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)]
isumm1[dig.treat == '', dig.treat := 'none']
isumm1[, dig.treat := relevel(factor(dig.treat), ref = 'none')]
```

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)
m1notreat <- lmer(e.rel.150 ~ (1|dig.ID) + (1|new.ID), data = isumm1)
m1nodig <- 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)
m2b <- lmer(e.rel.150 ~ (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
```

```r
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                      
```

2

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(m1)
```

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

```r
summary(m2)
```

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

```
## REML criterion at convergence: -141
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.2447 -0.5187  0.1327  0.4729  1.5858
##
## Random effects:
##  Groups           Name        Variance Std.Dev.
##  dig.treat:dig.ID (Intercept) 0.005960 0.07720
##  new.ID           (Intercept) 0.003555 0.05962
##  dig.ID           (Intercept) 0.013257 0.11514
##  Residual                     0.001676 0.04094
## Number of obs: 61, groups:  dig.treat:dig.ID, 15; new.ID, 4; dig.ID, 3
##
## Fixed effects:
##                       Estimate Std. Error t value
## (Intercept)            0.38753    0.08642   4.485
## dig.treat Acid        -0.01161    0.07746  -0.150
## dig.treat Dis          0.03652    0.10002   0.365
## dig.treat Dis + acid  -0.03615    0.10002  -0.361
## dig.treat MF liquid   -0.29670    0.09969  -2.976
## dig.treat MF slurry    0.09273    0.09969   0.930
## dig.treat Sep-D       -0.27869    0.07561  -3.686
## dig.treat Sep-D + acid -0.28412   0.10002  -2.841
## dig.treat Sep-S       -0.13617    0.07648  -1.780
## dig.treat Sep-S + acid -0.10922   0.10172  -1.074
##
## Correlation of Fixed Effects:
##            (Intr) dg.trA dg.trD dg.D+a dg.MFl dg.MFs dg.S-D d.S-D+a dg.S-S
## dig.tretAcd -0.310
## dig.treatDs -0.248  0.306
## dg.trtDs+ac -0.248  0.306  0.348
## dg.trtMFlqd -0.249  0.307  0.320  0.320
## dg.trtMFslr -0.249  0.307  0.320  0.320  0.344
## dig.trtSp-D -0.327  0.299  0.313  0.313  0.312  0.312
## dg.trSp-D+a -0.248  0.306  0.348  0.348  0.320  0.320  0.313
## dig.trtSp-S -0.317  0.416  0.318  0.318  0.336  0.336  0.318  0.318
## dg.trSp-S+a -0.242  0.359  0.160  0.160  0.165  0.165  0.167  0.160   0.332
```

```r
summary(m2b)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ (1 | dig.ID/dig.treat) + (1 | new.ID)
##    Data: isumm1
##
## REML criterion at convergence: -145.6
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.2192 -0.5986  0.1588  0.4905  1.6799
##
## Random effects:
##  Groups           Name        Variance Std.Dev.
##  dig.treat:dig.ID (Intercept) 0.020448 0.14300
```

```
##  new.ID          (Intercept) 0.003628 0.06024
##  dig.ID          (Intercept) 0.016501 0.12846
##  Residual                    0.001670 0.04086
## Number of obs: 61, groups:  dig.treat:dig.ID, 15; new.ID, 4; dig.ID, 3
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.28971    0.09093   3.186
```

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
```

AIC(m1, m2, m2b, m3)

```
##     df        AIC
```

```
## m1   13  -97.86348
## m2   14 -112.98432
## m2b   5 -135.58904
## m3   17 -102.74407
```

Check for treatment effect and interaction with likelihood ratio test.

```
anova(m1, m1notreat, test = 'Chisq')
```

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

```
## Data: isumm1
## Models:
## m1notreat: 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)
## m1notreat    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, m1nodig, test = 'Chisq')
```

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

```
## Data: isumm1
## Models:
## m1nodig: 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)
## m1nodig    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
```

```
anova(m2b, m1, test = 'Chisq')
```

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

```
## Data: isumm1
## Models:
## m2b: e.rel.150 ~ (1 | dig.ID/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)
## m2b    5 -138.76 -128.20 74.379  -148.76
## m1    13 -147.36 -119.92 86.678  -173.36 24.599  8   0.001817 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(m2b, m2, test = 'Chisq')
```

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

```
## Data: isumm1
## Models:
## m2b: e.rel.150 ~ (1 | dig.ID/dig.treat) + (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)
## m2b    5 -138.76 -128.20 74.379  -148.76
## m2    14 -152.17 -122.62 90.085  -180.17 31.413  9  0.0002514 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Plot to check treatment effect and interaction.

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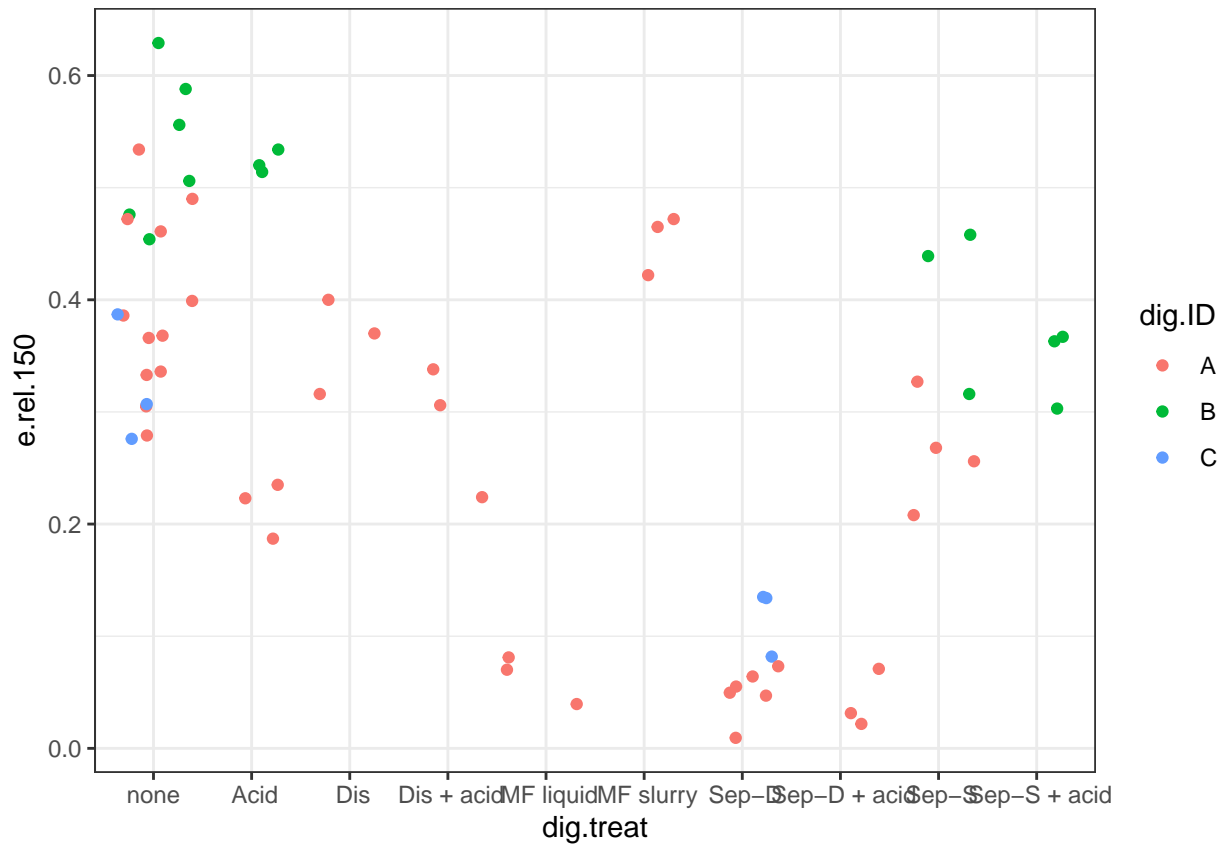
```r
table(isumm1[, .(dig.ID, dig.treat)])
```

```
##       dig.treat
## dig.ID none  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.

```r
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
```

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```
##   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
```

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```
##  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.

```r
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
```

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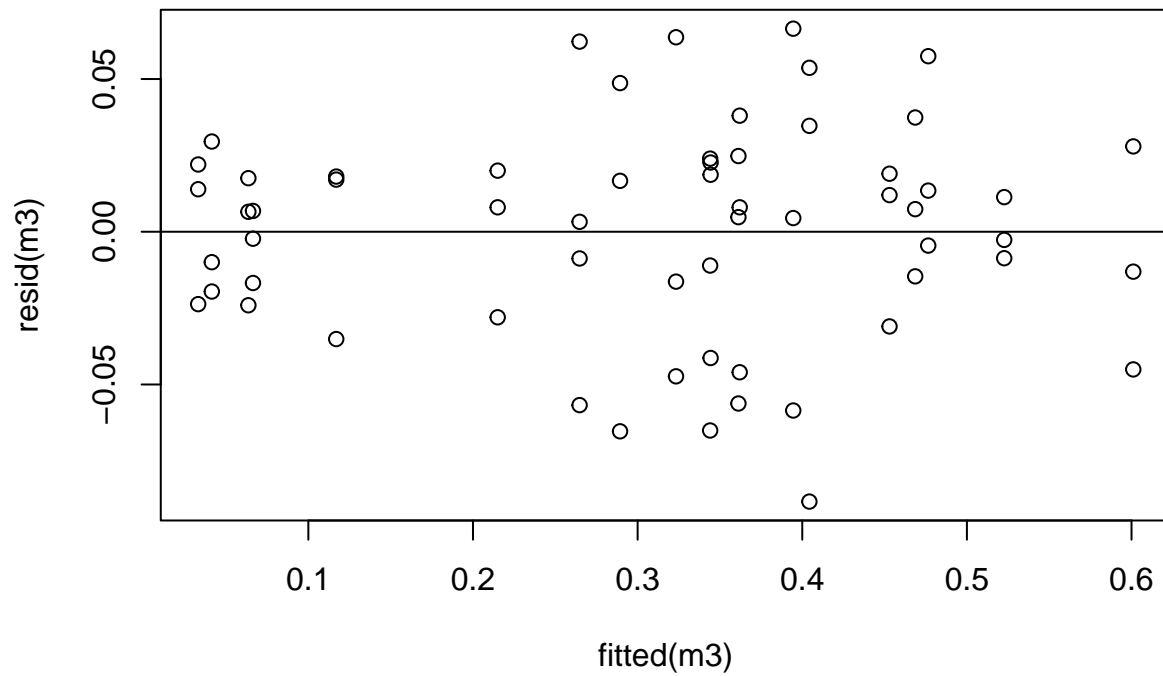
```
qqnorm(resid(m3))
qqline(resid(m3))
```

Normal Q–Q Plot
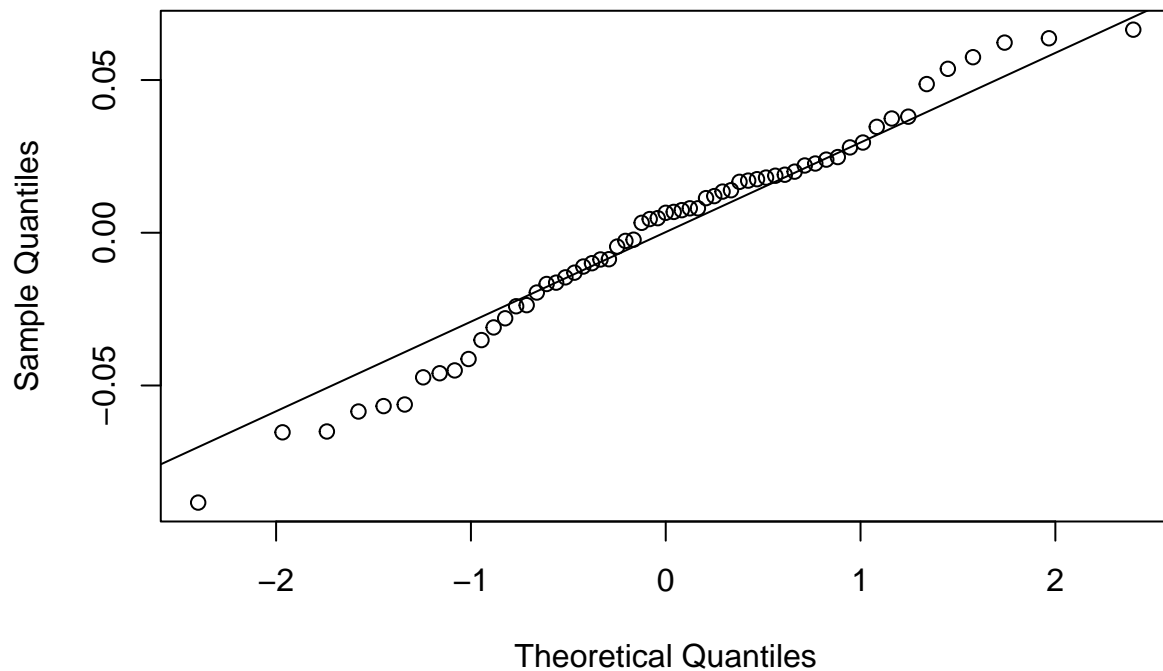
More on trials 1-4, DM and pH effects

Look for DM and pH explanation of digestate variability.

13

```
dref <- isumm1[dig.treat == 'none', ]
m4 <- lmer(e.rel.150 ~ (1|dig.ID) + (1|new.ID), data = dref)
m4b <- lmer(e.rel.150 ~ (1|dig.ID/new.ID), data = dref)
m5 <- lmer(e.rel.150 ~ (1|dig.ID) + (1|new.ID) + man.dm + man.ph, data = dref)
m6 <- lmer(e.rel.150 ~ (1|dig.ID/new.ID) + man.dm + man.ph, data = dref)
```

```
## boundary (singular) fit: see help('isSingular')
```

summary(m4)

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ (1 | dig.ID) + (1 | new.ID)
##    Data: dref
##
## REML criterion at convergence: -49.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.47340 -0.47349  0.02298  0.60460  1.39387
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  new.ID   (Intercept) 0.003812 0.06174
##  dig.ID   (Intercept) 0.018496 0.13600
##  Residual             0.002045 0.04523
## Number of obs: 21, groups:  new.ID, 4; dig.ID, 3
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.38646    0.08562   4.514
```

summary(m4b)

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ (1 | dig.ID/new.ID)
##    Data: dref
##
## REML criterion at convergence: -48.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.40190 -0.56096  0.00607  0.63643  1.39169
##
## Random effects:
##  Groups        Name        Variance Std.Dev.
##  new.ID:dig.ID (Intercept) 0.005363 0.07323
##  dig.ID        (Intercept) 0.007081 0.08415
##  Residual                  0.002002 0.04475
## Number of obs: 21, groups:  new.ID:dig.ID, 7; dig.ID, 3
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.42337    0.05855   7.231
```

```
summary(m5)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ (1 | dig.ID) + (1 | new.ID) + man.dm + man.ph
##    Data: dref
##
## REML criterion at convergence: -48.4
##
## Scaled residuals:
##      Min      1Q   Median      3Q      Max
## -1.42953 -0.58352  0.01923  0.62873  1.32172
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  new.ID   (Intercept) 0.001349 0.03673
##  dig.ID   (Intercept) 0.001390 0.03729
##  Residual             0.002064 0.04543
## Number of obs: 21, groups:  new.ID, 4; dig.ID, 3
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  1.82322    0.61703   2.955
## man.dm       0.04232    0.01132   3.740
## man.ph      -0.20688    0.07496  -2.760
##
## Correlation of Fixed Effects:
##        (Intr) man.dm
## man.dm -0.145
## man.ph -0.992  0.032
```

```
summary(m6)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ (1 | dig.ID/new.ID) + man.dm + man.ph
##    Data: dref
##
## REML criterion at convergence: -48.9
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.5803 -0.4847  0.0908  0.7587  1.3597
##
## Random effects:
##  Groups         Name        Variance Std.Dev.
##  new.ID:dig.ID (Intercept) 0.001500 0.03873
##  dig.ID        (Intercept) 0.000000 0.00000
##  Residual                  0.002002 0.04475
## Number of obs: 21, groups:  new.ID:dig.ID, 7; dig.ID, 3
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  2.364336   0.755467   3.130
```

```
## man.dm         0.037429    0.008942    4.186
## man.ph        -0.267593    0.093150   -2.873
##
## Correlation of Fixed Effects:
##         (Intr) man.dm
## man.dm -0.019
## man.ph -0.997 -0.054
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```r
AIC(m4, m5)
```

```
##    df       AIC
## m4  4 -41.88321
## m5  6 -36.39417
```

```r
anova(m4, m5, test = 'Chisq')
```

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

```
## Data: dref
## Models:
## m4: e.rel.150 ~ (1 | dig.ID) + (1 | new.ID)
## m5: e.rel.150 ~ (1 | dig.ID) + (1 | new.ID) + man.dm + man.ph
##     npar     AIC     BIC logLik deviance Chisq Df Pr(>Chisq)
## m4     4 -45.128 -40.950 26.564  -53.128
## m5     6 -54.238 -47.971 33.119  -66.238 13.11  2   0.001423 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

I do not like how AIC difference flips with ML and REML! But see reduction in dig.ID standard deviation when DM and pH are included. And see likelihood ratio tests below.

```r
m5noph <- update(m5, ~ . - man.ph)
m5nodm <- update(m5, ~ . - man.dm)
```

```r
m6noph <- update(m6, ~ . - man.ph)
```

```
## boundary (singular) fit: see help('isSingular')
```

```r
m6nodm <- update(m6, ~ . - man.dm)
```

```r
summary(m5noph)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ (1 | dig.ID) + (1 | new.ID) + man.dm
##     Data: dref
##
## REML criterion at convergence: -46.9
##
```

```
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.4247 -0.5232  0.1227  0.5865  1.5221
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  new.ID   (Intercept) 0.004851 0.06965
##  dig.ID   (Intercept) 0.004059 0.06371
##  Residual             0.002048 0.04526
## Number of obs: 21, groups:  new.ID, 4; dig.ID, 3
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.10914    0.12057   0.905
## man.dm       0.04611    0.01783   2.586
##
## Correlation of Fixed Effects:
##        (Intr)
## man.dm -0.900
```

```
summary(m5nodm)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ (1 | dig.ID) + (1 | new.ID) + man.ph
##    Data: dref
##
## REML criterion at convergence: -49.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.57949 -0.48978 -0.01658  0.70174  1.31183
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  new.ID   (Intercept) 0.002640 0.05138
##  dig.ID   (Intercept) 0.014155 0.11898
##  Residual             0.001972 0.04440
## Number of obs: 21, groups:  new.ID, 4; dig.ID, 3
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  1.62305    0.68550   2.368
## man.ph      -0.15157    0.08363  -1.812
##
## Correlation of Fixed Effects:
##        (Intr)
## man.ph -0.994
```

```
anova(m5, m5noph, test = 'Chisq')
```

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

```
## Data: dref
```

```
## Models:
## m5noph: e.rel.150 ~ (1 | dig.ID) + (1 | new.ID) + man.dm
## m5: e.rel.150 ~ (1 | dig.ID) + (1 | new.ID) + man.dm + man.ph
##          npar     AIC     BIC logLik deviance  Chisq Df Pr(>Chisq)
## m5noph    5 -47.936 -42.713 28.968  -57.936
## m5        6 -54.238 -47.971 33.119  -66.238 8.3024  1   0.003959 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(m5, m5nodm, test = 'Chisq')
```

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

```
## Data: dref
## Models:
## m5nodm: e.rel.150 ~ (1 | dig.ID) + (1 | new.ID) + man.ph
## m5: e.rel.150 ~ (1 | dig.ID) + (1 | new.ID) + man.dm + man.ph
##          npar     AIC     BIC logLik deviance  Chisq Df Pr(>Chisq)
## m5nodm    5 -46.496 -41.274 28.248  -56.496
## m5        6 -54.238 -47.971 33.119  -66.238 9.7418  1   0.001801 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(m6, m6noph, test = 'Chisq')
```

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

```
## Data: dref
## Models:
## m6noph: e.rel.150 ~ (1 | dig.ID/new.ID) + man.dm
## m6: e.rel.150 ~ (1 | dig.ID/new.ID) + man.dm + man.ph
##          npar     AIC     BIC logLik deviance Chisq Df Pr(>Chisq)
## m6noph    5 -48.726 -43.503 29.363  -58.726
## m6        6 -54.562 -48.295 33.281  -66.562 7.836  1   0.005121 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(m6, m6nodm, test = 'Chisq')
```

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

```
## Data: dref
## Models:
## m6nodm: e.rel.150 ~ (1 | dig.ID/new.ID) + man.ph
## m6: e.rel.150 ~ (1 | dig.ID/new.ID) + man.dm + man.ph
##          npar     AIC     BIC logLik deviance  Chisq Df Pr(>Chisq)
## m6nodm    5 -45.809 -40.586 27.904  -55.809
## m6        6 -54.562 -48.295 33.281  -66.562 10.753  1   0.001041 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
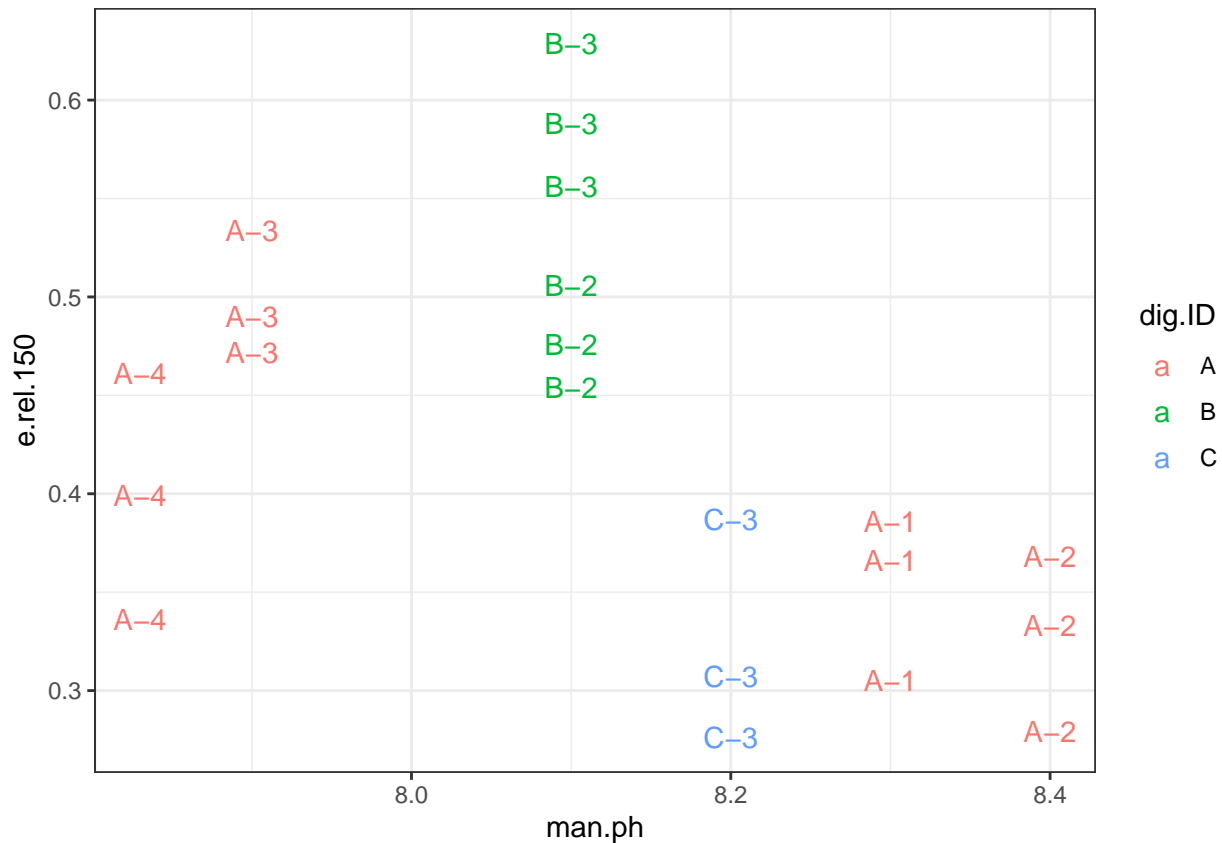
Plots to look at apparent effects.

```r
ggplot(dref, aes(man.dm, e.rel.150, colour = dig.ID)) +
  geom_text(aes(label = paste0(dig.ID, '-', new.ID))) +
  theme_bw()
```
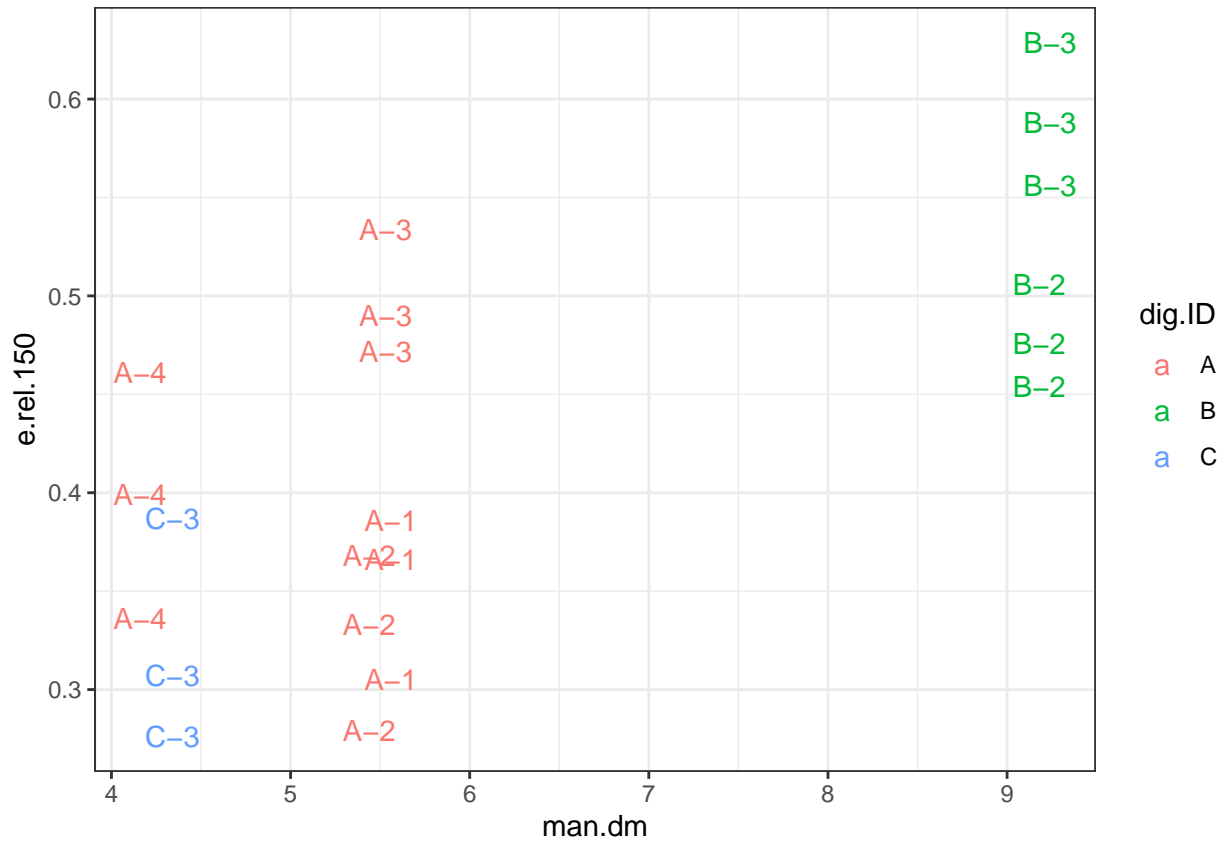


```r
ggplot(dref, aes(man.dm, e.rel.150, colour = man.ph)) +
  geom_text(aes(label = paste0(dig.ID, '-', new.ID))) +
  theme_bw()
```
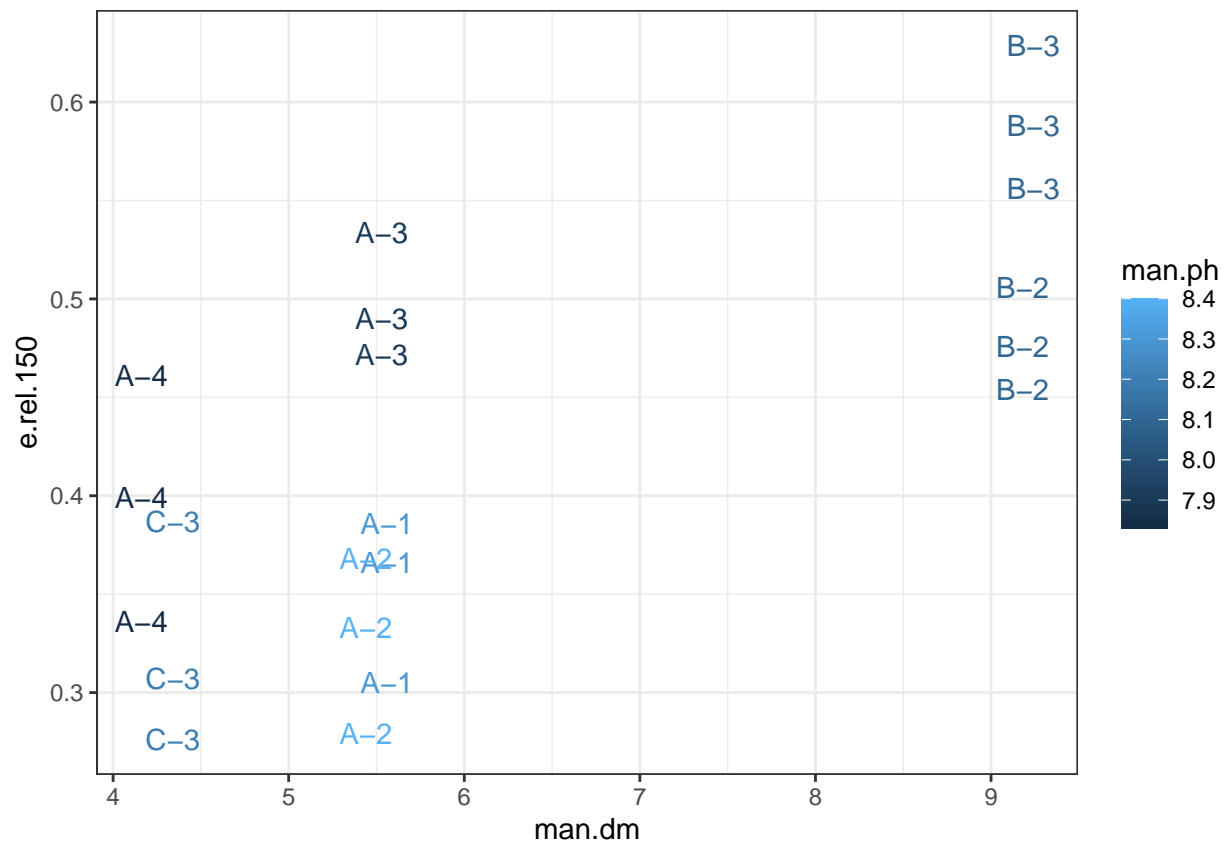
```
ggplot(dref, aes(man.ph, e.rel.150, colour = dig.ID)) +
  geom_text(aes(label = paste0(dig.ID, '-', new.ID))) +
  theme_bw()
```

Take means–I do not believe pH result.

```r
dmn <- dref[, .(e.rel.150 = mean(e.rel.150), man.dm = mean(man.dm), man.ph = mean(man.ph)),
    by = .(dig.ID, new.ID)]
```

```r
m10 <- lmer(e.rel.150 ~ (1|dig.ID), data = dmn)
m10b <- lm(e.rel.150 ~ 1, data = dmn)
m11 <- lm(e.rel.150 ~ man.dm + man.ph, data = dmn)
```

```r
summary(m10)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ (1 | dig.ID)
##    Data: dmn
##
## REML criterion at convergence: -9.3
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.9344 -0.5982 -0.2947  0.5724  1.2806
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  dig.ID   (Intercept) 0.007082 0.08415
##  Residual             0.006030 0.07765
## Number of obs: 7, groups:  dig.ID, 3
```

```
## 
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.42337    0.05855   7.231
```

```r
summary(m10b)
```

```
## 
## Call:
## lm(formula = e.rel.150 ~ 1, data = dmn)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.10086 -0.08469 -0.02552  0.06448  0.16681
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.42419    0.03837   11.05 3.26e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.1015 on 6 degrees of freedom
```

```r
summary(m11)
```

```
## 
## Call:
## lm(formula = e.rel.150 ~ man.dm + man.ph, data = dmn)
## 
## Residuals:
##          1          2          3          4          5          6          7
##  0.0009136 -0.0617638  0.0064977  0.0413327  0.0483238 -0.0091826 -0.0261214
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.364336   0.755467   3.130   0.0352 *
## man.dm       0.037429   0.008942   4.186   0.0139 *
## man.ph      -0.267593   0.093150  -2.873   0.0453 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.04655 on 4 degrees of freedom
## Multiple R-squared:  0.8598, Adjusted R-squared:  0.7897
## F-statistic: 12.27 on 2 and 4 DF,  p-value: 0.01965
```

```r
ggplot(dmn, aes(man.dm, e.rel.150, colour = man.ph)) +
  geom_text(aes(label = paste0(dig.ID, '-', new.ID))) +
  theme_bw()
```
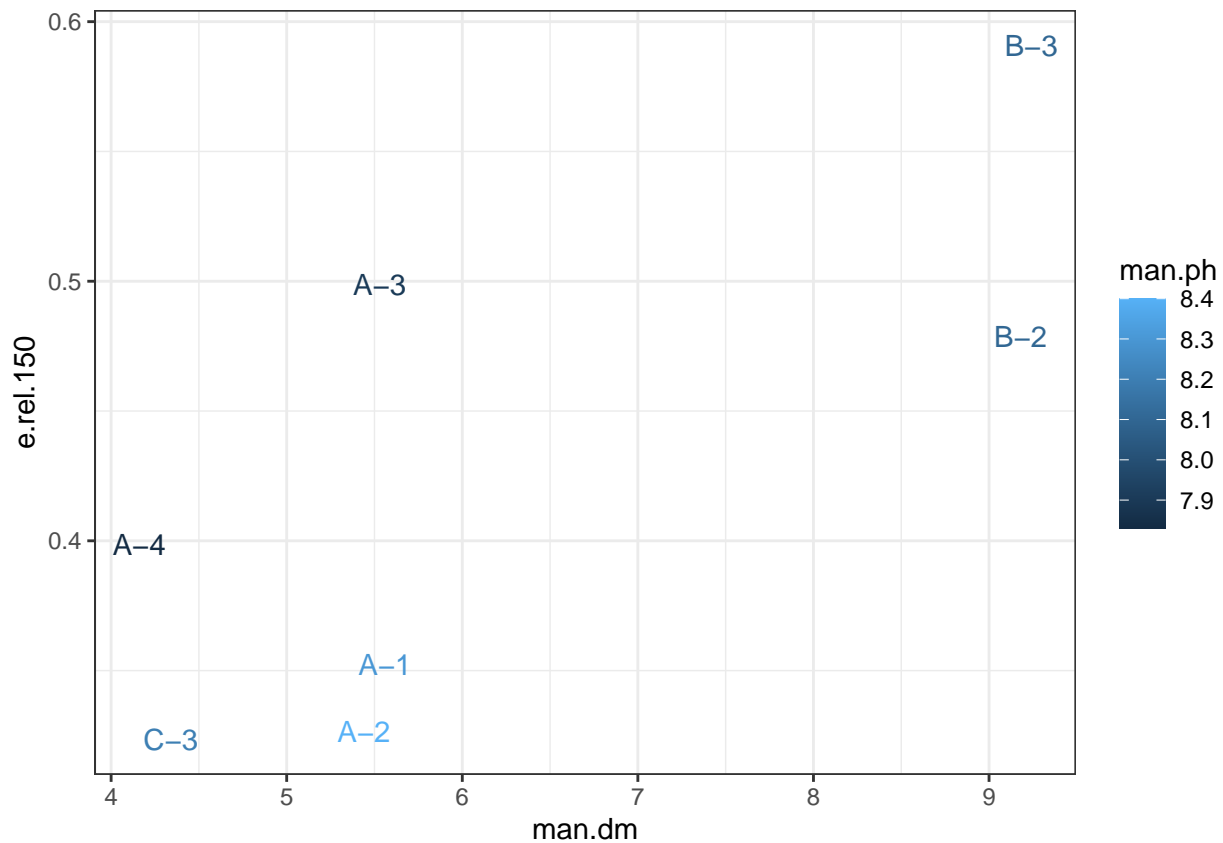
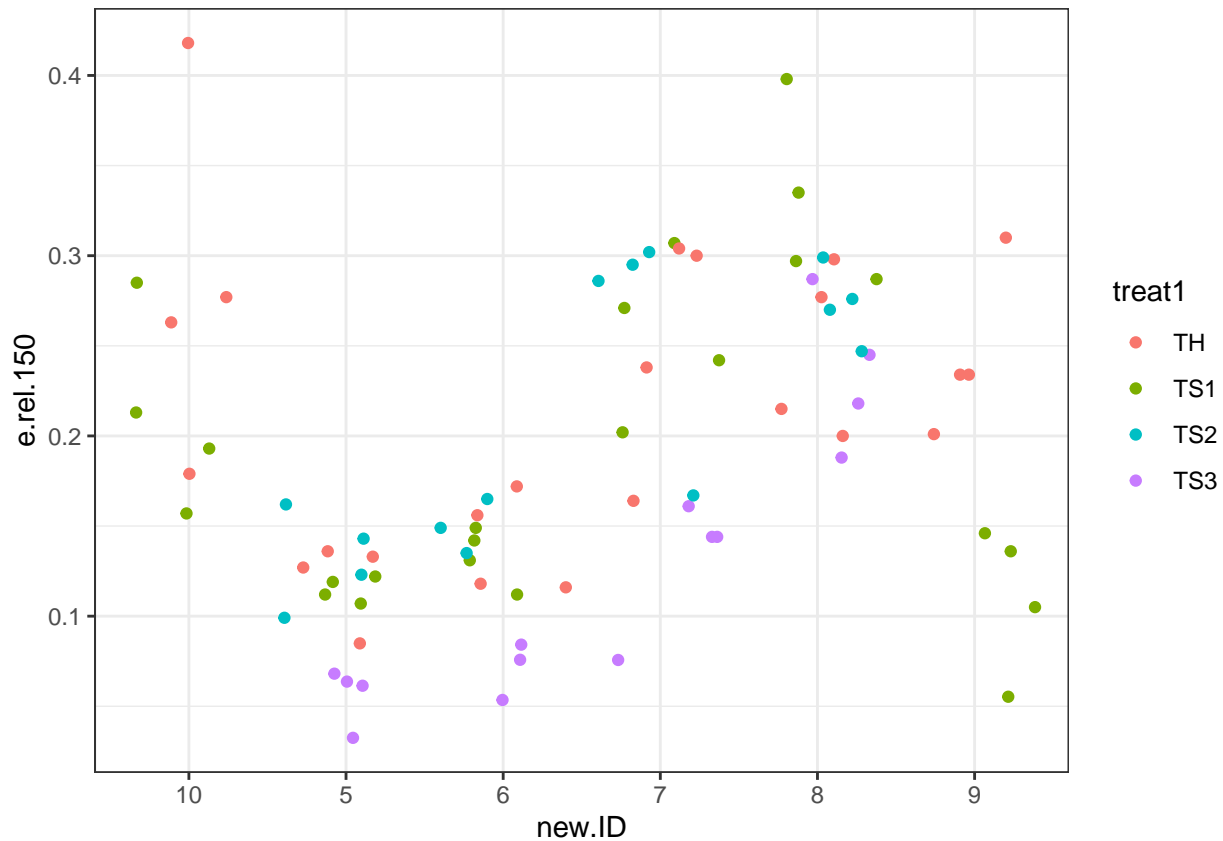## Trials 5-10 (app tech on winter wheat)

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.

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

```r
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)  0.214788   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.
```

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

And get a column for copy/paste into paper.

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

Add 11-12

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

```r
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.

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

```r
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'
```
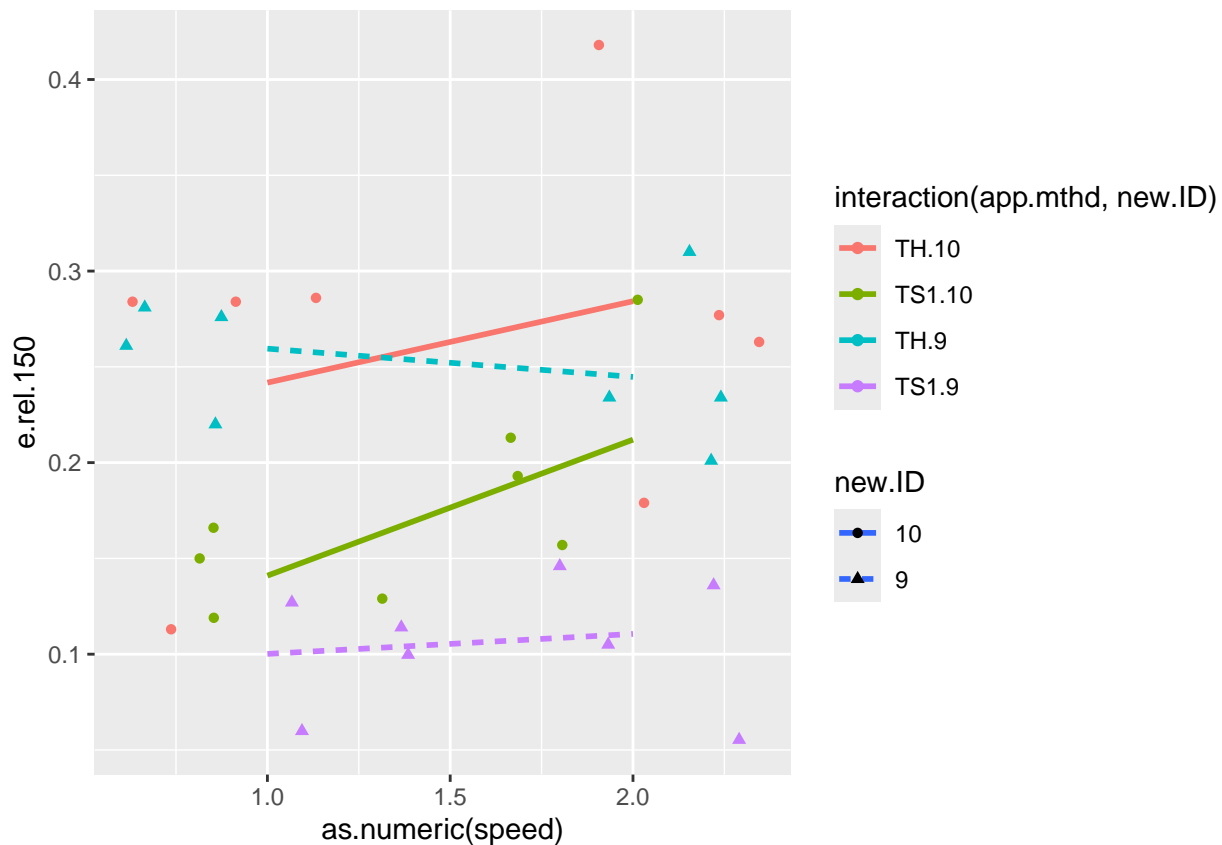
Fit model.

```r
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)
```

```r
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')
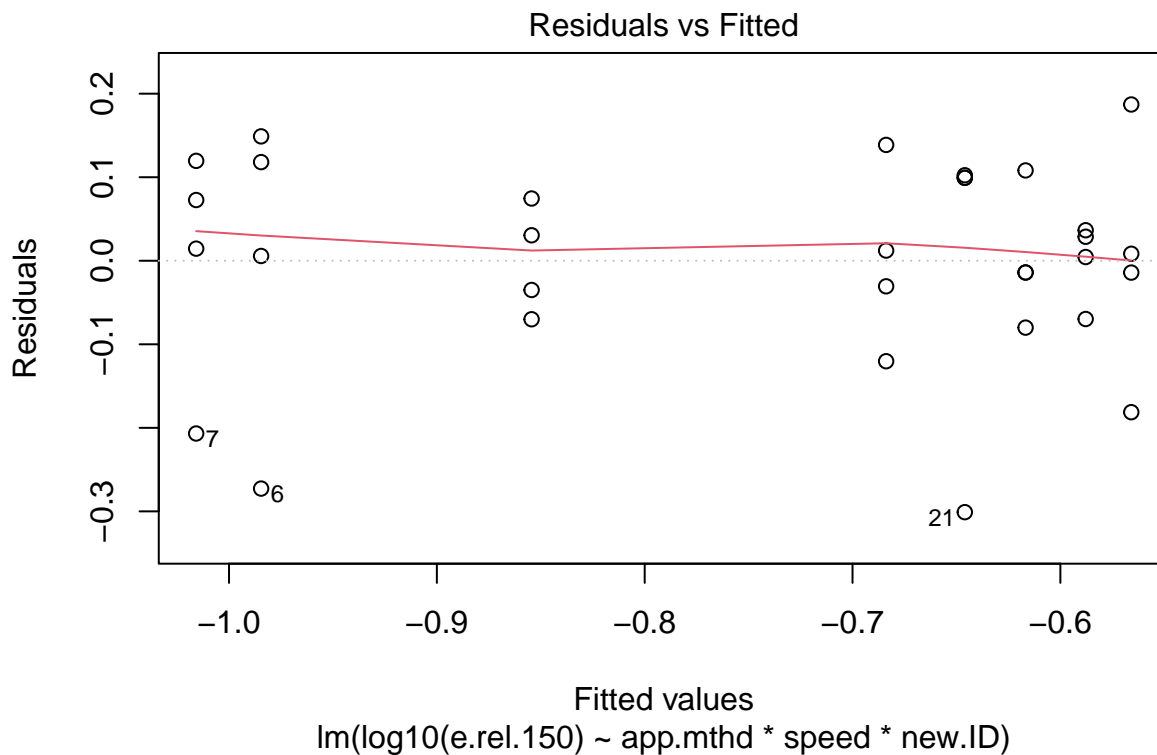
```
## Single term deletions
```
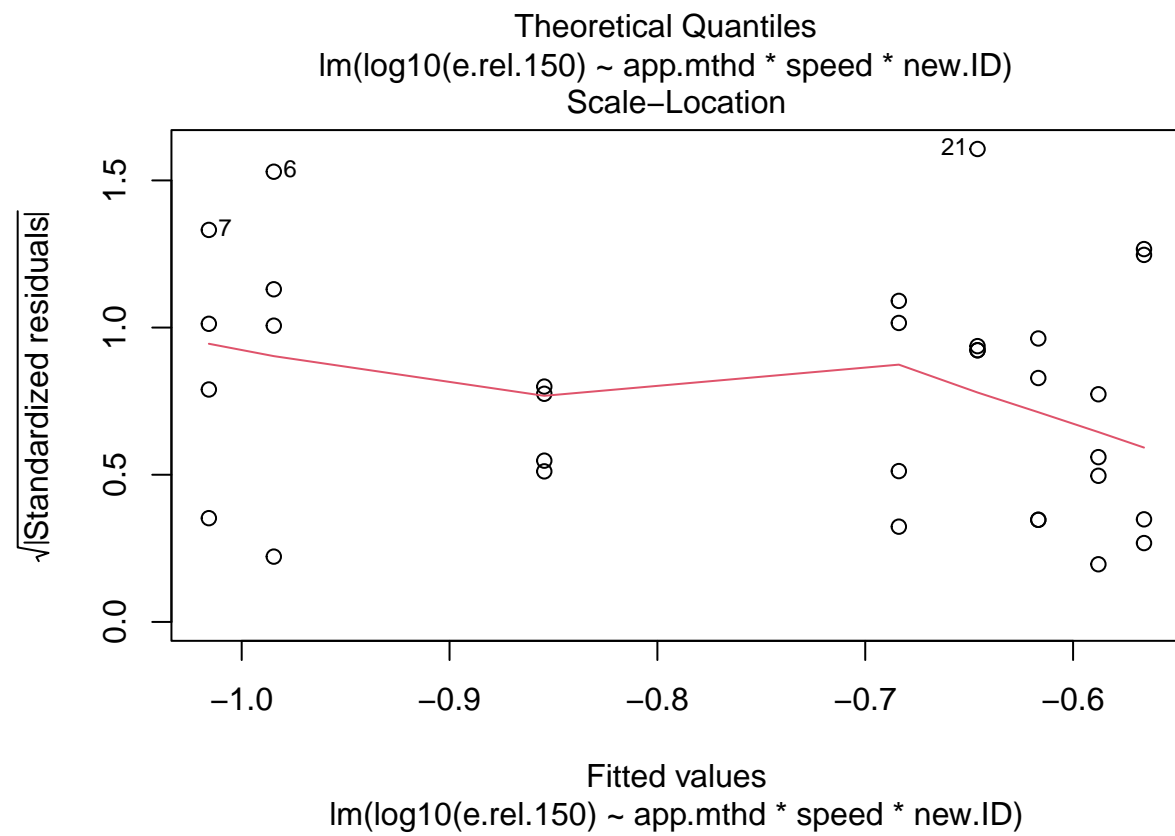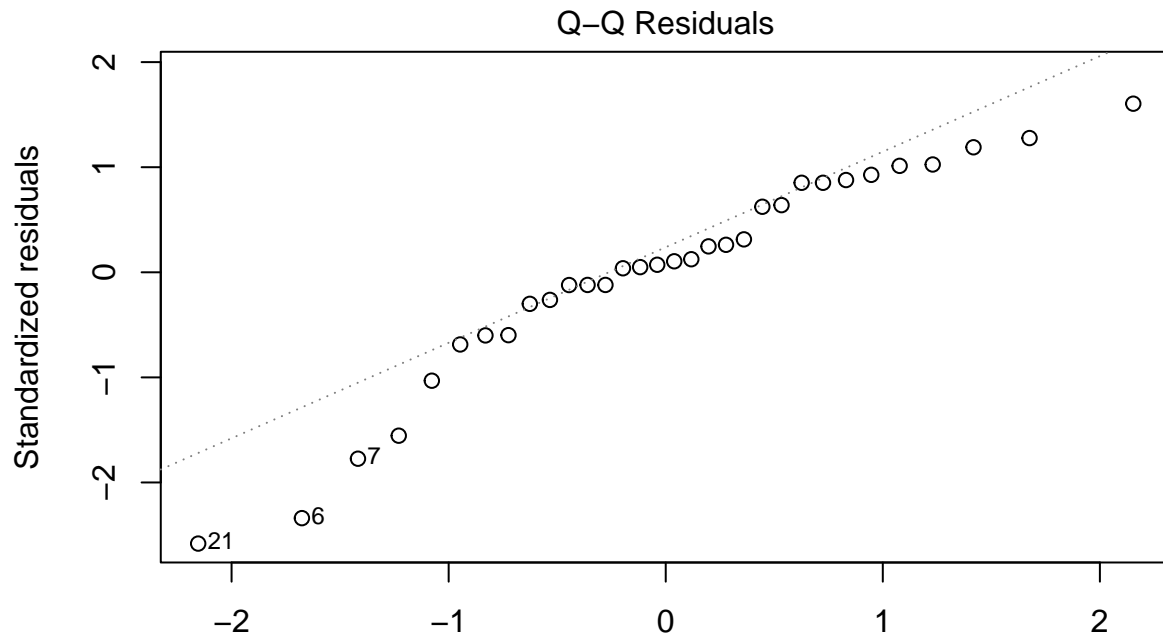
```
##
## Model:
## e.rel.150 ~ (app.mthd + speed + new.ID)^2
##                 Df Sum of Sq      RSS      AIC F value Pr(>F)
## <none>                      0.077852 -178.60
## app.mthd:speed   1 0.0014405 0.079292 -180.01  0.4626 0.5027
## app.mthd:new.ID  1 0.0072631 0.085115 -177.74  2.3324 0.1393
## speed:new.ID     1 0.0069414 0.084793 -177.87  2.2290 0.1480
```
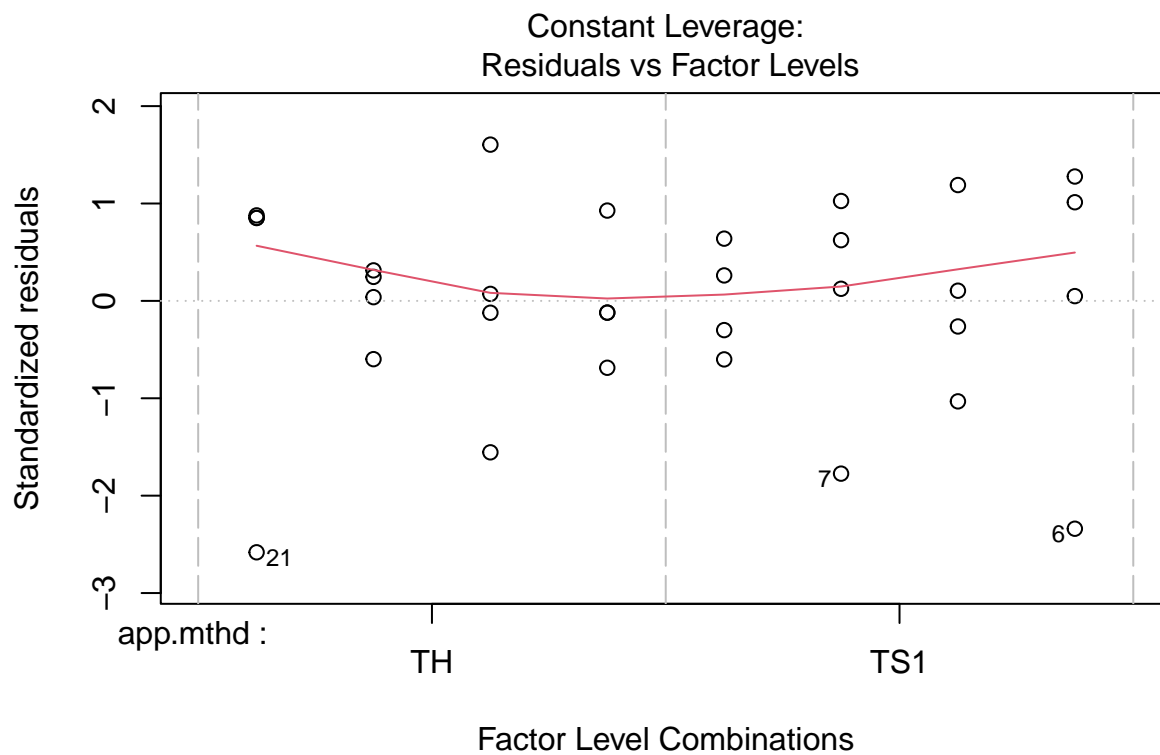
```r
summary(m3, test = 'F')
```

```
##                 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
```

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


Residuals vs Fitted

Fitted values
lm(log10(e.rel.150) ~ app.mthd * speed * new.ID)
```

Q–Q Residuals

Theoretical Quantiles
lm(log10(e.rel.150) ~ app.mthd * speed * new.ID)

Scale–Location

Fitted values
lm(log10(e.rel.150) ~ app.mthd * speed * new.ID)

Constant Leverage:
Residuals vs Factor Levels

```
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
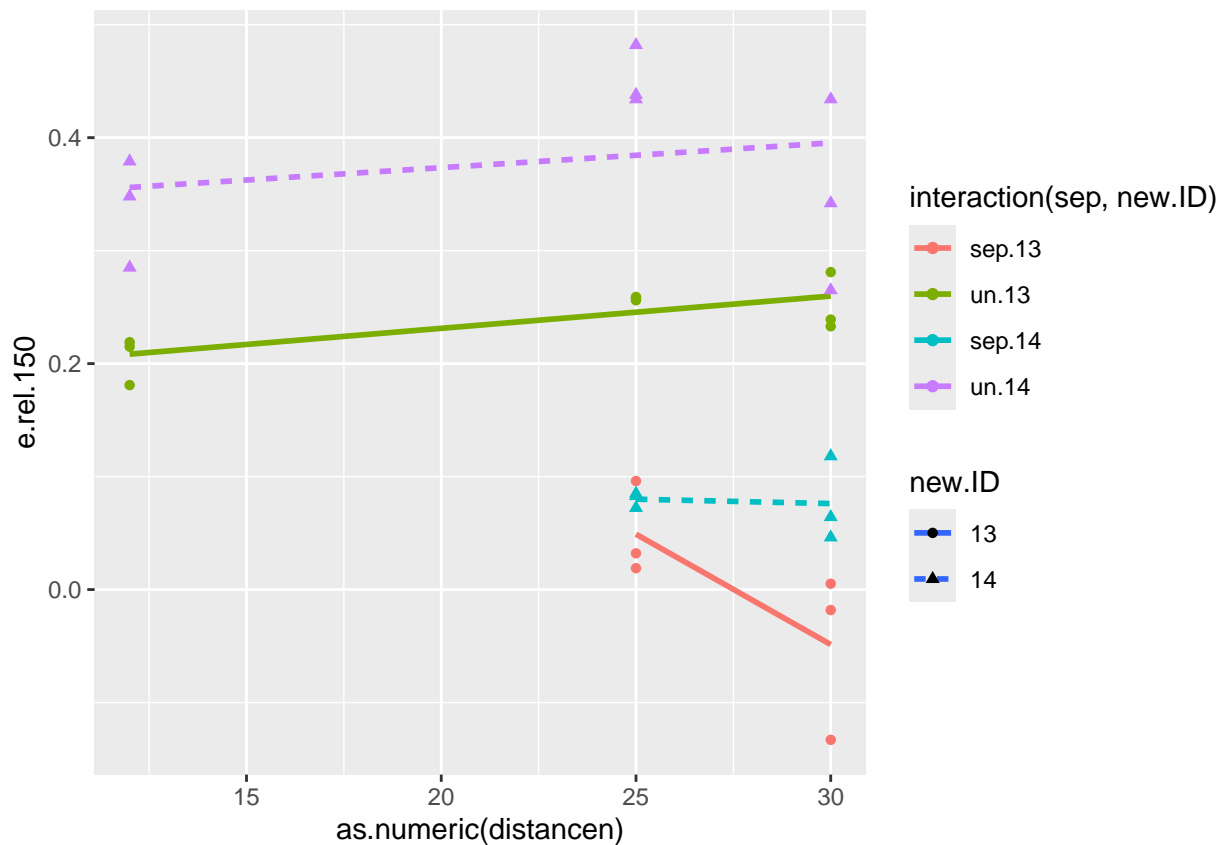## new.ID sep un
##     13   3  3
##     14   3  3
```

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
```

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```
## ---
## 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
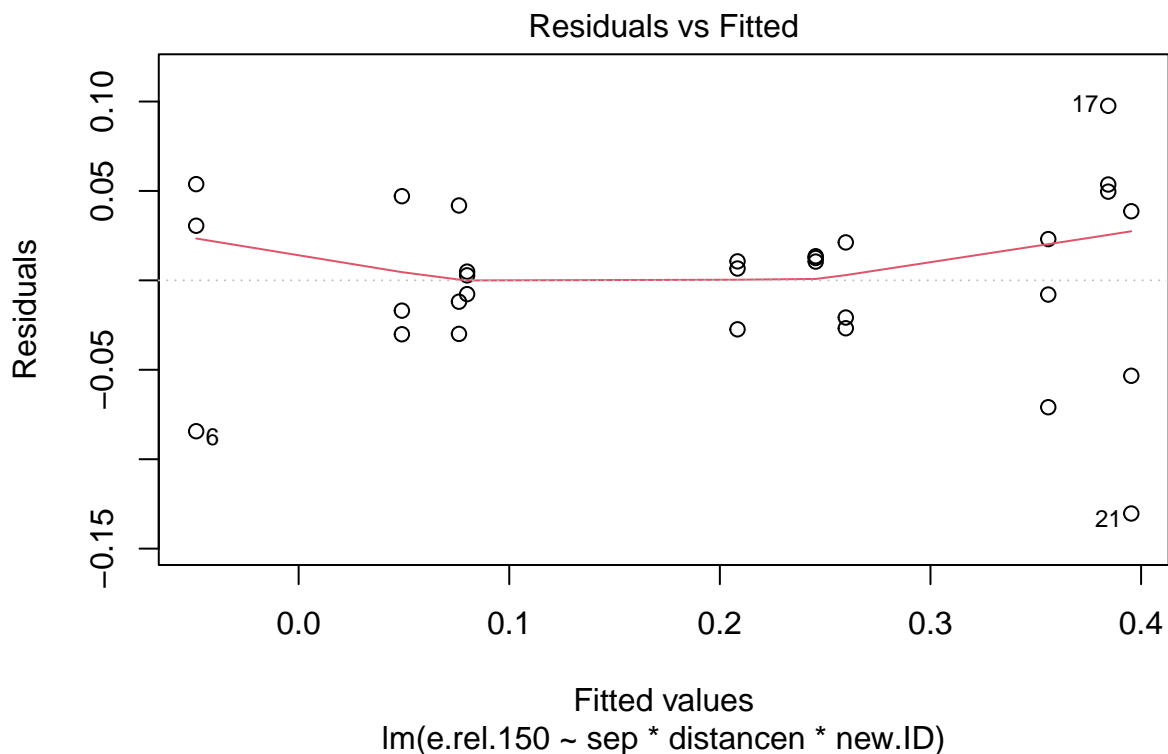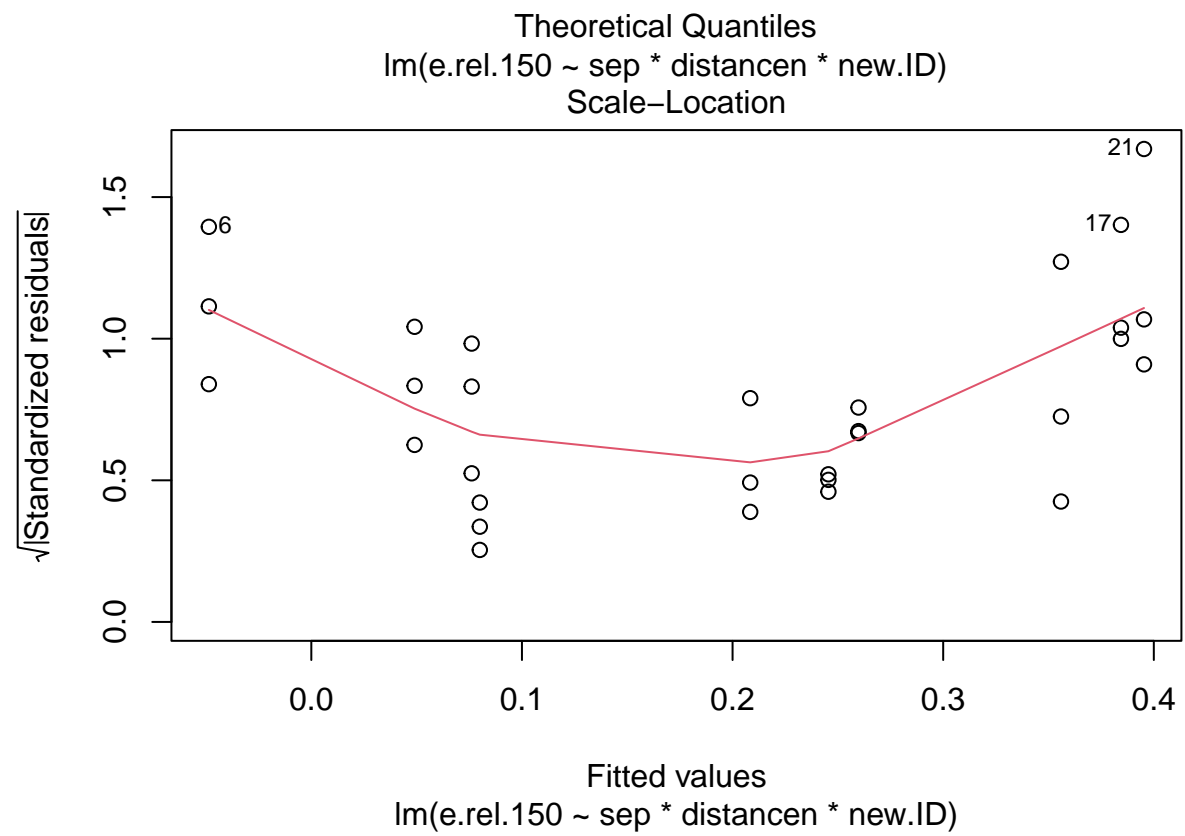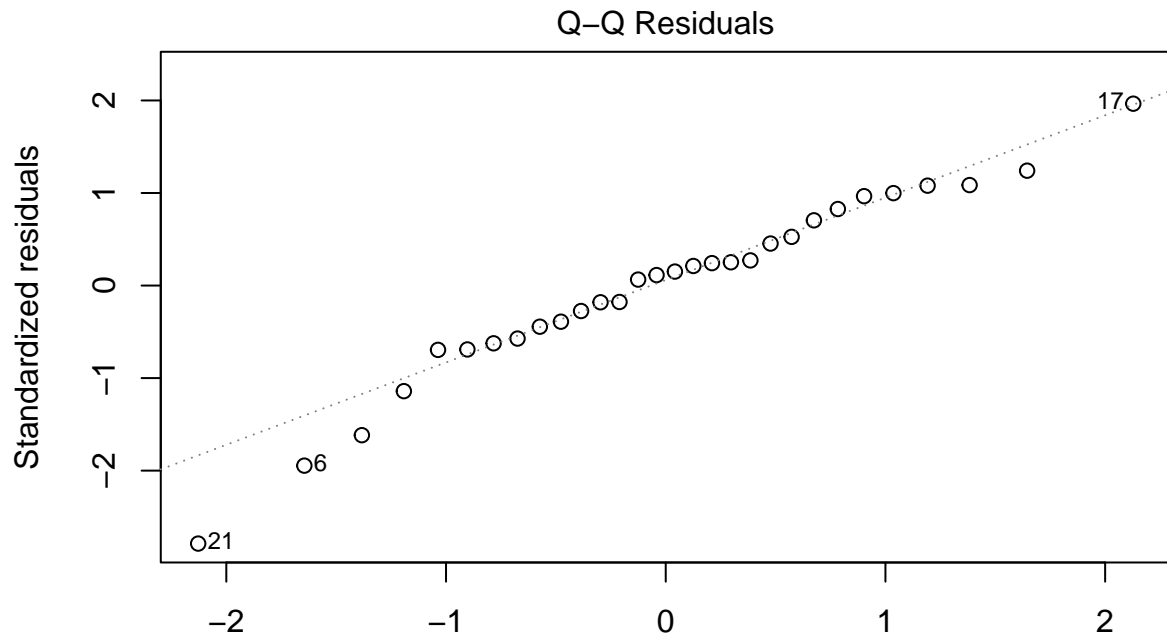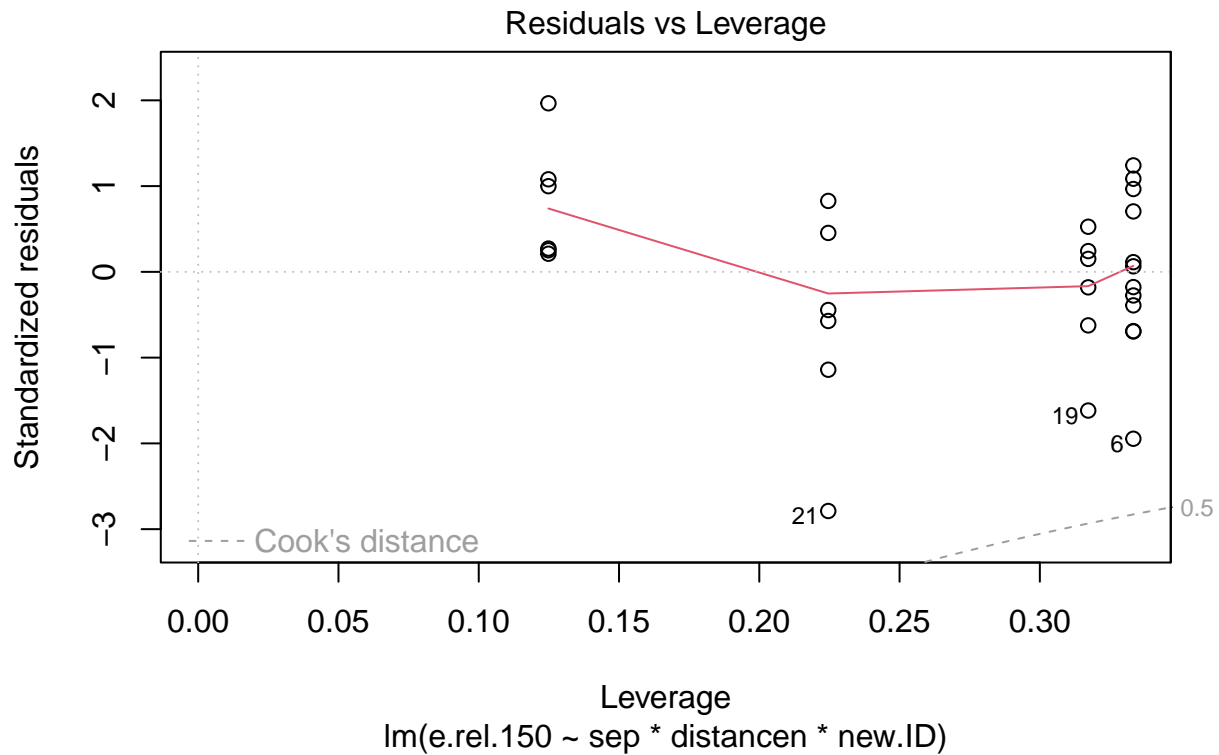```

**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)
```


Residuals vs Fitted

Fitted values
lm(e.rel.150 ~ sep * distancen * new.ID)

Q–Q Residuals

Theoretical Quantiles
lm(e.rel.150 ~ sep * distancen * new.ID)

Scale–Location

Fitted values
lm(e.rel.150 ~ sep * distancen * new.ID)

Residuals vs Leverage

lm(e.rel.150 ~ sep * distancen * new.ID)

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
```

Dunnett 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.ctrl')
```

```
##  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
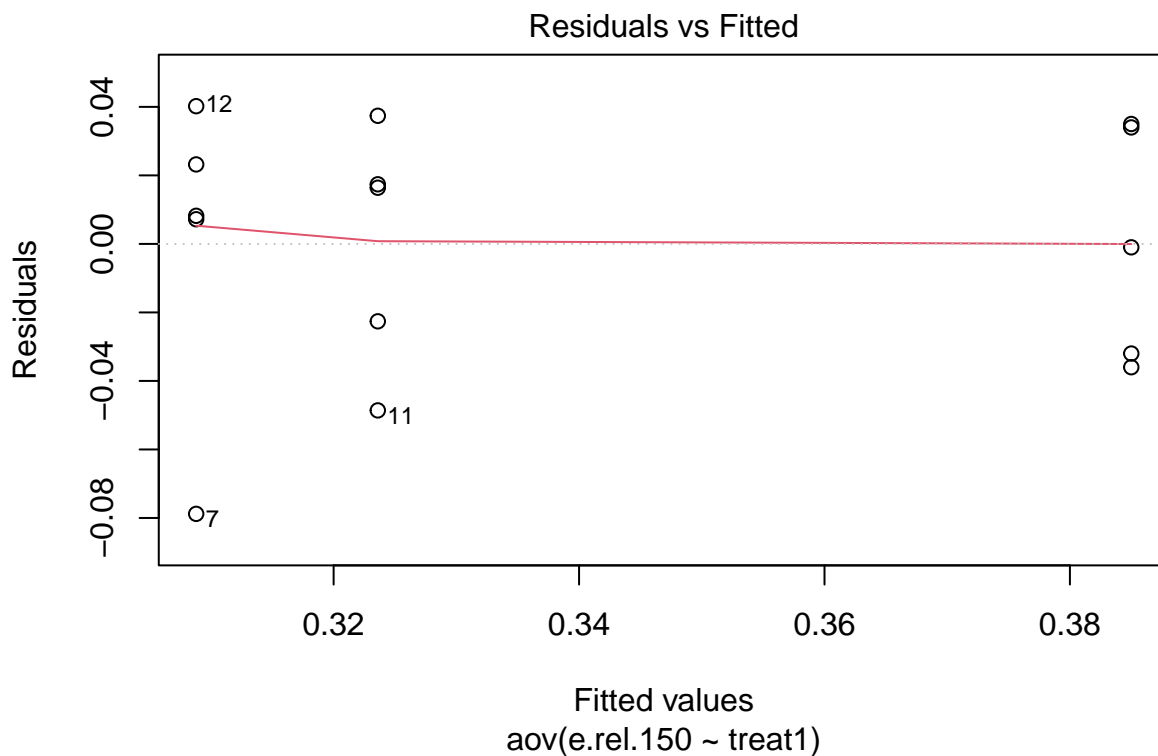```

Relative effects.

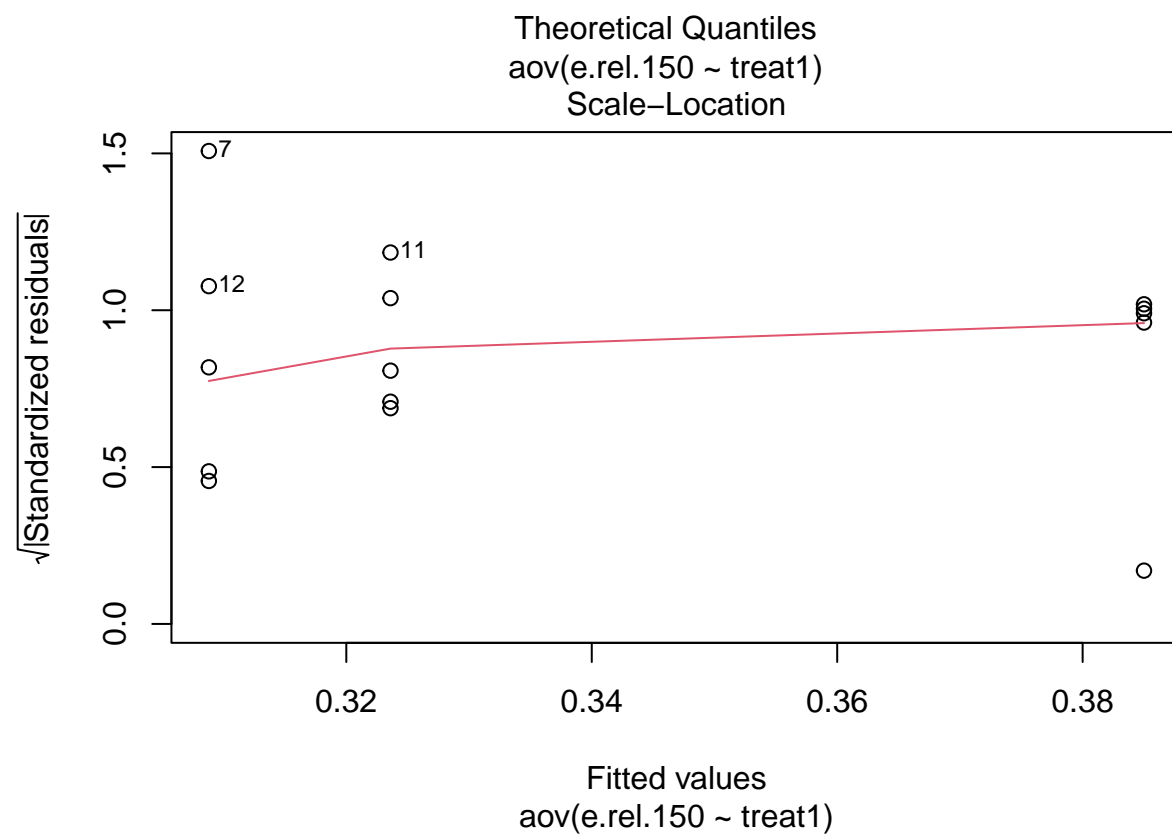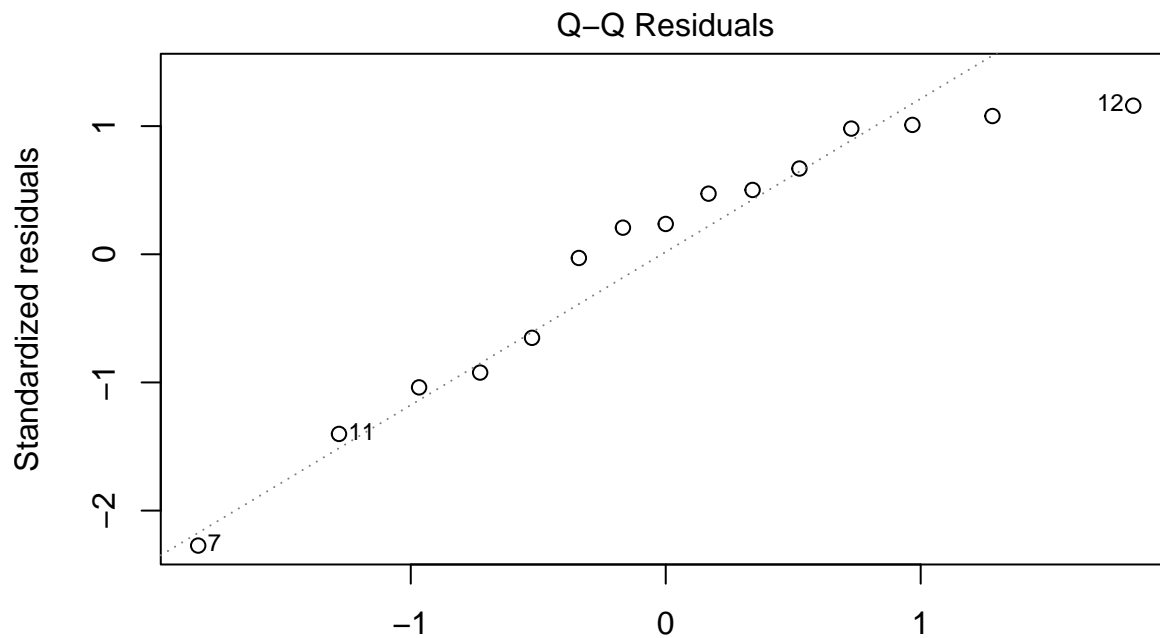```
coef(m1)
```

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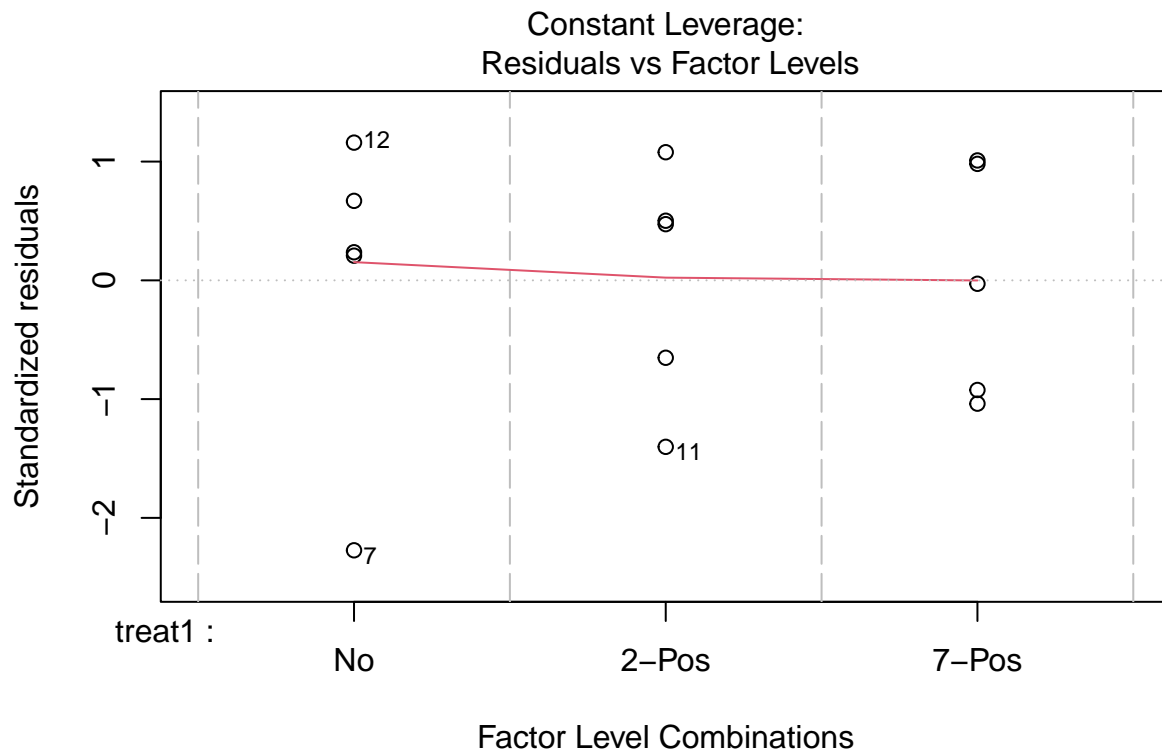## (Intercept) treat12-Pos treat17-Pos
##      0.3088      0.0148      0.0762
```

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

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

```
plot(m1)
```


Residuals vs Fitted

Fitted values
aov(e.rel.150 ~ treat1)

Q–Q Residuals

Standardized residuals

Theoretical Quantiles
aov(e.rel.150 ~ treat1)

Scale–Location

√|Standardized residuals|

Fitted values
aov(e.rel.150 ~ treat1)

Constant Leverage:
Residuals vs Factor Levels

Other stuff

I still need to sort this stuff out!

Then temperature stuff Add to supporting material