Replication

BIOE 498/598 PJ

Spring 2022

Why replication?

1. Reduce noise effects.
2. Estimate confidence intervals for effect sizes.
3. Analyze dispersion effects.

Does noise matter?

```r
data <- read.csv("LeafSpring.csv")
data1 <- data[ 1:16, ]
data2 <- data[17:32, ]
data3 <- data[33:48, ]
```

Effect sizes differ for each replicate

Replicate 1

```
##          B     .09937
##          C     .09313
##          Q    -.08688
##        C:Q    -.07563
##        B:Q     .07313
##          E     .07312
##      B:D:Q    -.06687
##          D     .05688
##        C:D     .04313
##        D:Q     .02312
```

Replicate 2

```
##          Q    -.14688
##          B     .12937
##          C     .11063
##        C:Q    -.07688
##        D:Q     .06687
##          E     .06312
##      C:D:Q    -.05063
##        B:Q     .04438
##        B:C     .04187
##        C:D    -.02812
```

Duplicates vs. Replicates

- We use replicates to estimate **confidence intervals** for effect sizes.
- More replicates = narrower confidence intervals
- Treating duplicates as replicates artificially narrows the confidence intervals for two reasons.
  1. Inflating the degrees of freedom fakes additional statistical power
  2. Duplicates typically have less variation than replicates

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- Treating duplicates as replicates artificially narrows the confidence intervals for two reasons.
    1. Inflating the degrees of freedom fakes additional statistical power
    2. Duplicates typically have less variation than replicates
- Statistical significance $\neq$ Practical significance

Sample variance across replicates

If a run is replicated r times with responses y_1, y_2, ..., y_r and mean $\bar{y}$,

$$\text{sample variance} = s^2 = \frac{\sum_i^r (y_i - \bar{y})^2}{r-1}$$

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For a factorial design with N *unreplicated* runs ($N = 2^k$ for a full factorial or $N = 2^{k-p}$ for a fractional factorial),

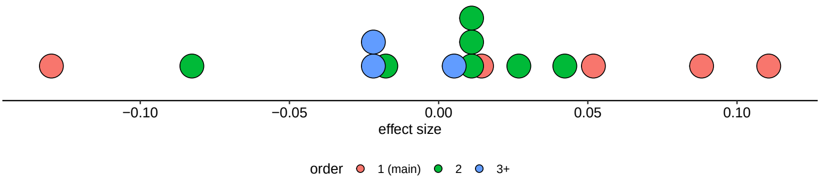
$$\text{standard error of effects} = SE(\beta_i) = \sqrt{\frac{\text{mean}(s^2)}{rN}}$$

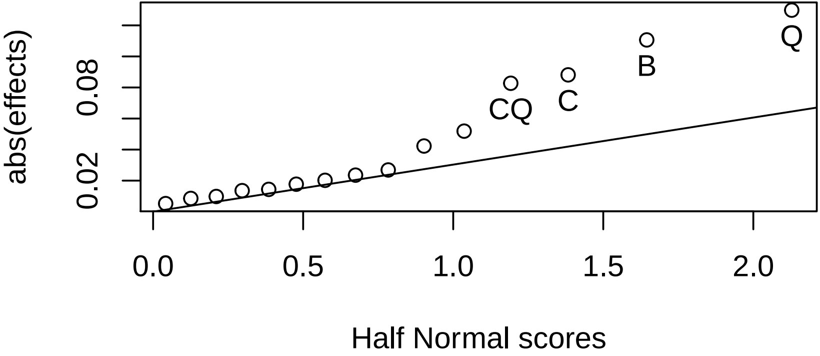
Linear models find the “best fit” effect sizes

```
model <- lm(height ~ B*C*D*E*Q, data=data)
show_model(model, n_coefs=17, show_fit=FALSE)
```

```
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  7.636042   0.018571 411.183  < 2e-16 ***
## Q           -0.129792   0.018571  -6.989 6.42e-08 ***
## B            0.110625   0.018571   5.957 1.23e-06 ***
## C            0.088125   0.018571   4.745 4.16e-05 ***
## C:Q         -0.082708   0.018571  -4.454 9.64e-05 ***
## E            0.051875   0.018571   2.793  0.00874 **
## B:Q          0.042292   0.018571   2.277  0.02959 *
## D:Q          0.026875   0.018571   1.447  0.15758
## C:D:Q       -0.023542   0.018571  -1.268  0.21406
## B:D:Q       -0.020208   0.018571  -1.088  0.28465
## C:D         -0.017708   0.018571  -0.954  0.34746
## D            0.014375   0.018571   0.774  0.44458
## E:Q          0.013542   0.018571   0.729  0.47119
## B:D          0.009792   0.018571   0.527  0.60165
## B:C          0.008542   0.018571   0.460  0.64866
## B:C:Q        0.005208   0.018571   0.280  0.78093
## B:E                NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Half-normal & dot plots — significance based only on effect size






```
## zscore= 0.0417893 0.1256613 0.2104284 0.2967378 0.3853205 0.4770404
```