

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)  
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 interaction likelihood ratio test.

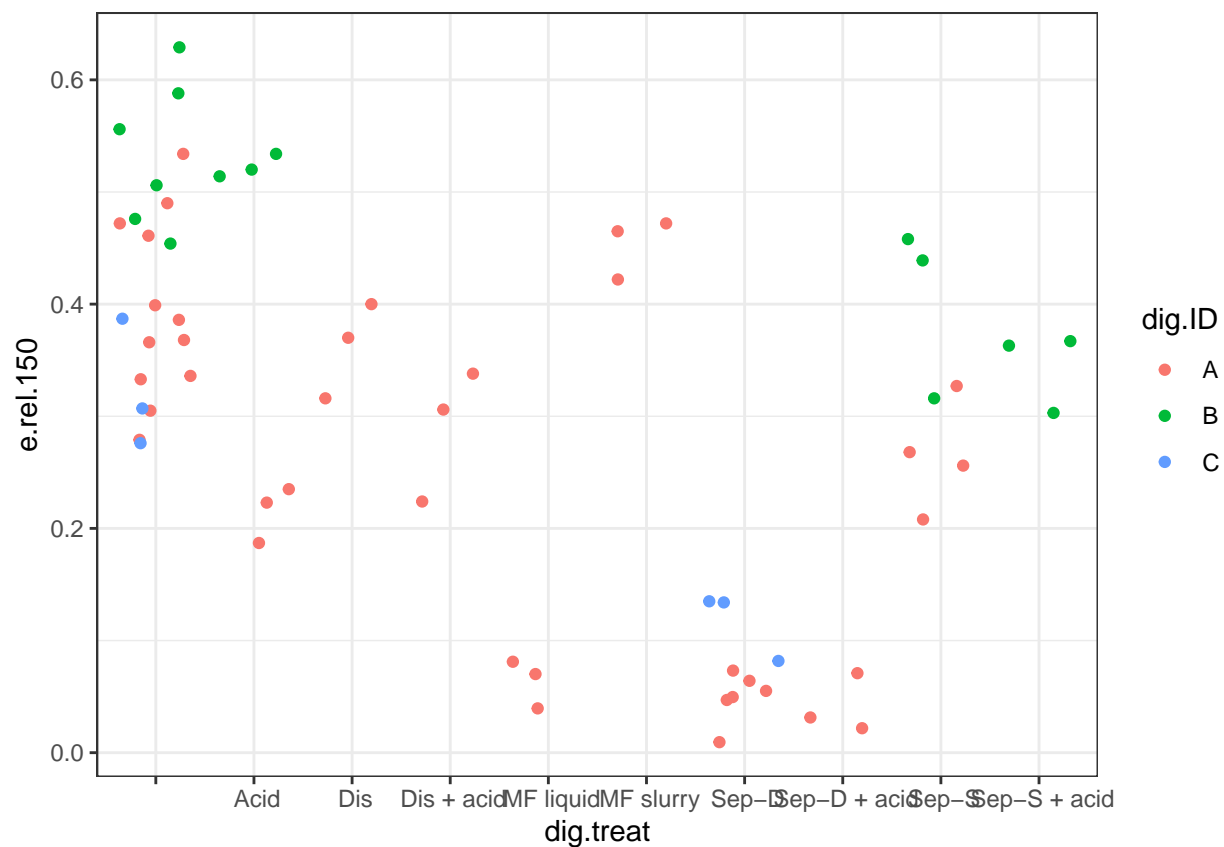
```
anova(m2, m1, test = 'Chisq')
```

```
## 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.

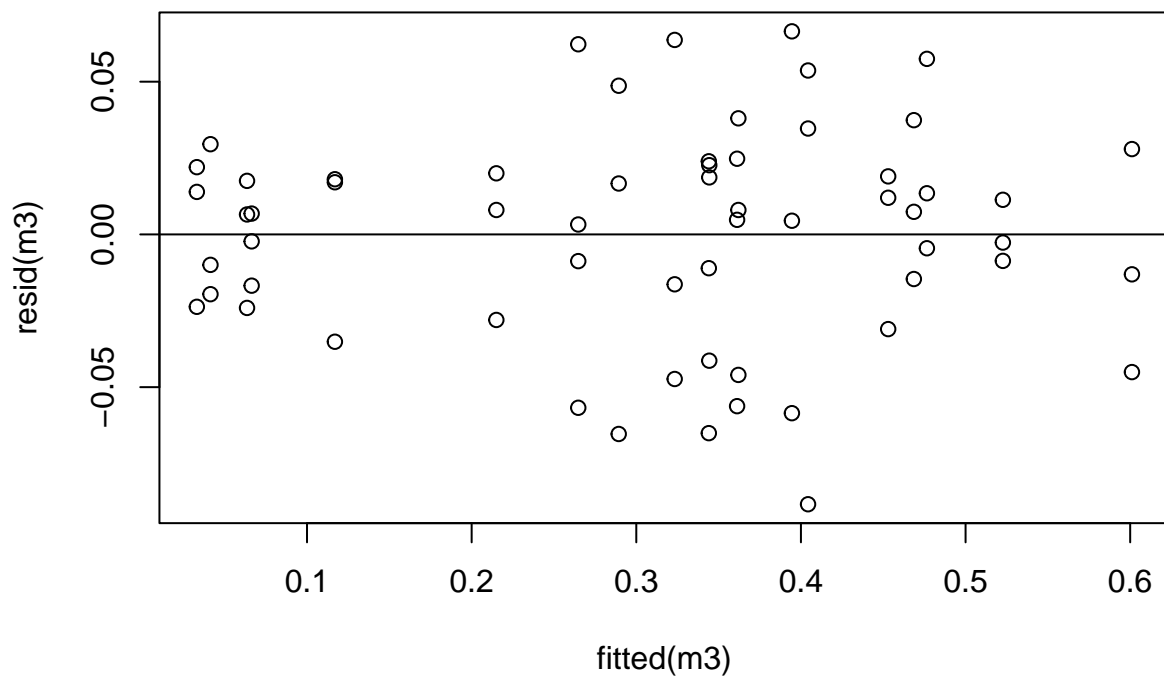
```
mmeans1_4 <- letters1_4[order(letters1_4$treat1), ]
```

And get a column for copy/paste into paper.

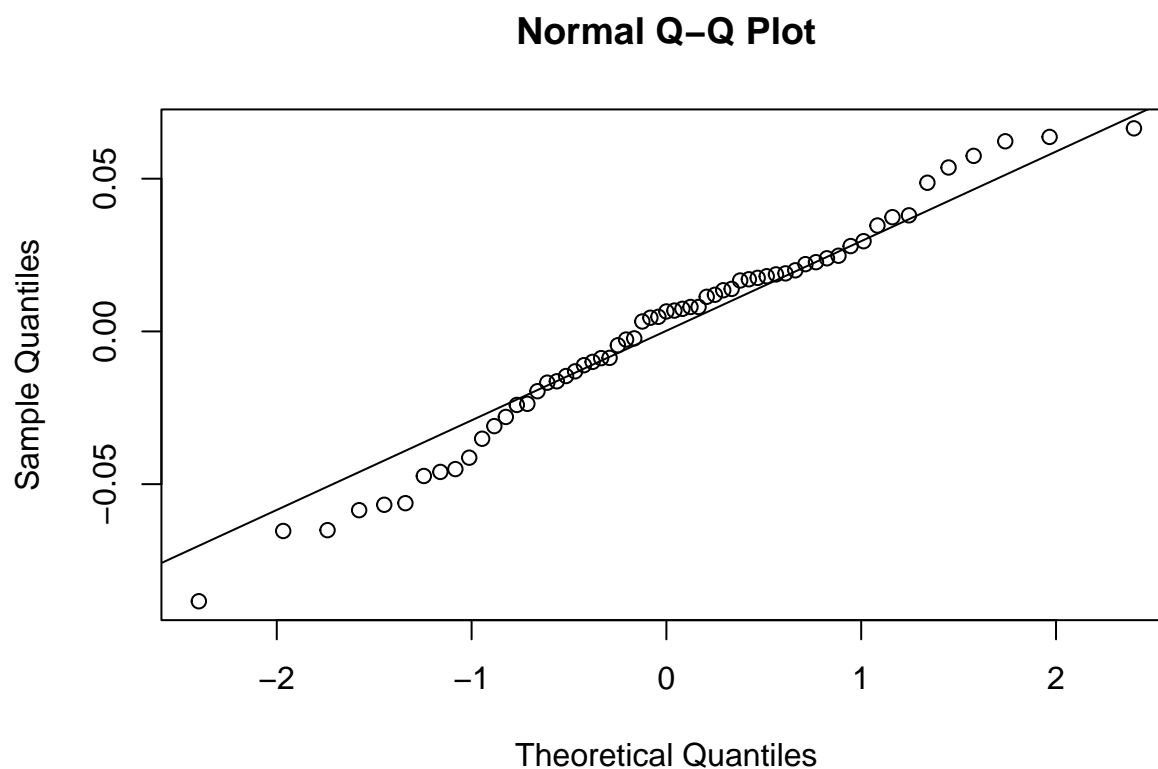
```
mmeans1_4$tabval <- paste(100 * signif(mmeans1_4$emmean, 3), gsub(' ', '', mmeans1_4$.group))
```

Residuals.

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



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



Trials 5-10 (app tech on winter wheat)

Subset.

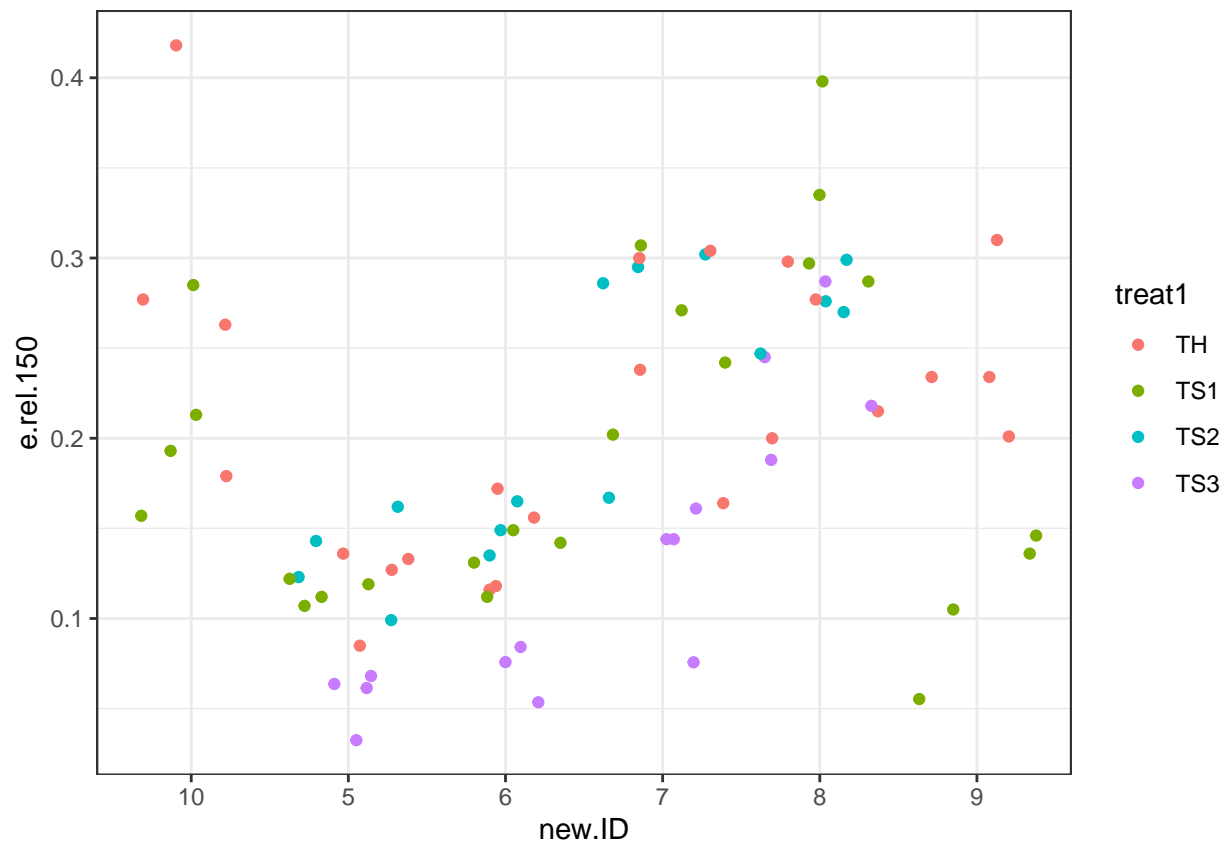
```
isumm1 <- droplevels(isumm[new.ID %in% c('5', '6', '7', '8', '9', '10') & !treat1 %in% c('TH-4', 'TS1-4')])

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$tabval <- paste(100 * signif(mmeans5_10$emmean, 3), 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
```

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