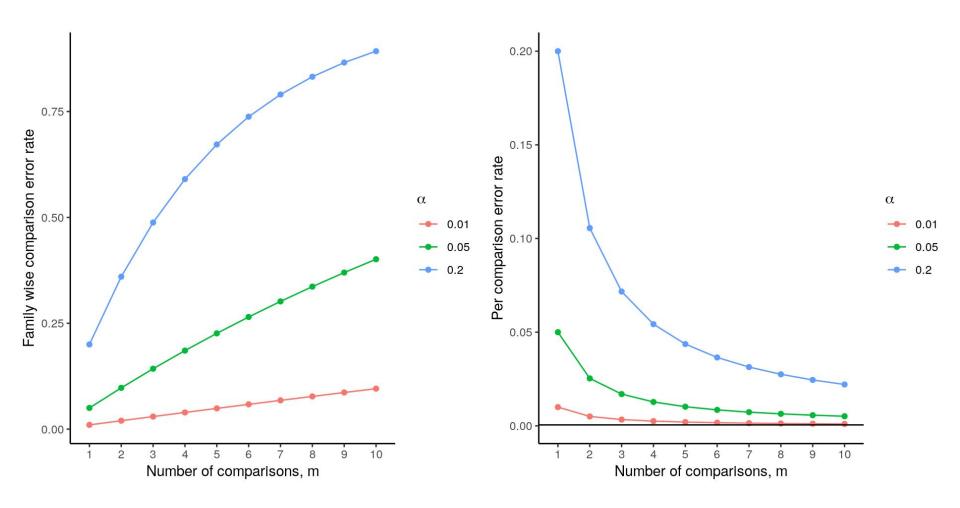


Multiple comparison

- Familywise error rate (FWER): the risk of making at least one Type I error (false positive) among the family of comparisons in the experiment
- Per comparison error rate (PCER): the probability of a Type I error in the absence of any multiple hypothesis testing correction
- False Discovery Rate (FDR) controls the expected (mean) proportion of false discoveries among the R (out of m) hypotheses declared "significant"



Calculating (95%) confidence intervals

Typically...

- Upper bound = estimate + (scale factor X SE)
- Lower bound = estimate (scale factor X SE)

Now, imagine our quantity of interest is the difference between means...

- Upper bound = difference + (scale factor X SED)
- Lower bound = difference (scale factor X SED)

Choice of scale factor (2) (2)





1. Fisher's



Bonferroni's



3. Tukey's



Fisher's Least Significant Difference (LSD)

Scale factor:
$$t_{\alpha=\frac{\alpha_c}{2},\mathrm{df}=N-m}$$

LSD:
$$t_{\alpha = \frac{\alpha_c}{2}, \text{df} = N - m}$$
 x sed

CI: Difference
$$\pm$$
 $t_{\alpha=\frac{\alpha_c}{2},\mathrm{df}=N-m}$ X SED

N is the number of observations $m \ \text{is the number of treatment groups}$ $\alpha_{\textbf{C}}$ is the PCER

Bonferroni correction

Scale factor:
$$t_{\alpha = \frac{\alpha_c}{2 \times k}, \text{df} = N - m}$$

LSD:
$$t_{\alpha = \frac{\alpha_c}{2 \times k}}$$
, df= $N-m$ X SED

CI: Difference
$$\pm t_{\alpha=\frac{\alpha_c}{2\times k}}, df=N-m \times SED$$

N is the number of observations

m is the number of treatment groups

$$\alpha_{c}$$
 is the PCER
$$k = \binom{m}{2}$$
 is the number of pairwise comparisons being made

Tukey's Honest Significant Difference (HSD)

CI: Difference

$$\pm \frac{q_{1-\alpha_c,m,\mathrm{df}=N-m}}{\sqrt{2}} \times \sqrt{\frac{2\hat{\sigma}^2}{n}}$$

N is the number of observations

m is the number of treatment groups

 $lpha_{c}$ is the PCER

n is the assumed equal number of replicates in each group

 $\hat{\sigma}^2$ is the residual mean square error

