Statistical analysis

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14:49 - 05 December, 2024

Data table

```
setDT(isumm)
```

Trials 1-4 (digestate treatment effects)

Subset.

```
isumm1 <- isumm[new.ID %in% as.character(1:4)]
```

Separate digestate type from treatment

```
isumm1[, dig.ID := substr(treat1, 1, 1)]
isumm1[, dig.treat := gsub('^[ABC]', '', treat1)]
```

Fit mixed-effects model and fixed-effects for comparison.

```
m0 <- lm(e.rel.150 ~ dig.treat * dig.ID + new.ID, data = isumm1)
mn <- lmer(e.rel.150 ~ (1|dig.ID) + (1|new.ID), data = isumm1)
m1 <- lmer(e.rel.150 ~ dig.treat + (1|dig.ID) + (1|new.ID), data = isumm1)
m2 <- lmer(e.rel.150 ~ dig.treat + (1|dig.ID/dig.treat) + (1|new.ID), data = isumm1)
m3 <- lmer(e.rel.150 ~ treat1 + (1|new.ID), data = isumm1)
```

```
summary(m0)
```

```
##
## Call:
## lm(formula = e.rel.150 ~ dig.treat * dig.ID + new.ID, data = isumm1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.08833 -0.01957  0.00625  0.02000  0.06763
##
## Coefficients: (15 not defined because of singularities)
##                                Estimate Std. Error t value Pr(>|t|)
## (Intercept)                    0.357632   0.020424  17.510  < 2e-16 ***
```

```
## dig.treat Acid                -0.126583   0.031198  -4.057 0.000205 ***
## dig.treat Dis                  0.004368   0.031198   0.140 0.889299
## dig.treat Dis + acid          -0.068298   0.031198  -2.189 0.034060 *
## dig.treat MF liquid           -0.329802   0.031198 -10.571 1.56e-13 ***
## dig.treat MF slurry            0.059632   0.031198   1.911 0.062635 .
## dig.treat Sep-D               -0.325770   0.023584 -13.813  < 2e-16 ***
## dig.treat Sep-D + acid        -0.316265   0.031198 -10.137 5.70e-13 ***
## dig.treat Sep-S               -0.128618   0.028884  -4.453 5.93e-05 ***
## dig.treat Sep-S + acid        -0.119417   0.031198  -3.828 0.000414 ***
## dig.IDB                        0.122167   0.023584   5.180 5.60e-06 ***
## dig.IDC                       -0.160417   0.031198  -5.142 6.35e-06 ***
## new.ID2                       -0.016048   0.028884  -0.556 0.581353
## new.ID3                        0.126118   0.028884   4.366 7.81e-05 ***
## new.ID4                        0.035737   0.023584   1.515 0.137008
## dig.treat Acid:dig.IDB         0.185500   0.040848   4.541 4.48e-05 ***
## dig.treat Dis:dig.IDB                NA         NA      NA       NA
## dig.treat Dis + acid:dig.IDB         NA         NA      NA       NA
## dig.treat MF liquid:dig.IDB          NA         NA      NA       NA
## dig.treat MF slurry:dig.IDB          NA         NA      NA       NA
## dig.treat Sep-D:dig.IDB              NA         NA      NA       NA
## dig.treat Sep-D + acid:dig.IDB       NA         NA      NA       NA
## dig.treat Sep-S:dig.IDB       -0.072965   0.042516  -1.716 0.093326 .
## dig.treat Sep-S + acid:dig.IDB       NA         NA      NA       NA
## dig.treat Acid:dig.IDC               NA         NA      NA       NA
## dig.treat Dis:dig.IDC                NA         NA      NA       NA
## dig.treat Dis + acid:dig.IDC         NA         NA      NA       NA
## dig.treat MF liquid:dig.IDC          NA         NA      NA       NA
## dig.treat MF slurry:dig.IDC          NA         NA      NA       NA
## dig.treat Sep-D:dig.IDC       0.119370   0.040848   2.922 0.005519 **
## dig.treat Sep-D + acid:dig.IDC       NA         NA      NA       NA
## dig.treat Sep-S:dig.IDC              NA         NA      NA       NA
## dig.treat Sep-S + acid:dig.IDC       NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04085 on 43 degrees of freedom
## Multiple R-squared:  0.9582, Adjusted R-squared:  0.9417
## F-statistic: 58.01 on 17 and 43 DF,  p-value: < 2.2e-16
```

```
anova(m0)
```

```
## Analysis of Variance Table
##
## Response: e.rel.150
##                  Df  Sum Sq  Mean Sq F value    Pr(>F)
## dig.treat         9 1.27757 0.141952  85.075 < 2.2e-16 ***
## dig.ID            2 0.24833 0.124167  74.416 1.088e-14 ***
## new.ID            3 0.05598 0.018659  11.182 1.493e-05 ***
## dig.treat:dig.ID  3 0.06357 0.021189  12.699 4.453e-06 ***
## Residuals        43 0.07175 0.001669
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(m1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ dig.treat + (1 | dig.ID) + (1 | new.ID)
##    Data: isumm1
##
## REML criterion at convergence: -123.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.2902 -0.7355  0.1204  0.5567  1.9408
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  new.ID   (Intercept) 0.002487 0.04987
##  dig.ID   (Intercept) 0.014034 0.11846
##  Residual             0.002945 0.05427
## Number of obs: 61, groups:  new.ID, 4; dig.ID, 3
##
## Fixed effects:
##                         Estimate Std. Error t value
## (Intercept)              0.41336    0.07456   5.544
## dig.treat Acid          -0.04325    0.03038  -1.424
## dig.treat Dis            0.01184    0.03921   0.302
## dig.treat Dis + acid    -0.06082    0.03921  -1.551
## dig.treat MF liquid     -0.33145    0.03793  -8.740
## dig.treat MF slurry      0.05799    0.03793   1.529
## dig.treat Sep-D         -0.30086    0.02434 -12.360
## dig.treat Sep-D + acid  -0.30879    0.03921  -7.875
## dig.treat Sep-S         -0.15722    0.02682  -5.862
## dig.treat Sep-S + acid  -0.15216    0.03972  -3.831
##
## Correlation of Fixed Effects:
##             (Intr) dg.trA dg.trD dg.D+a dg.MFl dg.MFs dg.S-D d.S-D+a dg.S-S
## dig.tretAcd -0.058
## dig.treatDs -0.073  0.026
## dg.trtDs+ac -0.073  0.026  0.362
## dg.trtMFlqd -0.067  0.027  0.085  0.085
## dg.trtMFslr -0.067  0.027  0.085  0.085  0.318
## dig.trtSp-D -0.124  0.034  0.285  0.285  0.252  0.252
## dg.trSp-D+a -0.073  0.026  0.362  0.362  0.085  0.085  0.285
## dig.trtSp-S -0.075  0.039  0.085  0.085  0.310  0.310  0.250  0.085
## dg.trSp-S+a -0.070  0.368  0.013  0.013  0.031  0.031  0.028  0.013   0.089
```

```
summary(m2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ dig.treat + (1 | dig.ID/dig.treat) + (1 | new.ID)
##    Data: isumm1
##
## REML criterion at convergence: -141
##
```

```
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.2447 -0.5187  0.1327  0.4729  1.5858
##
## Random effects:
##  Groups           Name        Variance Std.Dev.
##  dig.treat:dig.ID (Intercept) 0.005960 0.07720
##  new.ID           (Intercept) 0.003555 0.05962
##  dig.ID           (Intercept) 0.013257 0.11514
##  Residual                     0.001676 0.04094
## Number of obs: 61, groups:  dig.treat:dig.ID, 15; new.ID, 4; dig.ID, 3
##
## Fixed effects:
##                        Estimate Std. Error t value
## (Intercept)             0.38753    0.08642   4.485
## dig.treat Acid         -0.01161    0.07746  -0.150
## dig.treat Dis           0.03652    0.10002   0.365
## dig.treat Dis + acid   -0.03615    0.10002  -0.361
## dig.treat MF liquid    -0.29670    0.09969  -2.976
## dig.treat MF slurry     0.09273    0.09969   0.930
## dig.treat Sep-D        -0.27869    0.07561  -3.686
## dig.treat Sep-D + acid -0.28412    0.10002  -2.841
## dig.treat Sep-S        -0.13617    0.07648  -1.780
## dig.treat Sep-S + acid -0.10922    0.10172  -1.074
##
## Correlation of Fixed Effects:
##             (Intr) dg.trA dg.trD dg.D+a dg.MFl dg.MFs dg.S-D d.S-D+a dg.S-S
## dig.tretAcd -0.310
## dig.treatDs -0.248  0.306
## dg.trtDs+ac -0.248  0.306  0.348
## dg.trtMFlqd -0.249  0.307  0.320  0.320
## dg.trtMFslr -0.249  0.307  0.320  0.320  0.344
## dig.trtSp-D -0.327  0.299  0.313  0.313  0.312  0.312
## dg.trSp-D+a -0.248  0.306  0.348  0.348  0.320  0.320  0.313
## dig.trtSp-S -0.317  0.416  0.318  0.318  0.336  0.336  0.318  0.318
## dg.trSp-S+a -0.242  0.359  0.160  0.160  0.165  0.165  0.167  0.160   0.332
```

```
summary(m3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ treat1 + (1 | new.ID)
##    Data: isumm1
##
## REML criterion at convergence: -136.7
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.1636 -0.4793  0.1600  0.4899  1.6282
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  new.ID   (Intercept) 0.003794 0.06159
##  Residual             0.001667 0.04083
## Number of obs: 61, groups:  new.ID, 4
```

```
##
## Fixed effects:
##                          Estimate Std. Error t value
## (Intercept)             0.3940833  0.0329751  11.951
## treat1A Acid           -0.1290595  0.0307427  -4.198
## treat1A Dis             0.0007752  0.0307427   0.025
## treat1A Dis + acid     -0.0718915  0.0307427  -2.338
## treat1A MF liquid      -0.3309564  0.0307427 -10.765
## treat1A MF slurry       0.0584769  0.0307427   1.902
## treat1A Sep-D          -0.3281439  0.0231922 -14.149
## treat1A Sep-D + acid   -0.3198581  0.0307427 -10.404
## treat1A Sep-S          -0.1297731  0.0283938  -4.570
## treat1B                 0.1245406  0.0231922   5.370
## treat1B Acid            0.1786072  0.0307427   5.810
## treat1B Sep-S          -0.0721926  0.0307427  -2.348
## treat1B Sep-S + acid    0.0002738  0.0307427   0.009
## treat1C                -0.1531926  0.0307427  -4.983
## treat1C Sep-D          -0.3595926  0.0307427 -11.697

##
## Correlation matrix not shown by default, as p = 15 > 12.
## Use print(value, correlation=TRUE)  or
##     vcov(value)        if you need it
```

Check for treatment effect and interaction with likelihood ratio test.

```
anova(m1, mn, test = 'Chisq')
```

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

## Data: isumm1
## Models:
## mn: e.rel.150 ~ (1 | dig.ID) + (1 | new.ID)
## m1: e.rel.150 ~ dig.treat + (1 | dig.ID) + (1 | new.ID)
##    npar      AIC      BIC logLik deviance  Chisq Df Pr(>Chisq)
## mn    4  -50.419  -41.975 29.209  -58.419
## m1   13 -147.357 -119.915 86.678 -173.357 114.94  9  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

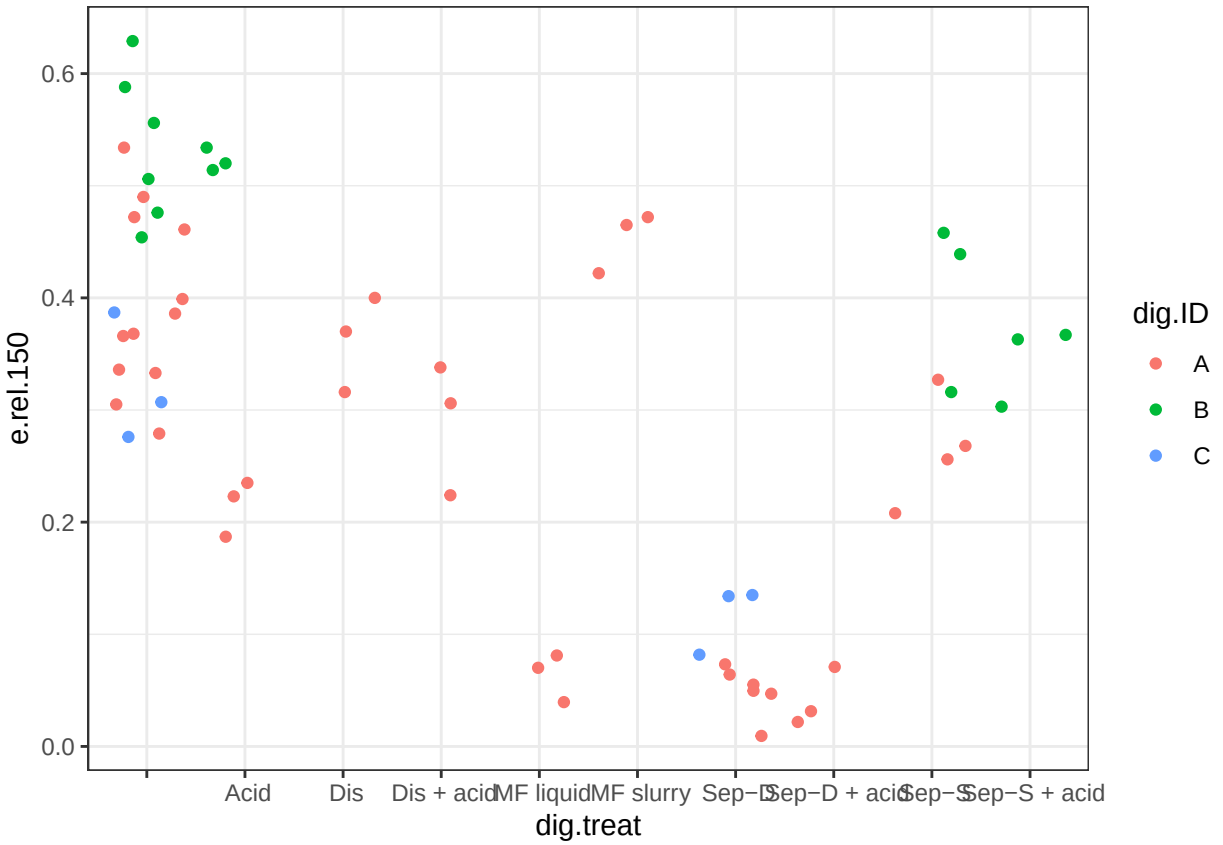
```
anova(m2, m1, test = 'Chisq')
```

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

## Data: isumm1
## Models:
## m1: e.rel.150 ~ dig.treat + (1 | dig.ID) + (1 | new.ID)
## m2: e.rel.150 ~ dig.treat + (1 | dig.ID/dig.treat) + (1 | new.ID)
##    npar     AIC     BIC logLik deviance  Chisq Df Pr(>Chisq)
## m1   13 -147.36 -119.92 86.678  -173.36
## m2   14 -152.17 -122.62 90.085  -180.17 6.8136  1   0.009047 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Plot to check.

```
ggplot(isumm1, aes(dig.treat, e.rel.150, colour = dig.ID)) +
  geom_jitter(height = 0) +
  theme_bw()
```




```
table(isumm1[, .(dig.ID, dig.treat)])
```

```
##       dig.treat
## dig.ID     Acid  Dis  Dis + acid  MF liquid  MF slurry  Sep-D  Sep-D + acid
##      A 12     3    3           3          3          3      6             3
##      B  6     3    0           0          0          0      0             0
##      C  3     0    0           0          0          0      3             0
##       dig.treat
## dig.ID  Sep-S  Sep-S + acid
##      A      4             0
##      B      3             3
##      C      0             0
```

Major imbalance. Get marginal means.

```
emmeans(m3, 'treat1')
```

```
##  treat1         emmean     SE   df lower.CL upper.CL
```

```
##  A              0.3941 0.0330 3.28   0.2941    0.494
##  A Acid         0.2650 0.0423 7.90   0.1672    0.363
##  A Dis          0.3949 0.0423 7.90   0.2970    0.493
##  A Dis + acid   0.3222 0.0423 7.90   0.2244    0.420
##  A MF liquid    0.0631 0.0423 7.90  -0.0347    0.161
##  A MF slurry    0.4526 0.0423 7.90   0.3547    0.550
##  A Sep-D        0.0659 0.0370 4.85  -0.0301    0.162
##  A Sep-D + acid 0.0742 0.0423 7.90  -0.0236    0.172
##  A Sep-S        0.2643 0.0407 6.76   0.1675    0.361
##  B              0.5186 0.0370 4.85   0.4226    0.615
##  B Acid         0.5727 0.0423 7.90   0.4748    0.671
##  B Sep-S        0.3219 0.0423 7.90   0.2240    0.420
##  B Sep-S + acid 0.3944 0.0423 7.90   0.2965    0.492
##  C              0.2409 0.0423 7.90   0.1430    0.339
##  C Sep-D        0.0345 0.0423 7.90  -0.0634    0.132
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

```
mmeans1_4 <- emmeans(m3, 'treat1')
mmeans1_4
```

```
##  treat1         emmean     SE   df lower.CL upper.CL
##  A              0.3941 0.0330 3.28   0.2941    0.494
##  A Acid         0.2650 0.0423 7.90   0.1672    0.363
##  A Dis          0.3949 0.0423 7.90   0.2970    0.493
##  A Dis + acid   0.3222 0.0423 7.90   0.2244    0.420
##  A MF liquid    0.0631 0.0423 7.90  -0.0347    0.161
##  A MF slurry    0.4526 0.0423 7.90   0.3547    0.550
##  A Sep-D        0.0659 0.0370 4.85  -0.0301    0.162
##  A Sep-D + acid 0.0742 0.0423 7.90  -0.0236    0.172
##  A Sep-S        0.2643 0.0407 6.76   0.1675    0.361
##  B              0.5186 0.0370 4.85   0.4226    0.615
##  B Acid         0.5727 0.0423 7.90   0.4748    0.671
##  B Sep-S        0.3219 0.0423 7.90   0.2240    0.420
##  B Sep-S + acid 0.3944 0.0423 7.90   0.2965    0.492
##  C              0.2409 0.0423 7.90   0.1430    0.339
##  C Sep-D        0.0345 0.0423 7.90  -0.0634    0.132
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

```
pairs(mmeans1_4)
```

```
##  contrast                          estimate     SE   df t.ratio p.value
##  A - A Acid                        0.129059 0.0313 45.0   4.118  0.0117
##  A - A Dis                        -0.000775 0.0313 45.0  -0.025  1.0000
##  A - (A Dis + acid)                0.071891 0.0313 45.0   2.294  0.5999
##  A - A MF liquid                   0.330956 0.0313 45.0  10.559  <.0001
##  A - A MF slurry                  -0.058477 0.0313 45.0  -1.866  0.8571
##  A - (A Sep-D)                     0.328144 0.0237 45.2  13.854  <.0001
##  A - (A Sep-D + acid)              0.319858 0.0313 45.0  10.205  <.0001
##  A - (A Sep-S)                     0.129773 0.0290 45.2   4.468  0.0041
```

```
##  A - B                              -0.124541 0.0237 45.2  -5.258  0.0003
##  A - B Acid                         -0.178607 0.0313 45.0  -5.699  0.0001
##  A - (B Sep-S)                       0.072193 0.0313 45.0   2.303  0.5934
##  A - (B Sep-S + acid)               -0.000274 0.0313 45.0  -0.009  1.0000
##  A - C                               0.153193 0.0313 45.0   4.888  0.0011
##  A - (C Sep-D)                       0.359593 0.0313 45.0  11.473  <.0001
##  A Acid - A Dis                     -0.129835 0.0444 45.8  -2.921  0.2252
##  A Acid - (A Dis + acid)            -0.057168 0.0444 45.8  -1.286  0.9922
##  A Acid - A MF liquid                0.201897 0.0444 45.8   4.542  0.0032
##  A Acid - A MF slurry               -0.187536 0.0444 45.8  -4.219  0.0086
##  A Acid - (A Sep-D)                  0.199084 0.0394 45.9   5.050  0.0006
##  A Acid - (A Sep-D + acid)           0.190799 0.0444 45.8   4.293  0.0069
##  A Acid - (A Sep-S)                  0.000714 0.0429 45.9   0.017  1.0000
##  A Acid - B                         -0.253600 0.0313 43.8  -8.114  <.0001
##  A Acid - B Acid                    -0.307667 0.0333 43.0  -9.229  <.0001
##  A Acid - (B Sep-S)                 -0.056867 0.0411 44.7  -1.385  0.9846
##  A Acid - (B Sep-S + acid)          -0.129333 0.0333 43.0  -3.880  0.0237
##  A Acid - C                          0.024133 0.0411 44.7   0.588  1.0000
##  A Acid - (C Sep-D)                  0.230533 0.0411 44.7   5.615  0.0001
##  A Dis - (A Dis + acid)              0.072667 0.0333 43.0   2.180  0.6764
##  A Dis - A MF liquid                 0.331732 0.0411 44.7   8.081  <.0001
##  A Dis - A MF slurry                -0.057702 0.0411 44.7  -1.406  0.9825
##  A Dis - (A Sep-D)                   0.328919 0.0313 43.8  10.523  <.0001
##  A Dis - (A Sep-D + acid)            0.320633 0.0333 43.0   9.618  <.0001
##  A Dis - (A Sep-S)                   0.130548 0.0393 44.9   3.320  0.0959
##  A Dis - B                          -0.123765 0.0394 45.9  -3.139  0.1433
##  A Dis - B Acid                     -0.177832 0.0444 45.8  -4.001  0.0161
##  A Dis - (B Sep-S)                   0.072968 0.0444 45.8   1.642  0.9395
##  A Dis - (B Sep-S + acid)            0.000501 0.0444 45.8   0.011  1.0000
##  A Dis - C                           0.153968 0.0444 45.8   3.464  0.0673
##  A Dis - (C Sep-D)                   0.360368 0.0444 45.8   8.108  <.0001
##  (A Dis + acid) - A MF liquid        0.259065 0.0411 44.7   6.310  <.0001
##  (A Dis + acid) - A MF slurry       -0.130368 0.0411 44.7  -3.176  0.1332
##  (A Dis + acid) - (A Sep-D)          0.256252 0.0313 43.8   8.198  <.0001
##  (A Dis + acid) - (A Sep-D + acid)   0.247967 0.0333 43.0   7.439  <.0001
##  (A Dis + acid) - (A Sep-S)          0.057882 0.0393 44.9   1.472  0.9741
##  (A Dis + acid) - B                 -0.196432 0.0394 45.9  -4.983  0.0008
##  (A Dis + acid) - B Acid            -0.250499 0.0444 45.8  -5.636  0.0001
##  (A Dis + acid) - (B Sep-S)          0.000301 0.0444 45.8   0.007  1.0000
##  (A Dis + acid) - (B Sep-S + acid)  -0.072165 0.0444 45.8  -1.624  0.9442
##  (A Dis + acid) - C                  0.081301 0.0444 45.8   1.829  0.8737
##  (A Dis + acid) - (C Sep-D)          0.287701 0.0444 45.8   6.473  <.0001
##  A MF liquid - A MF slurry          -0.389433 0.0333 43.0 -11.682  <.0001
##  A MF liquid - (A Sep-D)            -0.002812 0.0313 43.8  -0.090  1.0000
##  A MF liquid - (A Sep-D + acid)     -0.011098 0.0411 44.7  -0.270  1.0000
##  A MF liquid - (A Sep-S)            -0.201183 0.0312 43.0  -6.452  <.0001
##  A MF liquid - B                    -0.455497 0.0394 45.9 -11.554  <.0001
##  A MF liquid - B Acid               -0.509564 0.0444 45.8 -11.465  <.0001
##  A MF liquid - (B Sep-S)            -0.258764 0.0444 45.8  -5.822  0.0001
##  A MF liquid - (B Sep-S + acid)     -0.331230 0.0444 45.8  -7.452  <.0001
##  A MF liquid - C                    -0.177764 0.0444 45.8  -4.000  0.0162
##  A MF liquid - (C Sep-D)             0.028636 0.0444 45.8   0.644  1.0000
##  A MF slurry - (A Sep-D)             0.386621 0.0313 43.8  12.369  <.0001
##  A MF slurry - (A Sep-D + acid)      0.378335 0.0411 44.7   9.216  <.0001
```

```
##  A MF slurry - (A Sep-S)              0.188250 0.0312 43.0   6.037  <.0001
##  A MF slurry - B                     -0.066064 0.0394 45.9  -1.676  0.9298
##  A MF slurry - B Acid                -0.120130 0.0444 45.8  -2.703  0.3354
##  A MF slurry - (B Sep-S)              0.130669 0.0444 45.8   2.940  0.2170
##  A MF slurry - (B Sep-S + acid)       0.058203 0.0444 45.8   1.310  0.9908
##  A MF slurry - C                      0.211670 0.0444 45.8   4.762  0.0016
##  A MF slurry - (C Sep-D)              0.418069 0.0444 45.8   9.406  <.0001
##  (A Sep-D) - (A Sep-D + acid)        -0.008286 0.0313 43.8  -0.265  1.0000
##  (A Sep-D) - (A Sep-S)               -0.198371 0.0289 43.9  -6.852  <.0001
##  (A Sep-D) - B                       -0.452685 0.0337 46.0 -13.450  <.0001
##  (A Sep-D) - B Acid                  -0.506751 0.0394 45.9 -12.854  <.0001
##  (A Sep-D) - (B Sep-S)               -0.255951 0.0394 45.9  -6.493  <.0001
##  (A Sep-D) - (B Sep-S + acid)        -0.328418 0.0394 45.9  -8.331  <.0001
##  (A Sep-D) - C                       -0.174951 0.0394 45.9  -4.438  0.0045
##  (A Sep-D) - (C Sep-D)                0.031449 0.0394 45.9   0.798  1.0000
##  (A Sep-D + acid) - (A Sep-S)        -0.190085 0.0393 44.9  -4.834  0.0013
##  (A Sep-D + acid) - B                -0.444399 0.0394 45.9 -11.273  <.0001
##  (A Sep-D + acid) - B Acid           -0.498465 0.0444 45.8 -11.215  <.0001
##  (A Sep-D + acid) - (B Sep-S)        -0.247666 0.0444 45.8  -5.572  0.0001
##  (A Sep-D + acid) - (B Sep-S + acid) -0.320132 0.0444 45.8  -7.203  <.0001
##  (A Sep-D + acid) - C                -0.166665 0.0444 45.8  -3.750  0.0322
##  (A Sep-D + acid) - (C Sep-D)         0.039734 0.0444 45.8   0.894  0.9998
##  (A Sep-S) - B                       -0.254314 0.0376 46.0  -6.760  <.0001
##  (A Sep-S) - B Acid                  -0.308380 0.0429 45.9  -7.196  <.0001
##  (A Sep-S) - (B Sep-S)               -0.057580 0.0429 45.9  -1.344  0.9884
##  (A Sep-S) - (B Sep-S + acid)        -0.130047 0.0429 45.9  -3.035  0.1791
##  (A Sep-S) - C                        0.023419 0.0429 45.9   0.546  1.0000
##  (A Sep-S) - (C Sep-D)                0.229820 0.0429 45.9   5.363  0.0002
##  B - B Acid                          -0.054067 0.0313 43.8  -1.730  0.9119
##  B - (B Sep-S)                        0.196733 0.0313 43.8   6.294  <.0001
##  B - (B Sep-S + acid)                 0.124267 0.0313 43.8   3.976  0.0179
##  B - C                                0.277733 0.0313 43.8   8.886  <.0001
##  B - (C Sep-D)                        0.484133 0.0313 43.8  15.489  <.0001
##  B Acid - (B Sep-S)                   0.250800 0.0411 44.7   6.109  <.0001
##  B Acid - (B Sep-S + acid)            0.178333 0.0333 43.0   5.350  0.0003
##  B Acid - C                           0.331800 0.0411 44.7   8.082  <.0001
##  B Acid - (C Sep-D)                   0.538200 0.0411 44.7  13.110  <.0001
##  (B Sep-S) - (B Sep-S + acid)        -0.072467 0.0411 44.7  -1.765  0.8994
##  (B Sep-S) - C                        0.081000 0.0333 43.0   2.430  0.5079
##  (B Sep-S) - (C Sep-D)                0.287400 0.0333 43.0   8.621  <.0001
##  (B Sep-S + acid) - C                 0.153467 0.0411 44.7   3.738  0.0337
##  (B Sep-S + acid) - (C Sep-D)         0.359866 0.0411 44.7   8.766  <.0001
##  C - (C Sep-D)                        0.206400 0.0333 43.0   6.192  <.0001
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 15 estimates
```

Get letters.

```
letters1_4 <- cld(object = mmeans1_4,
                  adjust = "Tukey",
                  Letters = letters,
                  alpha = 0.05)
```

```
## Note: adjust = "tukey" was changed to "sidak"
## because "tukey" is only appropriate for one set of pairwise comparisons
```

```
letters1_4
```

```
##  treat1         emmean     SE   df lower.CL upper.CL .group
##  C Sep-D        0.0345 0.0423 7.90  -0.1402    0.209  a
##  A MF liquid    0.0631 0.0423 7.90  -0.1115    0.238  a
##  A Sep-D        0.0659 0.0370 4.85  -0.1313    0.263  a
##  A Sep-D + acid 0.0742 0.0423 7.90  -0.1004    0.249  a
##  C              0.2409 0.0423 7.90   0.0662    0.416   b
##  A Sep-S        0.2643 0.0407 6.76   0.0853    0.443   bc
##  A Acid         0.2650 0.0423 7.90   0.0904    0.440   b
##  B Sep-S        0.3219 0.0423 7.90   0.1472    0.497   bcd
##  A Dis + acid   0.3222 0.0423 7.90   0.1475    0.497   bcd
##  A              0.3941 0.0330 3.28   0.1430    0.645     d
##  B Sep-S + acid 0.3944 0.0423 7.90   0.2197    0.569    cd
##  A Dis          0.3949 0.0423 7.90   0.2202    0.570   bcde
##  A MF slurry    0.4526 0.0423 7.90   0.2779    0.627     def
##  B              0.5186 0.0370 4.85   0.3214    0.716      ef
##  B Acid         0.5727 0.0423 7.90   0.3980    0.747       f
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 15 estimates
## P value adjustment: tukey method for comparing a family of 15 estimates
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

Sort letters by treat1 and replace mmeans.

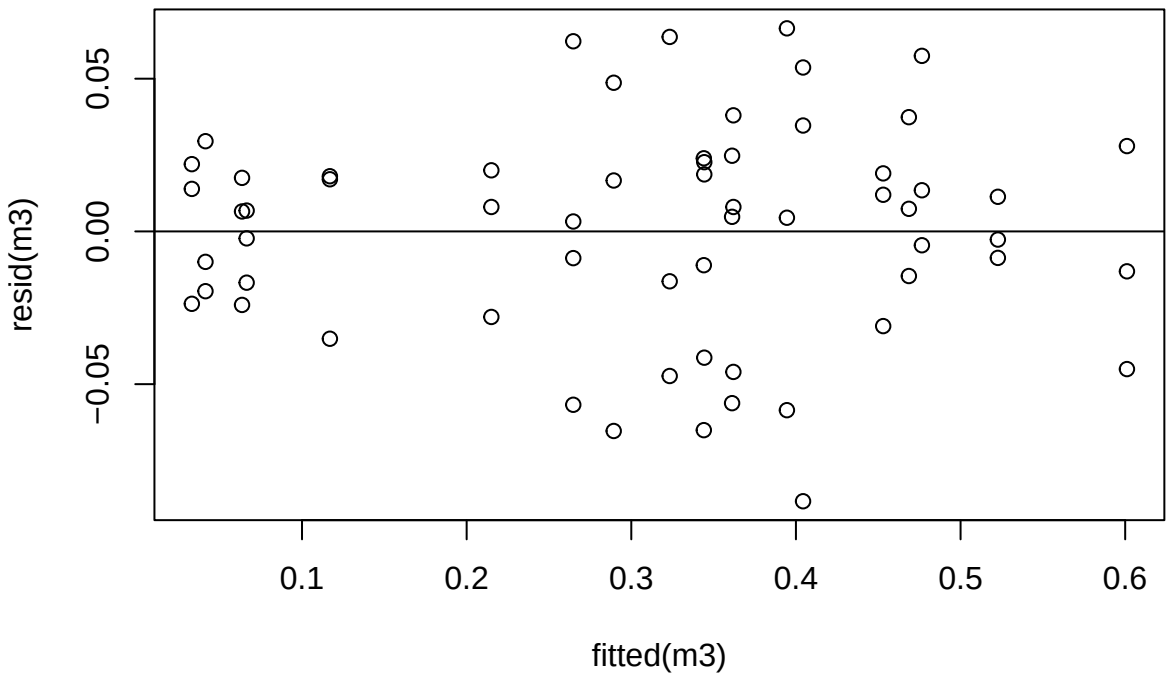
```
mmeans1_4 <- letters1_4[order(letters1_4$treat1), ]
```

And get a column for copy/paste into paper.

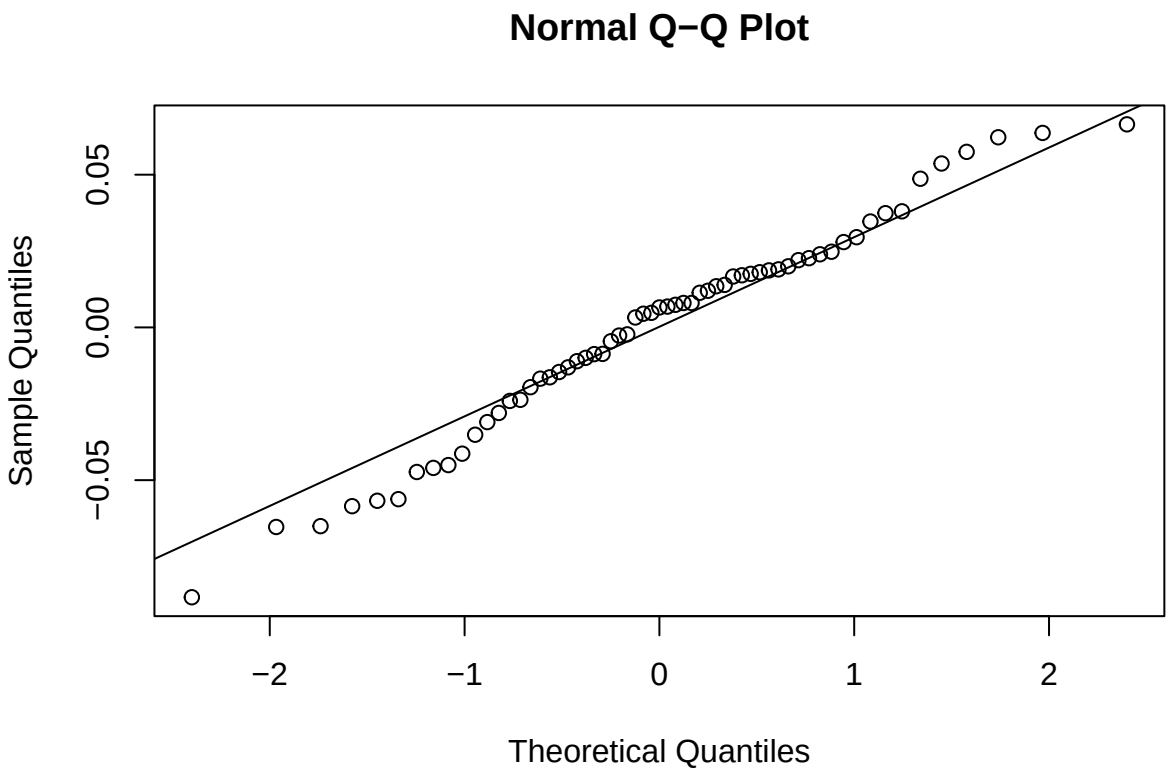
```
mmeans1_4$tabval <- paste(round(100 * mmeans1_4$emmean, 1), gsub(' ', '', mmeans1_4$.group))
```

Residuals.

```
plot(fitted(m3), resid(m3))
abline(0,0)
```




```
qqnorm(resid(m3))
qqline(resid(m3))
```



Trials 5-10 (app tech on winter wheat)

Subset.

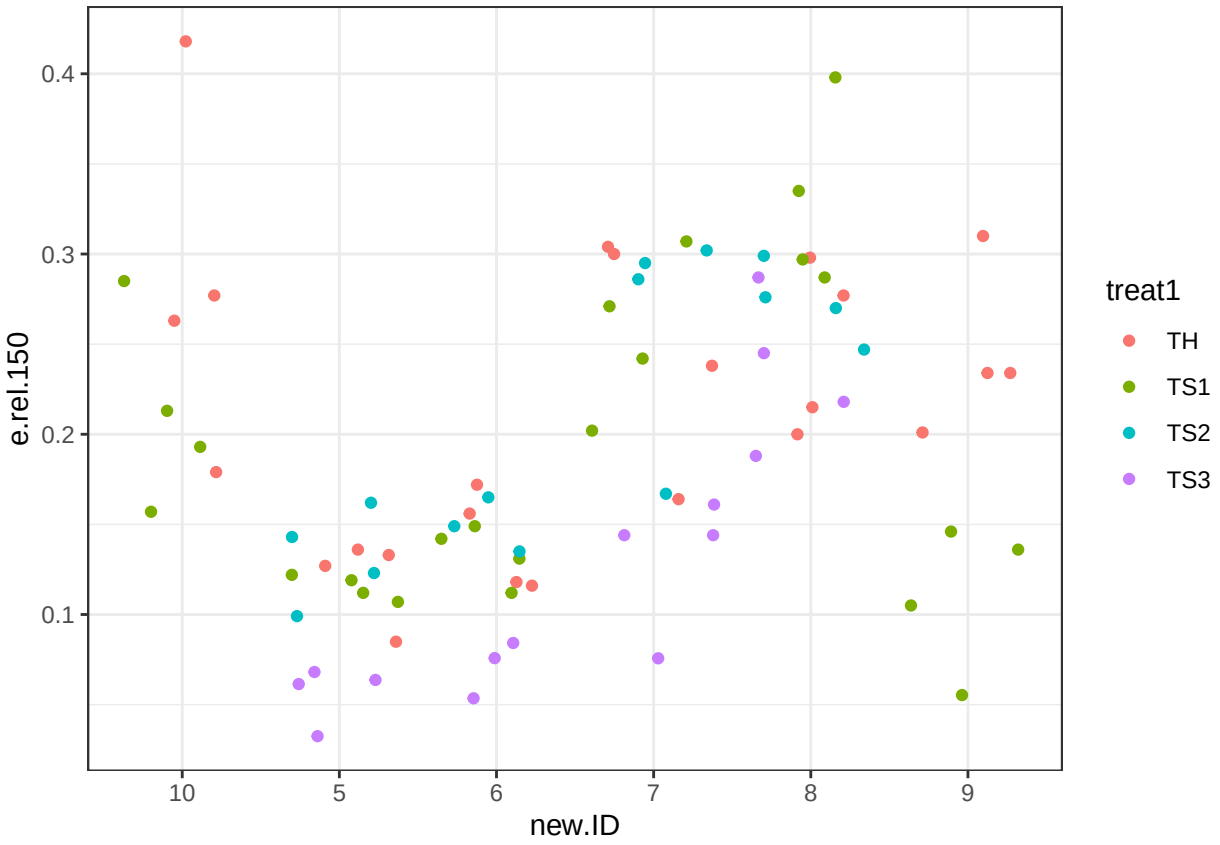
```
isumm1 <- droplevels(isumm[new.ID %in% c('5', '6', '7', '8', '9', '10') & !treat1 %in% c('TH-4', 'TS1-4
```

```
table(isumm1[, .(new.ID, treat1)])
```

```
##       treat1
## new.ID TH TS1 TS2 TS3
##     10  4   4   0   0
##     5   4   4   4   4
##     6   4   4   3   3
##     7   4   4   4   4
##     8   4   4   4   4
##     9   4   4   0   0
```

Close to balanced.

```
ggplot(isumm1, aes(new.ID, e.rel.150, colour = treat1)) +
  geom_jitter(height = 0) +
  theme_bw()
```



Fit mixed-effects model.

```
m1 <- lmer(e.rel.150 ~ treat1 + (1|new.ID), data = isumm1)
```

```
summary(m1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ treat1 + (1 | new.ID)
##    Data: isumm1
##
## REML criterion at convergence: -203.3
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.2137 -0.4155  0.0176  0.3447  3.1690
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  new.ID   (Intercept) 0.004217 0.06494
##  Residual             0.002613 0.05112
## Number of obs: 78, groups:  new.ID, 6
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  0.214787   0.028492   7.539
## treat1TS1   -0.022150   0.014756  -1.501
```

```
## treat1TS2   -0.006375   0.017576  -0.363
## treat1TS3   -0.087455   0.017576  -4.976
##
## Correlation of Fixed Effects:
##           (Intr) tr1TS1 tr1TS2
## treat1TS1 -0.259
## treat1TS2 -0.217  0.420
## treat1TS3 -0.217  0.420  0.436
```

Marginal means.

```
mmeans <- emmeans(m1, 'treat1')
mmeans
```

```
##  treat1 emmean     SE   df lower.CL upper.CL
##  TH      0.215 0.0285 5.99   0.1450    0.285
##  TS1     0.193 0.0285 5.99   0.1229    0.262
##  TS2     0.208 0.0301 7.36   0.1380    0.279
##  TS3     0.127 0.0301 7.36   0.0569    0.198
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

Need name for export.

Tukey's test

```
mmeans5_10 <- emmeans(m1, 'treat1')
pairs(mmeans5_10)
```

```
##  contrast  estimate     SE   df t.ratio p.value
##  TH - TS1   0.02215 0.0148 69.0   1.501  0.4424
##  TH - TS2   0.00638 0.0176 69.8   0.362  0.9837
##  TH - TS3   0.08746 0.0176 69.8   4.963  <.0001
##  TS1 - TS2 -0.01577 0.0176 69.8  -0.895  0.8074
##  TS1 - TS3  0.06531 0.0176 69.8   3.706  0.0023
##  TS2 - TS3  0.08108 0.0187 69.0   4.344  0.0003
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 4 estimates
```

```
letters5_10 <- cld(object = mmeans5_10,
                   adjust = "Tukey",
                   Letters = letters,
                   alpha = 0.05)
```

```
## Note: adjust = "tukey" was changed to "sidak"
## because "tukey" is only appropriate for one set of pairwise comparisons
```

```
letters5_10
```

```
##  treat1 emmean     SE   df lower.CL upper.CL .group
##  TS3     0.127 0.0301 7.36   0.0290    0.226  a
##  TS1     0.193 0.0285 5.99   0.0927    0.293   b
##  TS2     0.208 0.0301 7.36   0.1100    0.307   b
##  TH      0.215 0.0285 5.99   0.1149    0.315   b
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## Conf-level adjustment: sidak method for 4 estimates
## P value adjustment: tukey method for comparing a family of 4 estimates
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

```
mmeans5_10 <- letters5_10[order(letters5_10$treat1), ]
```

And get a column for copy/paste into paper.

```
mmeans5_10$tabval <- paste(round(100 * mmeans5_10$emmean, 1), gsub(' ', '', mmeans5_10$.group))
```

Add 11-12

```
isumm1 <- droplevels(isumm[new.ID %in% c('11', '12') & treat1 != 'TS1 + acid', ])
```

```
table(isumm1[, .(new.ID, treat1)])
```

```
##       treat1
## new.ID OSI TH TS1
##     11   4  4   4
##     12   4  4   4
```

Completely balanced and only two experiments, so no need for mixed-effects model.

```
m1 <- lm(e.rel.150 ~ treat1 + new.ID, data = isumm1)
```

```
summary(m1)
```

```
##
## Call:
## lm(formula = e.rel.150 ~ treat1 + new.ID, data = isumm1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.08313 -0.04784 -0.01006  0.03072  0.16487
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)  0.29213    0.02727  10.713 9.81e-10 ***
## treat1TH     0.12425    0.03340   3.720  0.00135 **
## treat1TS1    0.07063    0.03340   2.115  0.04720 *
## new.ID12    -0.04500    0.02727  -1.650  0.11450
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06679 on 20 degrees of freedom
## Multiple R-squared:  0.4543, Adjusted R-squared:  0.3725
## F-statistic: 5.551 on 3 and 20 DF,  p-value: 0.006143
```

Marginal means.

```
mmeans <- emmeans(m1, 'treat1')
mmeans
```

```
##  treat1 emmean     SE df lower.CL upper.CL
##  OSI     0.270 0.0236 20    0.220    0.319
##  TH      0.394 0.0236 20    0.345    0.443
##  TS1     0.340 0.0236 20    0.291    0.390
##
## Results are averaged over the levels of: new.ID
## Confidence level used: 0.95
```

Need name for export.

Tukey's test

```
mmeans11_12 <- emmeans(m1, 'treat1')
pairs(mmeans11_12)
```

```
##  contrast  estimate     SE df t.ratio p.value
##  OSI - TH   -0.1242 0.0334 20  -3.720  0.0037
##  OSI - TS1  -0.0706 0.0334 20  -2.115  0.1121
##  TH - TS1    0.0536 0.0334 20   1.606  0.2664
##
## Results are averaged over the levels of: new.ID
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
letters11_12 <- cld(object = mmeans11_12,
                    adjust = "Tukey",
                    Letters = letters,
                    alpha = 0.05)
```

```
## Note: adjust = "tukey" was changed to "sidak"
## because "tukey" is only appropriate for one set of pairwise comparisons
```

Order.

```
mmeans11_12 <- letters11_12[c(3, 2, 1), ]
```

And get a column for copy/paste into paper.

```
mmeans11_12$tabval <- paste(round(100 * mmeans11_12$emmean, 1), gsub(' ', '', mmeans11_12$.group))
```

9 and 10 driving speed may not have stats, may need it, section 3 supp Relative differences there

supp sec 4, bands hose distance, 13 and 14

chamber movement supp sec 5 trial 15

Then temperature stuff Add to supporting material