Getting over ANOVA: Estimation graphics for multi-group comparisons

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Abstract

Data analysis in experimental science mainly relies on null-hypothesis significance testing, despite its well-known limitations. A powerful alternative is estimation statistics, which focuses on effect-size quantification. However, current estimation tools struggle with the complex, multi-group comparisons common in biological research. Here we introduce DABEST 2.0, an estimation framework for complex experimental designs, including shared-control, repeated-measures, two-way factorial experiments, and meta-analysis of replicates.

Introduction

For decades, statisticians have pointed out the limitations of *null-hypothesis significance testing* (NHST) as a method for data analysis. The NHST framework turns research decision-making into a misleading dichotomy between so-called 'significance' and 'non-significance' (Berkson 1942; Cohen 1994; Nuzzo 2014). As a result, researchers often place undue confidence in NHST test results (Halsey et al. 2015; Button et al. 2013), contributing to poor experimental reproducibility (Collaboration 2015; Errington et al. 2021; Prinz et al. 2011). The emphasis on this dichotomy also discourages researchers from engaging in the critical task of effect quantification (Cumming and Calin-Jageman 2016).

An alternative to NHST is estimation statistics, a data analysis framework that comprises effect size estimation, precision intervals, data graphics and meta-analysis (Altman et al. 2000; Claridge-Chang and Assam 2016; Singh Chawla 2017; Calin-Jageman and Cumming 2019; Borenstein et al. 2009). The estimation framework has the potential to almost entirely replace NHST. However, realizing this transition will require the implementation of estimation methods, accessible software (**Supplementary Note 1**) and data graphics appropriate for all experimental types, including complex designs.

Conventional multi-group analysis is unfocused

In addition to the limitations of NHST in simple comparisons, multi-group experiments present greater challenges. Conventional multi-group analysis uses omnibus testing via Analysis of Variance (ANOVA, Fisher 1925) and its variants, followed by multiple comparisons (Dunn 1961). However, ANOVA tests a null hypothesis that is inherently unfocused, assuming "everything is the same" (all group means are equal). A rejection of this proposition provides no specific information about which groups differ, in which direction, or by how much (Rosenthal and Rosnow 1985). Consequently, researchers must embark on a second analytical step that requires multiple comparisons. Even a modest number of groups (g) requires the analyst to test m hypotheses; with $m = g(g-1)/2$ pairwise comparisons, the number of tests sharply increases. For example, a 6-group experiment requires the testing of 15 hypotheses. Thus, in a typical multi-group experiment, what may have begun as a focused research question sprawls into a complex web of subsidiary tests. Multiplicity is usually managed with adjustments such as Bonferroni correction, but these undermine the statistical power and make it harder to detect true effects (García-Pérez 2023).

Estimation can simplify multi-group analysis, for example, by comparing each test group only to a single control. For g groups, this means focusing on $g-1$ effect sizes, *e.g.* instead of 15 p values, a 6-group experiment considers only 5 effect sizes. Multi-group estimation graphics show the effect magnitudes and precision estimates—the information most relevant for understanding biological systems. We also remark that existing effect-size software tends to only facilitate the analysis of simpler two-group experimental designs. Here we introduce DABEST 2.0, software that extends the applicability of estimation graphics to more complex multi-group experiments, including longitudinal studies, two-way factorial designs, multi-group binary data, and meta-analyses of internal replicates.

Results

Repeated-measures estimation graphics display effect trajectories

DABEST 1.0 was introduced with an estimation graphic for the multi-group data normally analysed via one-way ANOVA (Ho et al. 2019). With DABEST 2.0, we first extended this functionality to repeated-measures experiments. Throughout this article, we demonstrate estimation graphics with fictional scenarios. Consider a time-course study on the total sleep time (TST) of insomnia patients during drug treatment. The researcher records each patient's sleep period at baseline and each day after treatment (**Figure 1a**). To analyse the data with a repeated-measures ANOVA, the researcher first calculates the F statistic and its p-value. If deemed 'significant', the data are analysed with several pairwise t-tests: each time point is compared against all others, generating several T-values (test statistic) and multiple-comparison-adjusted p values (**Figure 1b**, **Supplementary Table 2**).

The effect-size alternative is the repeated-measures estimation plot (**Figure 1c–d**). The top panel (**Figure 1c**) represents the observed values, while the bottom panel (**Figure 1d)** graphs the effect size for each time point, along with curves that indicate precision. The effect size plot allows the researcher to focus on the relevant time point versus the baseline comparison. The effect sizes

and their confidence intervals (CIs), calculated via bootstrapped resampling (DiCiccio and Efron 1996; Efron 1979) (**Supplementary Note 2**), are represented by the dots (effect size), vertical black lines (95CI), and the full distributions (half-violin curves). The estimation framework shifts the focus to the magnitude of the intervention effect size (compared to Figure 1a). Thus, the researcher can clearly see that total sleep time slightly increased on Day 1 (90.8 min [95CI 46.8, 139.0]), greatly increased by Day 2, and plateaued by Day 3 (247.8 min [95CI 219.5, 274.6], and 223.0 min [95CI 206.3, 263.1], respectively), before declining over the subsequent days.

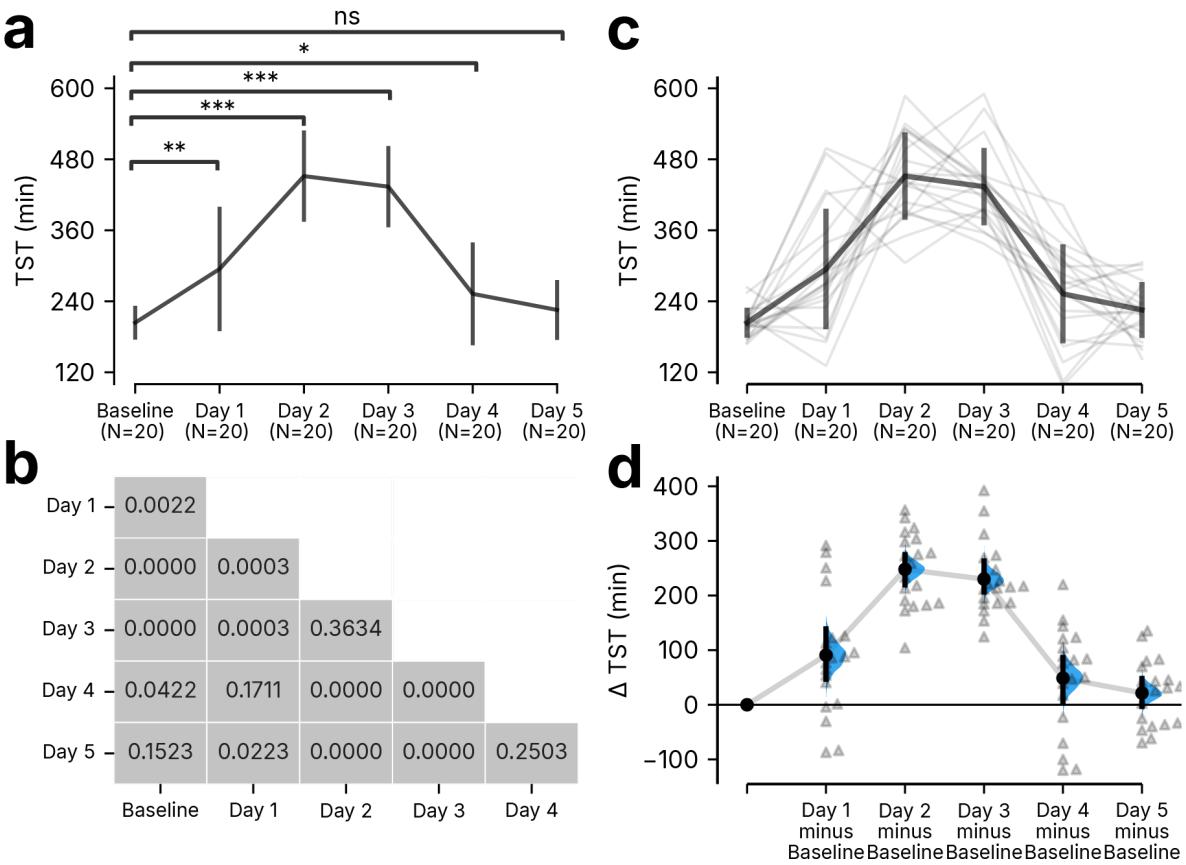

Figure 1. Estimation graphics for multiple group experimental designs

a, A conventional repeated measures plot of total sleep time (TST) in minutes (min) following treatment with an insomnia drug. One-way ANOVA with *post hoc* testing was used to generate corrected p values for all group comparisons. The *p* values for the comparison of each test day versus baseline are represented by asterisks (***: $p<0.001$; **: $0.001<p<0.01$; *: $0.01<p<0.05$, ns: $p\geq0.05$). **b**, The full *p* value table for the 15 comparisons. **c–d**, Repeated-measures plot of the same data as in **a**. Panel **c** shows subjects' data as connected lines. Panel **d** shows the bootstrapped distributions of the differences between test days and baseline. Black vertical bars indicate 95% confidence intervals. Triangles indicate individual deltas. In **a** and **c**, grey lines indicate the individual paired samples, while the black line indicates the mean and standard deviation.

Two-factor designs: delta-delta analysis

In complex experiments with two independent variables, researchers conventionally rely on two-way ANOVA (Fisher 1935), often including an interaction term for interdependent effects.

This approach still requires *post-hoc* tests for explicit group-to-group comparisons. DABEST 2.0 simplifies this analysis by introducing the delta-delta effect size, which focuses on the net effect of one primary variable within the context of a secondary variable (**Supplementary Note 3**).

Consider an experiment designed to test a drug's efficacy in treating test animals with a disease-causing mutation. This hypothetical experiment measures survival in both mutant (M) and wildtype (W) subjects given drug and placebo treatments. Key questions include (1) By how much does the drug improve survival in mutation carriers? (2) What placebo effect exists in mutation carriers? and (3) What is the drug's net effect after accounting for placebo effects? Two-way ANOVA (**Supplementary Table 3**) shows a significant interaction effect ($F(1,196) = 26.56$, $p = 6.21e^{-7}$), indicating that treatment effects depend on subject genotype, and Tukey's test is then performed (**Figure 2a**). In this case, of the six possible comparisons, four yield significant differences. Despite this, how much the drug specifically benefits mutation carriers remains unclear, making interpretation challenging.

Delta-delta analysis clearly depicts the two-way drug × genotype effect and reveals three key points (**Figure 2b**). First, mutation carriers given the placebo show reduced survival, by approximately −3.62 years [95CI −5.29, −2.01]; second, carriers given the drug treatment show improved survival, by about 2.1 years [95CI 0.76, 3.61]; and third, according to the delta-delta calculation (obtained by subtracting the placebo delta from the drug delta; **Methods**), which indicates the drug's net effect, the treatment improved survival by approximately 5.76 years [95CI 3.60, 7.89] in carriers, accounting for all background effects (**Supplementary Note 4**).

This approach should prove useful for researchers seeking to quantify specific treatment effects via 2×2 designs, using either original units or standardized effect sizes (**Methods**). For either paired data or independent groups, delta-delta graphics account for non-specific, background effects and distil a multifactorial problem into a single, focused effect size.

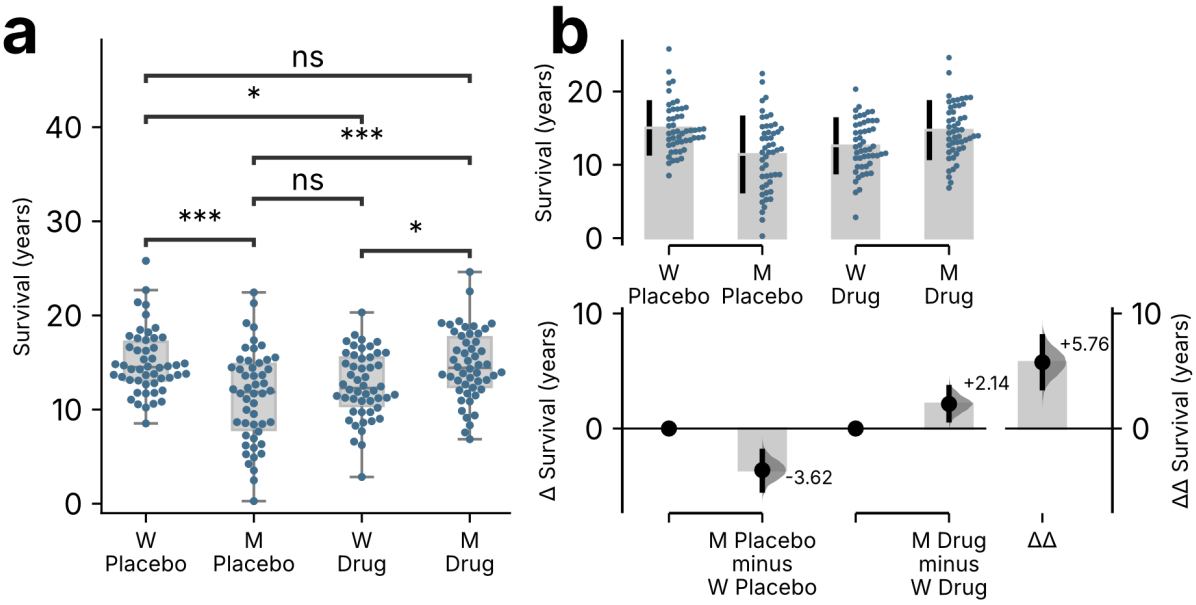

Figure 2. Estimation statistics for drug × genotype effects

a, A swarm and box plot of survival effects. The box shows the interquartile range (25th to 75th percentiles) with a horizontal line at the median (50th percentile). Vertical lines (whiskers) extend to 1.5 times the interquartile range from the upper and lower quartiles. Horizontal brackets with stars indicate the level of significance for comparisons with post-hoc Tukey's test (***: $p<0.001$; **: $0.001<p<0.01$; *:$0.01<p<0.05$). **b**, Estimation graphic of the survival effects between mutant (M) and wild type (W), calculated for the placebo and drug-treated groups; the delta-delta effect was calculated by subtracting the two primary deltas. The top panel is a swarm plot of the samples alongside a vertical bar, the gap indicates the mean of the sample, while the lines show the standard deviations. In the bottom panel, the left y-axis shows the bootstrapped distributions of the mean differences; the right y-axis shows the delta-delta effect size. Black vertical bars indicate 95% confidence intervals.

Differences of proportions

The NHST framework commonly employs Fisher's exact test or the Chi-squared test to analyse binary (or 'proportional') data (Kim 2017). Such results are frequently reported without effect sizes, error bars, or graphics (**Supplementary Table 4**).

To illustrate the differences between NHST and estimation analyses of proportional data, consider an experiment to test the efficacy of a drug in an animal model of spontaneous seizures. The drug is administered for 3 days, and seizure occurrence is scored as a binary outcome per animal (**Supplementary Table 5**). The researcher compares the seizure occurrence on day 3 in the placebo and drug-treated groups. Instead of a standard bar chart, which often omits error and effect statistics (**Figure 3a**), DABEST 2.0 provides a proportion plot incorporating error bars and the effect size. Compared to the placebo treatment, the drug reduced the number of spontaneous seizures in the model animals by 68% [95CI 53, 83] on day 3 (**Figure 3b**). DABEST 2.0 can also draw Sankey plots to illustrate changes in repeated-measures binary data (Kosara 2010; blogmaster_sev 2021). For example, changes in seizures over the 3 days relative to baseline can be visualized for the placebo (+5% [95CI −10, +18]) and drug groups (−60% [95CI −45, −78]) (**Figure 3c**). For reporting standardized effect sizes in binary data, DABEST can calculate Cohen's h (**Methods**).

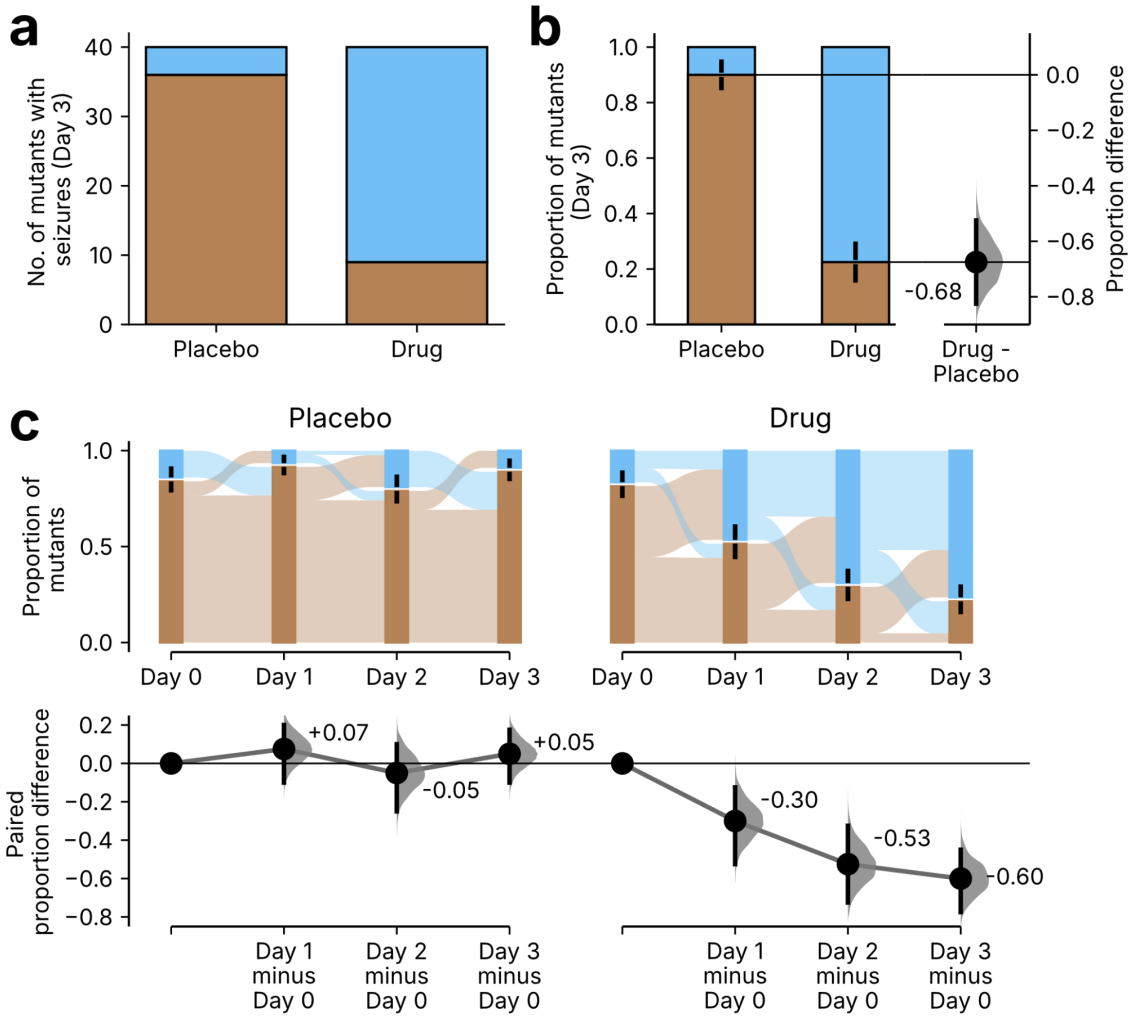

Figure 3. Graphical analyses of proportions and their differences

a, A bar chart that visualizes proportions without error bars or an effect size. **b,** Proportion plot generated using DABEST 2.0. The brown section of each bar represents the proportion of animals with seizures, while the blue section represents animals without seizures. **c,** Sankey-style estimation plots for repeated measures of proportions. The brown and blue bars illustrate the proportion of animals with and without seizures, respectively. The strip between each Sankey bar denotes categorical changes. Mean and ± standard deviation are represented by black vertical bars. Effect-size distributions are plotted as half-violin curves on either the right y-axis (**b**) or the x-axis (**c**, lower panel), alongside each mean (black dot) and 95% confidence interval (black line).

Simple meta-analysis of replicated experiments

Meta-analyses calculate more precise effect estimates, and resolve contradictions between studies (Glass 1976; O'Rourke 2007; Gurevitch et al. 2018). However, researchers rarely meta-analyse data from internally replicated experiments.

Consider evaluating a drug's effect on total sleep time in insomnia patients in three pilot trials (**Figure 4**). Two replicates show substantial effect sizes, while one does not. Without a way to synthesize this, researchers must either report only one experiment or combine all data into a single mega-analysis. Selective reporting conceals experiments, while clumping data lacks transparency about the experimental progression (including possible inter-experiment

modifications), magnifies errors when baselines vary, and can encourage *p*-hacking (Head et al. 2015).

To address these issues, several groups have argued for the use of a small-scale meta-analysis or 'minimeta' (Braver et al. 2014; Cumming 2014; Maner 2014; Goh et al. 2016) **(Supplementary Note 5**). To date, visualizing a series of replicated experiments still requires the use of standard meta-analysis tools (Goh et al. 2016). DABEST 2.0 introduces easy mini-meta-analysis, where users can display multiple instances of a series of experiments, their individual effect sizes, and the summary effect (**Figure 4**). The summary effect is calculated as a weighted delta using pooled replicate variances and a fixed-effects model suitable for replicates of similar experiments (**Methods**). Visualizing individual replicates shows both intra- and inter-experimental variations, while the averaged mean difference provides the overall most plausible effect size. The adoption of minimeta promotes the disclosure of seemingly contradictory results, encourages transparent reporting, and enhances reproducibility.

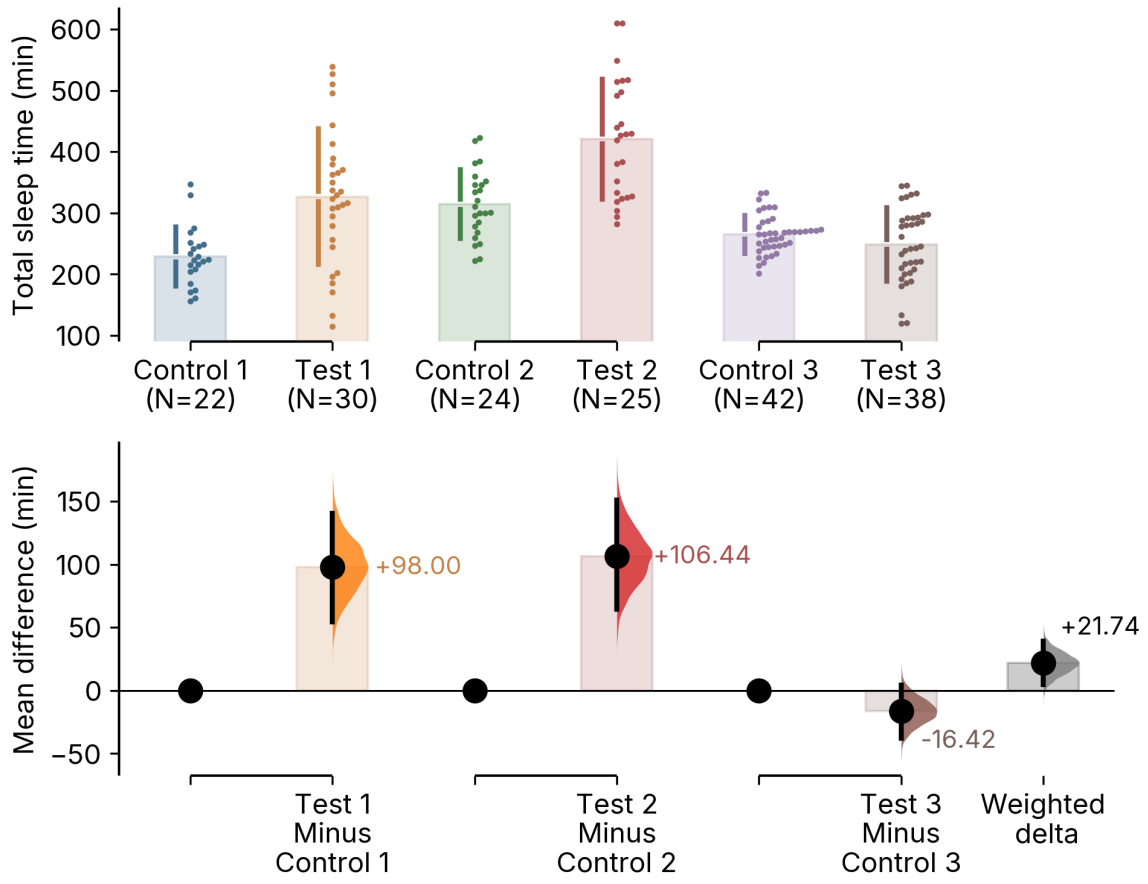

Figure 4. Example mini-meta-analysis of data from 3 two-group experiments

Top panel. Swarm plots of observed values from three experiments, with a vertical bar indicating the mean and standard deviation. **Lower panel.** The weighted-average delta resolves differences between replicates with positive effect sizes (Test 1 minus Control 1, +98.00 [95CI +54.25, +140.34]; Test 2 minus Control 2, +106.44 [95CI +64.44, +151.23]) and a negative effect size (Test 3 minus Control 3, −16.42 [95CI −37.69, 4.14]). The mean differences of the 3 experiments: half-violin curves show the bootstrapped

distribution of differences, and vertical bars show the 95% confidence intervals. The right-most column shows the weighted-average mean difference ($\Delta_w = +21.74$ [95CI +4.51, +39.32]).

Conclusion

DABEST 2.0 expands the applicability of estimation graphics with new tools for analysing repeated-measures experiments, two-way designs, and binary/proportional data. As well as providing alternatives to three major classes of significance tests, DABEST 2.0 also provides a solution for handling replicated experiments.

DABEST 2.0 is available as Python and R packages (with comprehensive documentation and tutorials) and as a web application, https://estimationstats.com. By providing robust estimation solutions for common multi-group experiments, DABEST 2.0 facilitates the transition from significance testing to more meaningful quantitative analysis.

Supplementary Notes

(1) Until recently, ready-to-use software tools for estimation graphics were not widely available; this changed with the release of the DABEST suite, providing tools suitable for both scripting and point-click workflows: DABEST for Python, dabestr for R, and estimationstats.com (Ho et al. 2019; Calin-Jageman and Cumming 2024). This advance was reinforced by changes in journal policy (Bernard 2019, 2021; Elkins et al. 2022) and a growing number of freely available software packages, including ESCI for R and Jamovi (Calin-Jageman and Cumming 2024), *t*-tests with effect sizes in JASP (JASP Team 2024), and Durga for R (Khan and McLean 2024) **(Supplementary Table 1**).

(2) Bootstrap resampling is used due to its computational simplicity, robustness for small samples and skewed/non-normal samples, and for allowing for calculation of the effect size and confidence intervals without assumption of the underlying sample distribution, thus allowing for more accurate estimation of statistics (Horowitz 2019; Hesterberg 2011).

(3) The delta-delta effect size is different from the interaction between the two independent variables. It represents the net effect of one variable within the other, where the former is the factor of primary importance. Together in the general spirit of contrast analysis, a delta-delta plot allows the researcher to ask focused questions on the main driver variable as well as the differentials by the secondary variable in a quantitative manner.

(4) Where an ANOVA user would have concluded that there is a statistically significant interaction between genotype and treatment ($p = 6.21e\text{-}7$) requiring further post-hoc testing, a delta-delta user concludes that the drug improved survival by 5.76 years [95% CI: 3.60, 7.89] in mutation carriers—an effect size that substantially exceeds the 2-year threshold typically considered clinically meaningful, with the confidence interval indicating that even the most conservative estimate represents substantial clinical benefit. Effect size estimation provides more information than NHST while maintaining statistical rigor.

(5) A lack of internal replication is thought to contribute to the reproducibility crisis, with over 80% of researchers citing insufficient within-lab replication as a factor in irreproducibility (Baker 2016). Compounding this issue is the fact that 'negative' replicates often remain unpublished—a well-known phenomenon known as 'the file-drawer problem' (Simonsohn et al. 2014).

Supplementary Table 1. Comparison between major packages with support for effect size calculation and visualization

Comparison of major packages across platform compatibility (R, Python, Excel, Matlab, Jamovi, web-based), cost (free vs. commercial), statistical capabilities (effect size metrics, group comparisons, proportions, meta-analysis, Bayesian methods), and visualization features (raw data plots, estimation plots). Date indicates year of release or major version. DABEST 2.0 is highlighted as the current package with comprehensive cross-platform support

Name	Platform			Free	Functionalities											Date	Docs	Citation
	R	Python	Other		numeric ES	Δ plot	raw plot	2 group	2x2	prop	minimeta	meta	correlation	Bayes				
esci 1.01	✘	✘	Excel	✘	✔	✔	✔	✔	✘	✘	✘	✘	✘	✘	2001	Link	Cumming and Calin-Jageman (2017)
MES	✘	✘	Matlab	✘	✔	✔	✘	✘	✘	✘	✘	✘	✘	✘	2011	Link	Hentschke and Stüttgen (2011)
DABEST 1.0	✔	✔	Web	✔	✔	✔	✔	✔	✘	✘	✘	✘	✘	✘	2016	Link	Ho et al. (2019)
BEST	✔	✔		✔	✔	✔	✘	✔	✘	✘	✘	✘	✘	✔	2017	Link	Kruschke (2013)
JASP	✘	✘	Rollapp	✔	✔	✘	✘	✘	✘	✘	✘	✔	✘	✘	2019	Link	
RESI	✔	✘		✔	✔	✔	✘	✘	✘	✘	✘	✘	✘	✘	2020	Link	Jones et al. (2023)
Prism 9	✘	✘	Prism 9	✘	✔	✔	✔	✔	✘	✘	✘	✘	✘	✘	2021	Link	
effectsize	✘	✔		✔	✔	✘	✘	✘	✘	✘	✘	✘	✘	✘	2022	Link	
Durga	✔	✘		✔	✔	✔	✔	✔	✘	✘	✘	✘	✘	✘	2023	Link	Khan and McLean (2024)
esci 1.01	✔	✘	Jamovi	✔	✔	✔	✔	✔	✔	✔	✘	✘	✔	✘	2023	Link	Calin-Jageman and Cumming (2024)
DABEST 2.0	✔	✔	Web	✔	✔	✔	✔	✔	✔	✔	✔	✘	✘	✘	2023	Link	This paper

Supplemental Table 2. Statistical analysis of the data presented in Figure 1A-B.
Here, multiple pairwise t-tests are performed with Benjamini/Hochberg FDR correction.

Group 1	Group 2	T statistic	Adjusted p-value	Reject H_0
Baseline	Day 1	-3.7655	0.0022	TRUE
	Day 2	-16.6801	0.0000	TRUE
	Day 3	-15.7577	0.0000	TRUE
	Day 4	-2.3300	0.0422	TRUE
	Day 5	-1.6192	0.1523	FALSE
Day 1	Day 2	-4.7033	0.0003	TRUE
	Day 3	-4.7597	0.0003	FALSE
	Day 4	1.5068	0.1711	FALSE
	Day 5	2.6785	0.0223	TRUE
Day 2	Day 3	0.9312	0.3634	TRUE
	Day 4	6.9478	0.0000	TRUE
	Day 5	10.9465	0.0000	TRUE
Day 3	Day 4	8.6813	0.0000	TRUE
	Day 5	11.6226	0.0000	TRUE
Day 4	Day 5	1.2302	0.2503	FALSE

Supplementary Table 3. An ANOVA table for the 2×2 design drug experiment.

There is a significant interaction effect between Genotype and Treatment, indicating that the treatment effect is specific to a genotype. Tukey's post-hoc HSD test was therefore performed to determine the specific locations of the significant effects, shown in Figure 2a.

	df	sum_sq	mean_sq	F	PR(>F)
C(Genotype)	1	27.33	27.33	1.75	0.19
C(Treatment)	1	9.48	9.48	0.61	0.44
C(Genotype) x C(Treatment)	1	414.31	414.31	26.56	6.21E-07
Residual	196	3057.44	15.6		

Supplementary Table 4. Types of visualizations and tests used to showcase proportion related data in literature.

The first search (yielding 40 articles) used the keywords "Fisher's exact test" in PubMed and Google Scholar from 2000 to 2024. These articles were further categorized based on the representation of how the Fisher's test results were conveyed, with or without visualizations. The second search (yielding 30 articles) focused on the keyword "Proportion" in PubMed and categorized the presence or absence of error bars/confidence intervals as well as the types of statistical tests that were performed. Details of the literature review can be found in the Methods.

Search type	Type of test	Visualization	Error	Count	%	Effect sizes
"Fisher's Exact test"	Fisher's	Graphics	N	19	47.5	0
			Y	10	25.0	0
	Fisher's	No Graphics	N	6	15.0	0
			Y	5	12.5	0
"Proportion"	Fisher's	Graphics	N	5	16.1	0
			Y	3	9.7	0
	Fisher's	No Graphics	N	1	3.2	0
			Y	4	12.9	0
	Mixed	Others	N	12	38.7	0
			Y	6	19.4	0

Supplementary Table 5. Example seizure occurrence drug trial data.

Number of animals with spontaneous seizures across 3 days of placebo/drug administration. A binary seizure/no seizure scoring system was adopted, thus yielding binary data. Day 0 refers to the baseline prior to placebo/drug administration. n=40 for each group.

	Day 0	Day 1	Day 2	Day 3
Placebo	34	37	32	36
Drug	33	21	12	9

Methods

Data simulation

Data analysed in this paper were simulated using the SciPy, NumPy, and Pandas packages. All code necessary to reproduce the results with DABEST-python is available in a separate Jupyter Notebook.

Effect size calculations

Bootstrap resampling and confidence interval estimation

In all examples in this paper, 5000 pairs of control and test samples were drawn for the control group and test group. The confidence intervals for effect size estimate across bootstrapped resamples are estimated as bias-corrected and accelerated (BCa) bootstrap confidence intervals (Efron 1987) using a custom implementation in DABEST-Python or boot.ci in dabestr.

Mean difference calculation

Mean difference is the bootstrapped mean difference between the control group and the test group:

$$\bar{X}_2 - \bar{X}_1$$

where $\bar{X}_2$ denotes the sample mean of the test group and $\bar{X}_1$ denotes the sample mean of the control group. Mean difference is also calculated for repeated measures, proportion plots, and two-group comparisons in delta-delta and mini-meta designs.

Delta-delta mean difference and modified Hedges' *g* calculations

In the text example for computing delta-delta effects in a 2×2 design over independent variables genotype ("wild type" or "mutant") and treatment ("placebo" or "drug"), two possible delta-delta effect sizes can be calculated:

$$\hat{\Delta}_P = \hat{X}_{P,M} - \hat{X}_{P,W}$$

$$\hat{\Delta}_D = \hat{X}_{D,M} - \hat{X}_{P,W}$$

$$\hat{\Delta}_{\Delta A} = \hat{\Delta}_D - \hat{\Delta}_P$$

where $\hat{X}$ denotes the sample mean and Δ denotes the difference of means.

$$\hat{\Delta}_W = \hat{X}_{D,W} - \hat{X}_{P,W}$$

$$\hat{\Delta}_M = \hat{X}_{D,M} - \hat{X}_{P,M}$$

$$\hat{\Delta}_{\Delta B} = \hat{\Delta}_M - \hat{\Delta}_W$$

where $\hat{X}$ denotes the sample mean and $\hat{\Delta}$ denotes the difference in means.

$\hat{\Delta}_{\Delta A}$ and $\hat{\Delta}_{\Delta B}$ have equal means but distinct variances.

In two-group analysis, standardized effect sizes such as Hedges' *g* can be computed for comparisons across measurements of different units. For reporting standardized delta-delta effect sizes, DABEST provides a modified Hedges' *g* calculated from normalization with pooled sample variance.

$$\hat{s}_{\Delta_\Delta} = \sqrt{\frac{(n_{A_2,B_1}-1)s^2_{A_2,B_1} + (n_{A_1,B_1}-1)s^2_{A_1,B_1} + (n_{A_2,B_2}-1)s^2_{A_2,B_2} + (n_{A_1,B_2}-1)s^2_{A_1,B_2}}{(n_{A_2,B_1}-1)+(n_{A_1,B_1}-1)+(n_{A_2,B_2}-1)+(n_{A_1,B_2}-1)}}$$

where s is the standard deviation and n is the sample size.

Weighted delta calculation in mini-meta

In a mini-meta experiment, the inverse-variance weighting method is used to calculate a weighted mean difference.

$$\hat{\Delta}_w = \frac{\sum \hat{\Delta}_i\, w_i}{\sum w_i}, \quad w_i = \frac{1}{\hat{\sigma}_i^2}, \quad \hat{\sigma}_i^2 = \mathrm{var}\big(\hat{\Delta}_i\big)$$

The variance used is calculated as the sample variance of the bootstrapped values of the mean difference.

$$\hat{\Delta}_w = \frac{\sum \hat{\Delta}_i\, \hat{w}_i}{\sum \hat{w}_i}, \quad \hat{w}_i = \frac{n_i - 1}{\sum_{r=1}^{n_i}\big(\hat{\Delta}_i^{(r)} - \bar{\Delta}_i^{\mathrm{b}}\big)^2}, \quad \bar{\Delta}_i^{\mathrm{b}} = \frac{1}{n_i}\sum_{r=1}^{n_i}\hat{\Delta}_i^{(r)}.$$

where $\hat{\Delta}_w$: estimated weighted delta; w_i: weight of mean difference for replicate i; $\hat{\sigma}_i^2$: sampling variance of the mean-difference estimator for replicate i; $\hat{\Delta}_i$: estimated mean difference for replicate i; $\hat{w}_i$: estimated weight of mean difference for replicate i; n_i: number of bootstrap replicates used for replicate i; $\hat{\Delta}_i^{(r)}$: the r-th bootstrap estimate of the mean difference for replicate i; $\bar{\Delta}_i^{\mathrm{b}}$: bootstrap mean of the mean differences for replicate i

Cohen's *h* calculation for binary data

Cohen's *h* is an effect size applicable to binary data.

$$h = 2arcsin\sqrt{p_2} - 2arcsin\sqrt{p_1}$$

Where p_2 denotes the proportion of successes in the test group and p_1 denotes that of the control group.

Visualization

Visualization of the raw data and effect size distributions was achieved with matplotlib and seaborn in DABEST-Python and ggplot2 in dabestr. Except for the Sankey diagram, designs are variations of either the Gardner-Altman plot (Gardner and Altman 1986; Ho et al. 2019) or the Cumming plot (Cumming 2011; Ho et al. 2019).

Sankey Diagrams

An alluvial design of the traditional Sankey plot (Kennedy and Sankey 1898) was implemented using matplotlib with inspiration from pySankey. A custom data transformation protocol utilized NumPy for numerical computations and pandas for efficient data handling, ensuring precision in managing large datasets. Parameters such as edge thickness and color opacity can be manually adjusted to enhance readability and interpret the dynamic transitions in the data effectively.

Literature review of proportion statistics usage

A total of 70 articles were sourced to identify the use of Fisher's exact test in scientific papers. Two types of searches were conducted: the first to break down how Fisher's exact tests were reported in papers, and the second was to compile a wide range of papers to identify the number of studies that generated proportion data and the visualization associated with it.

The first search (identifying 40 articles) used the keywords "Fisher's exact test" in PubMed (19,967 publications) and Google Scholar (17,900 publications) from Jan 2000 to May 2024, excluding books and meta-analysis. These articles were further categorized based on the representation of how Fisher's test results were conveyed, with or without visualizations. The second search (identifying 30 articles) focused on the keyword "Proportion" in PubMed (46,184 publications), also spanning from Jan 2000 to May 2024, and categorized by the presence or absence of error bars/confidence intervals as well as the types of statistical tests that were performed. It was found that about 40% of these papers used Fisher's exact test, with tables being the predominant form of visualization. Most of the other tests performed were either ANOVA or represented in percentages.

Software availability

DABEST is available in both Python and R. The Python package, DABEST-python, is hosted on PyPI, and its source code can be found on GitHub at https://github.com/ACCLAB/DABEST-python. A tutorial for the Python package can be found at https://acclab.github.io/DABEST-python/tutorials/. The R variation, dabestr, is available on CRAN (https://cran.r-project.org/web/packages/dabestr) and similarly has its source code accessible on GitHub (https://github.com/ACCLAB/dabestr). A tutorial for the R package is available at https://acclab.github.io/dabestr/. Both repositories are released under the Apache-2.0 license. In addition, www.estimationstats.com provides an online user interface and performs all the calculations using DABEST-Python.

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Competing interests

The authors declare no competing interests.

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