

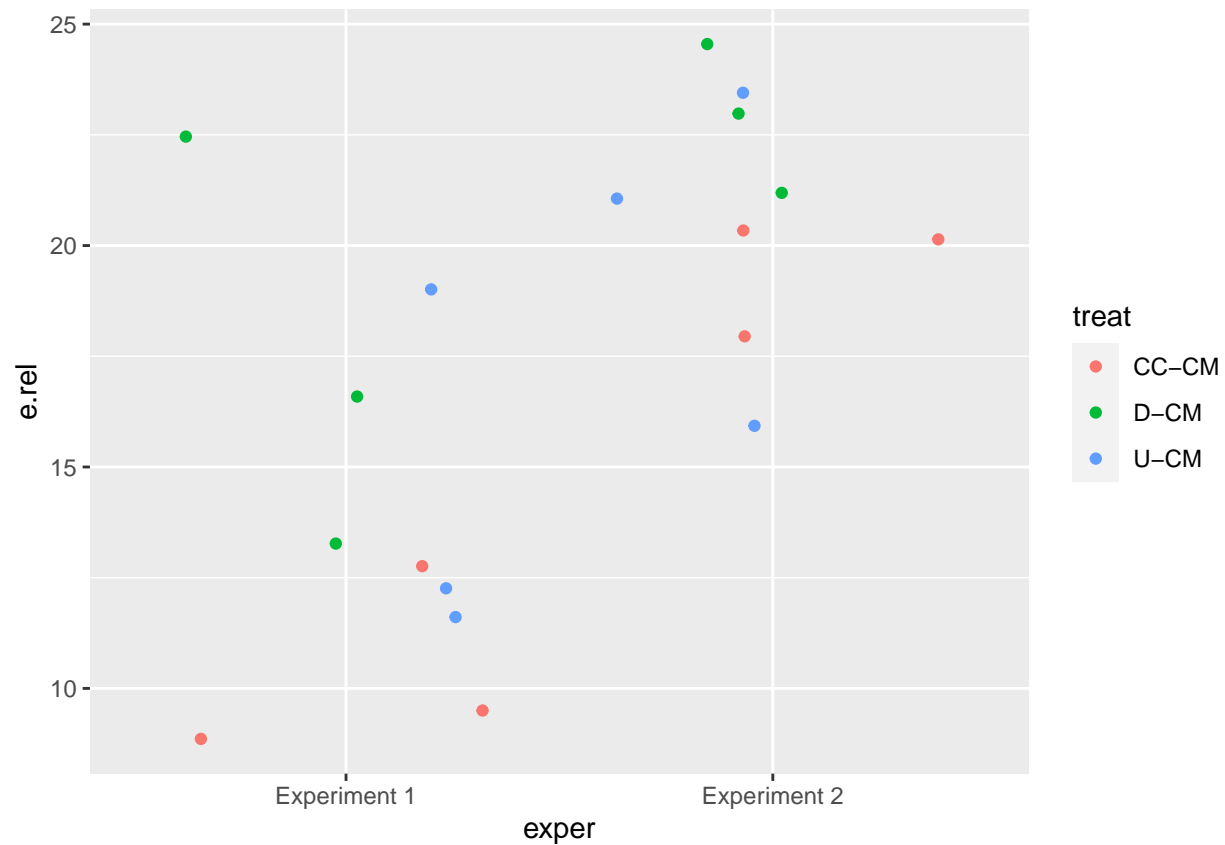
Data analysis for digestate experiments

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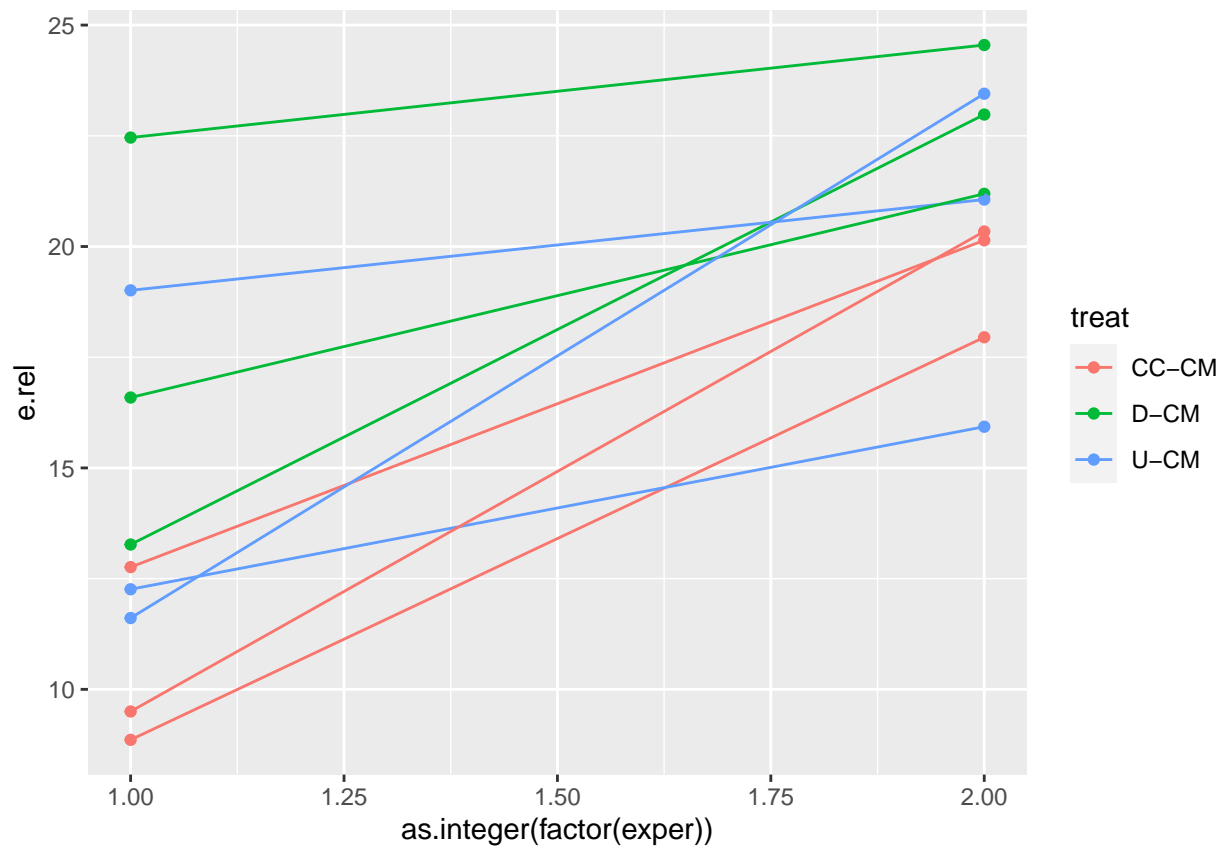
14 October, 2022

Plots

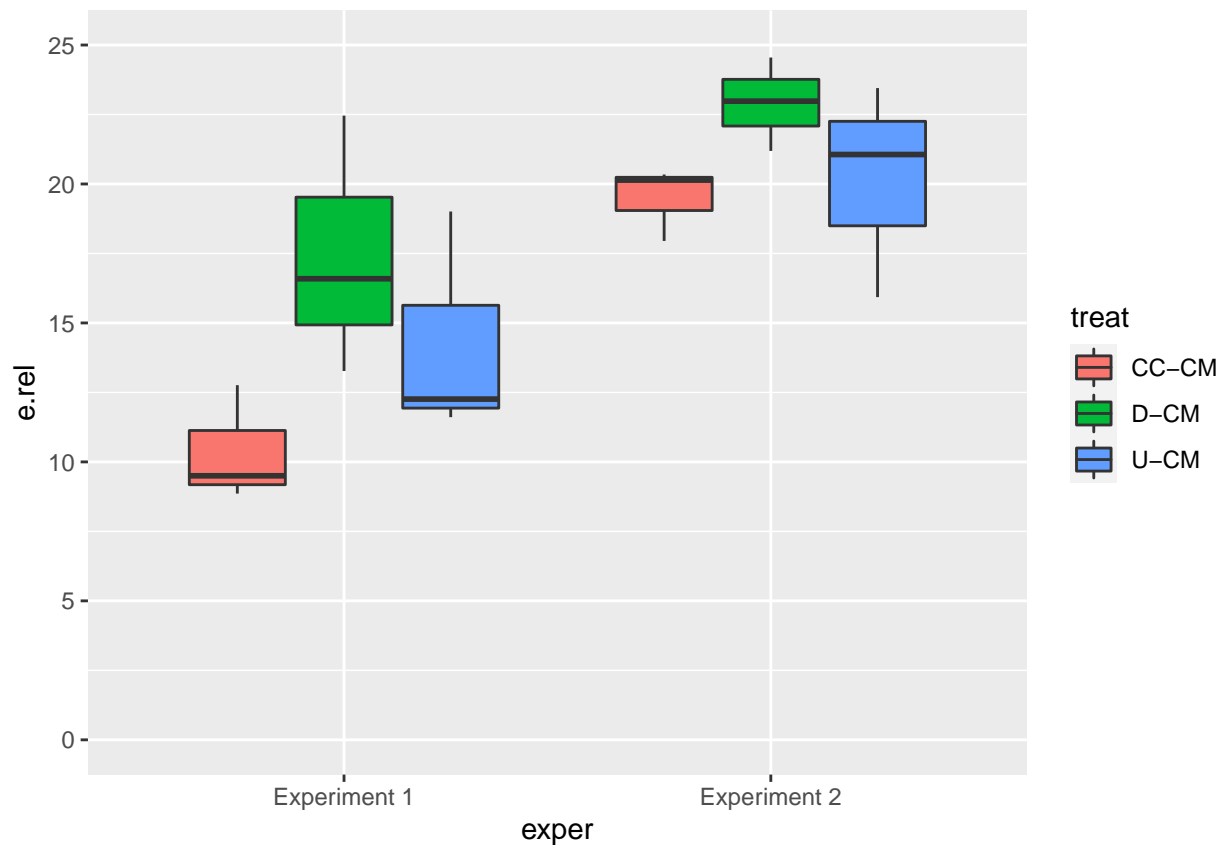
```
ggplot(dat, aes(exper, e.rel, colour = treat)) +  
  geom_jitter(height = 0)
```



```
ggplot(dat, aes(as.integer(factor(exper)), e.rel, colour = treat, group = interaction(treat, rep))) +  
  geom_point() +  
  geom_line()
```



```
ggplot(dat, aes(exper, e.rel, fill = treat)) +
  geom_boxplot() +
  ylim(0, 25)
```



Stats

Set reference to untreated cattle manure.

```
dat$treat <- factor(dat$treat, levels = c('U-CM', 'CC-CM', 'D-CM'))
```

```
m1 <- aov(e.rel ~ treat + exper, data = dat)
```

```
summary(m1)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## treat         2   83.07    41.53    4.266 0.035753 *
## exper         1  208.56   208.56   21.421 0.000391 ***
## Residuals    14  136.31     9.74
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary.lm(m1)
```

```
##
## Call:
## aov(formula = e.rel ~ treat + exper, data = dat)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.6939 -2.1599 -0.2792  1.6681  5.6906
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)          13.816      1.471    9.393 2.02e-07 ***
## treatCC-CM           -2.295      1.801   -1.274 0.223428
## treatD-CM            2.953      1.801    1.639 0.123404
## experExperiment 2     6.808      1.471    4.628 0.000391 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.12 on 14 degrees of freedom
## Multiple R-squared:  0.6815, Adjusted R-squared:  0.6132
## F-statistic: 9.984 on 3 and 14 DF,  p-value: 0.0008875
```

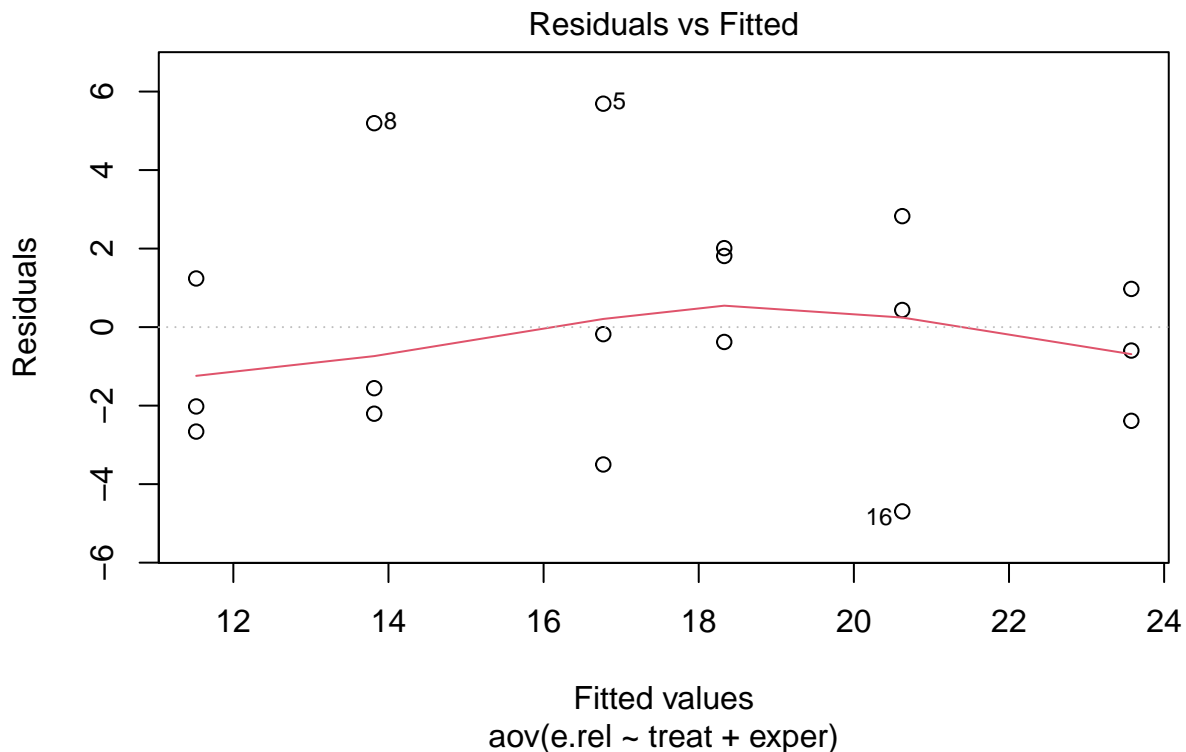
```
TukeyHSD(m1, 'treat')
```

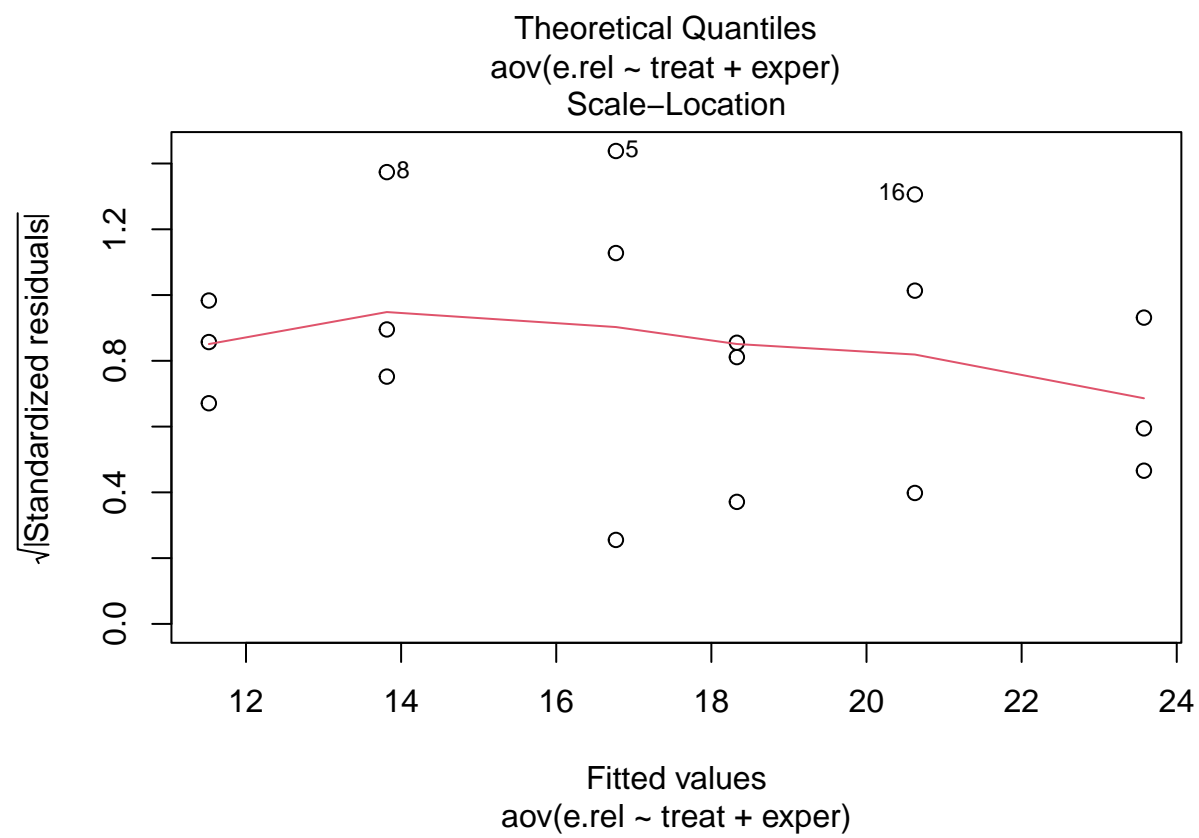
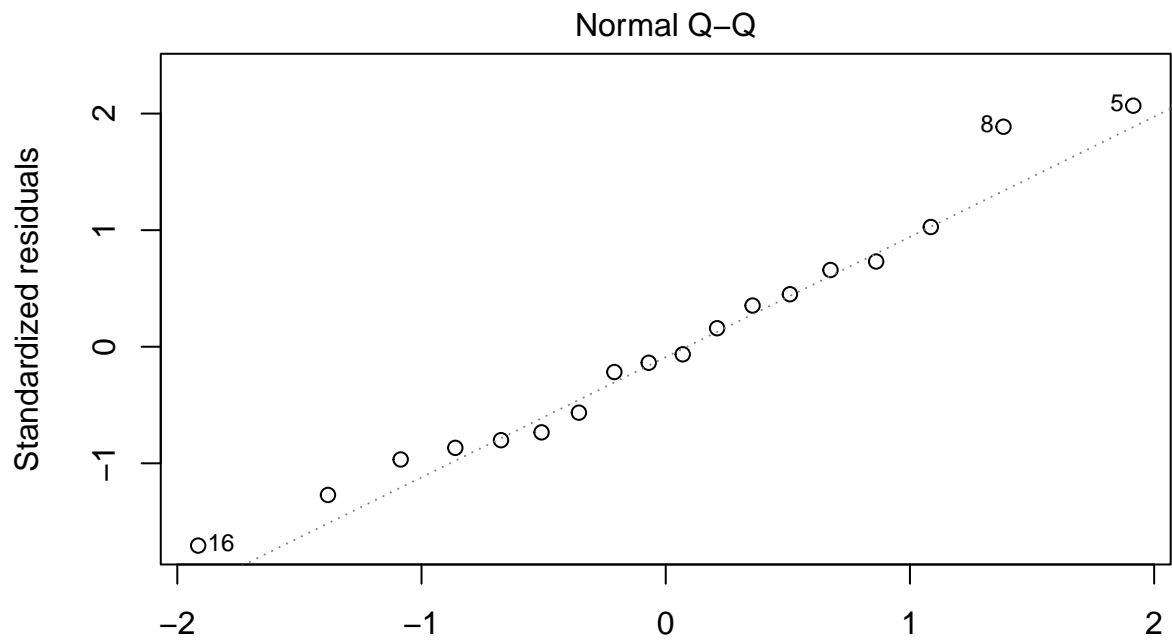
```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = e.rel ~ treat + exper, data = dat)
##
## $treat
##          diff          lwr          upr      p adj
## CC-CM-U-CM -2.295000 -7.0100259 2.420026 0.4319990
## D-CM-U-CM   2.953333 -1.7616926 7.668359 0.2624483
## D-CM-CC-CM  5.248333  0.5333074 9.963359 0.0286801
```

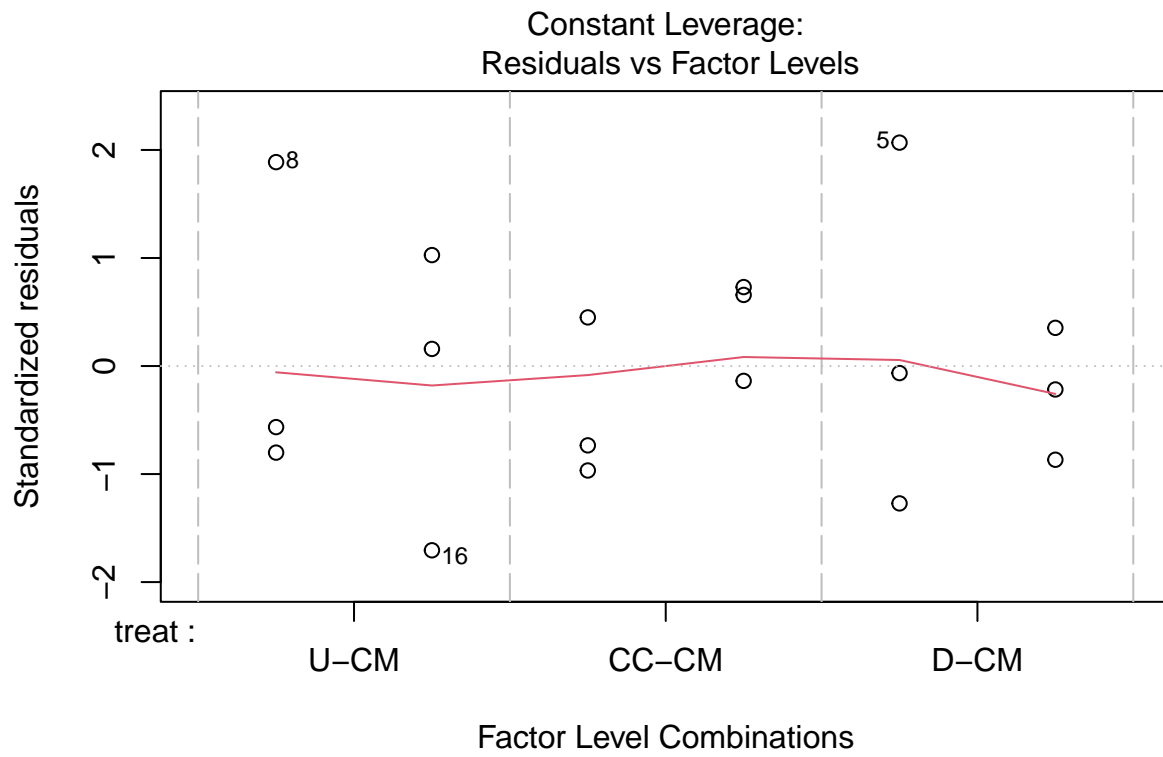
CC-CM and D-CM are clearly different. But neither is clearly different from the reference. Makes interpretation just a bit tricky. Some evidence of a difference but presumably digestion pH effect is moderated by low DM, and variability was high, so power is low.

Check residuals.

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







Looks fine, no need to transform.