

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
```

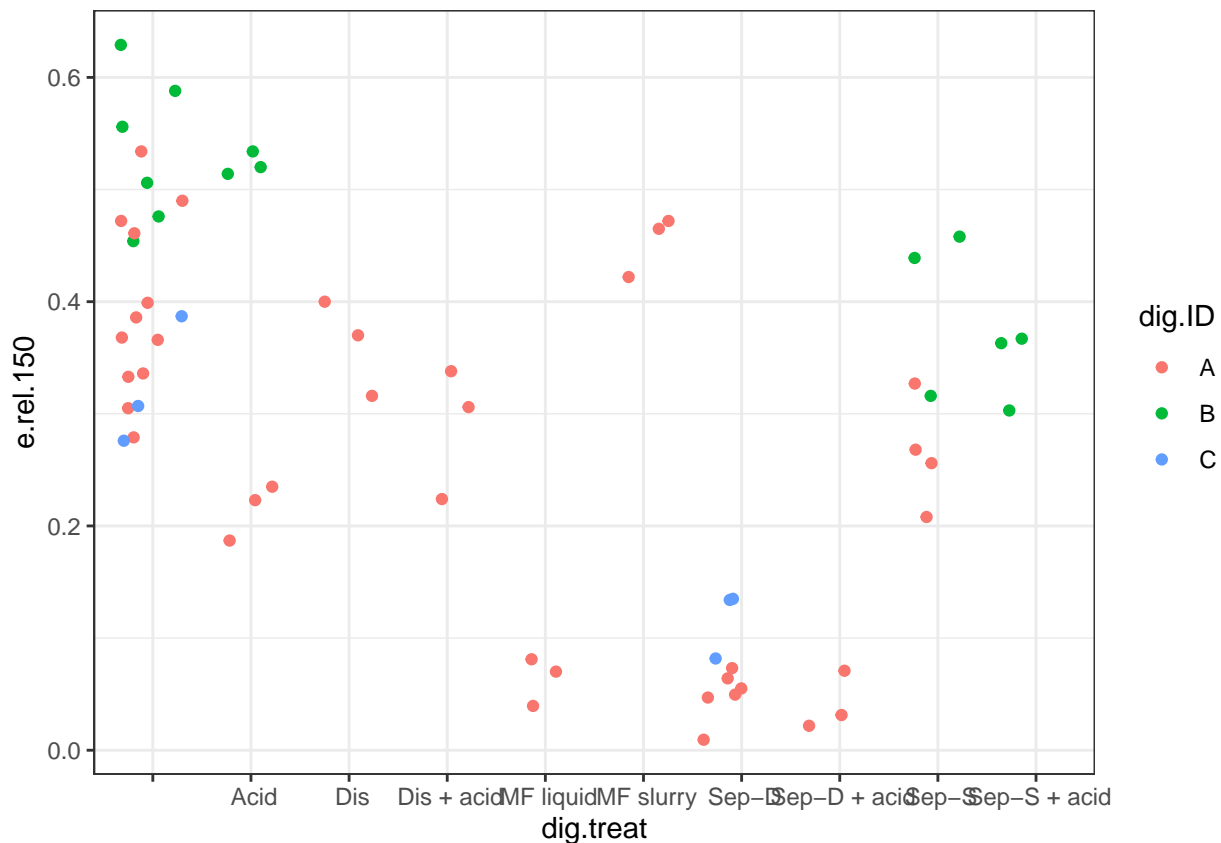
```
## m2    14 -152.17 -122.62 90.085  -180.17 6.8136  1  0.009047 **
```

```
## ---
```

```
## 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.

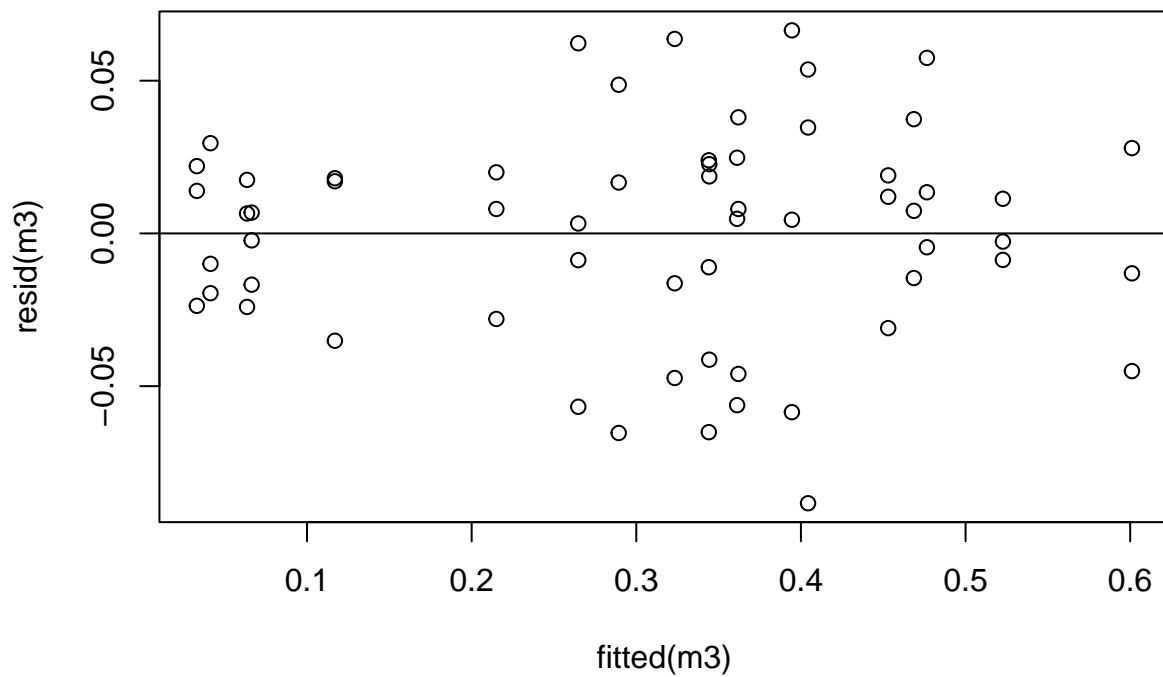
```
mmeans1_4 <- letters1_4[order(letters1_4$treat1), ]
```

And get a column for copy/paste into paper.

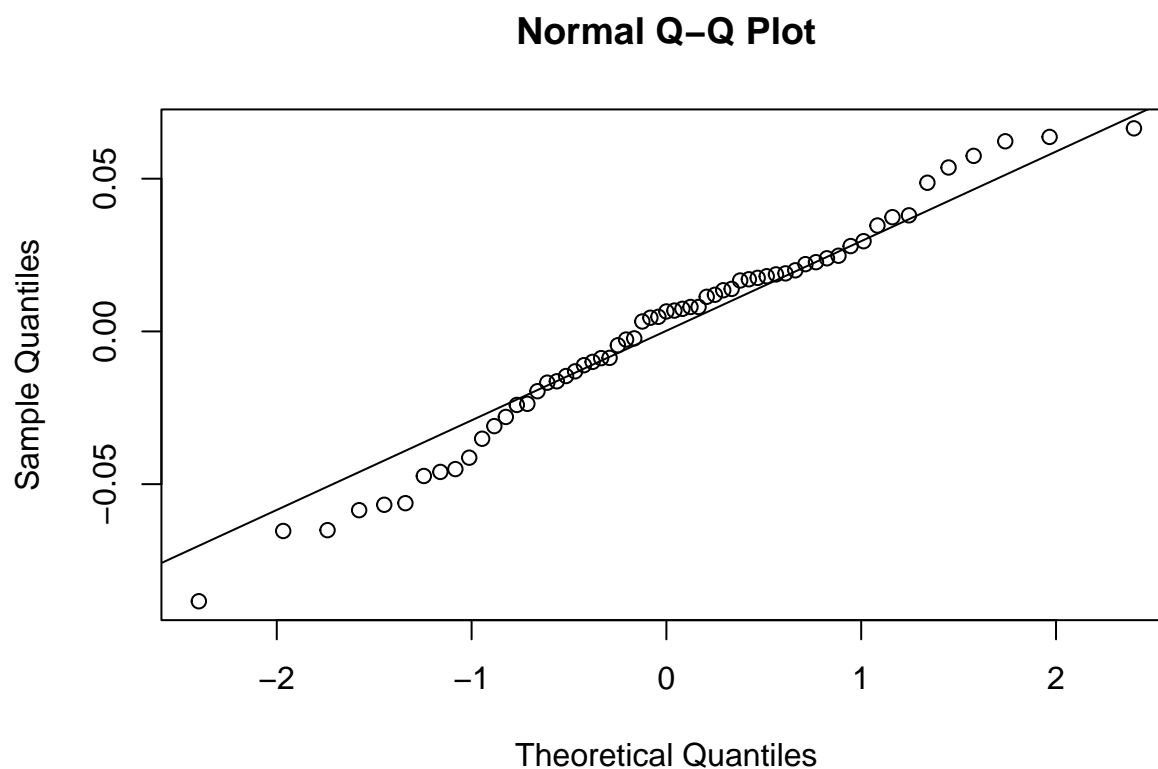
```
mmeans1_4$tabval <- paste(round(100 * mmeans1_4$emmean, 1), gsub(' ', '', mmeans1_4$.group))
```

Residuals.

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



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



Trials 5-10 (app tech on winter wheat)

Subset.

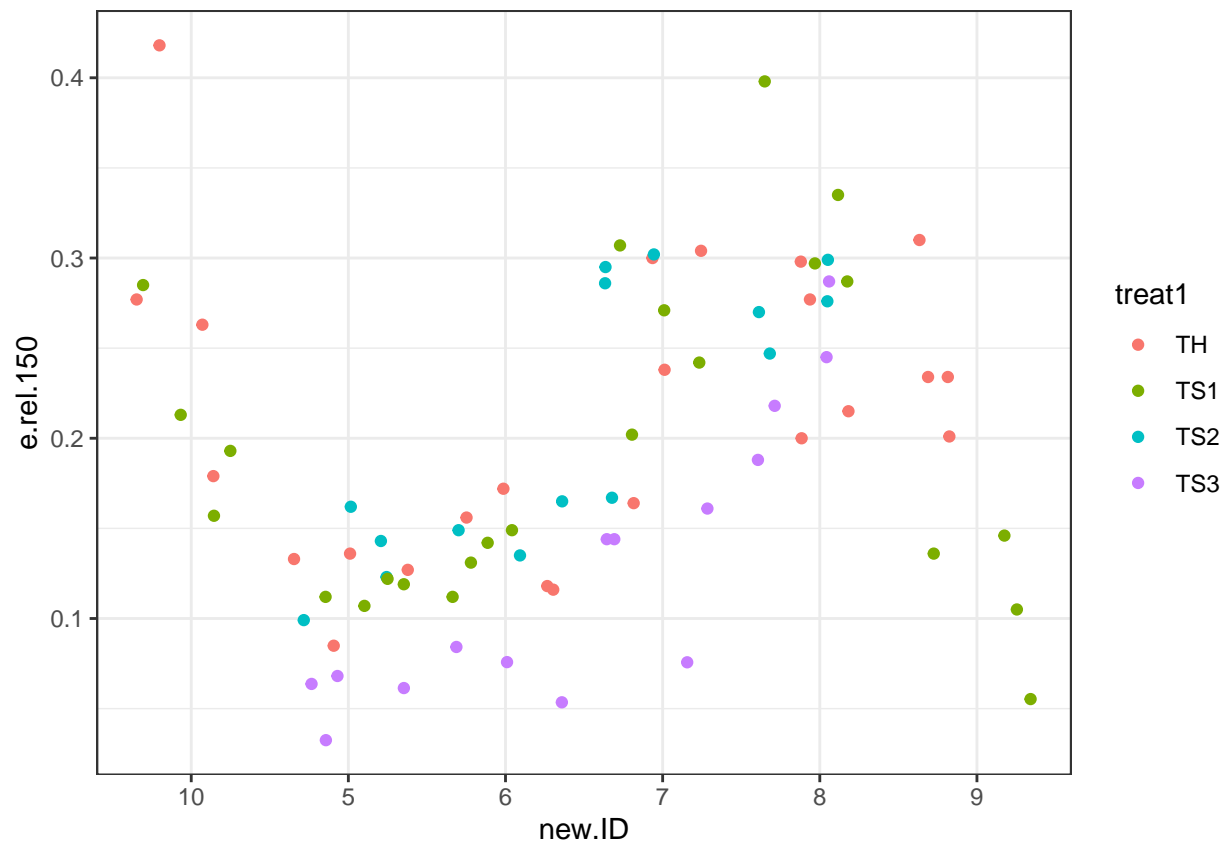
```
isumm1 <- droplevels(isumm[new.ID %in% c('5', '6', '7', '8', '9', '10') & !treat1 %in% c('TH-4', 'TS1-4')])

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)])
```

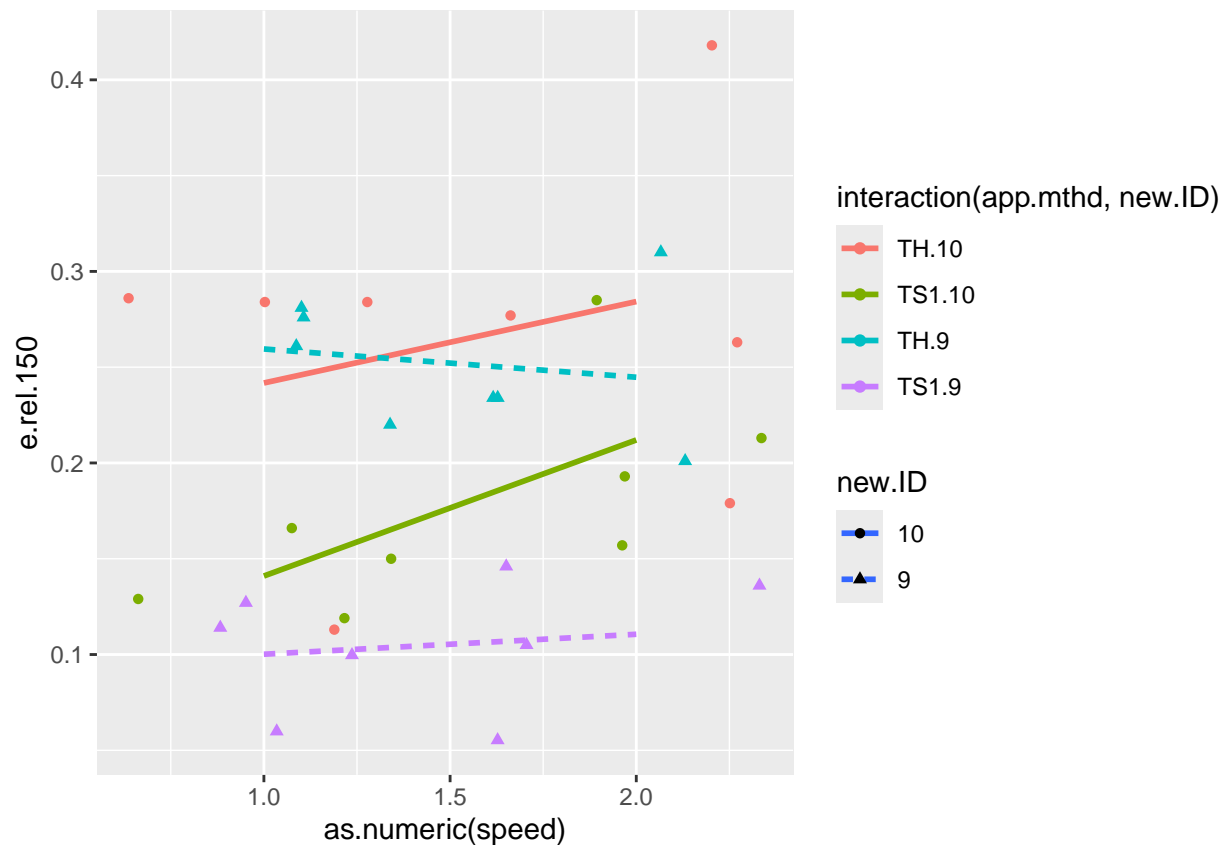
```
## , , speed = 4
##
##      app.mthd
## new.ID TH TS1
##     10  4  4
##     9   4  4
##
## , , speed = 12
##
##      app.mthd
## new.ID TH TS1
##     10  4  4
##     9   4  4
```

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
```

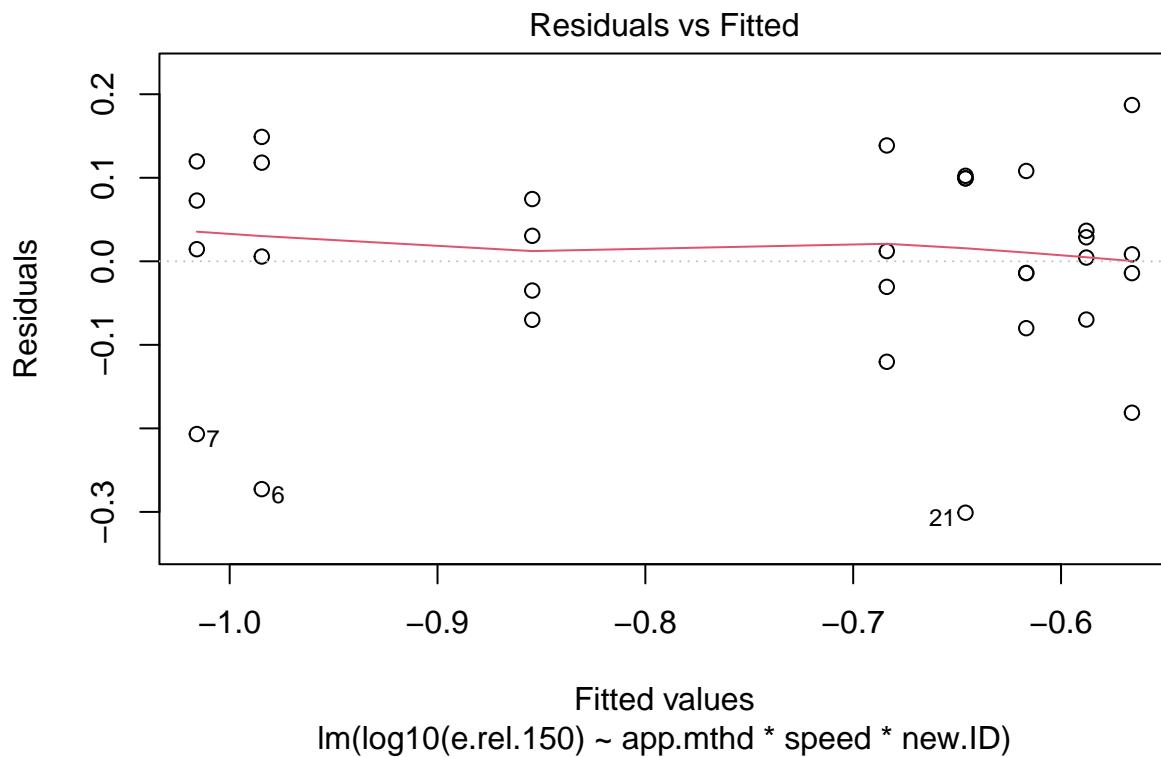
```
drop1(m3, test = 'F')
```

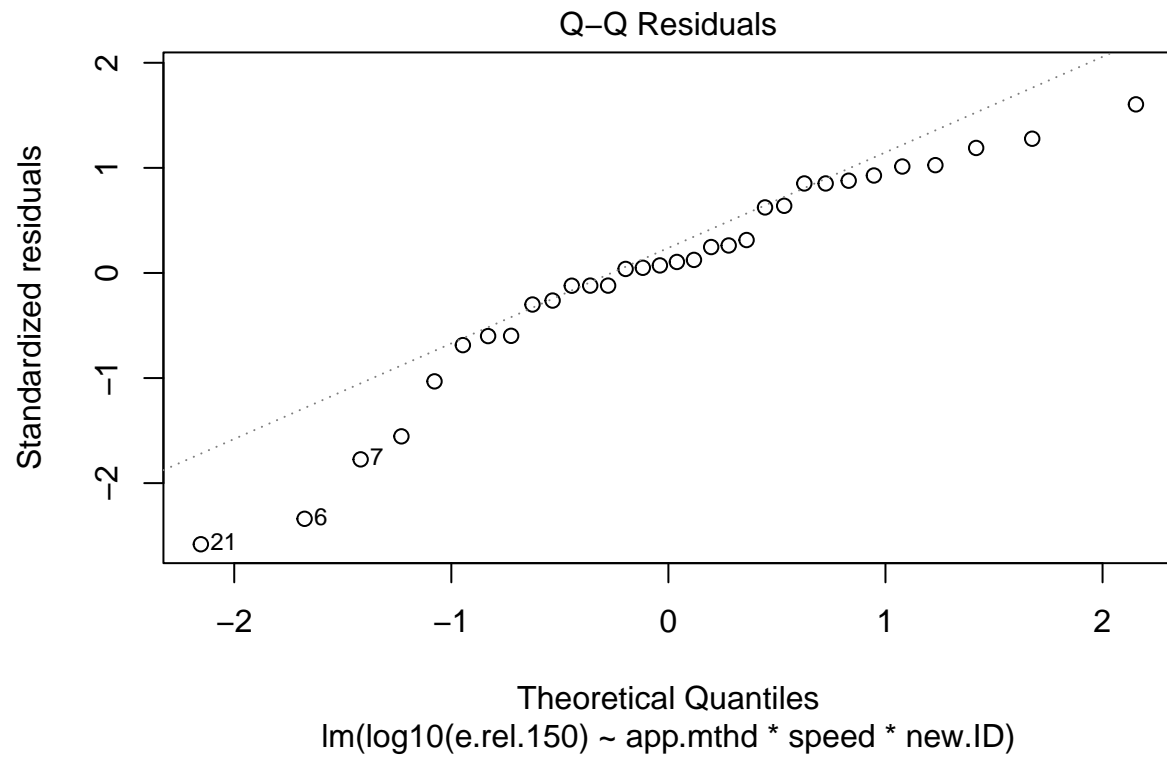
```
## Single term deletions
##
## Model:
## e.rel.150 ~ (app.mthd + speed + new.ID)^2
##           Df Sum of Sq      RSS      AIC F value Pr(>F)
## <none>                0.077852 -178.60
## app.mthd:speed      1 0.0014405 0.079292 -180.01   0.4626 0.5027
## app.mthd:new.ID     1 0.0072631 0.085115 -177.74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

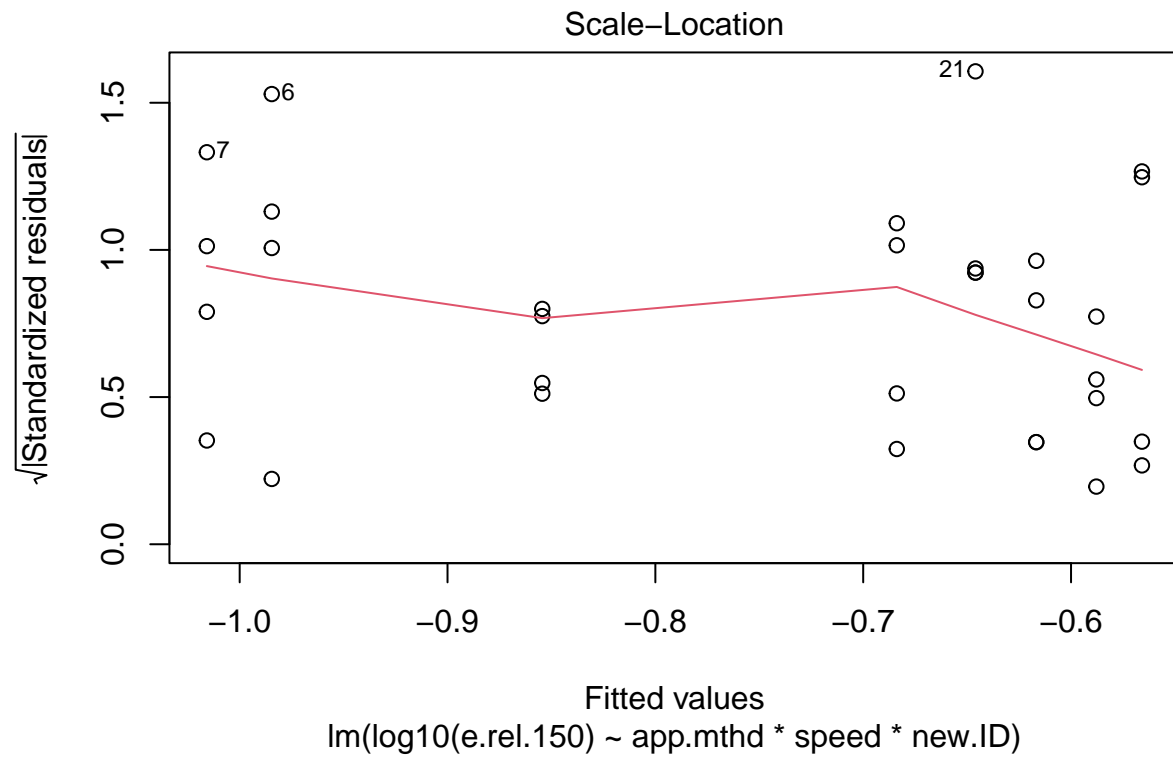
```
summary(m3, test = 'F')
```

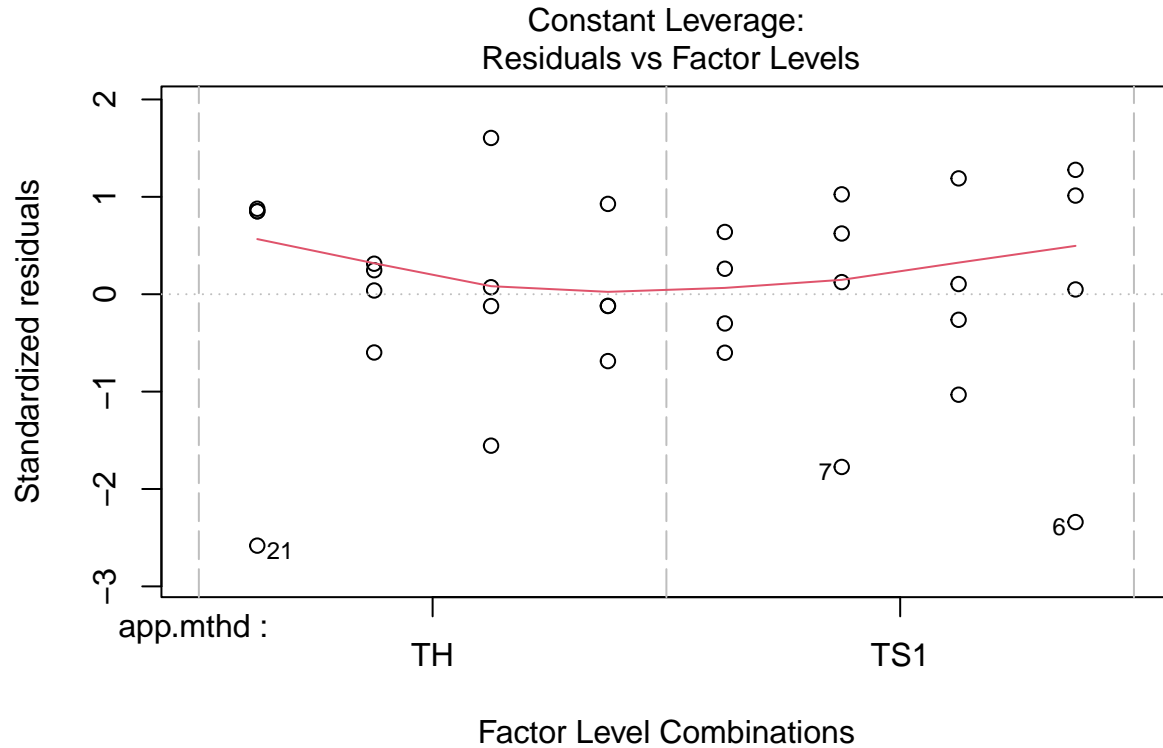
```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## app.mthd      1 0.10882  0.10882   34.946 3.61e-06 ***
## speed          1 0.00596  0.00596    1.914   0.1788
## new.ID         1 0.01345  0.01345    4.320   0.0481 *
## app.mthd:speed 1 0.00144  0.00144    0.463   0.5027
## app.mthd:new.ID 1 0.00726  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)

```

```

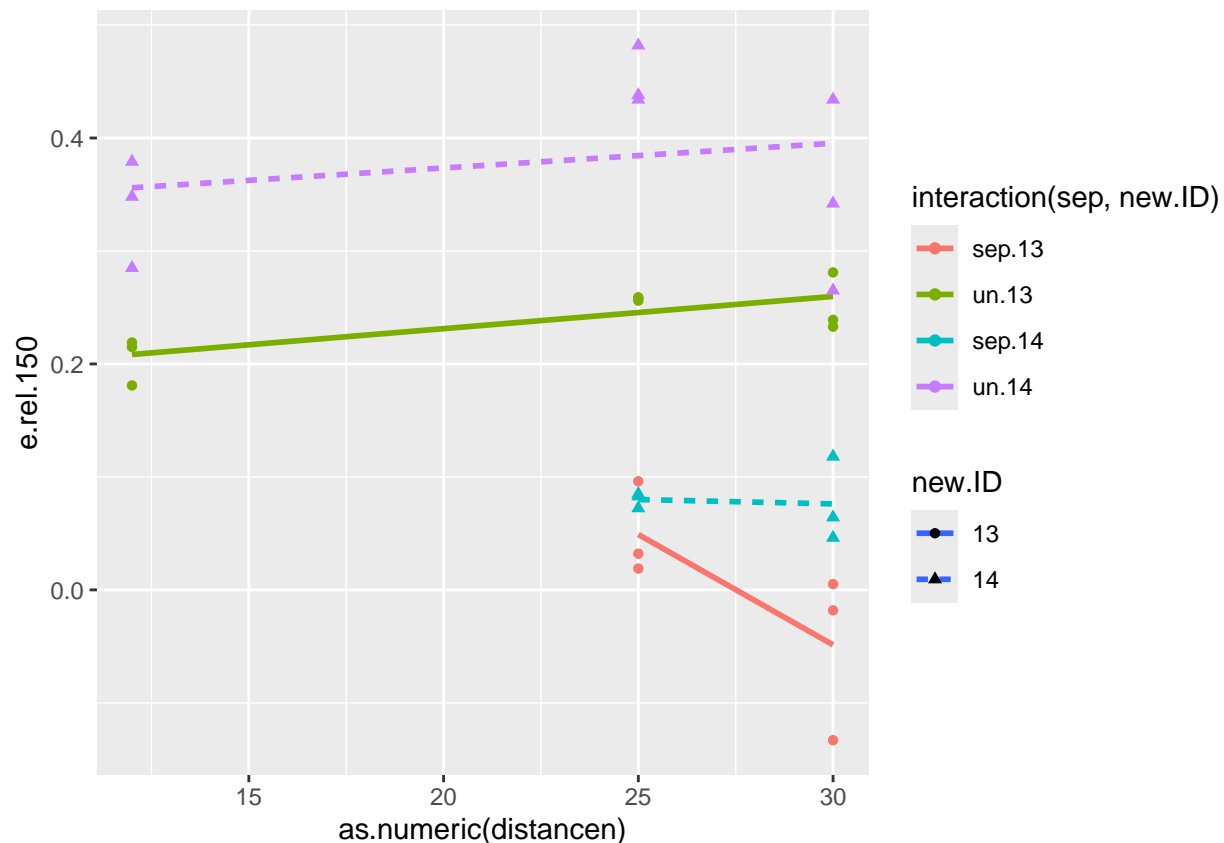
## Warning in geom_point(height = 0): Ignoring unknown parameters: 'height'

```

```

## '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')
```

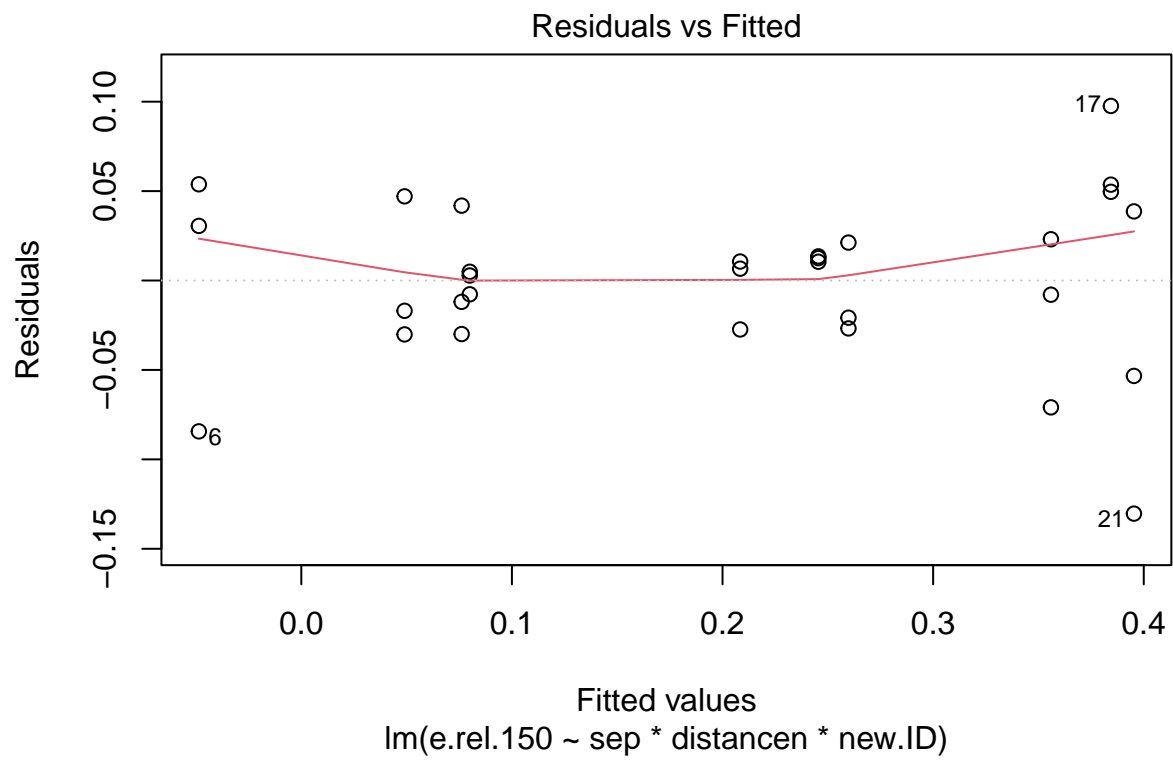
```
## Single term deletions
##
## Model:
## e.rel.150 ~ (sep + distancen + new.ID)^2
##
##          Df Sum of Sq    RSS      AIC F value Pr(>F)
## <none>                0.068606 -168.42
## sep:distancen    1 0.0112402 0.079847 -165.87  3.7682 0.06459 .
## sep:new.ID        1 0.0067105 0.075317 -167.62  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
```

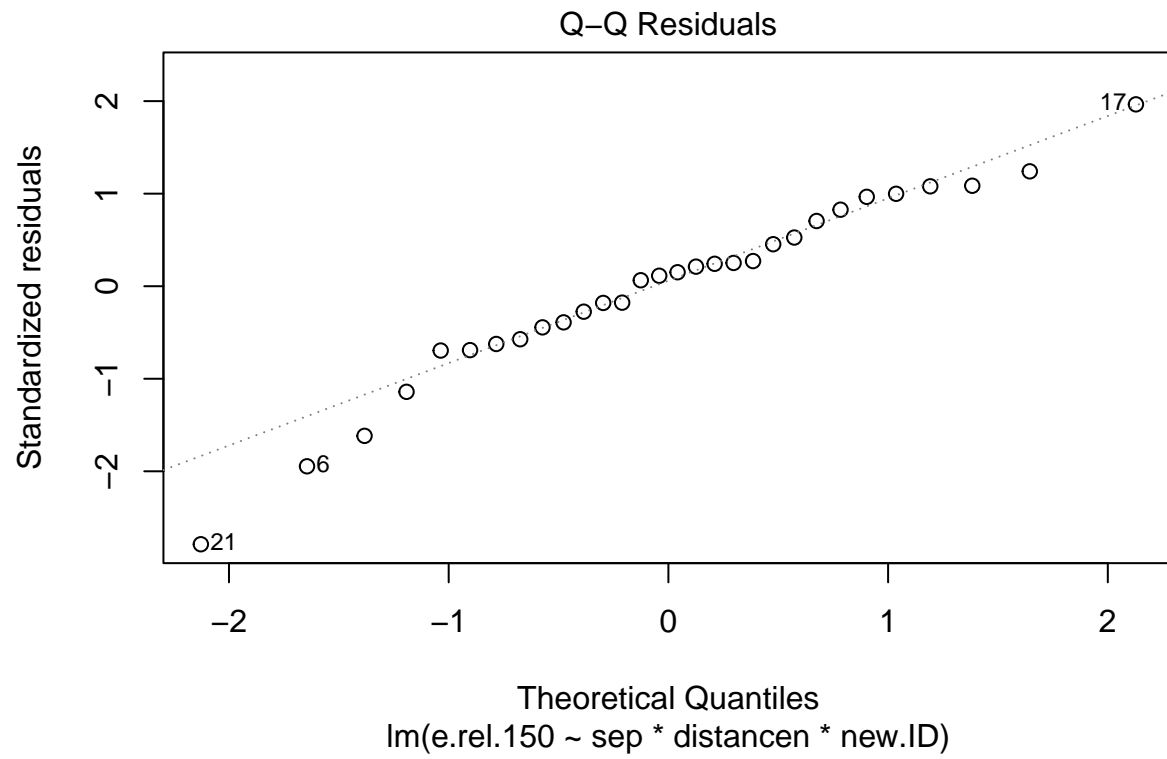
```
summary(m2b)
```

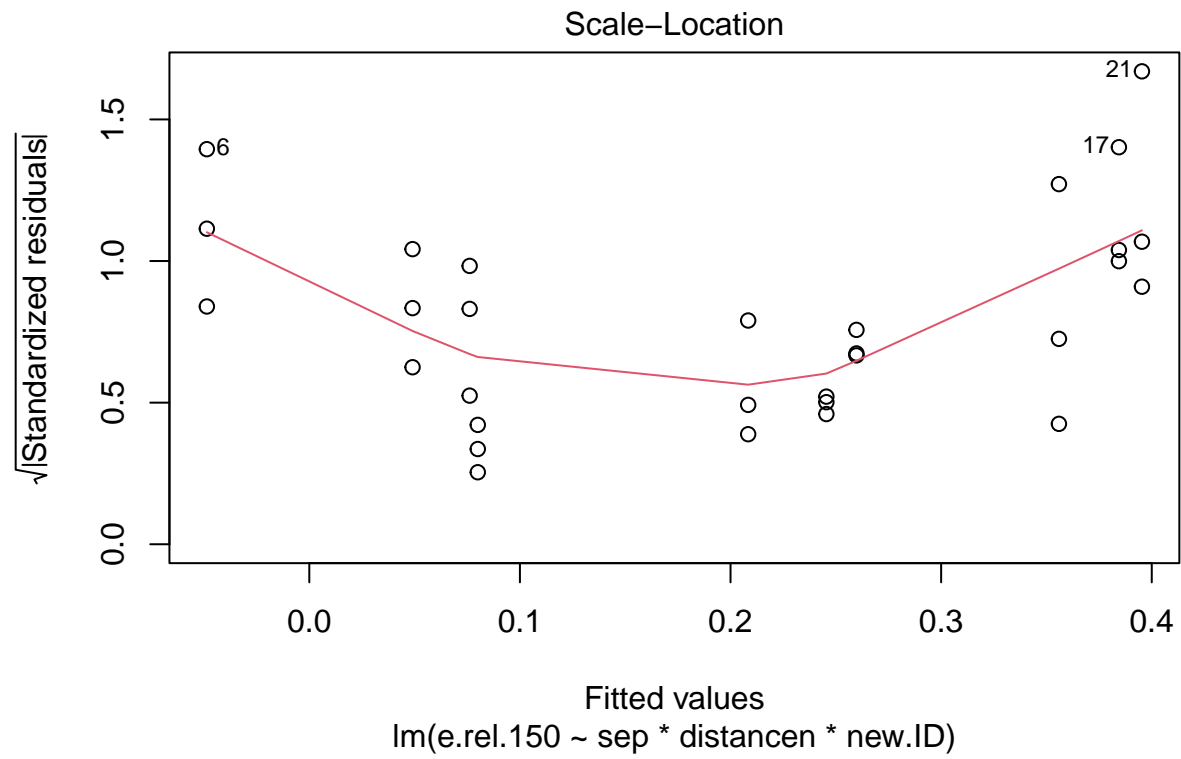
```
##
## Call:
## lm(formula = e.rel.150 ~ (sep + distancen + new.ID)^2, data = isumm1,
##     subset = sep != "sep" | new.ID != 13)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.130344 -0.022284  0.005761  0.021680  0.097605
##
## Coefficients: (1 not defined because of singularities)
##              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
```

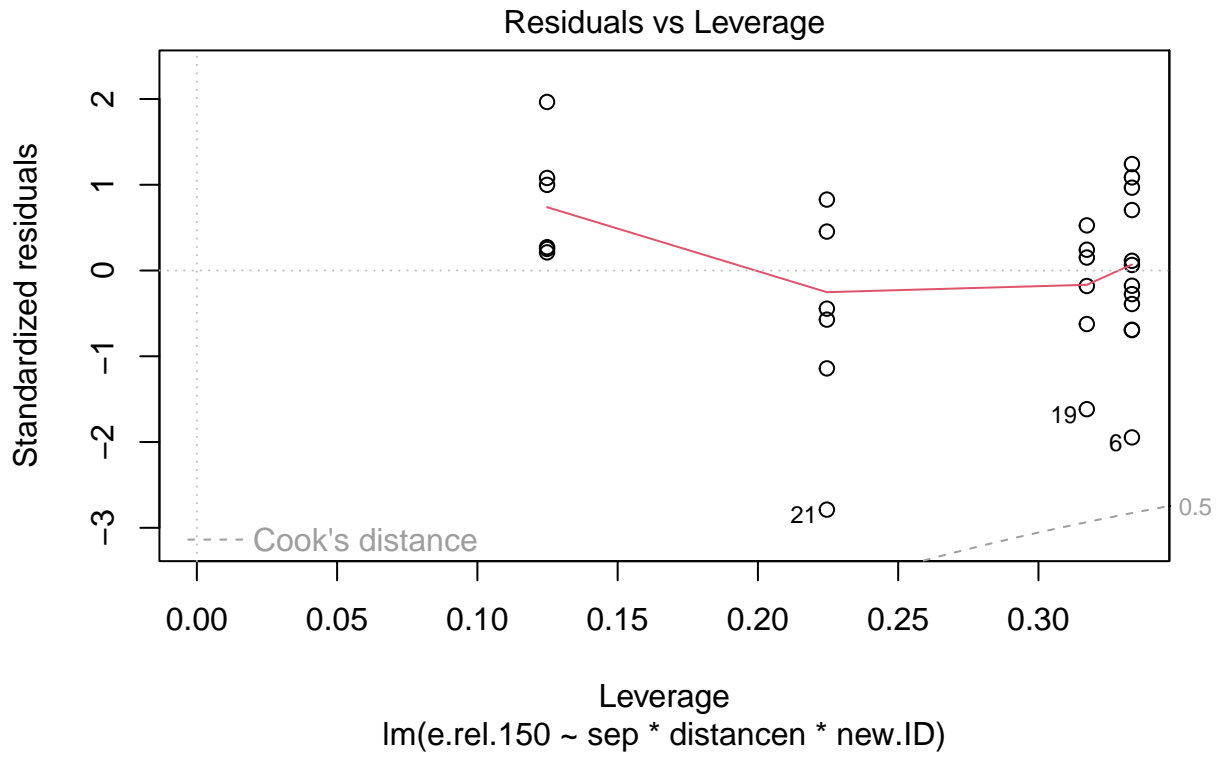
No clear distance effects, marginal interaction evidence, but all related to those negative values.

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









Means.

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

	new.ID	sep	distancef	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

Trial 15, chamber movement

Subset.

```
isumm1 <- isumm[new.ID == 15, ]
```

Set reference.


```
isumm1[, treat1 := factor(treat1, levels = c('No', '2-Pos', '7-Pos'))]
```

Fit model.

```
m1 <- aov(e.rel.150 ~ treat1, data = isumm1)
```

Tukey's test.

```
summary(m1)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## treat1        2 0.01633 0.008163   5.433 0.0209 *
## Residuals    12 0.01803 0.001502
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
TukeyHSD(m1)
```

```
##      Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = e.rel.150 ~ treat1, data = isumm1)
##
## $treat1
##              diff              lwr              upr              p adj
## 2-Pos-No      0.0148 -0.050599854 0.08019985 0.8207809
## 7-Pos-No      0.0762  0.010800146 0.14159985 0.0228266
## 7-Pos-2-Pos   0.0614 -0.003999854 0.12679985 0.0664770
```

Dunnnett test.

```
mmeans15 <- emmeans(m1, 'treat1')
mmeans15
```

```
##   treat1 emmean      SE df lower.CL upper.CL
##   No      0.309 0.0173 12    0.271    0.347
##   2-Pos   0.324 0.0173 12    0.286    0.361
##   7-Pos   0.385 0.0173 12    0.347    0.423
##
## Confidence level used: 0.95
```

```
contrast(mmeans15, 'trt.vs.ctrl1')
```

```
##   contrast      estimate      SE df t.ratio p.value
## (2-Pos) - No    0.0148 0.0245 12    0.604 0.7681
## (7-Pos) - No    0.0762 0.0245 12    3.108 0.0172
##
## P value adjustment: dunnettx method for 2 tests
```

```
contrast(mmeans15, 'tukey')
```

```
## contrast      estimate      SE df t.ratio p.value
## No - (2-Pos)    -0.0148 0.0245 12  -0.604  0.8208
## No - (7-Pos)    -0.0762 0.0245 12  -3.108  0.0228
## (2-Pos) - (7-Pos) -0.0614 0.0245 12  -2.505  0.0665
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
pairs(mmeans15)
```

```
## contrast      estimate      SE df t.ratio p.value
## No - (2-Pos)    -0.0148 0.0245 12  -0.604  0.8208
## No - (7-Pos)    -0.0762 0.0245 12  -3.108  0.0228
## (2-Pos) - (7-Pos) -0.0614 0.0245 12  -2.505  0.0665
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Relative effects.

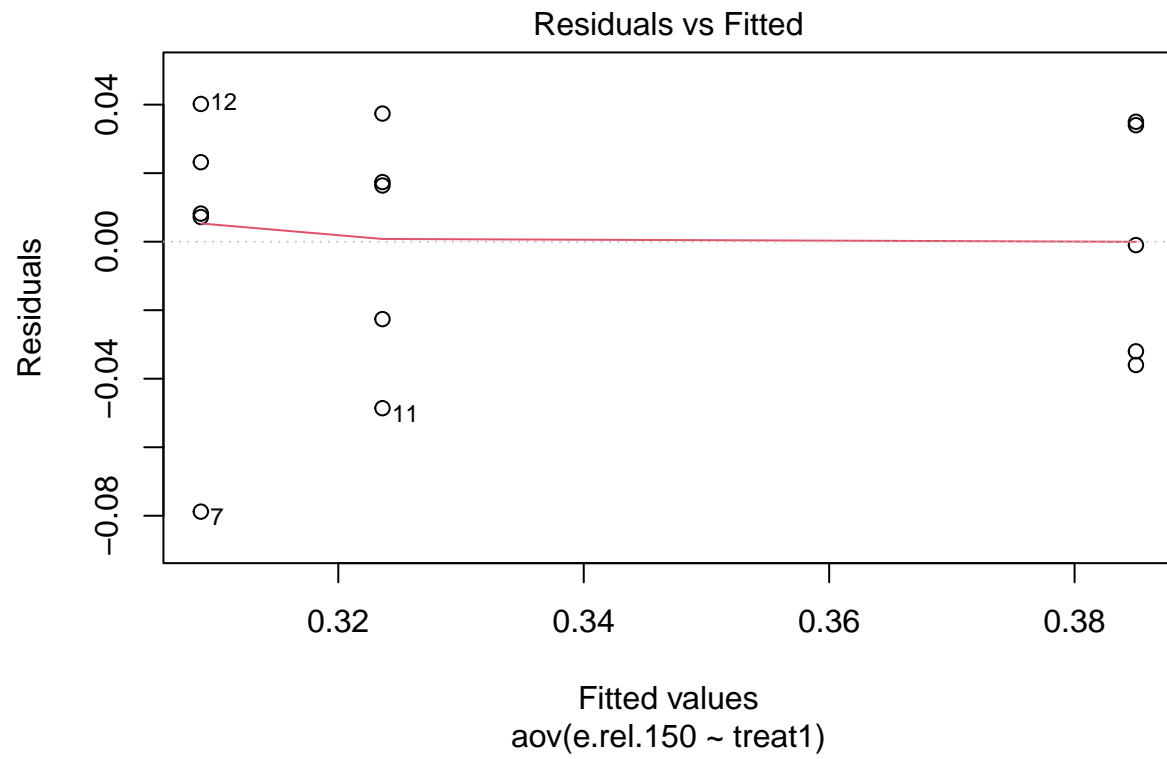
```
coef(m1)
```

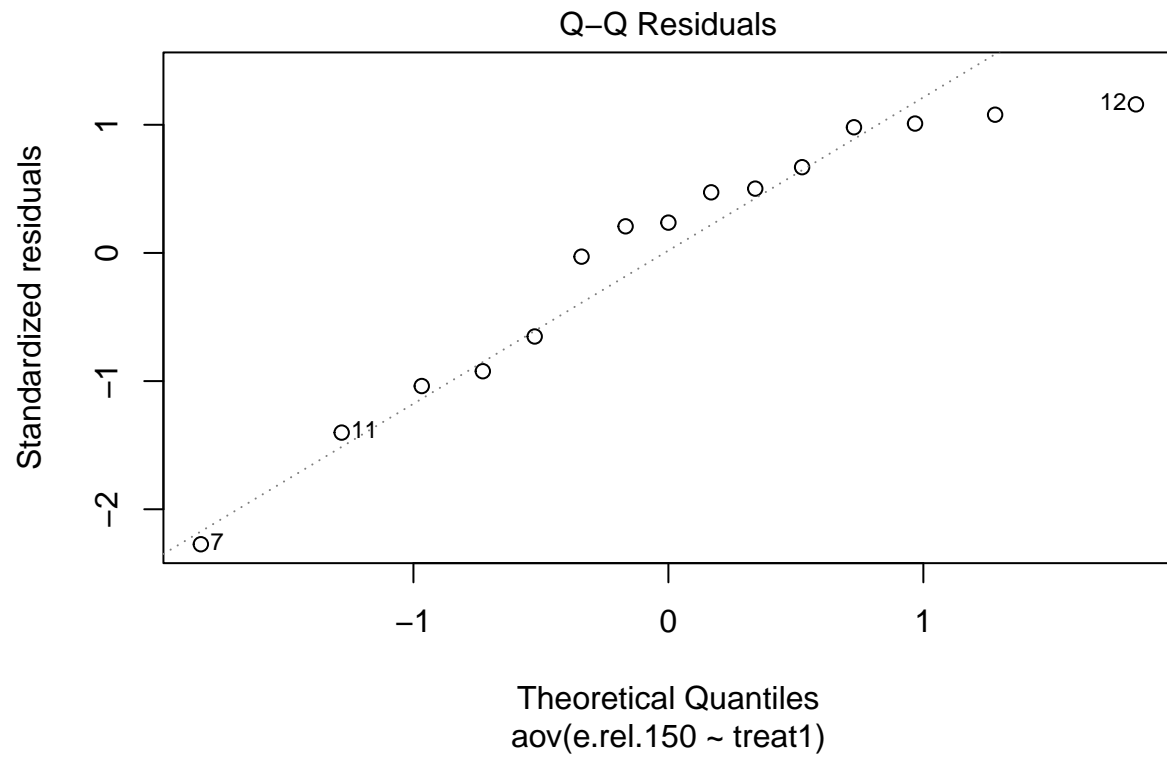
```
## (Intercept) treat12-Pos treat17-Pos
##      0.3088      0.0148      0.0762
```

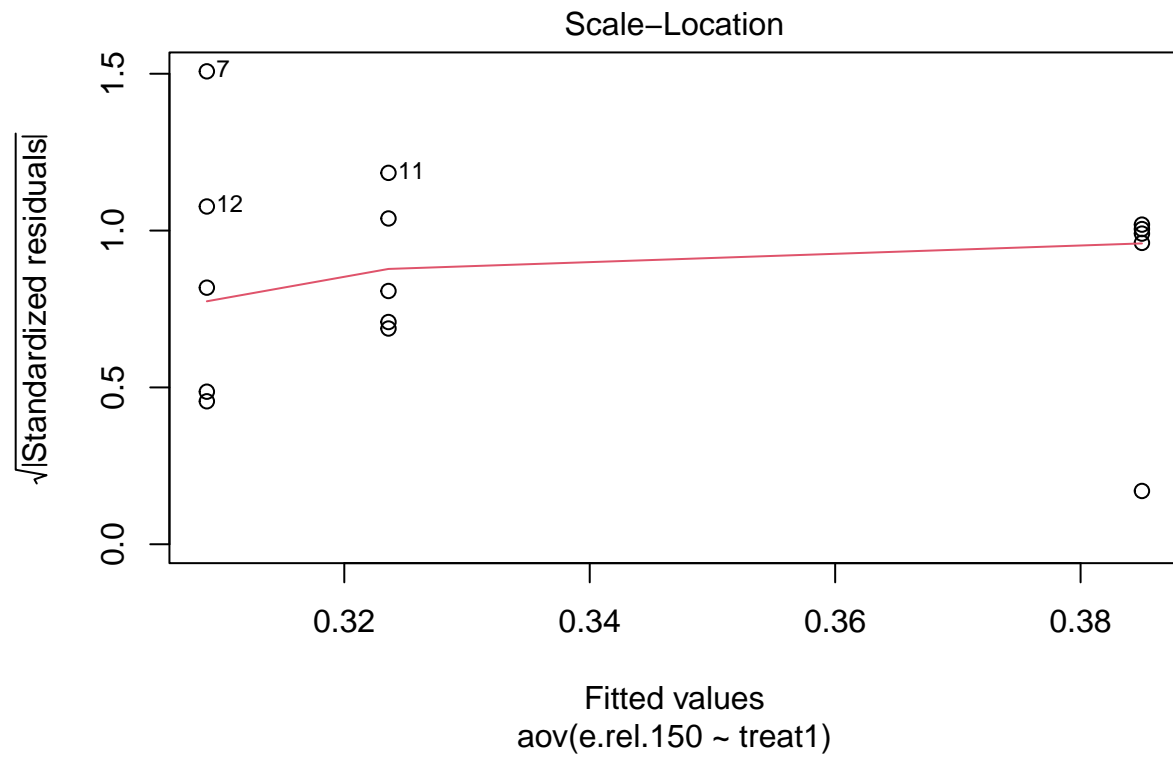
```
coef(m1) / coef(m1)[1]
```

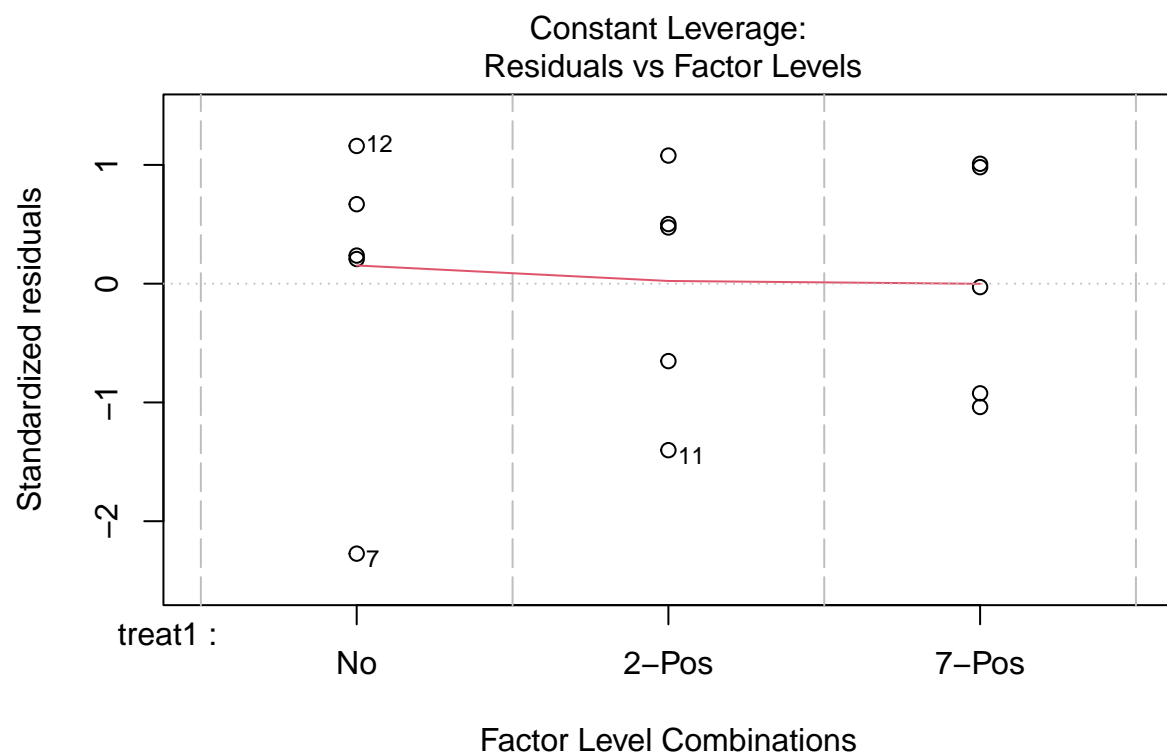
```
## (Intercept) treat12-Pos treat17-Pos
## 1.00000000 0.04792746 0.24676166
```

```
plot(m1)
```









Other stuff

I still need to sort this stuff out!

Then temperature stuff Add to supporting material