Statistical analysis

Sasha D. Hafner

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Data table

```
setDT(isumm)
```

Trials 1-4 (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.

```
m1 <- lmer(e.rel.150 ~ dig.treat + (1|dig.ID), data = isumm1)
m2 <- lmer(e.rel.150 ~ dig.treat + (1|dig.ID/dig.treat), data = isumm1)
```

```
summary(m1)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ dig.treat + (1 | dig.ID)
##    Data: isumm1
##
## REML criterion at convergence: -115.8
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.7502 -0.6560  0.1046  0.4727  2.5661
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  dig.ID   (Intercept) 0.010730 0.10359
##  Residual             0.003904 0.06248
```

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```
## Number of obs: 61, groups:  dig.ID, 3
##
## Fixed effects:
##                       Estimate Std. Error t value
## (Intercept)            0.43276    0.06161   7.024
## dig.treat Acid        -0.09302    0.02951  -3.152
## dig.treat Dis         -0.01167    0.03943  -0.296
## dig.treat Dis + acid  -0.08434    0.03943  -2.139
## dig.treat MF liquid   -0.31010    0.03943  -7.864
## dig.treat MF slurry    0.07933    0.03943   2.012
## dig.treat Sep-D       -0.30184    0.02609 -11.570
## dig.treat Sep-D + acid -0.33230   0.03943  -8.427
## dig.treat Sep-S       -0.12468    0.02769  -4.503
## dig.treat Sep-S + acid -0.20570   0.04179  -4.922
##
## 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 -0.095
## dig.treatDs -0.062  0.148
## dg.trtDs+ac -0.062  0.148  0.163
## dg.trtMFlqd -0.062  0.148  0.163  0.163
## dg.trtMFslr -0.062  0.148  0.163  0.163  0.163
## dig.trtSp-D -0.127  0.182  0.198  0.198  0.198  0.198
## dg.trSp-D+a -0.062  0.148  0.163  0.163  0.163  0.163  0.198
## dig.trtSp-S -0.099  0.261  0.168  0.168  0.168  0.168  0.207  0.168
## dg.trSp-S+a -0.076  0.217  0.055  0.055  0.055  0.055  0.070  0.055   0.210
```

summary(m2)

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: e.rel.150 ~ dig.treat + (1 | dig.ID/dig.treat)
##    Data: isumm1
##
## REML criterion at convergence: -122.4
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.0310 -0.5222  0.1171  0.4283  2.5808
##
## Random effects:
##  Groups           Name        Variance Std.Dev.
##  dig.treat:dig.ID (Intercept) 0.003286 0.05733
##  dig.ID           (Intercept) 0.011537 0.10741
##  Residual                     0.003057 0.05529
## Number of obs: 61, groups:  dig.treat:dig.ID, 15; dig.ID, 3
##
## Fixed effects:
##                       Estimate Std. Error t value
## (Intercept)           0.420186   0.071655   5.864
## dig.treat Acid       -0.076441   0.060889  -1.255
## dig.treat Dis         0.006601   0.079240   0.083
## dig.treat Dis + acid -0.066065   0.079240  -0.834
## dig.treat MF liquid  -0.291832   0.079240  -3.683
## dig.treat MF slurry   0.097601   0.079240   1.232
```

```
## dig.treat Sep-D        -0.281026   0.059784  -4.701
## dig.treat Sep-D + acid -0.314032   0.079240  -3.963
## dig.treat Sep-S        -0.110120   0.060313  -1.826
## dig.treat Sep-S + acid -0.190816   0.081197  -2.350
##
## 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 -0.288
## dig.treatDs -0.220  0.306
## dg.trtDs+ac -0.220  0.306  0.314
## dg.trtMFlqd -0.220  0.306  0.314  0.314
## dg.trtMFslr -0.220  0.306  0.314  0.314  0.314
## dig.trtSp-D -0.303  0.300  0.300  0.300  0.300  0.300
## dg.trSp-D+a -0.220  0.306  0.314  0.314  0.314  0.314  0.300
## dig.trtSp-S -0.291  0.423  0.312  0.312  0.312  0.312  0.306  0.312
## dg.trSp-S+a -0.217  0.330  0.152  0.152  0.152  0.152  0.157  0.152   0.329
```

Check for interaction with odds ratio test (?).

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

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

```
## Data: isumm1
## Models:
## m1: e.rel.150 ~ dig.treat + (1 | dig.ID)
## m2: e.rel.150 ~ dig.treat + (1 | dig.ID/dig.treat)
##     npar     AIC     BIC logLik deviance  Chisq Df Pr(>Chisq)
## m1    12 -140.87 -115.54 82.436  -164.87
## m2    13 -139.54 -112.10 82.769  -165.54 0.6652  1     0.4147
```

No evidence, good!

Plot to check.

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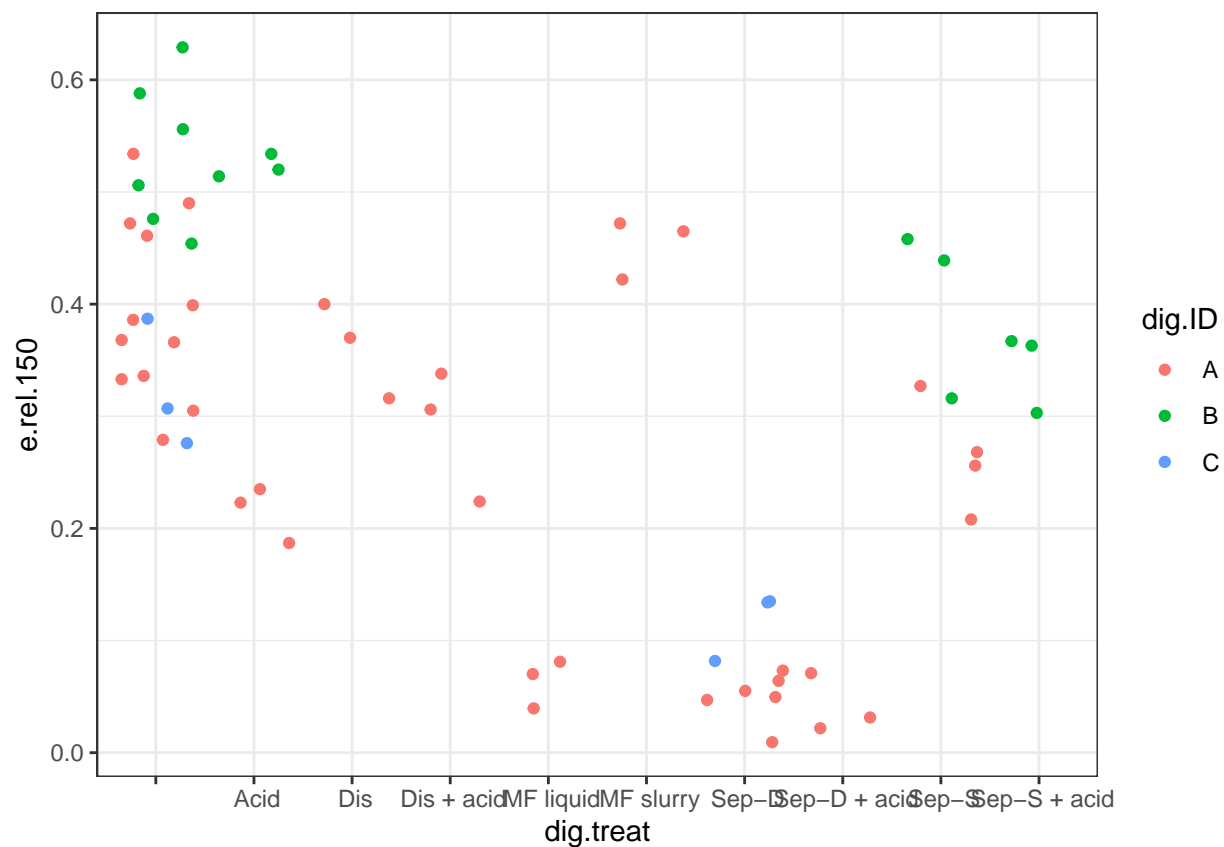
Hmm.

```
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
```

Not close to balanced.

Marginal means.

```
mmeans <- emmeans(m1, 'dig.treat')
mmeans
```

```
##  dig.treat      emmean      SE   df  lower.CL  upper.CL
##               0.433  0.0616 2.08    0.1772     0.688
##   Acid        0.340  0.0658 2.69    0.1159     0.564
##   Dis         0.421  0.0711 3.66    0.2161     0.626
```

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```
##    Dis + acid    0.348 0.0711 3.66    0.1434    0.553
##    MF liquid     0.123 0.0711 3.66   -0.0823    0.328
##    MF slurry     0.512 0.0711 3.66    0.3071    0.717
##    Sep-D         0.131 0.0638 2.39   -0.1049    0.367
##    Sep-D + acid  0.100 0.0711 3.66   -0.1045    0.305
##    Sep-S         0.308 0.0651 2.57    0.0800    0.536
##    Sep-S + acid  0.227 0.0720 3.79    0.0228    0.431
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

Need name for export.

Dunnett's test, all compared to untreated.

```
contrast(mmeans, 'dunnett', ref = '')
```

```
##  contrast            estimate     SE   df t.ratio p.value
##   Acid -              -0.0930 0.0296 49.2  -3.145  0.0211
##   Dis -               -0.0117 0.0395 49.1  -0.296  0.9978
##  ( Dis + acid) -      -0.0843 0.0395 49.1  -2.136  0.2161
##   MF liquid -         -0.3101 0.0395 49.1  -7.855  <.0001
##   MF slurry -          0.0793 0.0395 49.1   2.010  0.2714
##  ( Sep-D) -           -0.3018 0.0262 49.4 -11.514  <.0001
##  ( Sep-D + acid) -    -0.3323 0.0395 49.1  -8.418  <.0001
##  ( Sep-S) -           -0.1247 0.0277 49.2  -4.495  0.0004
##  ( Sep-S + acid) -    -0.2057 0.0420 49.5  -4.895  0.0001
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: dunnettx method for 9 tests
```

Residuals.

```
res <- resid(m1)
plot(fitted(m1), res)
abline(0,0)
```

```r
qqnorm(res)
qqline(res)
```

Normal Q–Q Plot
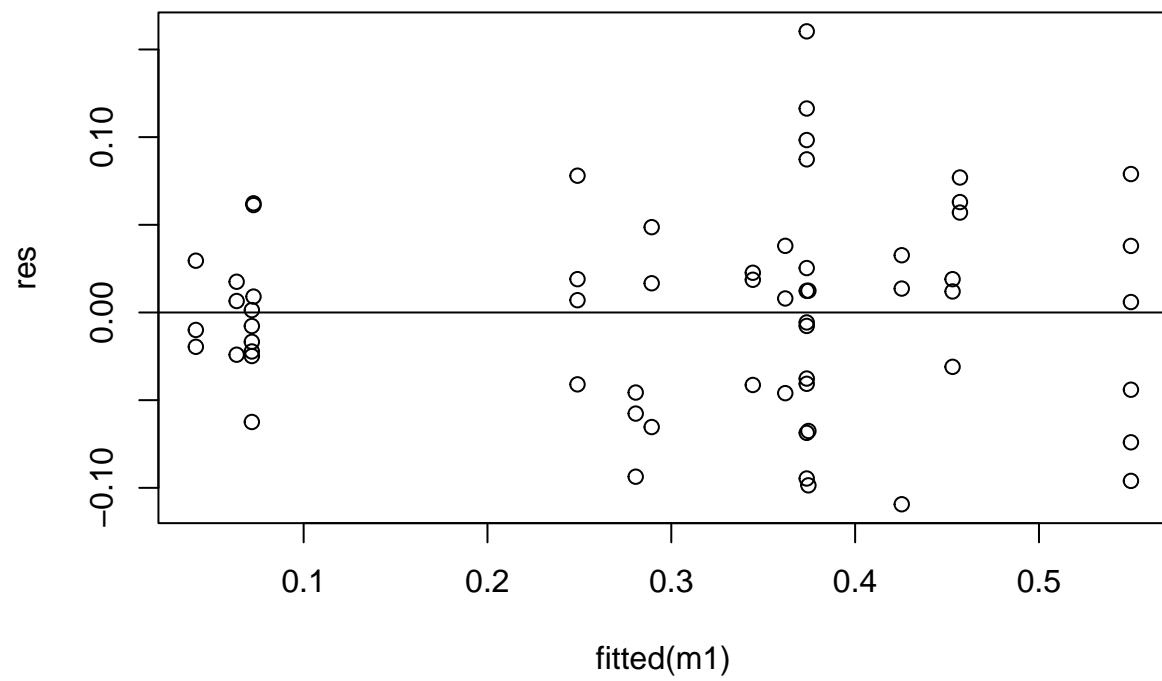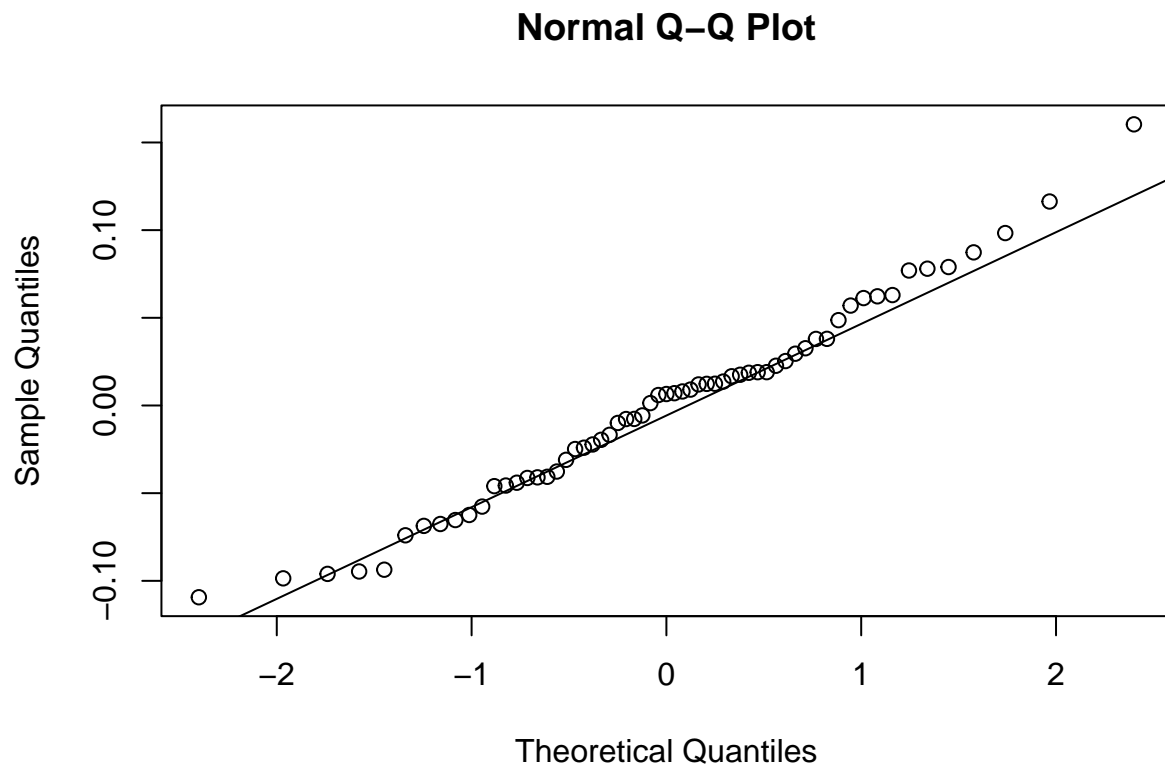
Trials 5-10 (app tech on winter wheat)

Subset.

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

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.
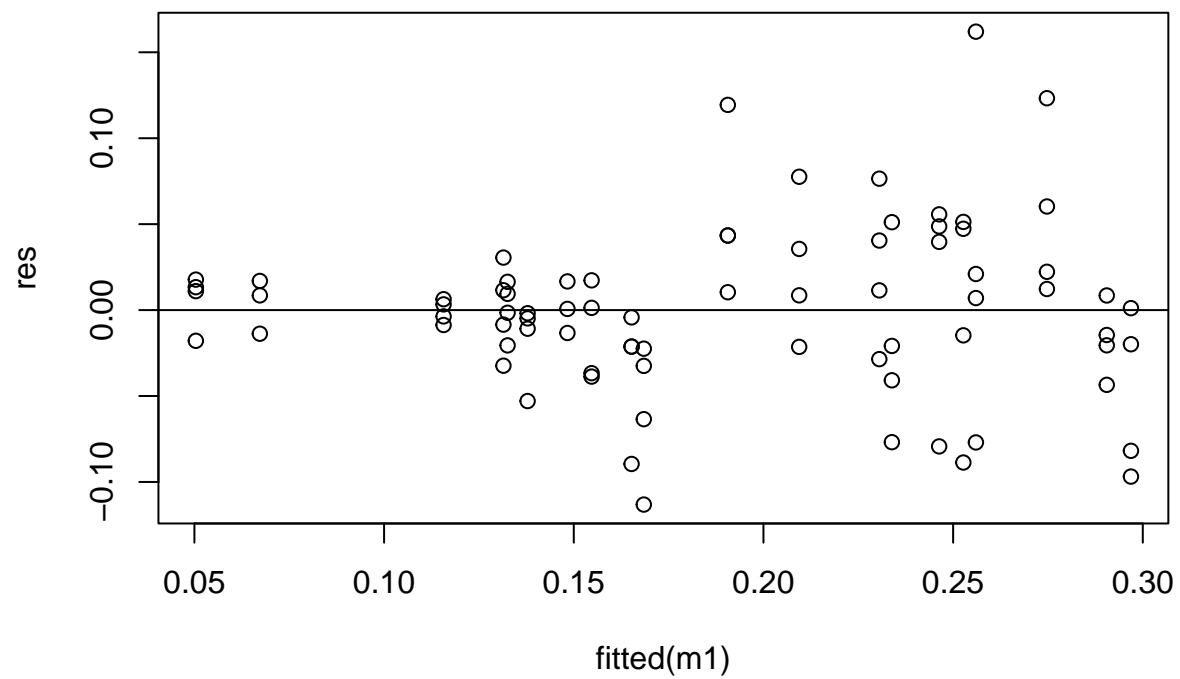
Tukey's test

```
pairs(mmeans)
```

```
##  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
```
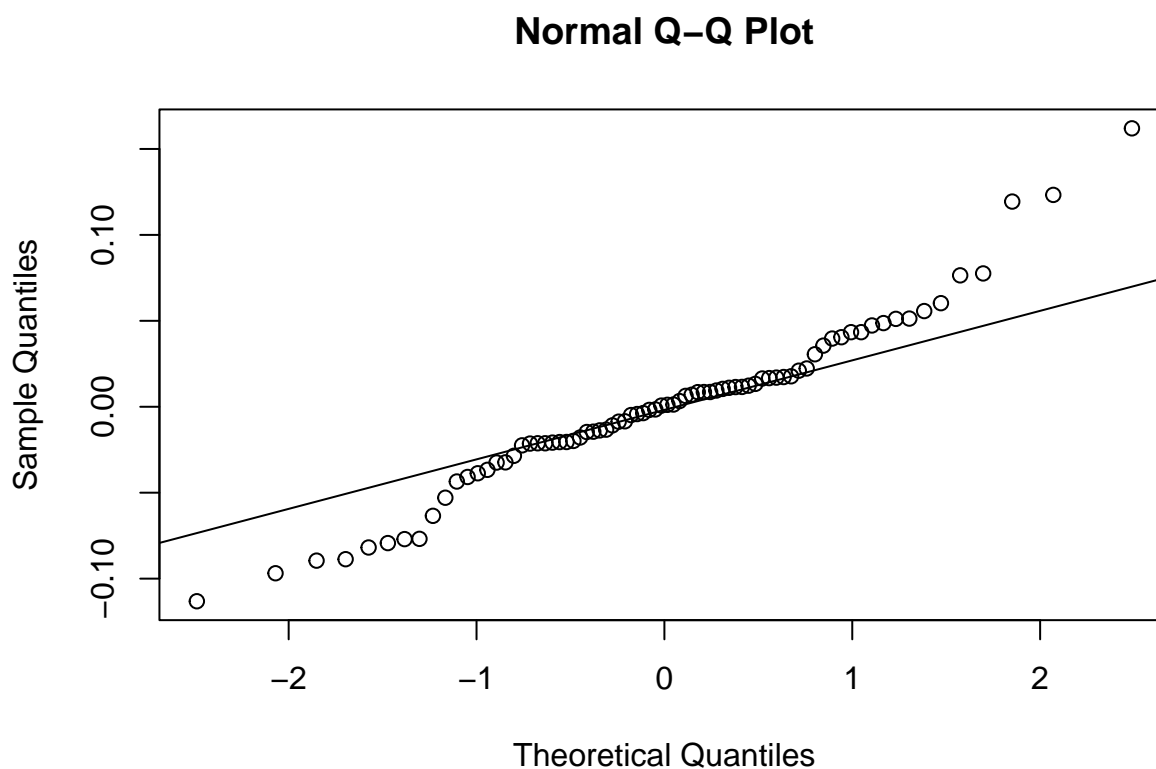
Residuals.

```r
res <- resid(m1)
plot(fitted(m1), res)
abline(0,0)
```



```r
qqnorm(res)
qqline(res)
```

Normal Q–Q Plot

Marginal means, export, save?

```
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
```

Tukey's test

```
pairs(mmeans)
```

```
##  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
```