

Statistical analysis

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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)  
m1 <- lmer(e.rel.150 ~ dig.treat + (1|dig.ID) + (1|new.ID), data = isumm1)  
minotreat <- lmer(e.rel.150 ~ (1|dig.ID) + (1|new.ID), data = isumm1)  
minodig <- lmer(e.rel.150 ~ dig.treat + (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.MF1 dg.MFs dg.S-D d.S-D+a dg.S-S
## dig.tretAcid -0.058
## dig.treatDs -0.073 0.026
## dg.trtDs+ac -0.073 0.026 0.362
## dg.trtMF1qd -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.MF1 dg.MFs dg.S-D d.S-D+a dg.S-S
## dig.tretAcid -0.310
## dig.treatDs -0.248  0.306
## dg.trtDs+ac -0.248  0.306  0.348
## dg.trtMF1qd -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, minotreat, test = 'Chisq')
```

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

## Data: isumm1
## Models:
## minotreat: 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)
## minotreat   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(m1, minodig, test = 'Chisq')
```

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

## Data: isumm1
## Models:
## minodig: e.rel.150 ~ dig.treat + (1 | new.ID)
## m1: e.rel.150 ~ dig.treat + (1 | dig.ID) + (1 | new.ID)
##           npar      AIC      BIC logLik deviance Chisq Df Pr(>Chisq)
## minodig    12 -106.00 -80.668 64.999 -130.00
## m1          13 -147.36 -119.915 86.678 -173.36 43.359 1 4.557e-11 ***
## ---
## 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
```

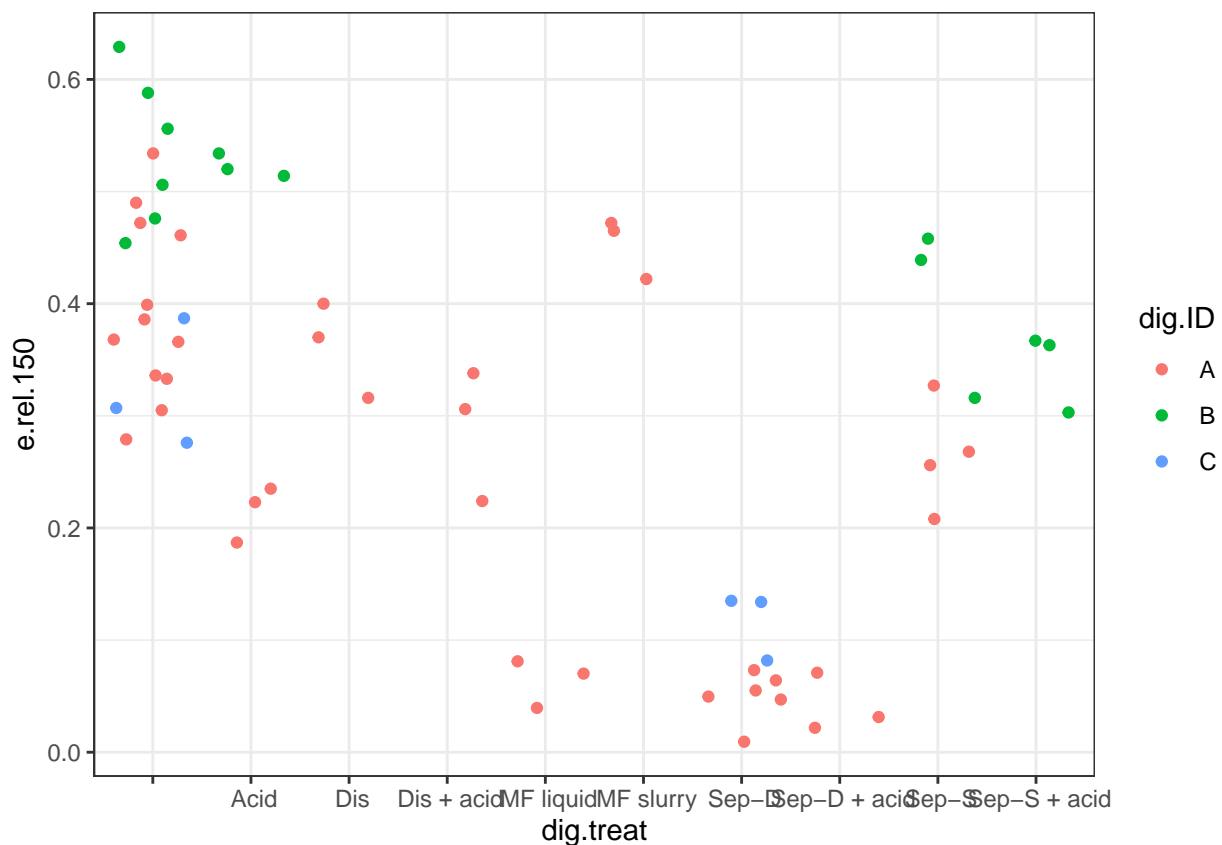
```
## m2    14 -152.17 -122.62 90.085  -180.17 6.8136  1  0.009047 **
```

```
## ---
```

```
## 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.

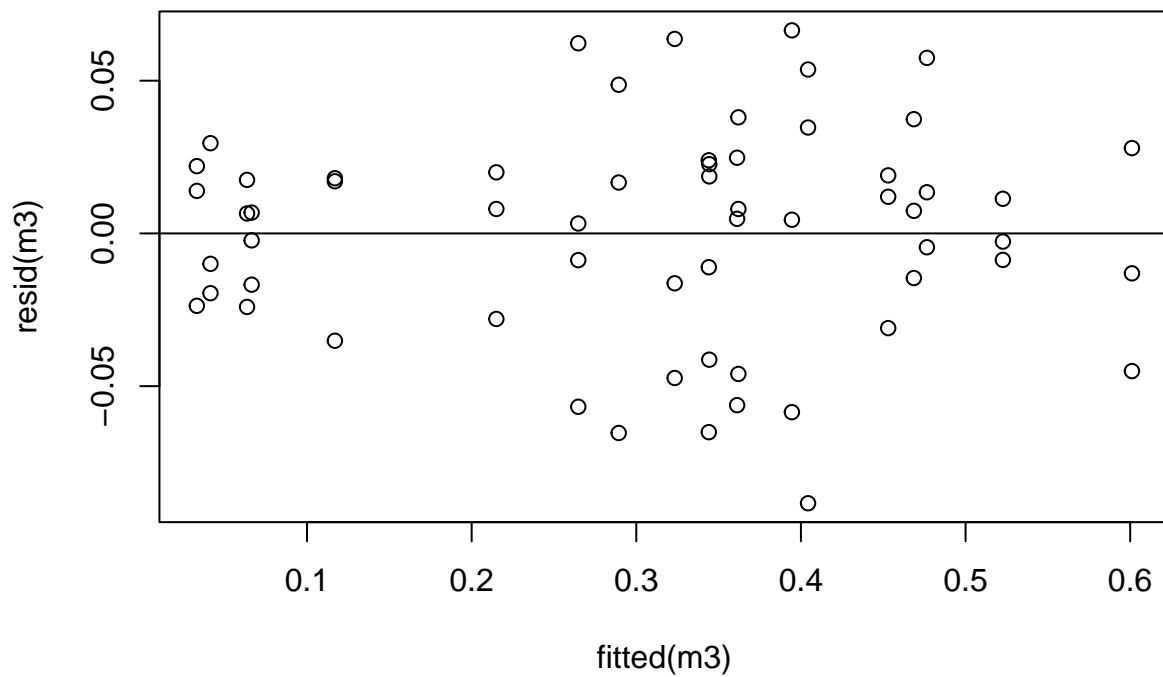
```
mmeans1_4 <- letters1_4[order(letters1_4$treat1), ]
```

And get a column for copy/paste into paper.

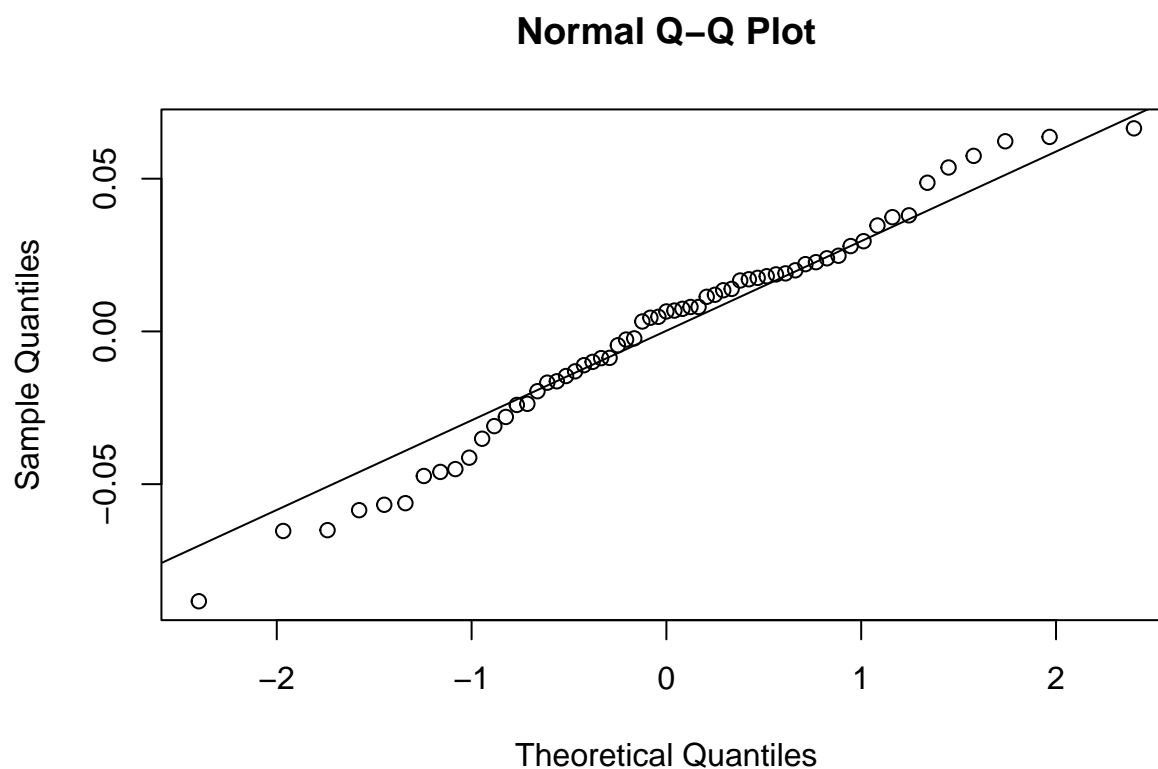
```
mmeans1_4$tabval <- paste(round(100 * mmeans1_4$emmean, 1), gsub(' ', '', mmeans1_4$.group))
```

Residuals.

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



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



Trials 5-10 (app tech on winter wheat)

Subset.

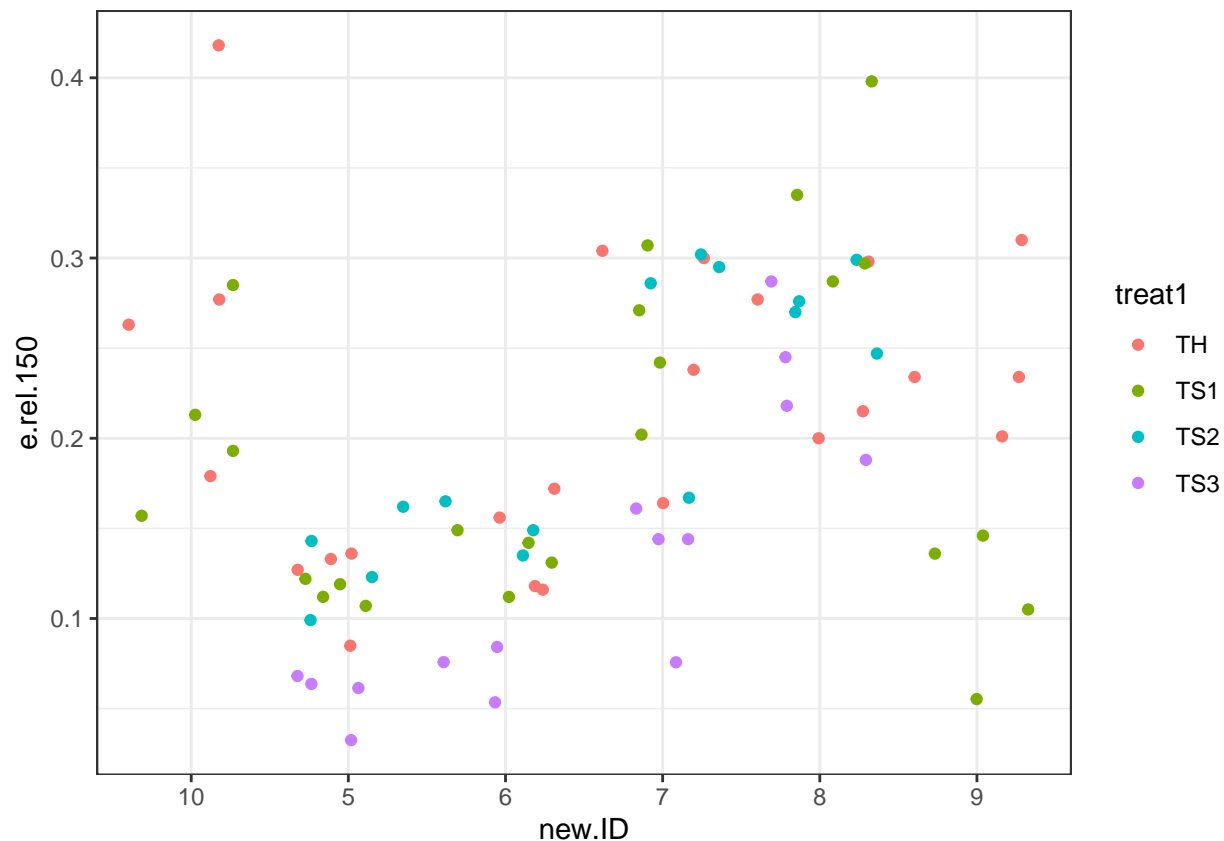
```
isumm1 <- droplevels(isumm[new.ID %in% c('5', '6', '7', '8', '9', '10') & !treat1 %in% c('TH-4', 'TS1-4')])

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))
```

Trials 9 and 10 for driving speed

Subset.

```
isumm1 <- isumm[new.ID %in% as.character(c(9, 10))]
```

Extract driving speed and application method.

```
table(isumm1$treat)
```

```
##
##      TH  TH-4    TS1 TS1-4
##       8     8     8     8
```

```
isumm1[, speed := factor('12', levels = c(4, 12))]
isumm1[grepl('-4', treat1), speed := '4']
```

```
isumm1[, app.mthd := factor(sub('-4', '', treat1), levels = c('TH', 'TS1'))]
```

```
table(isumm1[, .(new.ID, app.mthd, speed)])
```

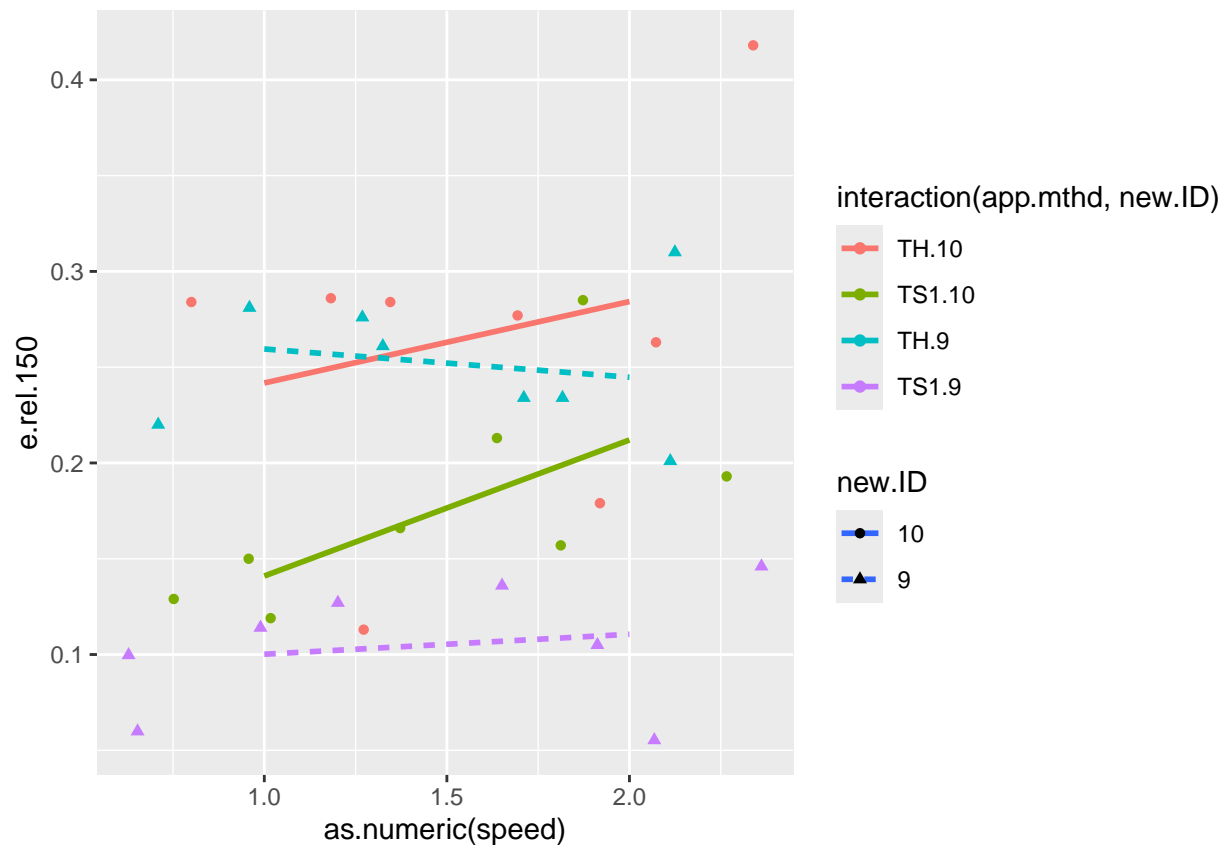
```
## , , speed = 4
##
##      app.mthd
## new.ID TH TS1
##     10  4  4
##     9   4  4
##
## , , speed = 12
##
##      app.mthd
## new.ID TH TS1
##     10  4  4
##     9   4  4
```

Completely crossed, perfectly balanced.

Plot.

```
ggplot(isumm1, aes(as.numeric(speed), e.rel.150, colour = interaction(app.mthd, new.ID), shape = new.ID))
  geom_smooth(method = lm, se = FALSE) +
  geom_jitter(height = 0)
```

```
## 'geom_smooth()' using formula = 'y ~ x'
```



Fit model.

```
m1 <- lm(log10(e.rel.150) ~ app.mthd * speed * new.ID, data = isumm1)
m2 <- aov(log10(e.rel.150) ~ (app.mthd + speed + new.ID)^2, data = isumm1)
m3 <- aov(e.rel.150 ~ (app.mthd + speed + new.ID)^2, data = isumm1)
```

```
summary(m1)
```

```
##
## Call:
## lm(formula = log10(e.rel.150) ~ app.mthd * speed * new.ID, data = isumm1)
##
## Residuals:
```

| ## | Min | 1Q | Median | 3Q | Max |
|----|----------|----------|---------|---------|---------|
| ## | -0.30094 | -0.04368 | 0.01029 | 0.09930 | 0.18706 |

```
##
## Coefficients:
```

| ## | Estimate | Std. Error | t value | Pr(> t) |
|------------------------|----------|------------|---------|--------------|
| ## (Intercept) | -0.64598 | 0.06731 | -9.598 | 1.09e-09 *** |
| ## app.mthdTS1 | -0.20844 | 0.09519 | -2.190 | 0.0385 * |
| ## speed12 | 0.08010 | 0.09519 | 0.841 | 0.4084 |
| ## new.ID9 | 0.05815 | 0.09519 | 0.611 | 0.5470 |
| ## app.mthdTS1:speed12 | 0.09049 | 0.13461 | 0.672 | 0.5079 |
| ## app.mthdTS1:new.ID9 | -0.21953 | 0.13461 | -1.631 | 0.1160 |
| ## speed12:new.ID9 | -0.10902 | 0.13461 | -0.810 | 0.4260 |

```
## app.mthdTS1:speed12:new.ID9 -0.03032    0.19037  -0.159   0.8748
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1346 on 24 degrees of freedom
## Multiple R-squared:  0.6785, Adjusted R-squared:  0.5847
## F-statistic: 7.236 on 7 and 24 DF,  p-value: 0.0001066
```

```
anova(m1)
```

```
## Analysis of Variance Table
##
## Response: log10(e.rel.150)
##
##          Df Sum Sq Mean Sq F value    Pr(>F)
## app.mthd      1  0.62960  0.62960  34.7448 4.419e-06 ***
## speed          1  0.03201  0.03201   1.7662  0.19635
## new.ID         1  0.10343  0.10343   5.7077  0.02510 *
## app.mthd:speed  1  0.01135  0.01135   0.6263  0.43647
## app.mthd:new.ID  1  0.11016  0.11016   6.0791  0.02122 *
## speed:new.ID    1  0.03084  0.03084   1.7020  0.20440
## app.mthd:speed:new.ID 1  0.00046  0.00046   0.0254  0.87477
## Residuals     24  0.43490  0.01812
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
drop1(m1, test = 'F')
```

```
## Single term deletions
##
## Model:
## log10(e.rel.150) ~ app.mthd * speed * new.ID
##
##          Df Sum of Sq    RSS      AIC F value Pr(>F)
## <none>                                0.43490 -121.55
## app.mthd:speed:new.ID  1  0.00045978  0.43536 -123.51  0.0254 0.8748
```

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

```
## Single term deletions
##
## Model:
## log10(e.rel.150) ~ (app.mthd + speed + new.ID)^2
##
##          Df Sum of Sq    RSS      AIC F value Pr(>F)
## <none>                                0.43536 -123.51
## app.mthd:speed  1  0.011349  0.44671 -124.69  0.6517 0.4271
## app.mthd:new.ID  1  0.110157  0.54551 -118.30  6.3257 0.0187 *
## speed:new.ID    1  0.030842  0.46620 -123.32  1.7710 0.1953
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

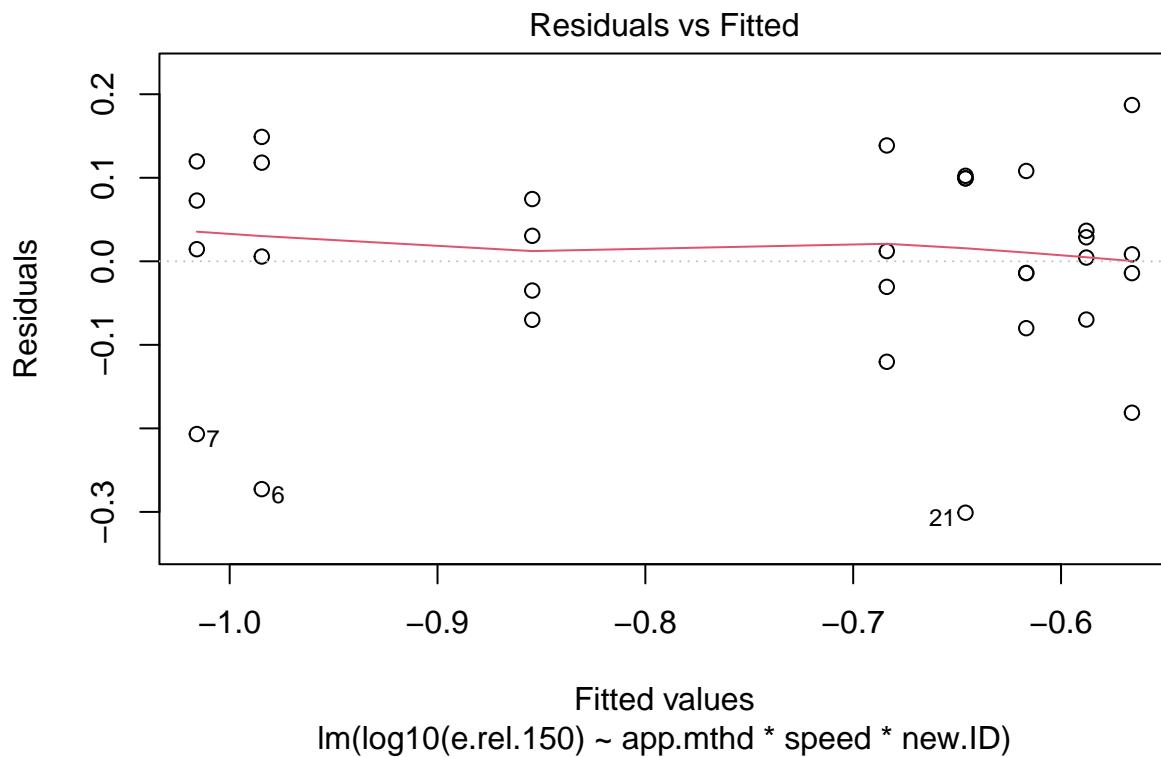
```
drop1(m3, test = 'F')
```

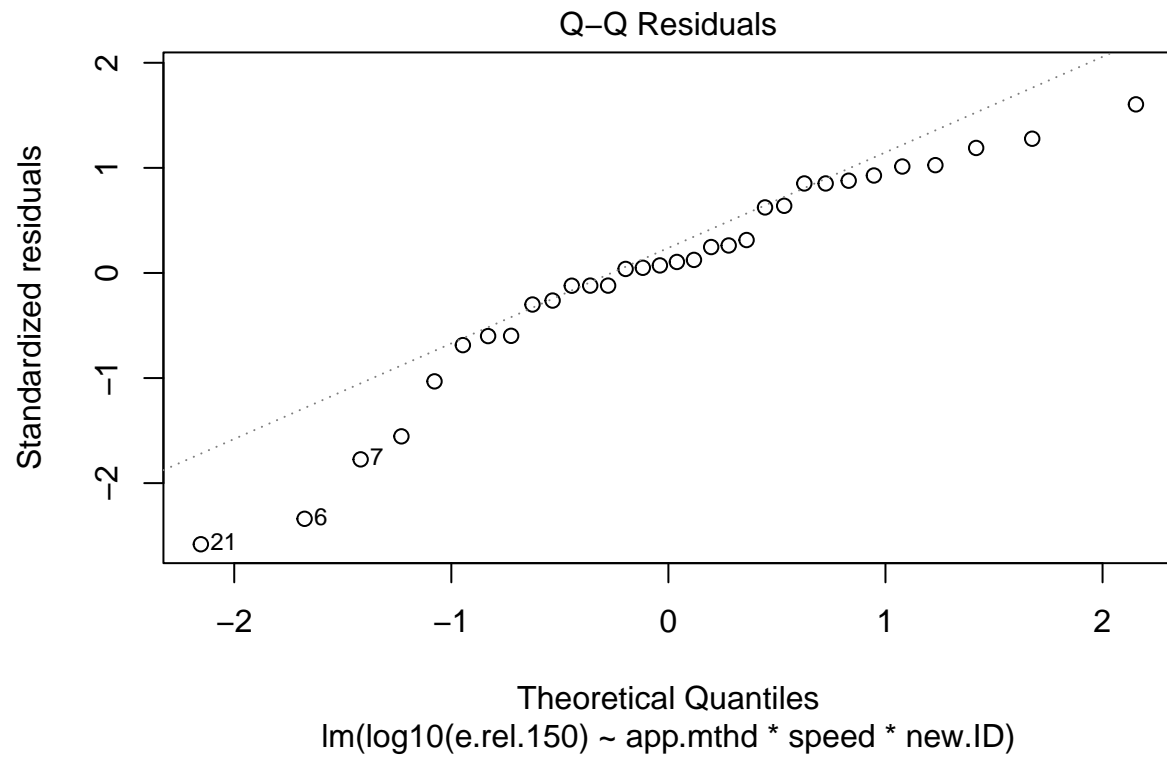
```
## Single term deletions
##
## Model:
## e.rel.150 ~ (app.mthd + speed + new.ID)^2
##           Df Sum of Sq    RSS    AIC F value Pr(>F)
## <none>                 0.077852 -178.60
## app.mthd:speed      1 0.0014405 0.079292 -180.01  0.4626 0.5027
## app.mthd:new.ID     1 0.0072631 0.085115 -177.74  2.3324 0.1393
## speed:new.ID        1 0.0069414 0.084793 -177.87  2.2290 0.1480
```

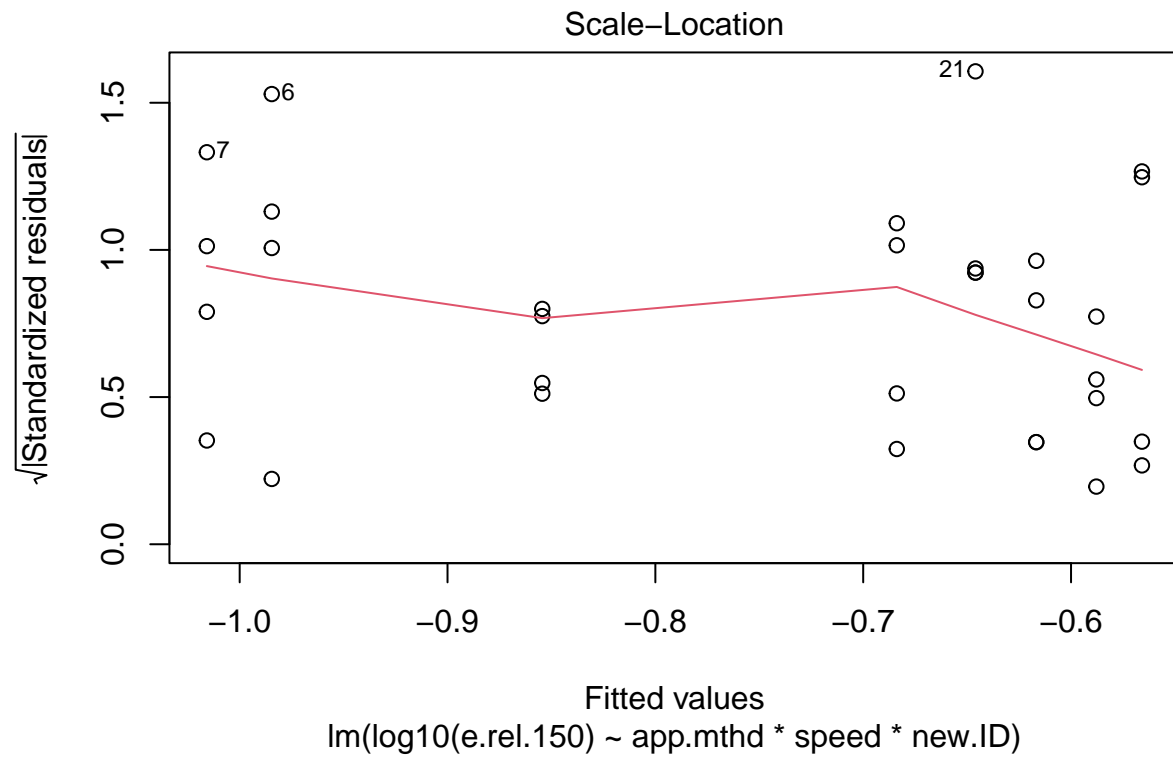
```
summary(m3, test = 'F')
```

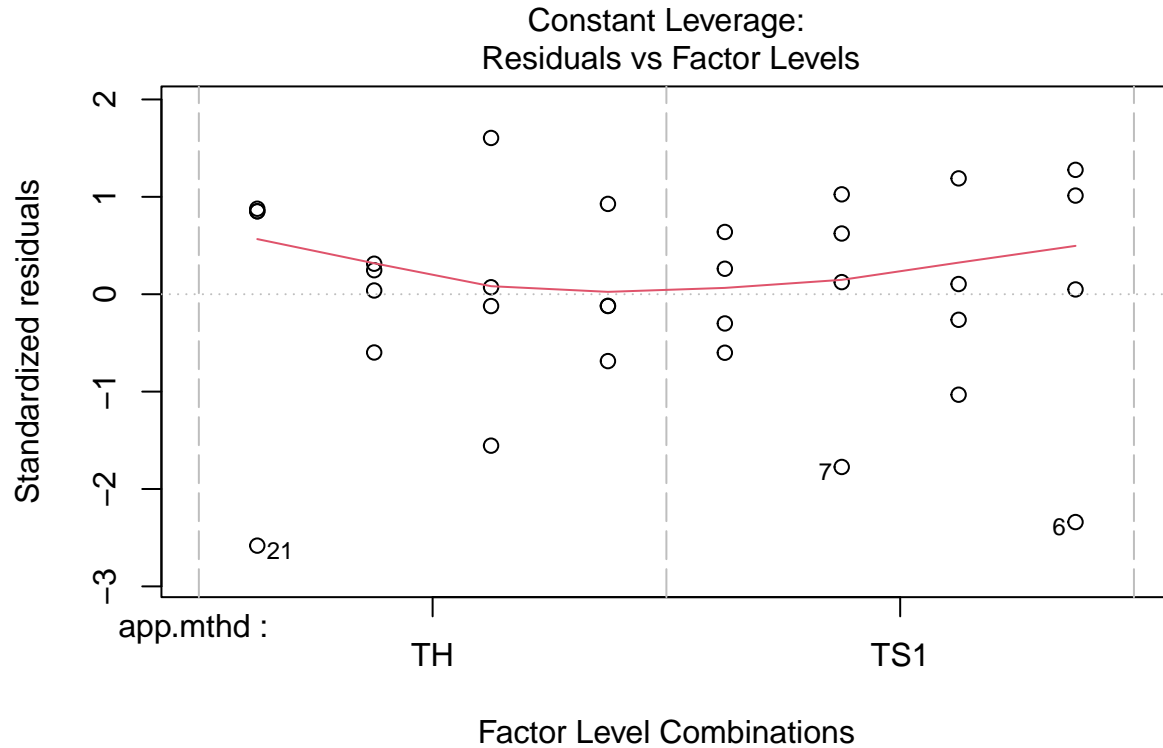
```
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## app.mthd      1 0.10882  0.10882   34.946 3.61e-06 ***
## speed          1 0.00596  0.00596    1.914  0.1788
## new.ID         1 0.01345  0.01345    4.320  0.0481 *
## app.mthd:speed 1 0.00144  0.00144    0.463  0.5027
## app.mthd:new.ID 1 0.00726  0.00726    2.332  0.1393
## speed:new.ID   1 0.00694  0.00694    2.229  0.1480
## Residuals     25 0.07785  0.00311
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(m1, ask = FALSE)
```









```
model.tables(m2, 'means')
```

```
## Tables of means
## Grand mean
##
## -0.7443791
##
## app.mthd
## app.mthd
##      TH      TS1
## -0.6041 -0.8846
##
## speed
## speed
##      4      12
## -0.7760 -0.7128
##
## new.ID
## new.ID
##     10     9
## -0.6875 -0.8012
##
## app.mthd:speed
##      speed
## app.mthd 4      12
```

```
##      TH  -0.6169 -0.5913
##      TS1 -0.9351 -0.8342
##
## app.mthd:new.ID
##      new.ID
## app.mthd 10      9
##      TH  -0.6059 -0.6023
##      TS1 -0.7691 -1.0002
##
## speed:new.ID
##      new.ID
## speed 10      9
##      4  -0.7502 -0.8018
##      12 -0.6249 -0.8007
```

More useful means.

```
isumm1[, .(mn = mean(e.rel.150), sd = sd(e.rel.150)), by = .(new.ID, app.mthd, speed)]
```

```
##      new.ID app.mthd speed      mn      sd
##      <char>  <fctr> <fctr>    <num>    <num>
## 1:      9      TH     12 0.244750 0.04619794
## 2:      9      TS1     12 0.110575 0.04077486
## 3:      9      TS1      4 0.100150 0.02905747
## 4:      9      TH      4 0.259500 0.02767068
## 5:     10      TS1      4 0.141000 0.02108712
## 6:     10      TH      4 0.241750 0.08583851
## 7:     10      TH     12 0.284250 0.09911399
## 8:     10      TS1     12 0.212000 0.05390114
```

Trials 13 and 14 for hose distance effect

Subset.

```
isumm1 <- isumm[new.ID %in% as.character(c(13, 14))]
```

Extract separation status and hose distance.

```
table(isumm1$treat)
```

```
##
## Sep25 Sep30 Un12 UN25 Un30
##      6      6      6      6      6
```

```
class(isumm1)
```

```
## [1] "data.table" "data.frame"
```



```

isumm1[, treat1 := tolower(treat1)]
isumm1[, distancef := factor(sub('sep|un', '', treat1))]
isumm1[, distancen := as.numeric(sub('sep|un', '', treat1))]
isumm1[, sep := factor(sub('[0-9]+$', '', treat1))]

```

```

table(isumm1[, .(new.ID, sep, distancef)])

```

```

## , , distancef = 12
##
##      sep
## new.ID sep un
##    13   0  3
##    14   0  3
##
## , , distancef = 25
##
##      sep
## new.ID sep un
##    13   3  3
##    14   3  3
##
## , , distancef = 30
##
##      sep
## new.ID sep un
##    13   3  3
##    14   3  3

```

Subset is completely crossed, perfectly balanced. But un has an additional distance of 12 cm.

Plot.

```

ggplot(isumm1, aes(as.numeric(distancen), e.rel.150, colour = interaction(sep, new.ID), shape = new.ID,
  geom_smooth(method = lm, se = FALSE) +
  geom_point(height = 0)

```

```

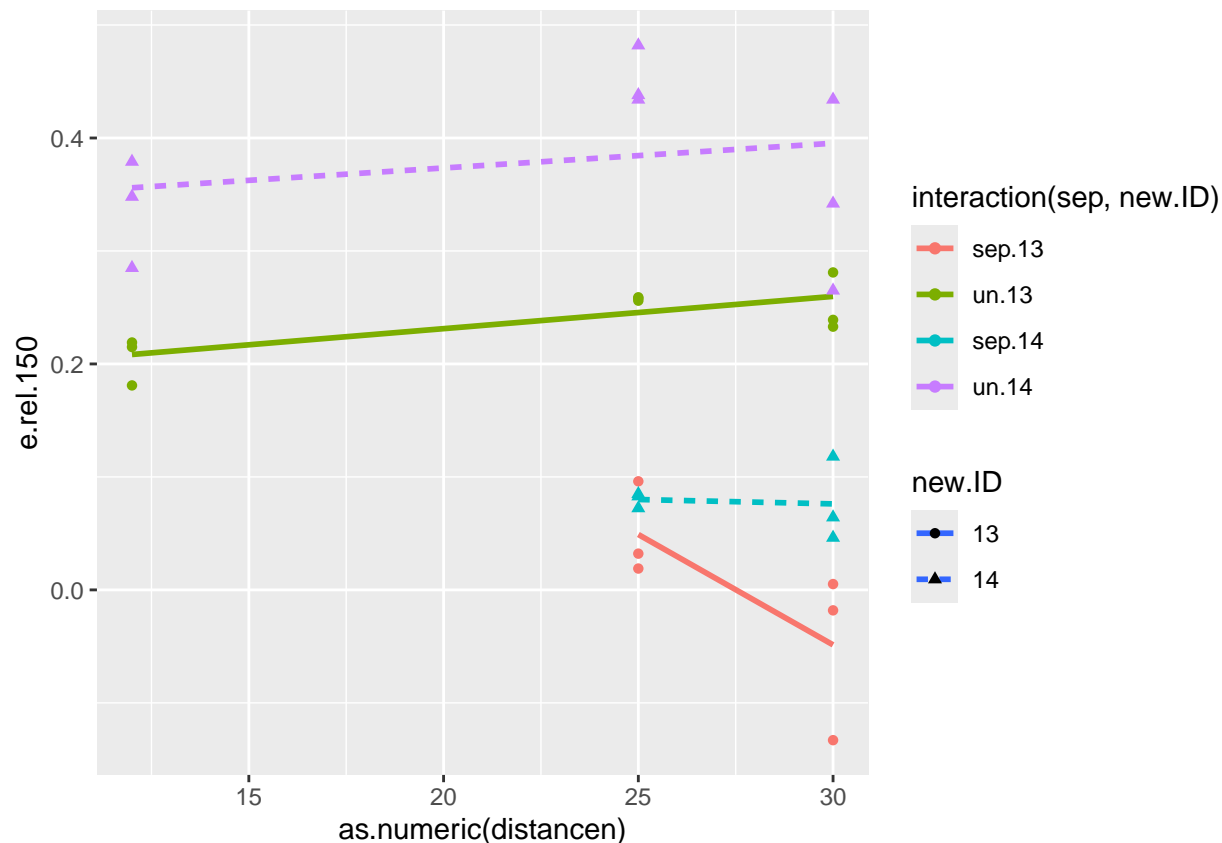
## Warning in geom_point(height = 0): Ignoring unknown parameters: 'height'

```

```

## 'geom_smooth()' using formula = 'y ~ x'

```



Hmm, might be some interactions. Fit model.

```
m1 <- lm(e.rel.150 ~ sep * distancen * new.ID, data = isumm1)
m2 <- lm(e.rel.150 ~ (sep + distancen + new.ID)^2, data = isumm1)
m2b <- lm(e.rel.150 ~ (sep + distancen + new.ID)^2, data = isumm1, subset = sep != 'sep' | new.ID != 13)
```

```
summary(m1)
```

```
##
## Call:
## lm(formula = e.rel.150 ~ sep * distancen * new.ID, data = isumm1)
##
## Residuals:
```

| ## | Min | 1Q | Median | 3Q | Max |
|----|-----------|-----------|----------|----------|----------|
| ## | -0.130344 | -0.025284 | 0.005761 | 0.028678 | 0.097605 |

```
##
## Coefficients:
```

| ## | Estimate | Std. Error | t value | Pr(> t) |
|-----------------------|-----------|------------|---------|----------|
| ## (Intercept) | 0.537433 | 0.239393 | 2.245 | 0.0352 * |
| ## sepun | -0.363325 | 0.245634 | -1.479 | 0.1533 |
| ## distancen | -0.019536 | 0.008669 | -2.253 | 0.0345 * |
| ## new.ID14 | -0.438100 | 0.338553 | -1.294 | 0.2091 |
| ## sepun:distancen | 0.022392 | 0.008978 | 2.494 | 0.0206 * |
| ## sepun:new.ID14 | 0.593641 | 0.347379 | 1.709 | 0.1015 |
| ## distancen:new.ID14 | 0.018763 | 0.012260 | 1.530 | 0.1402 |

```
## sepun:distancen:new.ID14 -0.019429  0.012696  -1.530  0.1402
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05309 on 22 degrees of freedom
## Multiple R-squared:  0.9129, Adjusted R-squared:  0.8851
## F-statistic: 32.93 on 7 and 22 DF,  p-value: 3.107e-10
```

```
anova(m1)
```

```
## Analysis of Variance Table
##
## Response: e.rel.150
##
##          Df Sum Sq Mean Sq F value    Pr(>F)
## sep          1  0.52136  0.52136  184.9781 3.464e-12 ***
## distancen    1  0.00309  0.00309   1.0954  0.30663
## new.ID       1  0.10014  0.10014  35.5289 5.342e-06 ***
## sep:distancen 1  0.01124  0.01124   3.9880  0.05834 .
## sep:new.ID    1  0.00710  0.00710   2.5182  0.12681
## distancen:new.ID 1  0.00012  0.00012   0.0411  0.84127
## sep:distancen:new.ID 1  0.00660  0.00660   2.3416  0.14021
## Residuals    22  0.06201  0.00282
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
drop1(m1, test = 'F')
```

```
## Single term deletions
##
## Model:
## e.rel.150 ~ sep * distancen * new.ID
##
##          Df Sum of Sq    RSS    AIC F value Pr(>F)
## <none>                0.062006 -169.45
## sep:distancen:new.ID  1 0.0065998 0.068606 -168.42  2.3416 0.1402
```

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

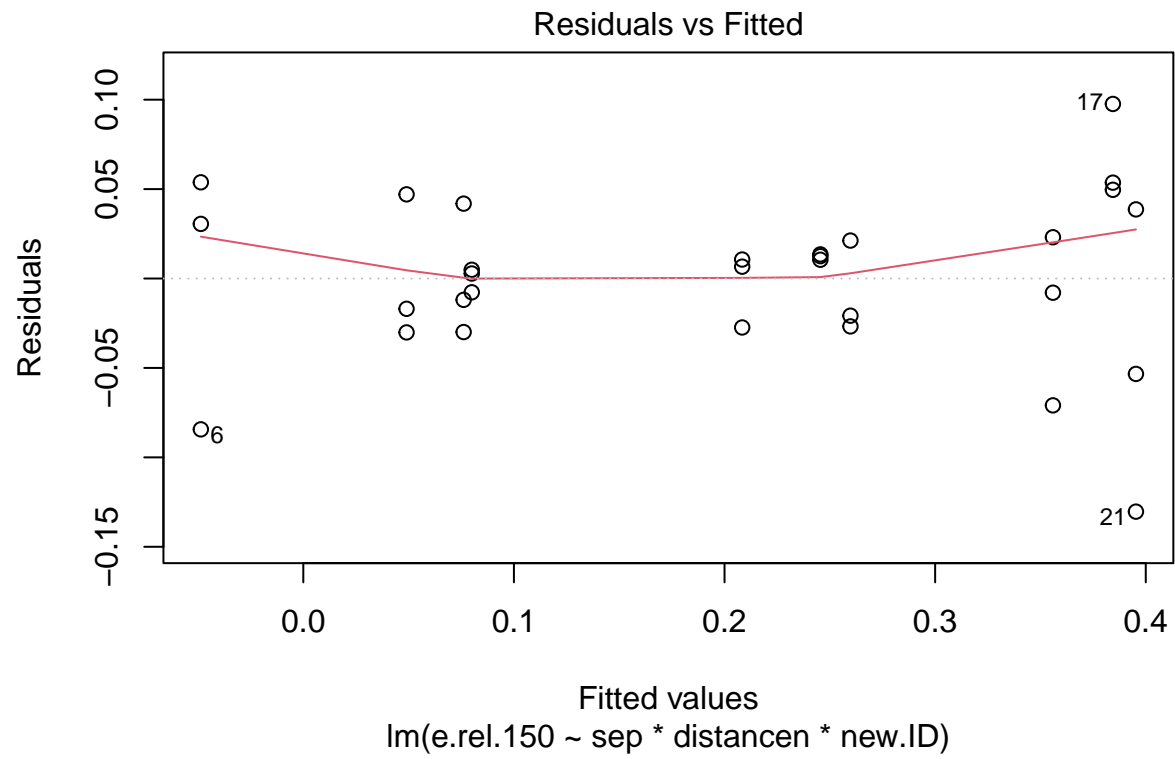
```
## Single term deletions
##
## Model:
## e.rel.150 ~ (sep + distancen + new.ID)^2
##
##          Df Sum of Sq    RSS    AIC F value  Pr(>F)
## <none>                0.068606 -168.42
## sep:distancen    1 0.0112402 0.079847 -165.87  3.7682 0.06459 .
## sep:new.ID       1 0.0067105 0.075317 -167.62  2.2497 0.14725
## distancen:new.ID 1 0.0001157 0.068722 -170.37  0.0388 0.84557
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

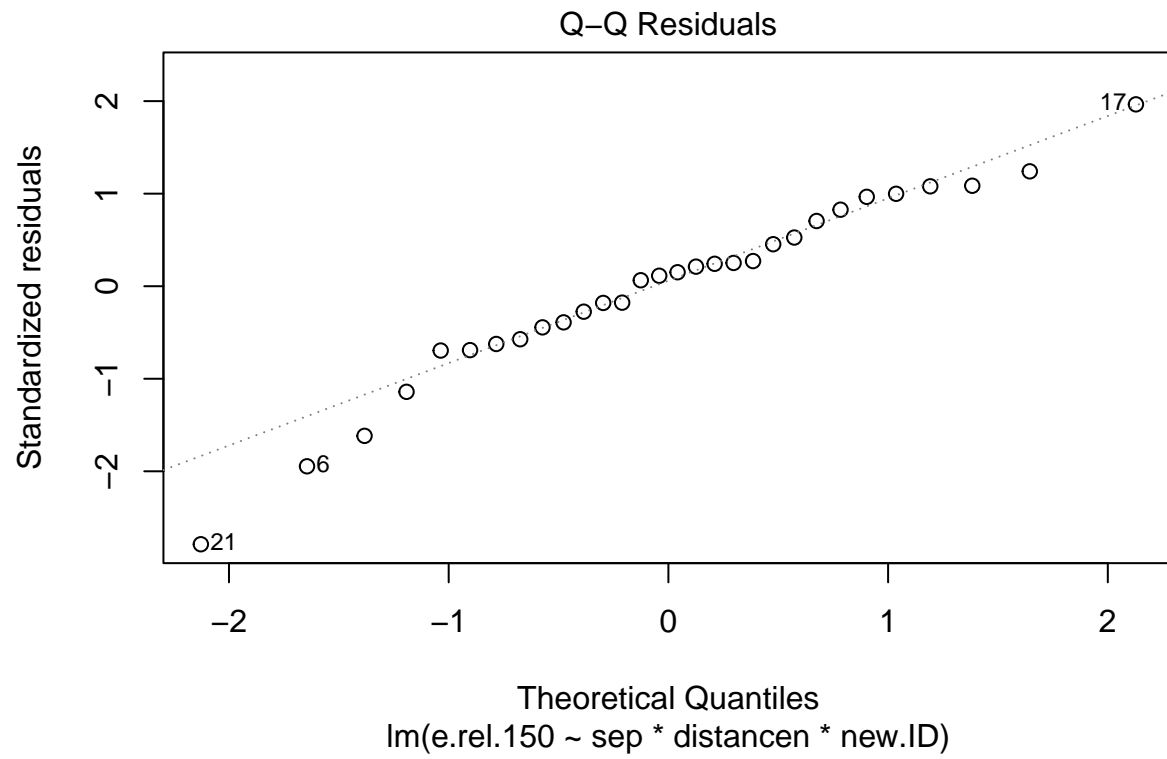
```
summary(m2b)
```

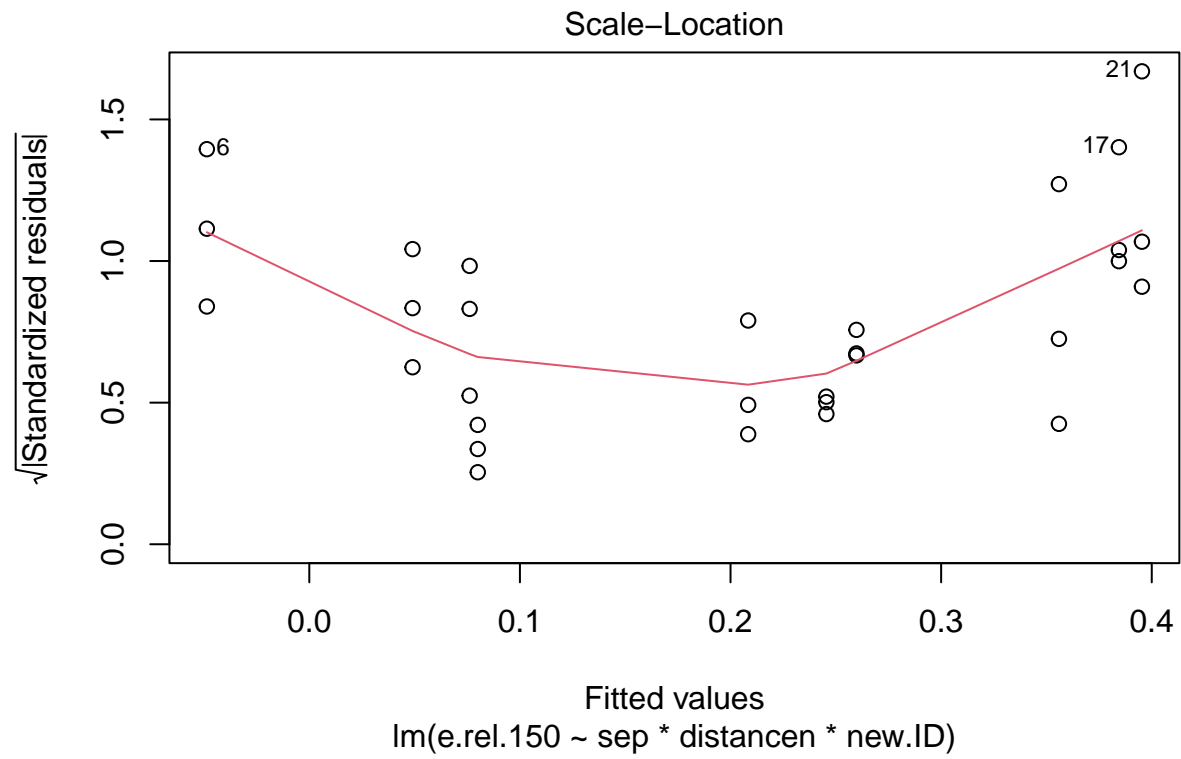
```
##
## Call:
## lm(formula = e.rel.150 ~ (sep + distancen + new.ID)^2, data = isumm1,
##     subset = sep != "sep" | new.ID != 13)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.130344 -0.022284  0.005761  0.021680  0.097605
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.0562079  0.2439600  -0.230   0.8204
## sepun         0.2303160  0.2380613   0.967   0.3461
## distancen    -0.0001073  0.0089899  -0.012   0.9906
## new.ID14      0.1555412  0.0754094   2.063   0.0539 .
## sepun:distancen  0.0029632  0.0087010   0.341   0.7374
## sepun:new.ID14      NA         NA         NA      NA
## distancen:new.ID14 -0.0006660  0.0031971  -0.208   0.8373
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05145 on 18 degrees of freedom
## Multiple R-squared:  0.8752, Adjusted R-squared:  0.8405
## F-statistic: 25.24 on 5 and 18 DF,  p-value: 1.516e-07
```

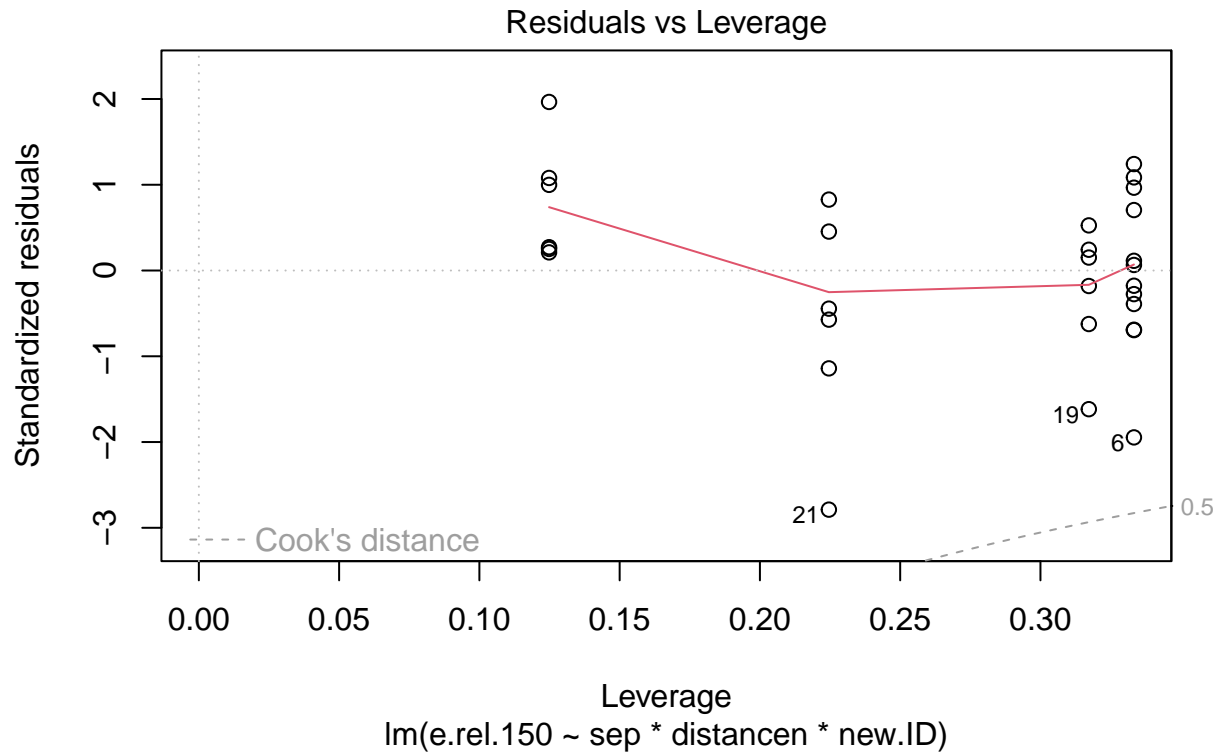
No clear distance effects, marginal interaction evidence, but all related to those negative values.

```
plot(m1, ask = FALSE)
```









Means.

```
isumm1[, .(mn = mean(e.rel.150), sd = sd(e.rel.150)), by = .(new.ID, sep, distancen)]
```

| ## | new.ID | sep | distancen | mn | sd |
|--------|--------|--------|-----------|-------------|-------------|
| ## | <char> | <fctr> | <fctr> | <num> | <num> |
| ## 1: | 13 | un | 30 | 0.25100000 | 0.026153394 |
| ## 2: | 13 | un | 25 | 0.25766667 | 0.001527525 |
| ## 3: | 13 | sep | 25 | 0.04903333 | 0.041291807 |
| ## 4: | 13 | sep | 30 | -0.04864667 | 0.073972093 |
| ## 5: | 13 | un | 12 | 0.20500000 | 0.020880613 |
| ## 6: | 14 | un | 12 | 0.33733333 | 0.047899200 |
| ## 7: | 14 | un | 25 | 0.45133333 | 0.026633312 |
| ## 8: | 14 | sep | 30 | 0.07613333 | 0.037357909 |
| ## 9: | 14 | sep | 25 | 0.08000000 | 0.006750556 |
| ## 10: | 14 | un | 30 | 0.34700000 | 0.084610874 |

Other stuff

I still need to sort this stuff out!

supp sec 4, bands hose distance, 13 and 14

chamber movement supp sec 5 trial 15

Then temperature stuff Add to supporting material