Stats to parse out DM and pH effects
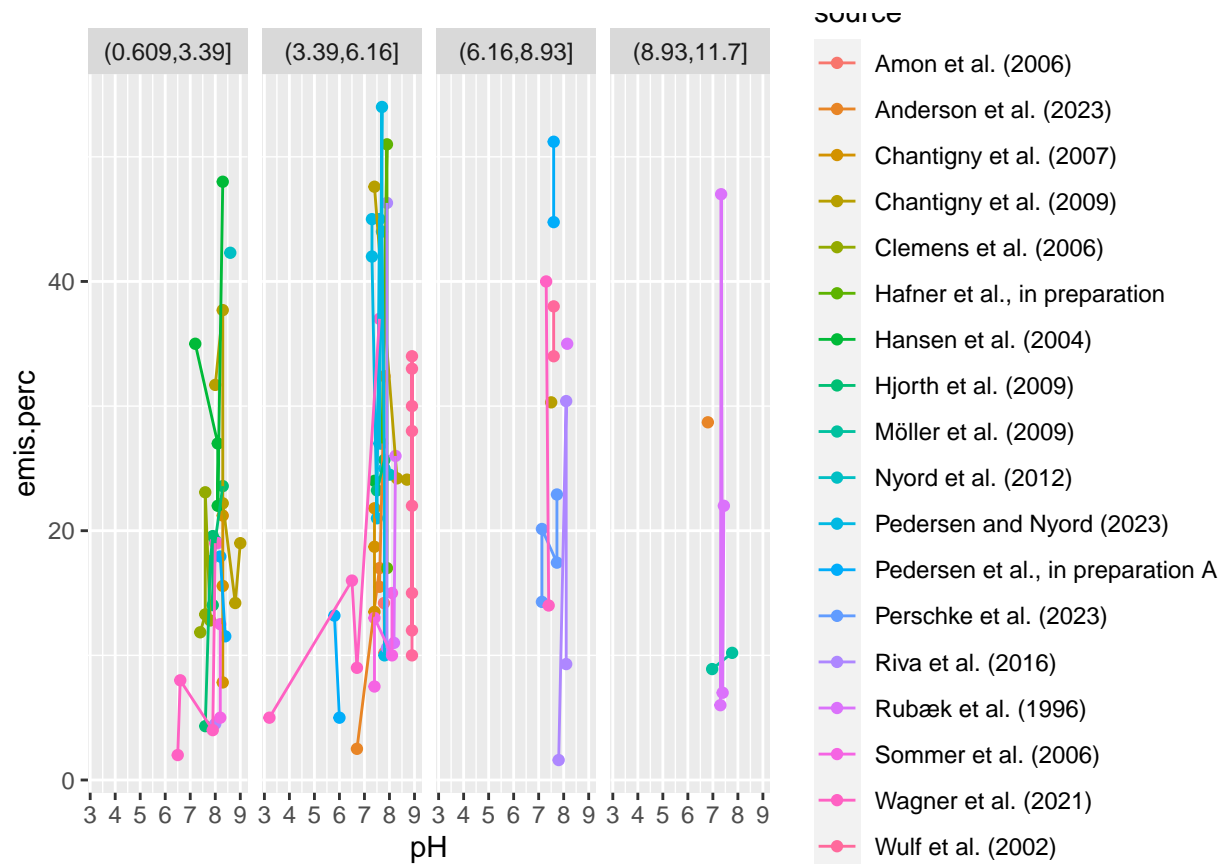
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Plots

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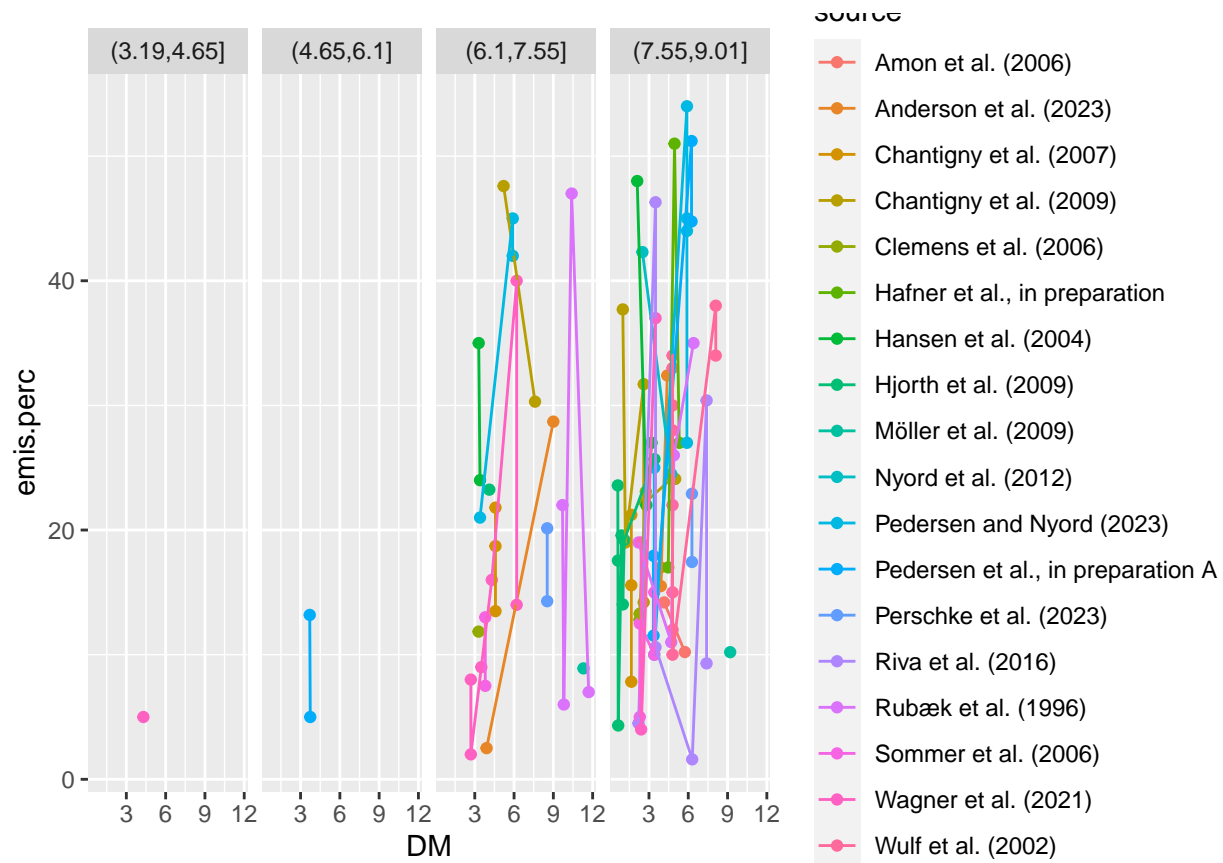
```r
ggplot(dd, aes(pH, emis.perc, colour = source)) +
  geom_point() +
  geom_line() +
  facet_wrap(~ DMgrp, ncol = 4)
```



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

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

```
## `geom_line()`: Each group consists of only one observation.
## i 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()
```
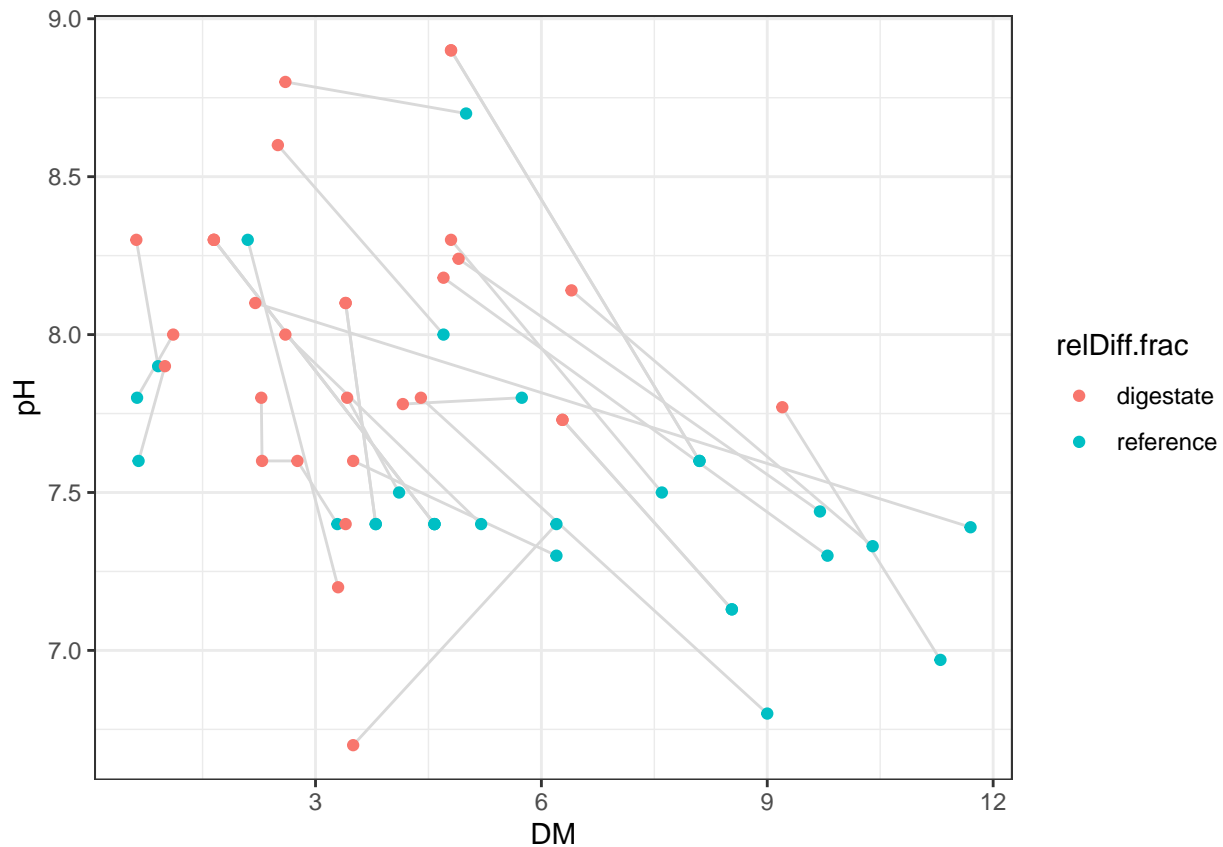
Generally increased pH and decreased DM, as expected in the absence of added high DM substrates.

Models

Summary.

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

```
##
##   119 rows and 6 columns
##   119 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>    4.43    7.75
## Unique (excld. NA)                           20                     6      68      36
## Missing values                                0                     4       2      14
## Sorted                                    FALSE                 FALSE   FALSE   FALSE
##
##                    relDiff.frac emis.perc
## Class                 character   numeric
## Minimum               digestate       1.6
## Maximum               reference        60
## Mean                       <NA>      22.9
## Unique (excld. NA)            2        95
## 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
## 50 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
## 62 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
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
## 16 observations deleted due to missingness
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
cc <- coef(m3)[1:3]
cc

## (Intercept)          pH          DM
##  -25.475142    4.205796    2.109639
confint(m3)[1:3, ]

##                   2.5 %     97.5 %
## (Intercept) -63.6388860  12.688603
## pH            0.5939860   7.817605
## DM            0.7787866   3.440491
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).

```
plot(m3, ask = FALSE)

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

Residuals vs Fitted

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

Normal Q–Q

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

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Scale–Location

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

Residuals vs Leverage

lm(emis.perc ~ pH + DM + source + app.meth)
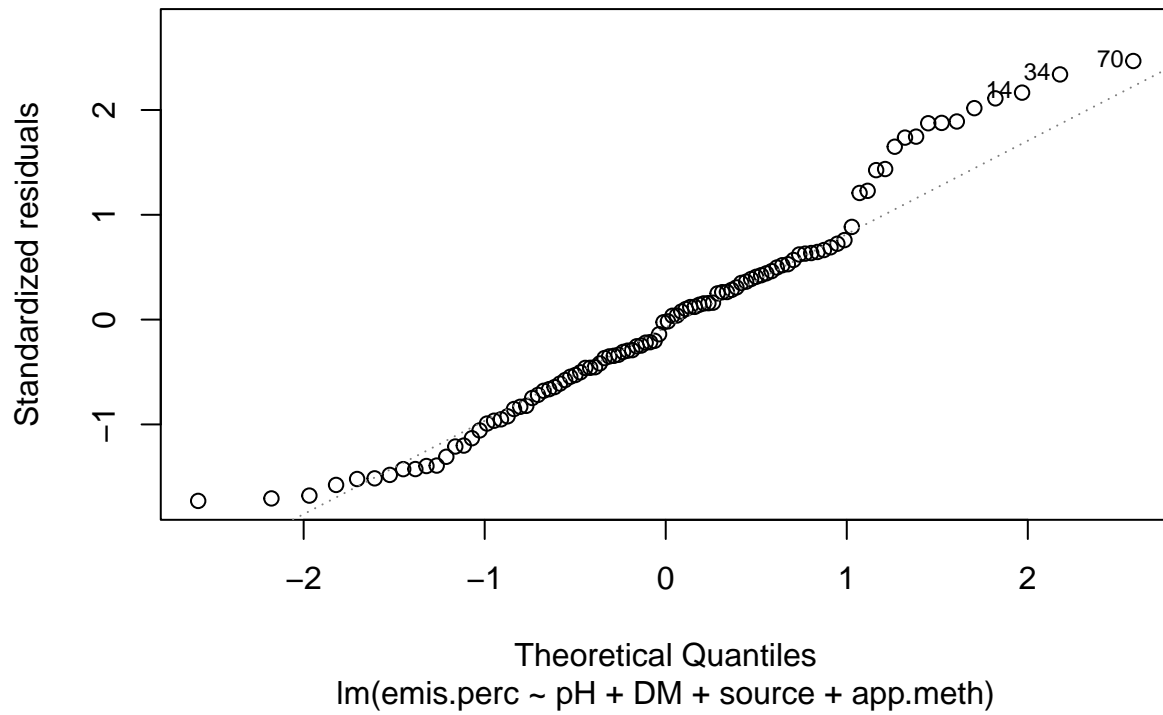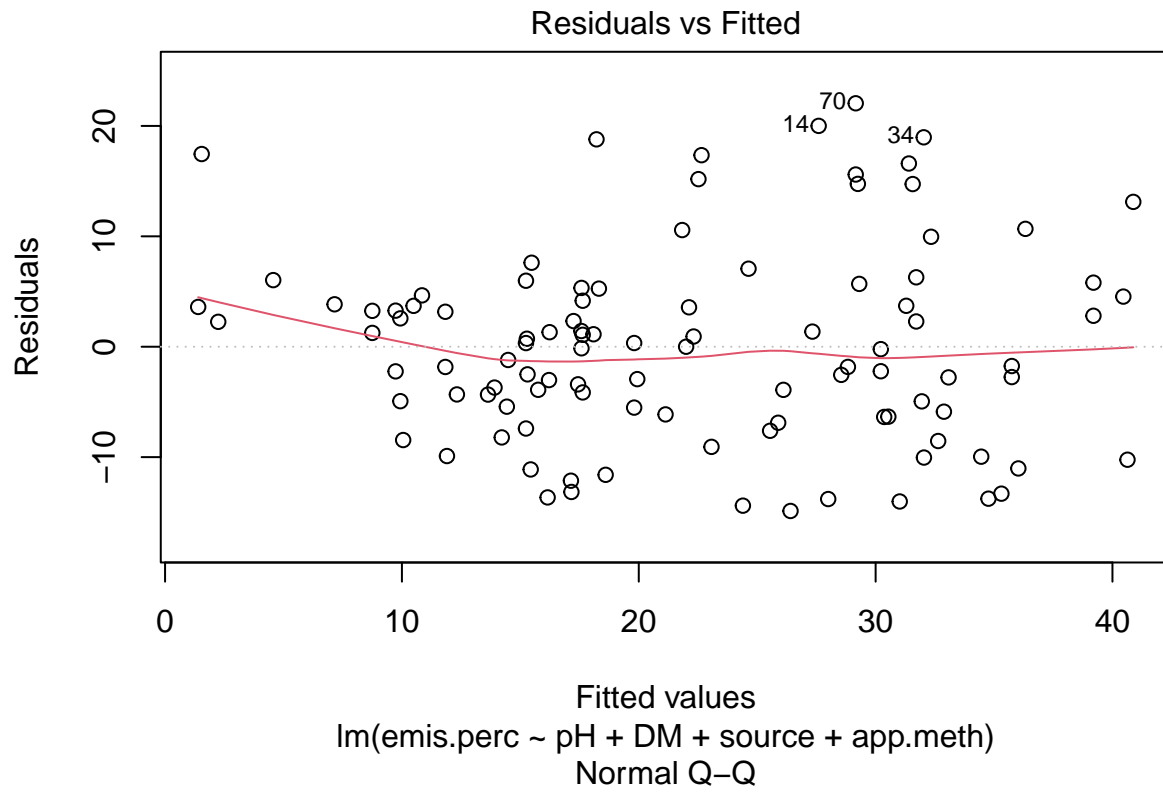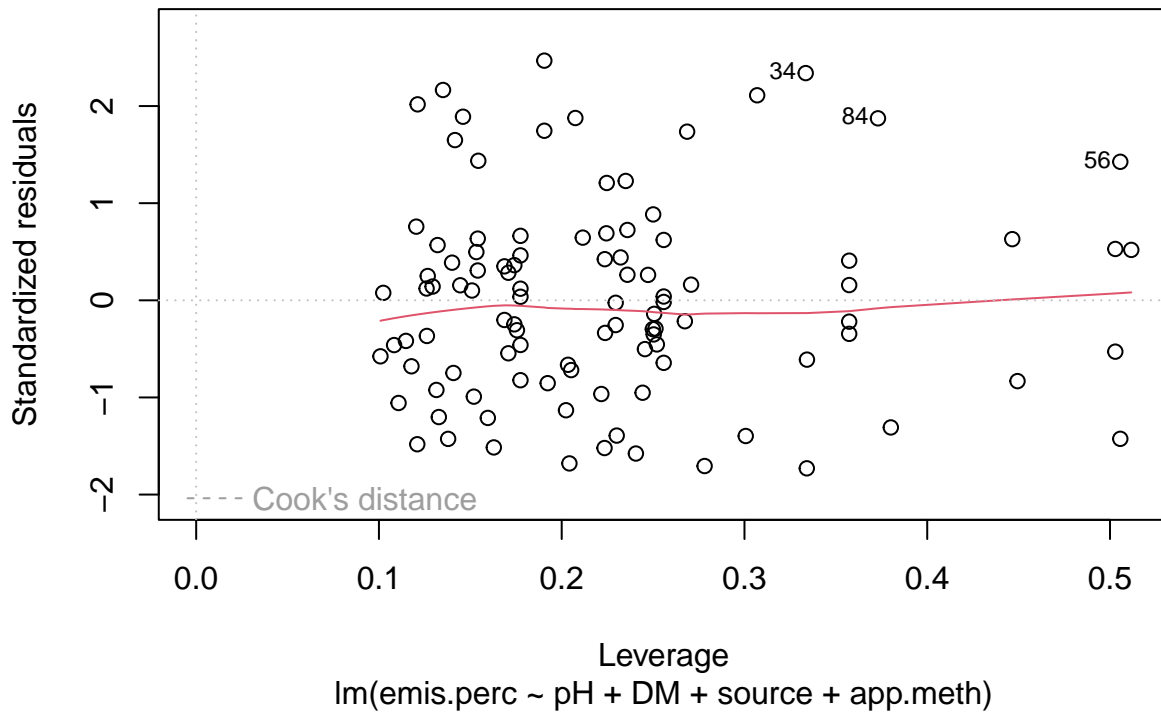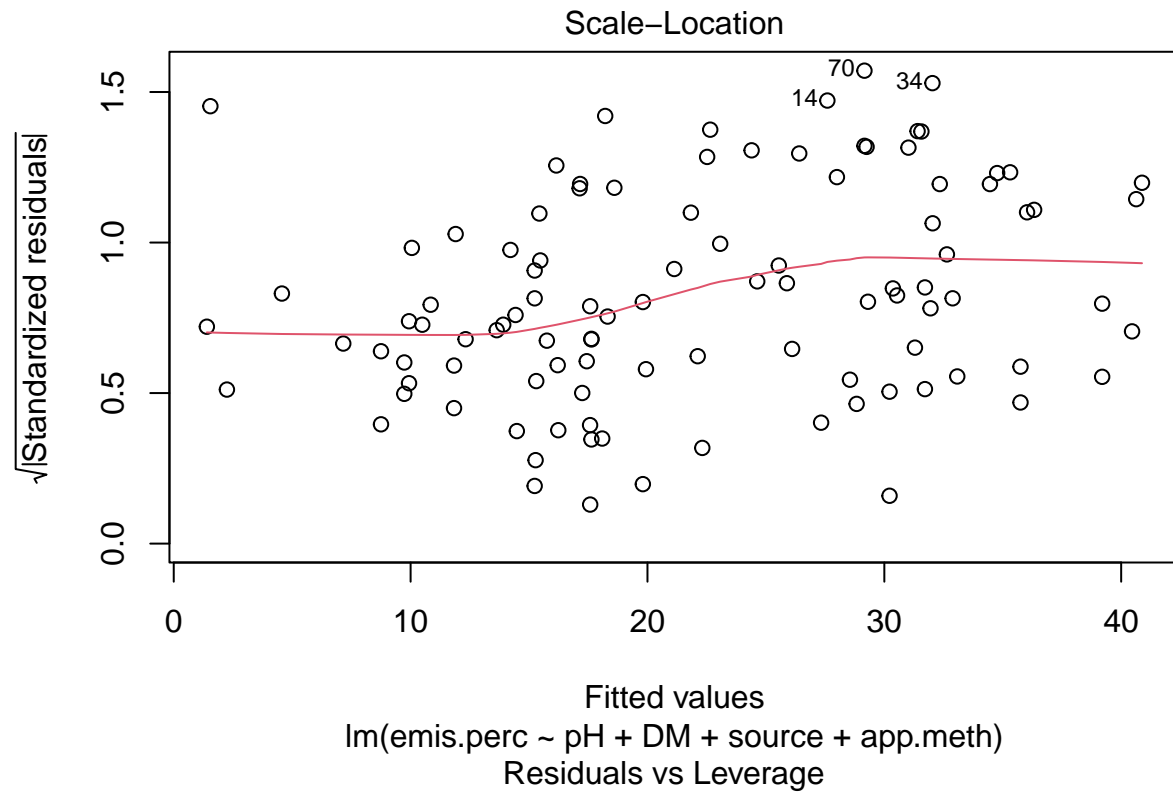
We might look at relative effect.

```
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
## 16 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
```


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Normal Q–Q

Standardized residuals

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

Scale–Location

√|Standardized residuals|

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

Residuals vs Leverage

lm(log10(emis.perc) ~ pH + DM + source + app.meth)
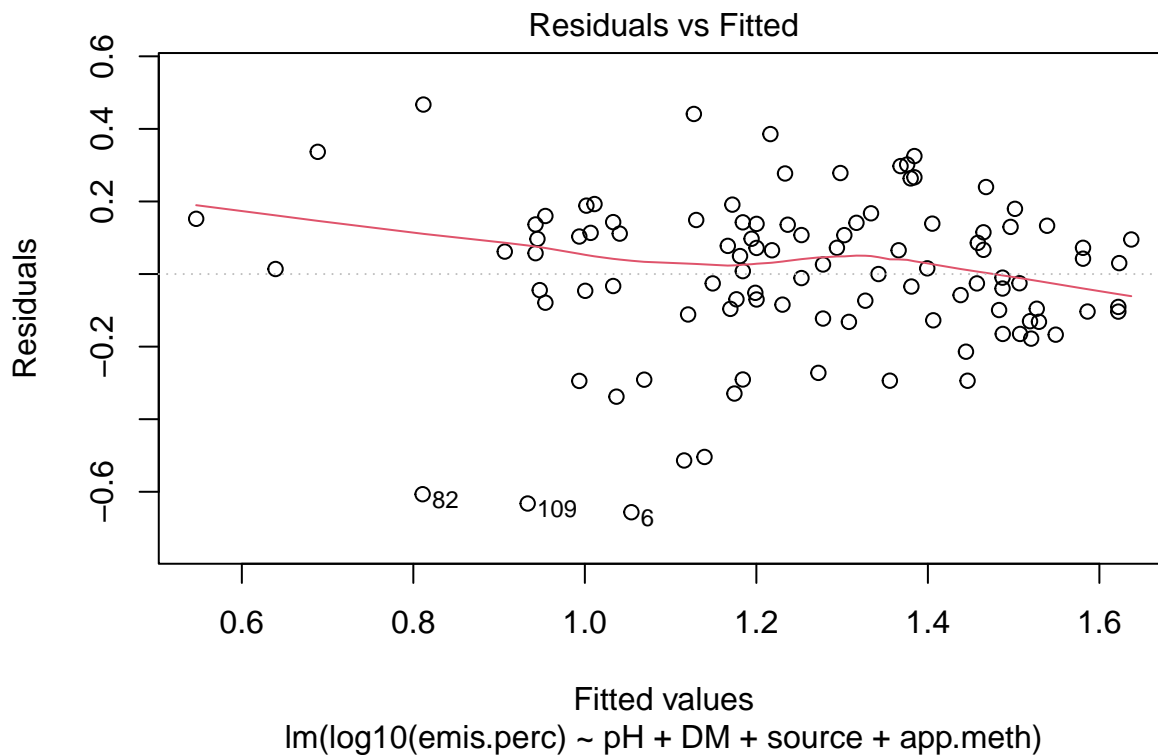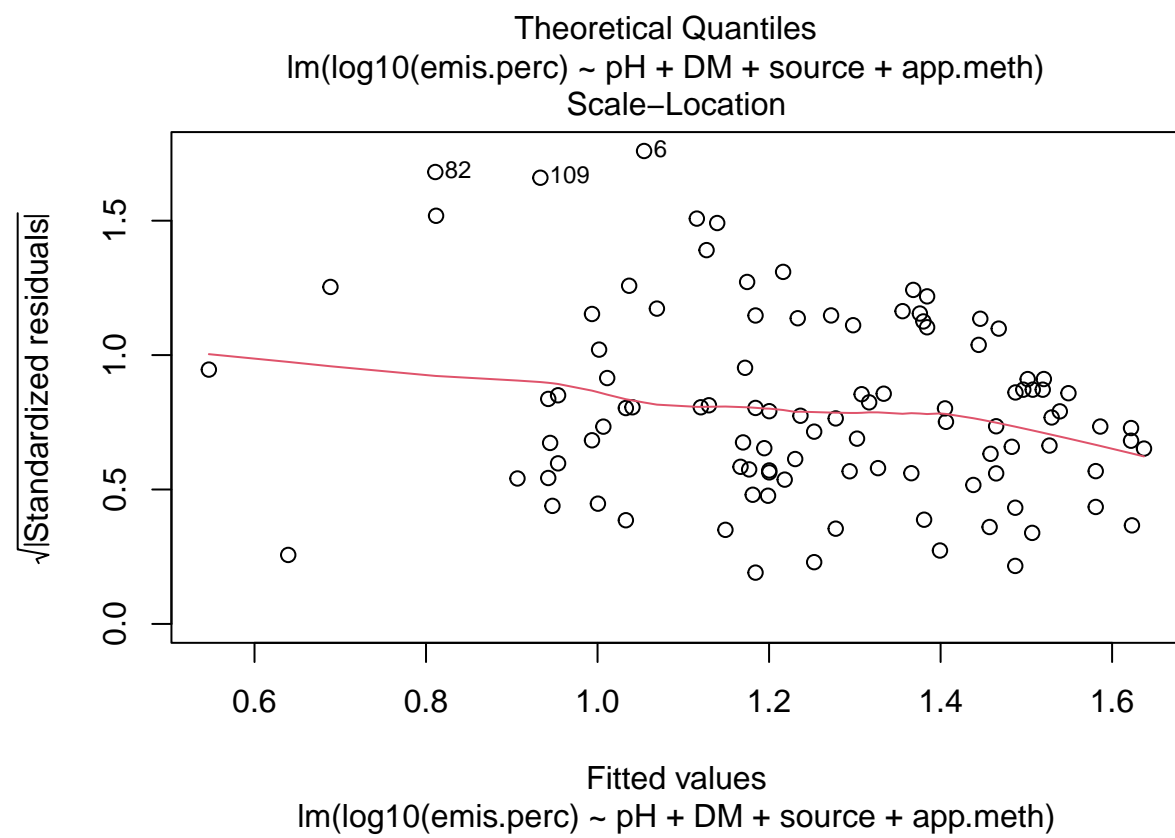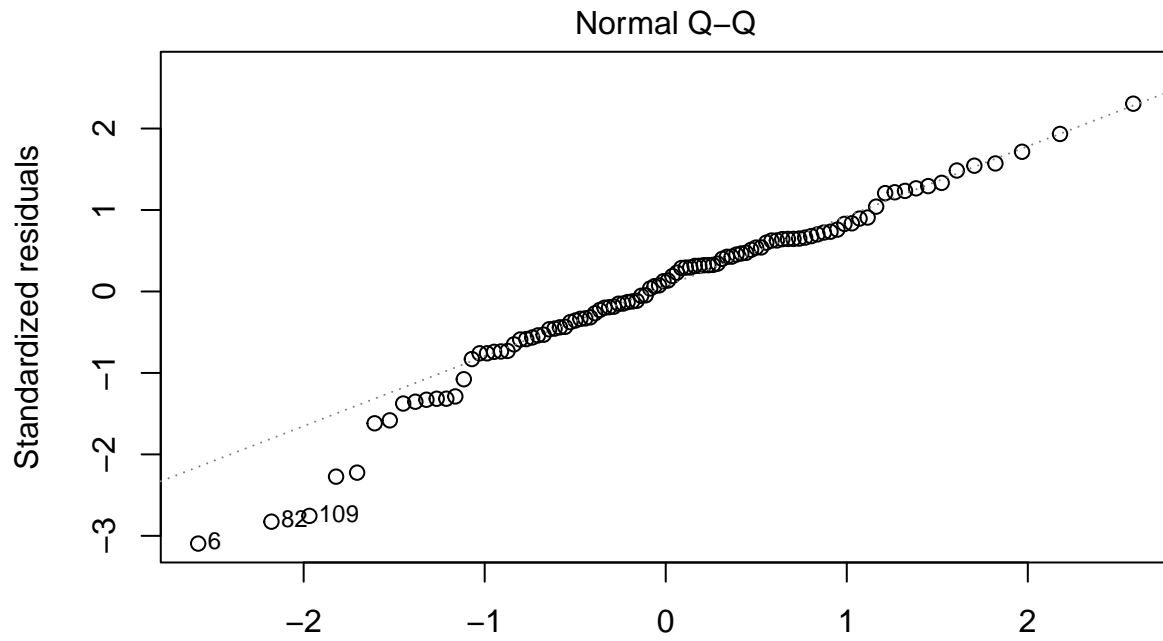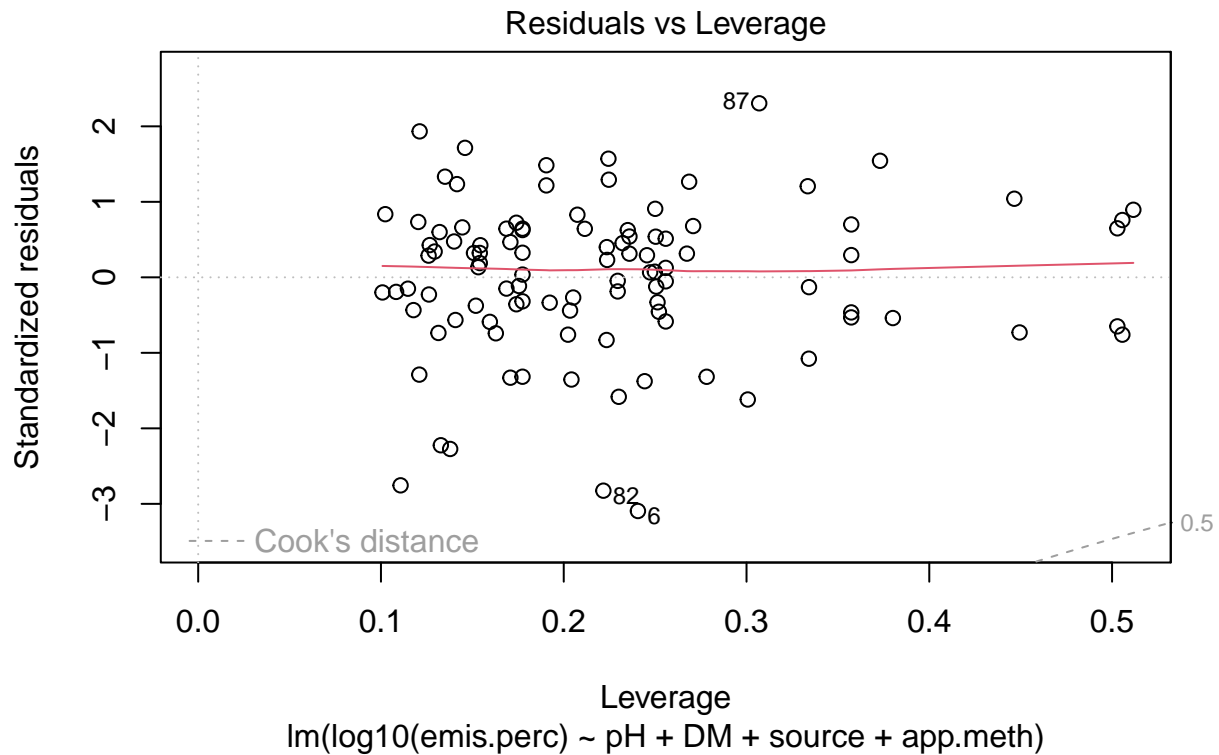
Mixed-effects model

As Johanna pointed out, `source` is really a random effect.

```
dfsumm(dd[, c('pH', 'DM', 'app.meth', 'source')])
```

```
##
##   59 rows and 4 columns
##   49 unique rows
##                      pH      DM       app.meth              source
## Class           numeric numeric      character           character
## Minimum             6.7    0.62      broadcast Amon et al. (2006)
## Maximum             8.9    11.7 trailing shoe Wulf et al. (2002)
## Mean               7.77    4.72          <NA>                <NA>
## Unique (excld. NA)   27      43             4                  14
## Missing values        0       0             2                   0
## Sorted            FALSE   FALSE         FALSE                TRUE
##
```

```
dsub <- subset(dat, !is.na(emis.perc) & !is.na(app.meth))
m5 <- lmer(log10(emis.perc) ~  relDiff.frac + app.meth + (1|source), data = dsub)
```

And there are multiple observations from each source.

```
table(dsub$source)
```

```
##
##               Amon et al. (2006)          Anderson et al. (2023)
##                                2                               5
##           Chantigny et al. (2007)         Chantigny et al. (2009)
##                                6                               9
```

```
##            Clemens et al. (2006)    Hafner et al., in preparation
##                        4                                3
##            Hansen et al. (2004)            Hjorth et al. (2009)
##                        5                                8
##          Neerackal et al. (2015)          Nyord et al. (2012)
##                        8                                2
##         Pedersen and Nyord (2023)       Pedersen et al. (2021)
##                        9                                4
## Pedersen et al., in preparation A      Perschke et al. (2023)
##                        6                                4
##               Riva et al. (2016)         Rubæk et al. (1996)
##                        6                                8
##              Sommer et al. (2006)        Wagner et al. (2021)
##                        6                               10
##                Wulf et al. (2002)
##                       10
```

```r
summary(m5)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: log10(emis.perc) ~ relDiff.frac + app.meth + (1 | source)
##    Data: dsub
##
## REML criterion at convergence: -2.5
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.2292 -0.4857  0.0590  0.6099  1.6787
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  source   (Intercept) 0.02839  0.1685
##  Residual             0.03507  0.1873
## Number of obs: 69, groups:  source, 15
##
## Fixed effects:
##                          Estimate Std. Error t value
## (Intercept)              1.303680   0.101085  12.897
## relDiff.fracreference   -0.002955   0.045499  -0.065
## app.methopen slot injection -0.285128   0.107897  -2.643
## app.methtrailing hose    0.087273   0.108850   0.802
## app.methtrailing shoe   -0.136058   0.216767  -0.628
##
## Correlation of Fixed Effects:
##            (Intr) rlDff. app.si app.mh
## rlDff.frcrf -0.224
## app.mthpnsi -0.529  0.002
## app.mthtrlh -0.828  0.005  0.568
## app.mthtrls -0.455  0.052  0.247  0.386
```

```r
ccm <- 100 * (10^fixef(m5) - 1)
ccm
```

```
##             (Intercept)       relDiff.fracreference
##             1912.2427561                  -0.6781026
## app.methopen slot injection       app.methtrailing hose
```

```
##                 -48.1353250                    22.2568885
##       app.methtrailing shoe
##                 -26.8958799
```

```r
100 * (10^confint(m5) - 1)
```

```
## Computing profile confidence intervals ...

##                                 2.5 %      97.5 %
## .sig01                        19.34601    76.96722
## .sigma                        42.42857    68.09626
## (Intercept)                 1183.98821  3039.32502
## relDiff.fracreference         -19.19513    21.85180
## app.methopen slot injection   -67.74775   -16.80177
## app.methtrailing hose         -24.99057    98.81704
## app.methtrailing shoe         -71.20792    89.58999
```

```r
dfsumm(dd[, c('pH', 'DM', 'app.meth', 'source')])
```

```
##
##  59 rows and 4 columns
##  49 unique rows
##                        pH       DM       app.meth              source
## Class             numeric  numeric      character           character
## Minimum               6.7     0.62      broadcast Amon et al. (2006)
## Maximum               8.9     11.7 trailing shoe Wulf et al. (2002)
## Mean                 7.77     4.72           <NA>                <NA>
## Unique (excld. NA)     27       43              4                  14
## Missing values          0        0              2                   0
## Sorted              FALSE    FALSE          FALSE                TRUE
##
```

```r
dsub <- subset(dat, !is.na(pH) & !is.na(DM) & !is.na(app.meth))
m6 <- lmer(log10(emis.perc) ~ pH + DM + app.meth + (1|source), data = dsub)
```

```r
summary(m6)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: log10(emis.perc) ~ pH + DM + app.meth + (1 | source)
##     Data: dsub
##
## REML criterion at convergence: 35.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.69602 -0.37275  0.00472  0.58206  1.67428
##
## Random effects:
##  Groups    Name         Variance Std.Dev.
##  source    (Intercept)  0.01438  0.1199
##  Residual               0.05913  0.2432
## Number of obs: 103, groups:  source, 17
##
## Fixed effects:
##                              Estimate Std. Error t value
## (Intercept)                  -0.02950    0.35422  -0.083
## pH                            0.15097    0.03999   3.775
```

```
## DM                                0.04846    0.01355   3.575
## app.methclosed slot injection    -0.63499    0.13515  -4.699
## app.methopen slot injection      -0.35685    0.14158  -2.520
## app.methtrailing hose            -0.06463    0.09715  -0.665
## app.methtrailing shoe            -0.05203    0.12593  -0.413
## app.methtrailing shoe + harrowing -0.20991    0.26252  -0.800
##
## Correlation of Fixed Effects:
##            (Intr) pH     DM     app.mthcsi app.mthpsi app.mh app.ms
## pH         -0.961
## DM         -0.405  0.281
## app.mthclsi -0.089 -0.017 -0.034
## app.mthpnsi -0.210  0.088 -0.079  0.280
## app.mthtrlh -0.375  0.194 -0.040  0.412     0.575
## app.mthtrls -0.281  0.134  0.018  0.317     0.539      0.608
## app.mthts+h -0.024 -0.038 -0.015  0.184     0.160      0.240  0.187
```

```r
ccm <- 100 * (10^fixef(m6) - 1)
ccm
```

```
##                   (Intercept)                              pH
##                     -6.566185                       41.569348
##                            DM       app.methclosed slot injection
##                     11.805280                      -76.825600
##     app.methopen slot injection           app.methtrailing hose
##                    -56.030607                      -13.827757
##         app.methtrailing shoe app.methtrailing shoe + harrowing
##                    -11.290429                      -38.328382
```

```r
100 * (10^confint(m6)[4:5, ] - 1)
```

```
## Computing profile confidence intervals ...
```

```
##        2.5 %    97.5 %
## pH 19.334246 69.27394
## DM  5.430987 18.50035
```

```r
ccm['pH'] / ccm['DM']
```

```
##       pH
## 3.521251
```

Large t statistics and similar coefficients as classical linear model `m4`. Compare:

```r
cc
```

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

```r
ccm
```

```
##                   (Intercept)                              pH
##                     -6.566185                       41.569348
##                            DM       app.methclosed slot injection
##                     11.805280                      -76.825600
##     app.methopen slot injection           app.methtrailing hose
##                    -56.030607                      -13.827757
##         app.methtrailing shoe app.methtrailing shoe + harrowing
##                    -11.290429                      -38.328382
```

But, let's try likelihood ratio test (I think that's what `anova()` is doing here).

```
m0 <- lmer(log10(emis.perc) ~ app.meth + (1|source), data = dsub)
m0pH <- lmer(log10(emis.perc) ~ DM + app.meth + (1|source), data = dsub)
m0DM <- lmer(log10(emis.perc) ~ pH + app.meth + (1|source), data = dsub)
anova(m6, m0pH)
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: dsub
## Models:
## m0pH: log10(emis.perc) ~ DM + app.meth + (1 | source)
## m6: log10(emis.perc) ~ pH + DM + app.meth + (1 | source)
##       npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## m0pH     9 39.919 63.631 -10.9594  21.9189
## m6      10 27.293 53.641  -3.6466   7.2932 14.626  1  0.0001311 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(m6, m0DM)
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: dsub
## Models:
## m0DM: log10(emis.perc) ~ pH + app.meth + (1 | source)
## m6: log10(emis.perc) ~ pH + DM + app.meth + (1 | source)
##       npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## m0DM     9 38.512 62.225 -10.2561  20.5123
## m6      10 27.293 53.641  -3.6466   7.2932 13.219  1  0.0002771 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(m6, m0)
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: dsub
## Models:
## m0: log10(emis.perc) ~ app.meth + (1 | source)
## m6: log10(emis.perc) ~ pH + DM + app.meth + (1 | source)
##      npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
## m0      8 44.082 65.160 -14.0409  28.0817
## m6     10 27.293 53.641  -3.6466   7.2932 20.788  2  3.061e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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)))
m7 <- lm(log10(emis.perc) ~ pH + DM + si + app.meth, data = dat)
coef(m7)
```

```
##                     (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                          si12
##                       0.42117908                    0.70218532
##                            si14                          si15
##                       0.26718720                    0.11573208
##                            si16                          si17
##                       0.20769066                    0.25782185
##                            si18                          si19
##                      -0.01567678                    0.14392388
##                            si20      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', 'DM', 'pH'), si = factor(19),
                      app.meth = 'trailing hose',
                      DM = c(6.5, 5.1, 5.1, 6.5), pH = c(7, 7.9, 7, 7.9))
preddat$emis <- 10^predict(m7, newdata = preddat)
preddat$rcDM <- 100 * ((preddat$emis - preddat$emis[1]) / preddat$emis[1]) / (preddat$DM - preddat$DM[]
preddat$rcpH <- 100 * ((preddat$emis - preddat$emis[1]) / preddat$emis[1]) / (preddat$pH - preddat$pH[]
```

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

scenario	si	app.meth	DM	pH	emis	rcDM	rcpH
ref	19	trailing hose	6.5	7.0	15.44346	NaN	NaN
dig	19	trailing hose	5.1	7.9	17.67028	-10.29939	16.02127
DM	19	trailing hose	5.1	7.0	13.19986	10.37702	-Inf
pH	19	trailing hose	6.5	7.9	20.67372	Inf	37.63014

Different approach

```
ddw <- subset(dw, !is.na(emis.perc.ref + emis.perc.dig + DM.ref + DM.dig + pH.ref + pH.dig))
ddw$demis <- ddw$emis.perc.dig - ddw$emis.perc.ref
ddw$dpH <- ddw$pH.dig - ddw$pH.ref
ddw$dDM <- ddw$DM.dig - ddw$DM.ref
```

```
m8 <- lm(log10(emis.perc.dig) ~ log10(emis.perc.ref) + dpH + dDM, data = ddw)
summary(m8)
```

```
##
## Call:
## lm(formula = log10(emis.perc.dig) ~ log10(emis.perc.ref) + dpH +
##     dDM, data = ddw)
##
## Residuals:
```

15
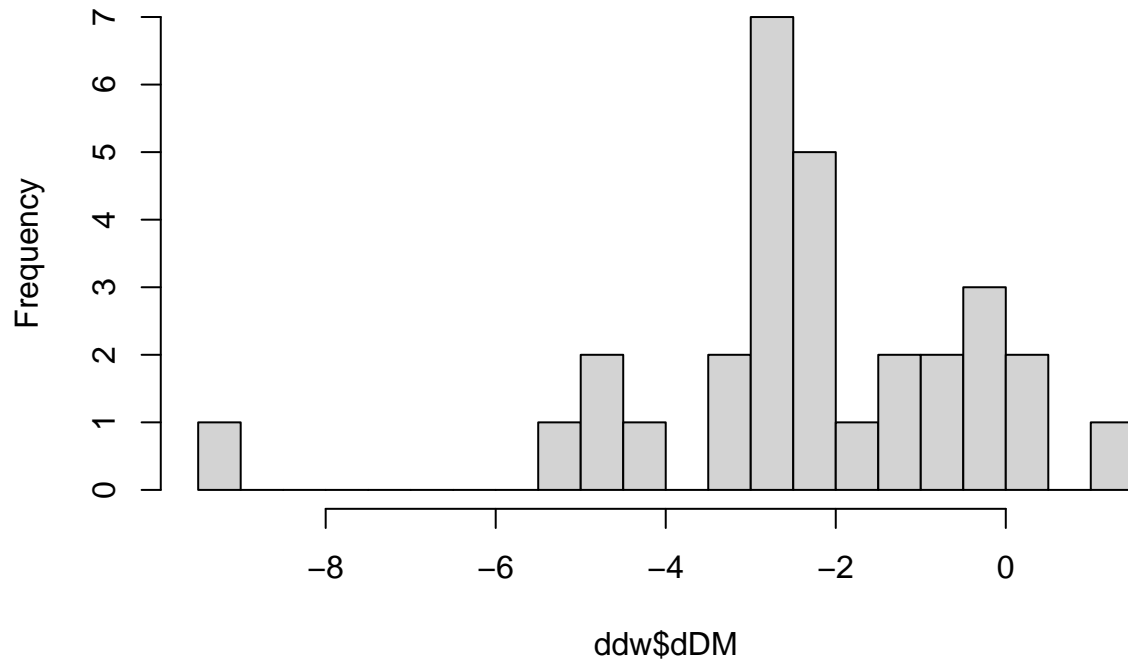
```
##       Min       1Q   Median       3Q      Max
## -0.33780 -0.05069  0.00758  0.07053  0.26165
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)          0.57702    0.12075   4.779 6.03e-05 ***
## log10(emis.perc.ref) 0.55047    0.09142   6.021 2.33e-06 ***
## dpH                  0.01750    0.05700   0.307    0.761
## dDM                 -0.00567    0.01393  -0.407    0.687
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1364 on 26 degrees of freedom
## Multiple R-squared:  0.5862, Adjusted R-squared:  0.5385
## F-statistic: 12.28 on 3 and 26 DF,  p-value: 3.42e-05
```

```r
m9 <- lm(demis ~ dpH + dDM, data = ddw)
summary(m9)
```

```
##
## Call:
## lm(formula = demis ~ dpH + dDM, data = ddw)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -16.083  -4.786   1.936   3.240  17.662
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.8593     2.3139  -0.371    0.713
## dpH           1.2468     3.3006   0.378    0.709
## dDM          -0.1133     0.8066  -0.140    0.889
##
## Residual standard error: 7.9 on 27 degrees of freedom
## Multiple R-squared:  0.0103, Adjusted R-squared:  -0.06301
## F-statistic: 0.1405 on 2 and 27 DF,  p-value: 0.8695
```
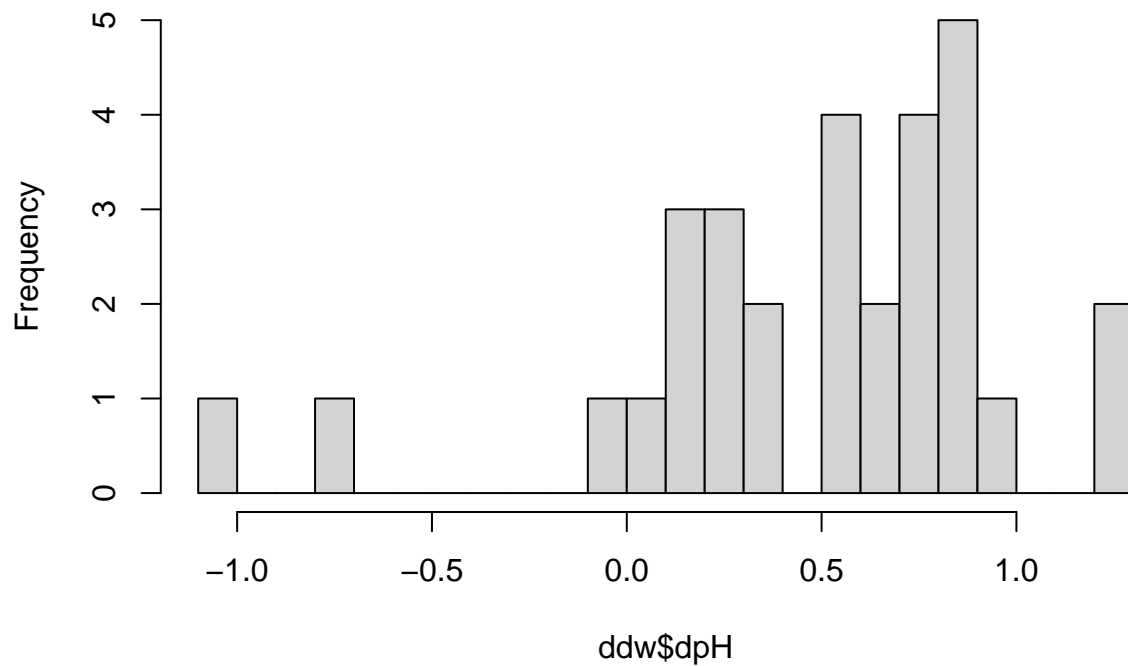
Wow. Nothing going on.

```r
hist(ddw$dDM, breaks = 20)
```

Histogram of ddw$dDM


```r
hist(ddw$dpH, breaks = 20)
```

Histogram of ddw$dpH

Include interaction.

```r
m10 <- lm(log10(emis.perc.dig) ~ log10(emis.perc.ref) + dpH*dDM, data = ddw)
summary(m10)
```

```
##
## Call:
## lm(formula = log10(emis.perc.dig) ~ log10(emis.perc.ref) + dpH *
##     dM, data = ddw)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.34652 -0.06666 -0.00179  0.06010  0.28448
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)            0.64078    0.12425   5.157 2.48e-05 ***
## log10(emis.perc.ref)   0.51054    0.09248   5.521 9.75e-06 ***
## dpH                   -0.03484    0.06465  -0.539    0.595
## dDM                    0.01932    0.02087   0.926    0.363
## dpH:dDM               -0.04188    0.02660  -1.574    0.128
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1327 on 25 degrees of freedom
## Multiple R-squared:  0.6235, Adjusted R-squared:  0.5633
## F-statistic: 10.35 on 4 and 25 DF,  p-value: 4.371e-05
```

Better to use mixed-effects model.

```r
m11 <- lmer(demis ~ dpH + dDM + (1|source), data = ddw)
summary(m11)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: demis ~ dpH + dDM + (1 | source)
##    Data: ddw
##
## REML criterion at convergence: 191.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.34194 -0.41053  0.03202  0.35965  1.62213
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  source   (Intercept) 49.36    7.026
##  Residual             25.34    5.034
## Number of obs: 30, groups:  source, 14
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  -3.3834     2.9617  -1.142
## dpH           0.3909     3.3565   0.116
## dDM          -1.5697     0.8808  -1.782
##
## Correlation of Fixed Effects:
##     (Intr) dpH
## dpH -0.322
## dDM  0.470  0.334
```

```
confint(m11)
```

```
## Computing profile confidence intervals ...

##                 2.5 %      97.5 %
## .sig01       2.226036 10.9701800
## .sigma       3.526253  7.5739994
## (Intercept) -9.353064  2.3565819
## dpH         -6.020312  6.9034389
## dDM         -3.342465  0.5623619
```