Data analysis for digestate experiments

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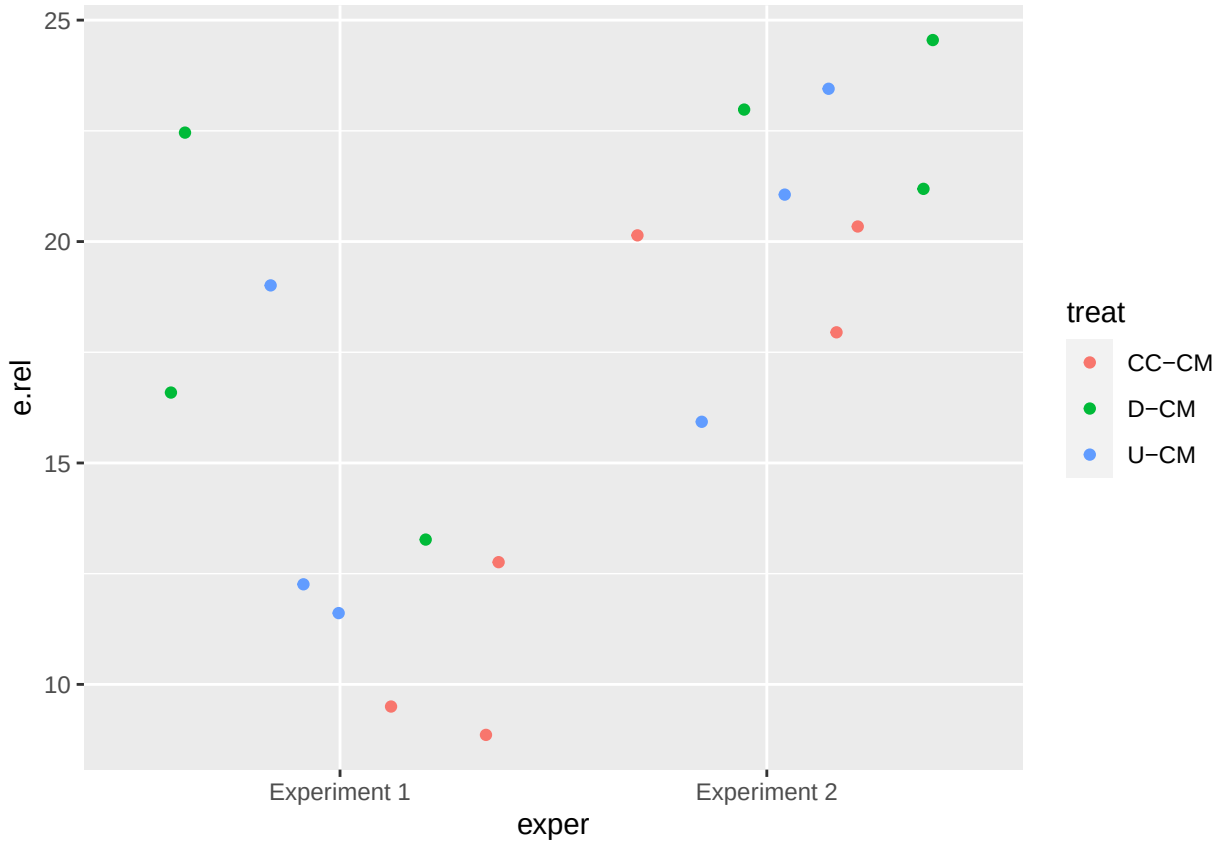
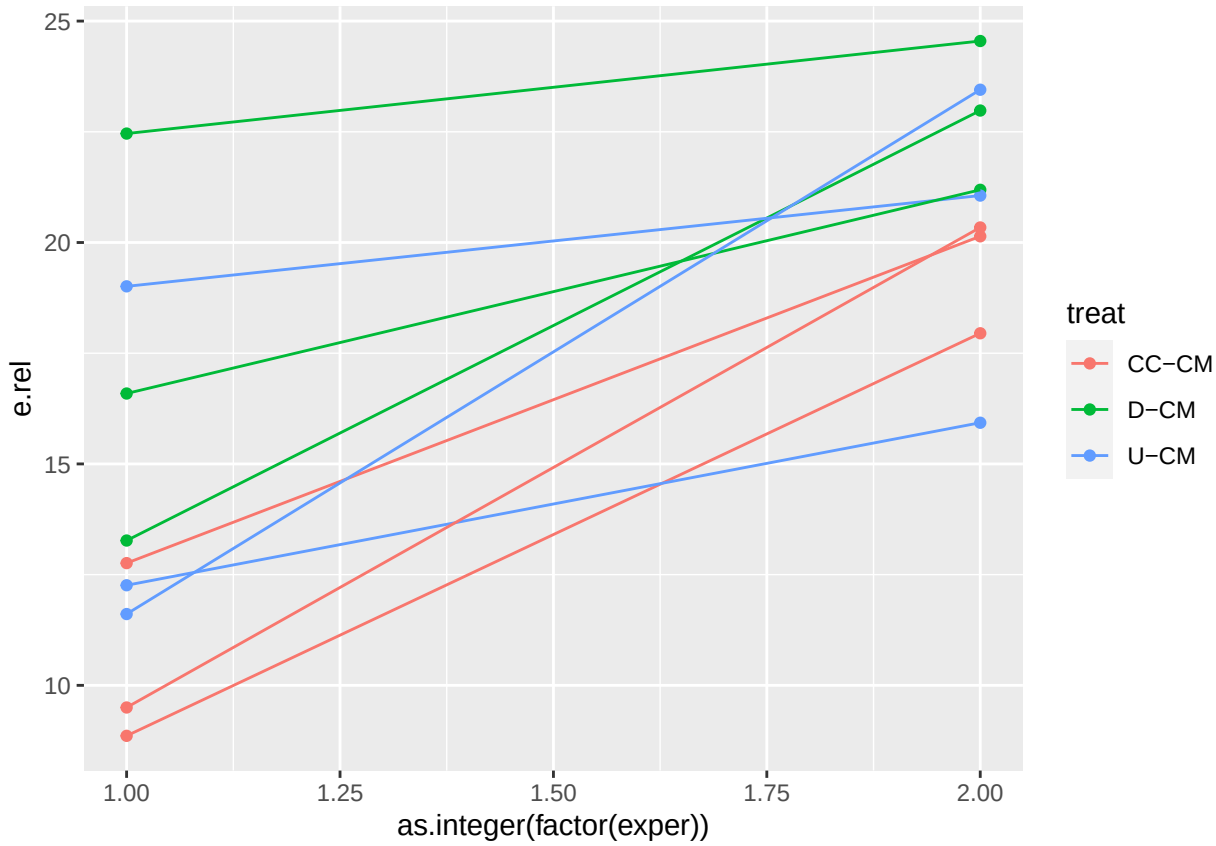
Plots

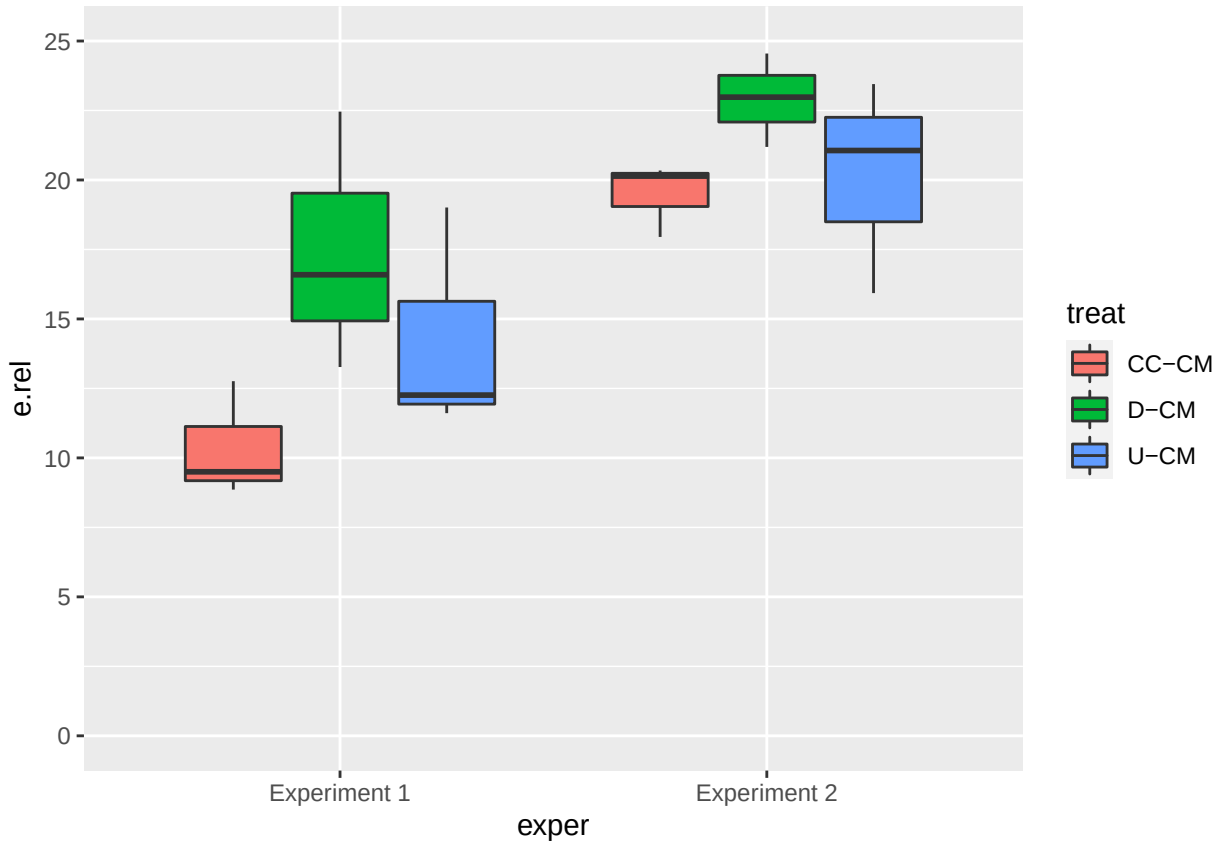
```
ggplot(dat, aes(exper, e.rel, colour = treat)) +
  geom_jitter(height = 0)
```




```
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

```
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)        11.521      1.471   7.833 1.75e-06 ***
## treatD-CM           5.248      1.801   2.913 0.011340 *
```

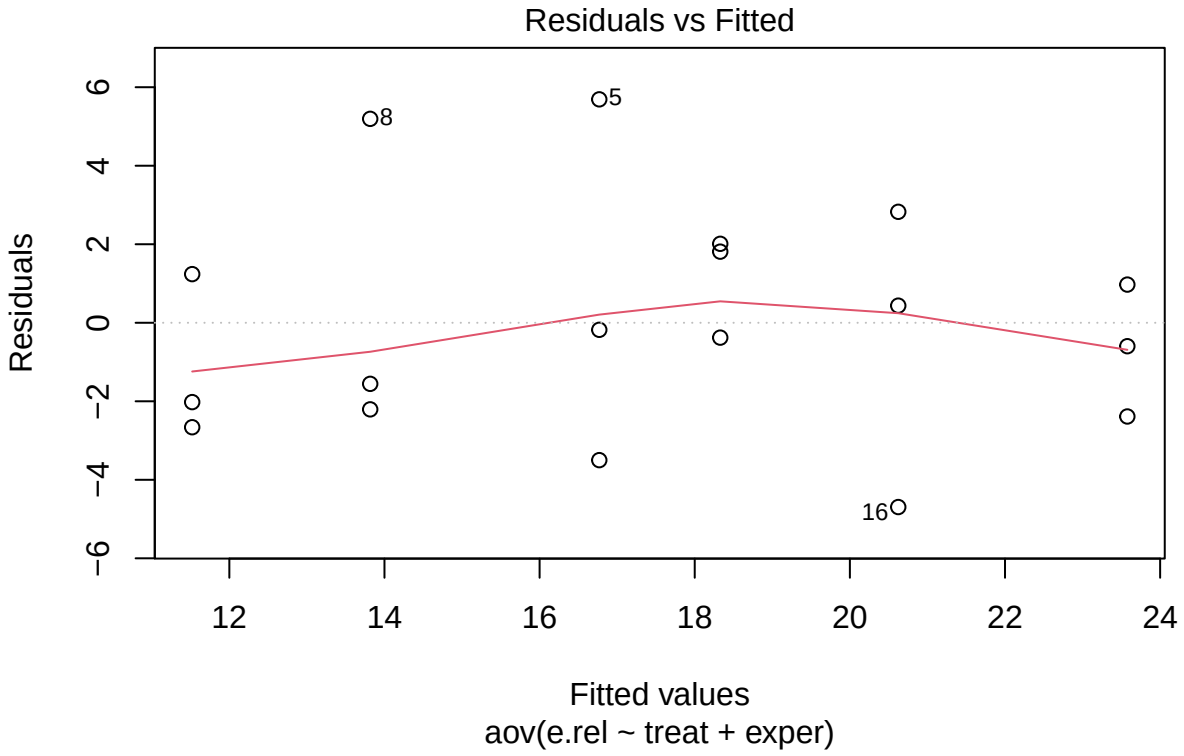
```
## treatU-CM            2.295      1.801   1.274 0.223428
## experExperiment 2    6.808      1.471   4.628 0.000391 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.12 on 14 degrees of freedom
## Multiple R-squared:  0.6815, Adjusted R-squared:  0.6132
## F-statistic: 9.984 on 3 and 14 DF,  p-value: 0.0008875
```

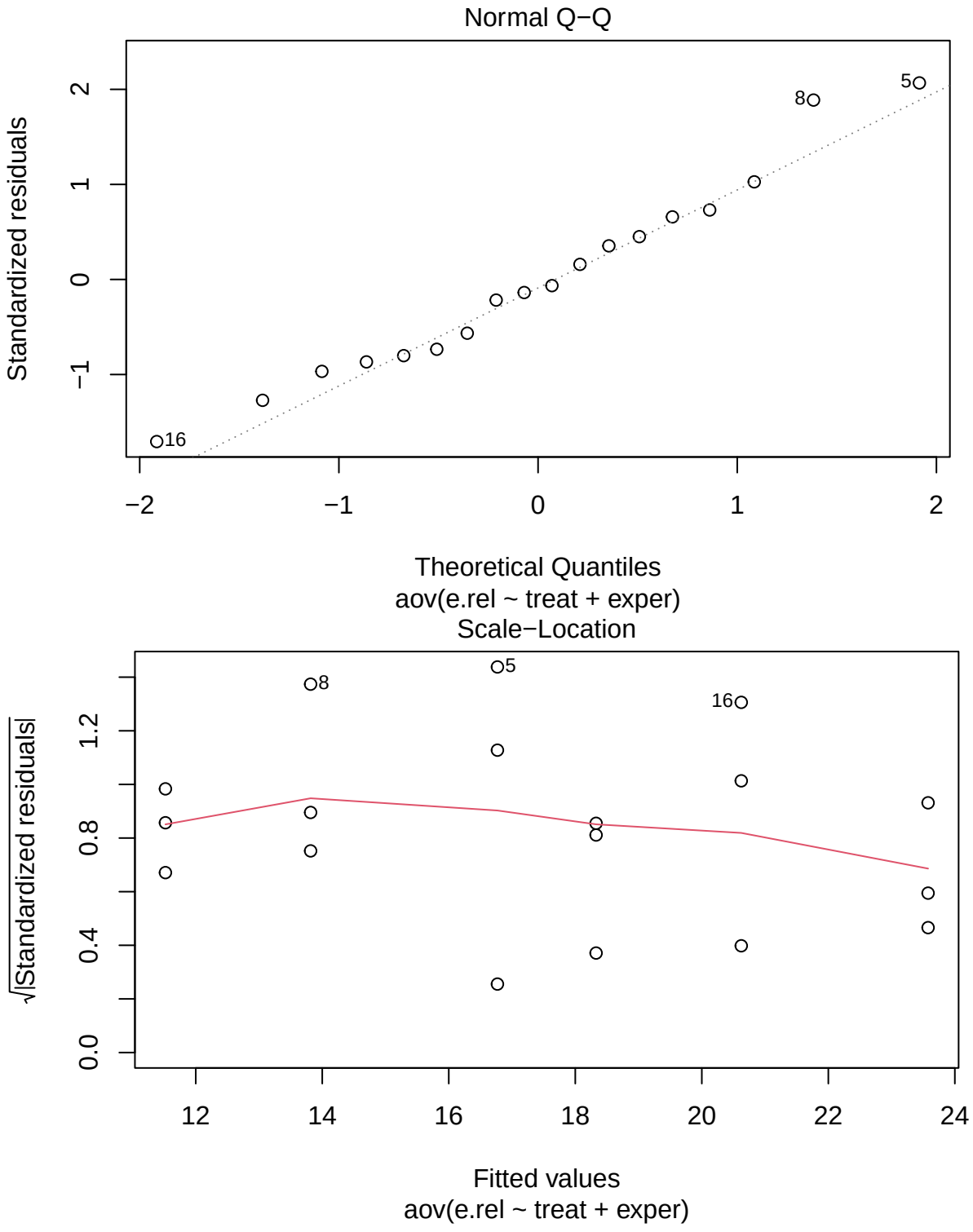
```
TukeyHSD(m1, 'treat')
```

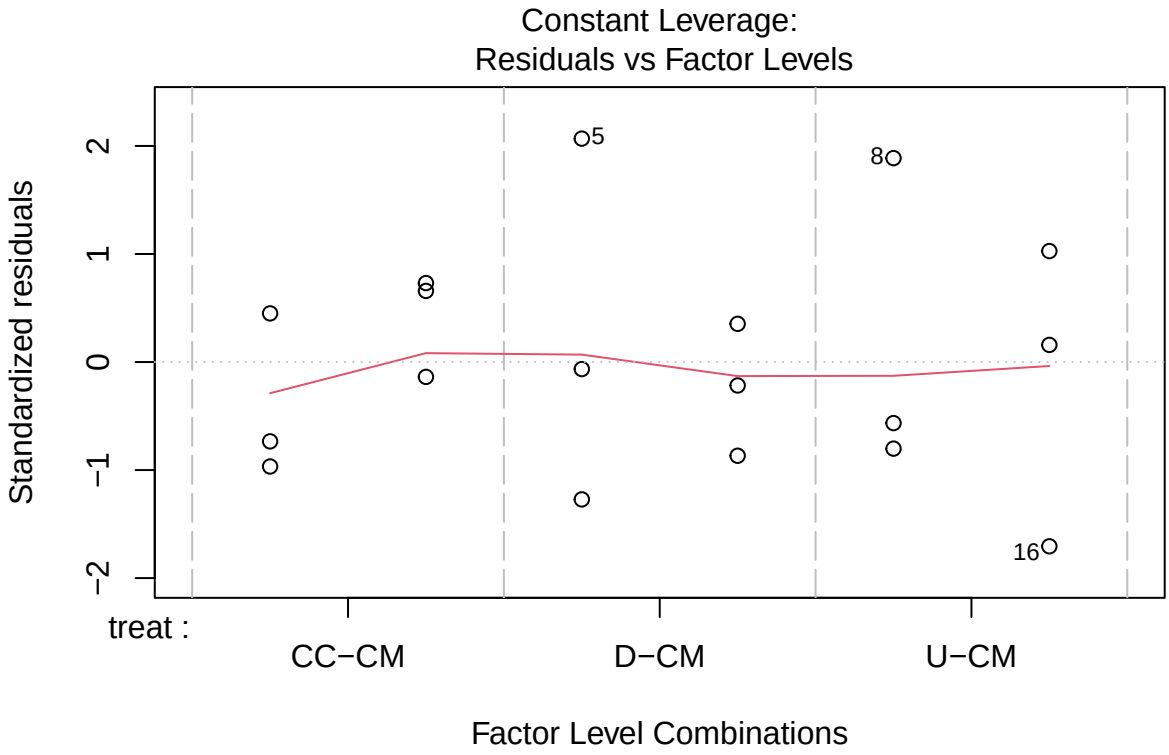
```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = e.rel ~ treat + exper, data = dat)
##
## $treat
##                 diff        lwr      upr     p adj
## D-CM-CC-CM  5.248333  0.5333074 9.963359 0.0286801
## U-CM-CC-CM  2.295000 -2.4200259 7.010026 0.4319990
## U-CM-D-CM  -2.953333 -7.6683592 1.761693 0.2624483
```

Check residuals.

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




Normal Q−Q
Standardized residuals
Theoretical Quantiles
aov(e.rel ~ treat + exper)
Scale−Location
√|Standardized residuals|
Fitted values
aov(e.rel ~ treat + exper)



Looks fine, no need to transform.

CC-CM and D-CM are clearly different.