GREIFSWALD

Sample Size Calculation with Unequal Group Sizes for Dunnett's Testing Marcus Vollmer

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A multiple comparison test

Dunnett's Test - What's that?

Multiple comparison test by Charles Dunnett (1955)¹ Post-hoc-Test after ANOVA

Compare k treatment arms against a control group

 $\mathsf{H}_{0i}: \mu_i = \mu_0$

Similar to performing multiple t-tests

Purpose

The three Rs

Principles were developed over 50 years ago as a framework for humane animal research

Replacement

Methods which avoid or

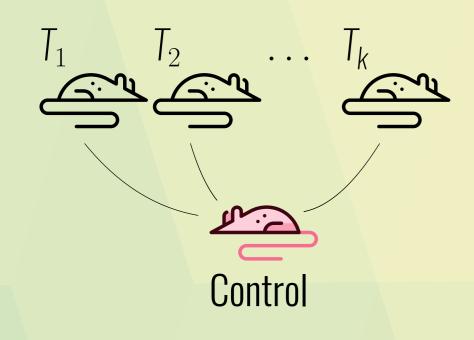
Reduction

Methods which minimise

Refinement

Methods which minimise

Designed to hold the family-wise error rate FWER=P(number of falsely rejected $H_0 > 1$) < α



«I don't have any hypothesis about the effect size - it's a pilot study. Why do I need sample size justification?»

replace the use of animals

the number of animals used per experiment

the suffering and improve animal welfare

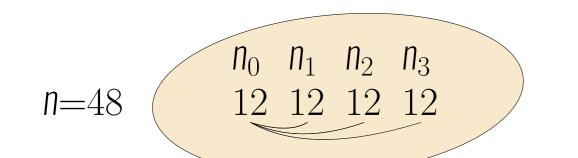
The importance of sample size estimation

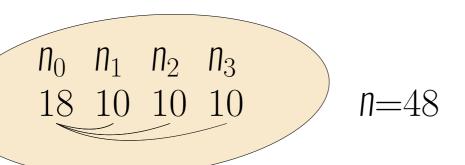
Which difference is of biological importance? Which statistical test should I conduct? And how many animals do I need to show a difference? Is this feasible (cages, animal keeper, laboratory space, costs)? Expectations may not always been fulfilled – if so, then you can publish significant results!

Reduction by imbalanced testing

Balanced vs. imbalanced sample sizes

Interestingly, in animal experiments equal sample sizes have been frequently proposed. However, the same statistical power can be achieved by unequally distributed group sizes with a reduction of the total sample size:

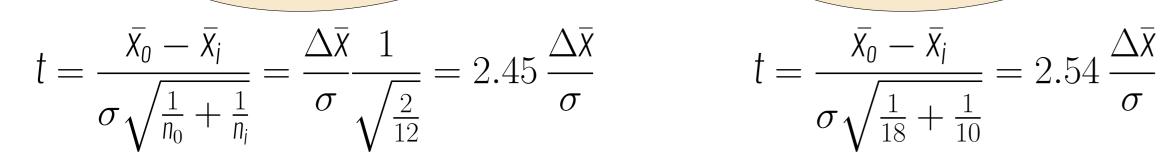


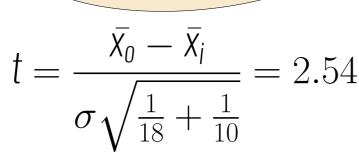


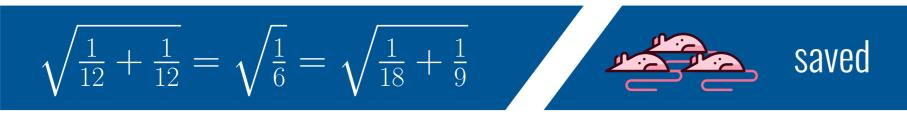
Available methods in R

Currently, two packages are available in R, R:multcomp² and R:DTK³, to perform the special testing problem with unequal group sizes. The computation of the p-values includes the consideration of a multidimensional t-distribution and the adjustment for multiple testing. Unfortunately, a procedure for sample size estimation is missing.

R:DunnettTests⁴ conducts a sample size calculation, but with identical treatment effect size and pre-specified sample allocation ratio only. In other situations, simulation-based evaluation is suggested, which needs great computational effort.





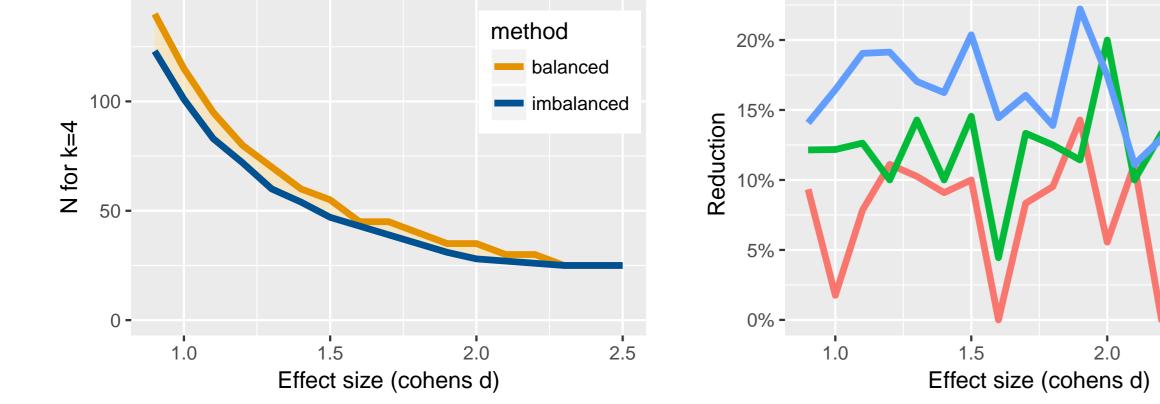


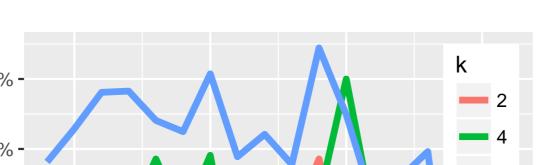
A general rule for equal effect sizes and equal variances says: $\frac{n_0}{n} \approx \sqrt{k} \frac{\sigma_0}{\sigma}$

What is the optimal set of sample sizes?

Statistical Power

Benefit of imbalanced sample sizes



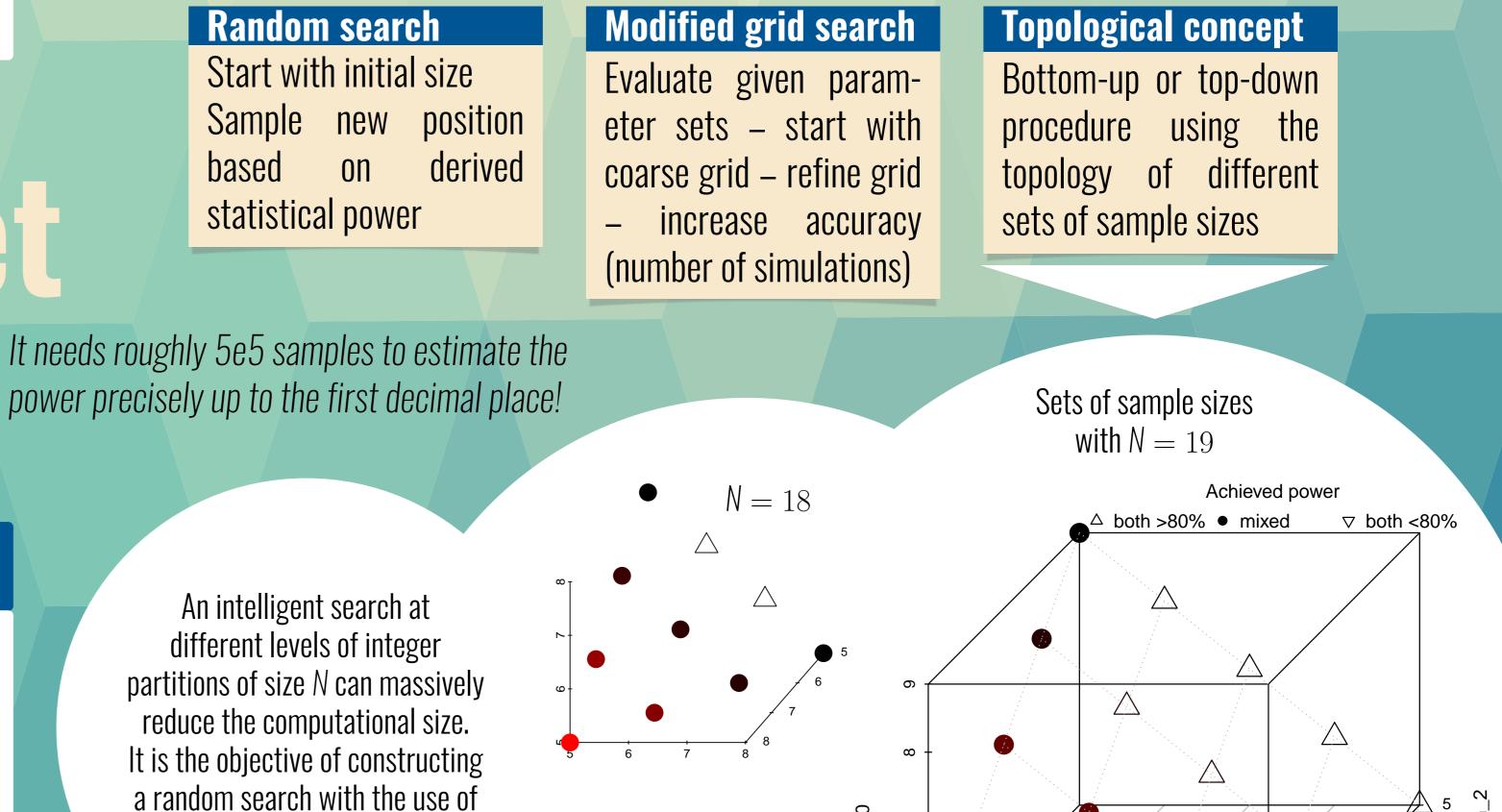


Simulation Study

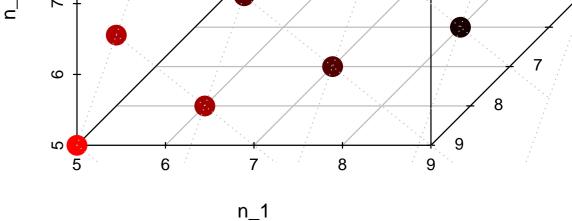
An intelligent search at different levels of integer partitions of size *N* can massively reduce the computational size. It is the objective of constructing a random search with the use of

A simulation study

The aim is to determine the sample sizes for multiple treatment groups with different effect sizes (different means and unequal variances). A necessary statistical power of 80% is expected. Ideas for finding the minimal set of group sizes in Monte Carlo experiments:







Treatment effect sizes: $C_d^1 = 1.85$, $C_d^2 = 2.25$

Passive immunization with glycoforms of IgG

2.5

Grid search results sorted by average power

[1] C. W. Dunnett, "Pairwise multiple comparisons in the unequal variance case," Journal of the American Statistical Association, vol. 75, no. 372, pp. 796–800, 1980. [2] T. Hothorn, F. Bretz, P. Westfall, R. M. Heiberger, A. Schuetzenmeister, and S. Scheibe, "Package 'multcomp'." Website, 2016. https://cran.r-project.org/package=multcomp [3] M. K. Lau, "Package 'DTK'." Website, 2013. https://cran.r-project.org/package=DTK. [4] F. Xia, "Package 'DunnettTests'." Website, 2013.

https://cran.r-project.org/package=DunnettTests.

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Mice experiment, immunization, Pneumococcal infection **IVIS Spectrum Imaging**

Negative control - Pre-immune IgG: $\mu_0 = 4.58$ Negative control - Post-immune: $\mu_1 = 5.73$ **3** Glycoforms: $\mu_{2,3,4} = 3.57$ equal variance: $\sigma = 0.96$

n0 n1 n2 power p1 p2 p4 34 12 18 100 0.851 0.785 0.780 0.768 0.79600 34 12 19 103 0.868 0.772 0.762 0.783 0.79625 32 11 20 103 0.798 0.809 0.800 0.789 0.79900 33 10 20 103 0.776 0.808 0.807 0.812 0.80075 33 12 19 102 0.843 0.779 0.797 0.785 0.80100 11 20 104 0.814 0.804 0.803 0.812 0.80825 32 12 19 101 0.862 0.792 0.800 0.785 0.80975 33 12 20 105 0.864 0.803 0.795 0.806 0.81700 34 11 20 105 0.812 0.807 0.825 0.831 0.81875 R^GMarcus_Vollmer +49 (0)3834 86-5444 marcus.vollmer@uni-greifswald.de

