. Effect of pH here 3x DM effect. Seems more plausible.

```r
plot(m4, ask = FALSE)
```

```
## Warning: not plotting observations with leverage one:
##   102
```


Residuals vs Fitted

lm(log10(emis.perc) ~ pH + DM + source + app.meth)

Normal Q-Q

lm(log10(emis.perc) ~ pH + DM + source + app.meth)

Scale-Location

lm(log10(emis.perc) ~ pH + DM + source + app.meth)

Residuals vs Leverage

lm(log10(emis.perc) ~ pH + DM + source + app.meth)
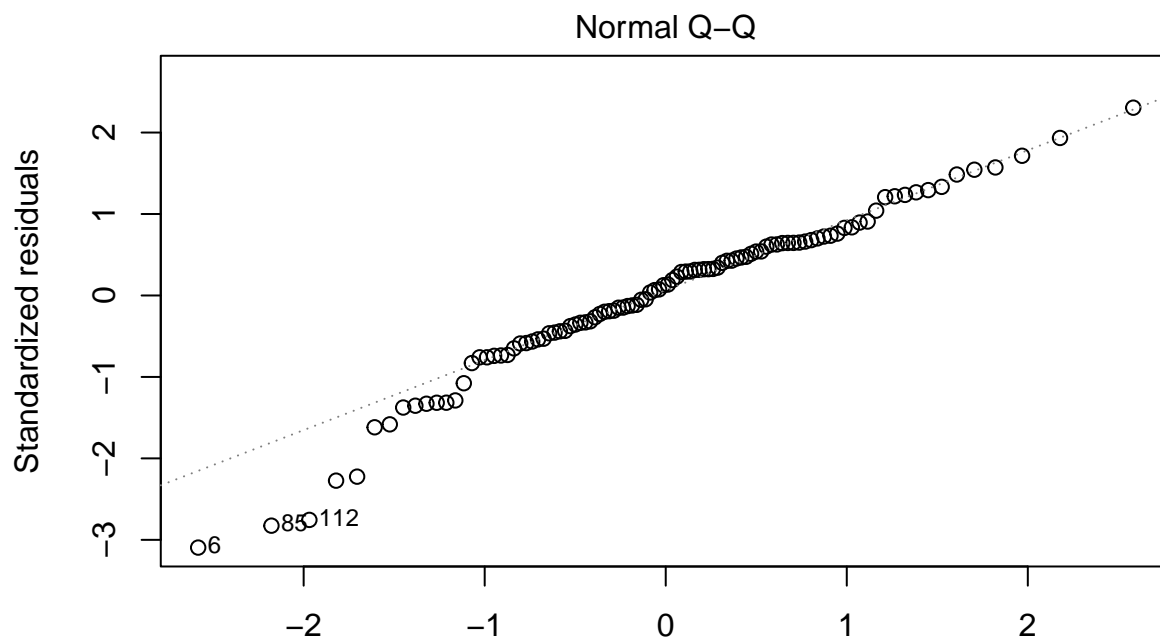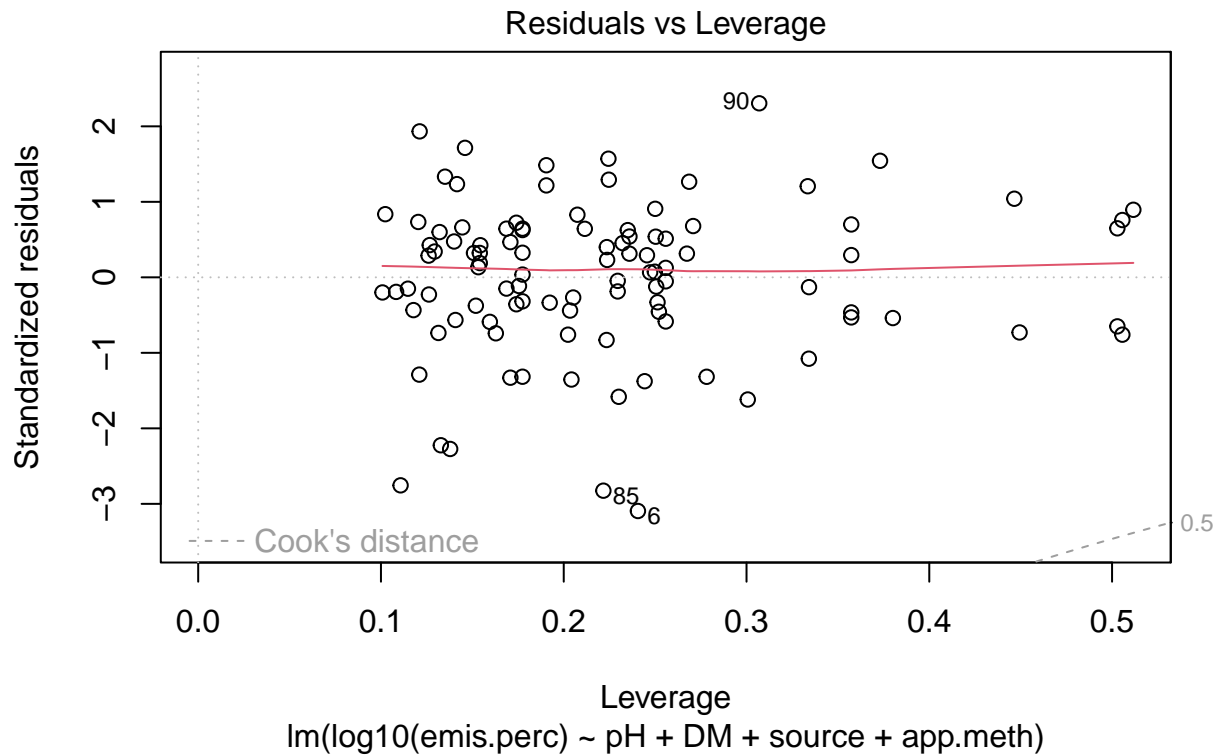
Predictions

Might be interesting to see how predictions here stack up against current DK EFs (based on ALFAM2).

```
dat$si <- factor(as.integer(factor(dat$source)))
m5 <- lm(log10(emis.perc) ~ pH + DM + si + app.meth, data = dat)
coef(m5)
```

```
##              (Intercept)                            pH
##              -0.12193204                      0.14074882
##                       DM                            si2
##               0.04869660                      0.17827981
##                      si3                            si4
##               0.05756898                      0.20300552
##                      si5                            si6
##               0.40397579                      0.37177705
##                      si7                            si8
##               0.48801250                      0.29512484
##                     si11                           si14
##               0.42117908                      0.26718720
##                     si15                           si16
##               0.70218532                      0.11573208
##                     si17                           si18
##               0.20769066                      0.25782185
##                     si19                           si20
##              -0.01567678                      0.14392388
##                     si21            app.methclosed slot injection
##               0.25760194                     -0.67956909
##     app.methopen slot injection            app.methtrailing hose
##              -0.57136678                     -0.13501678
```

```
##              app.methtrailing shoe app.methtrailing shoe + harrowing
##                   -0.31414078                       -0.27965539
```

```
preddat <- data.frame(scenario = c('ref', 'dig', 'dig+'), si = factor(19), app.meth = 'trailing hose',
                    DM = c(6.5, 5.1, 6.5), pH = c(7, 7.9, 7.9))
preddat$emis <- 10^predict(m5, newdata = preddat)
```

```
knitr::kable(preddat)
```

scenario	si	app.meth	DM	pH	emis
ref	19	trailing hose	6.5	7.0	10.69409
dig	19	trailing hose	5.1	7.9	12.23609
dig+	19	trailing hose	6.5	7.9	14.31588