



pwr4exp: An R package for robust statistical power analysis

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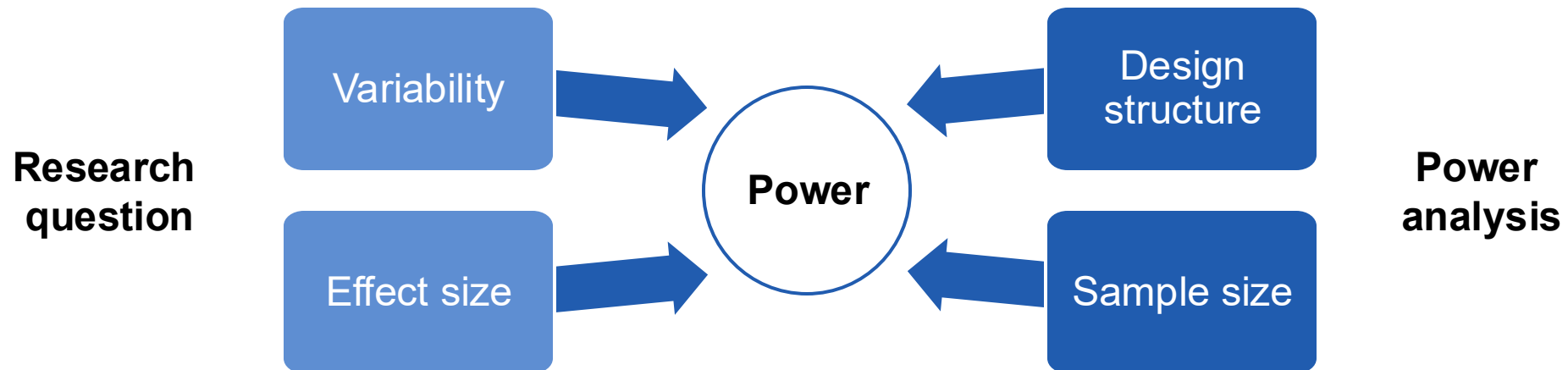
Power analysis is essential for hypothesis testing

	H_0 true	H_A true
Fail to reject H_0		Type II error False negative
Reject H_0	Type I error False positive	Power

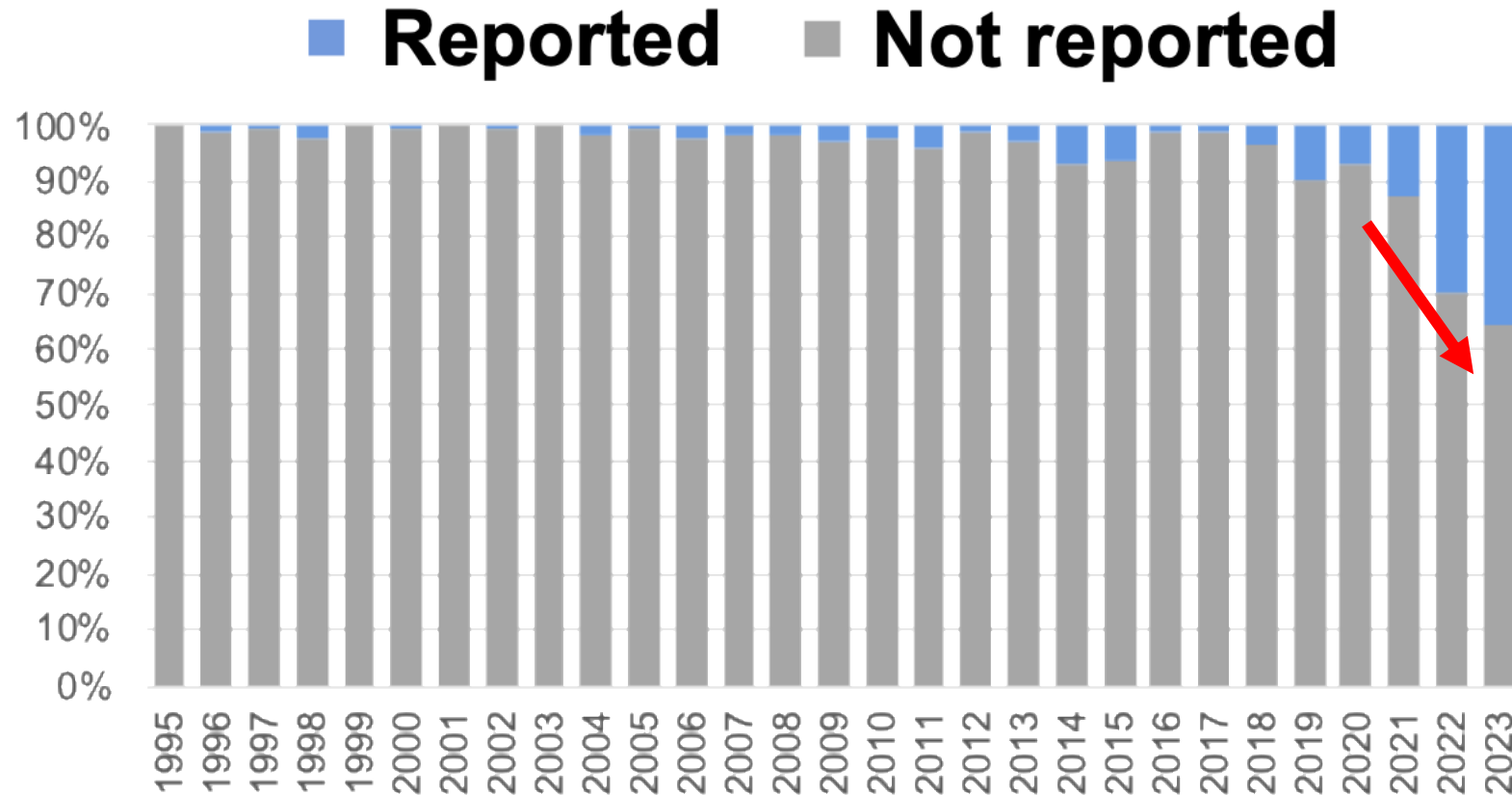
■ In controlled experiment

- H_0 : The treatment has no effect
- H_A : The treatment does have an effect

■ Power: $P[\text{reject } H_0 \mid H_A \text{ holds}]$

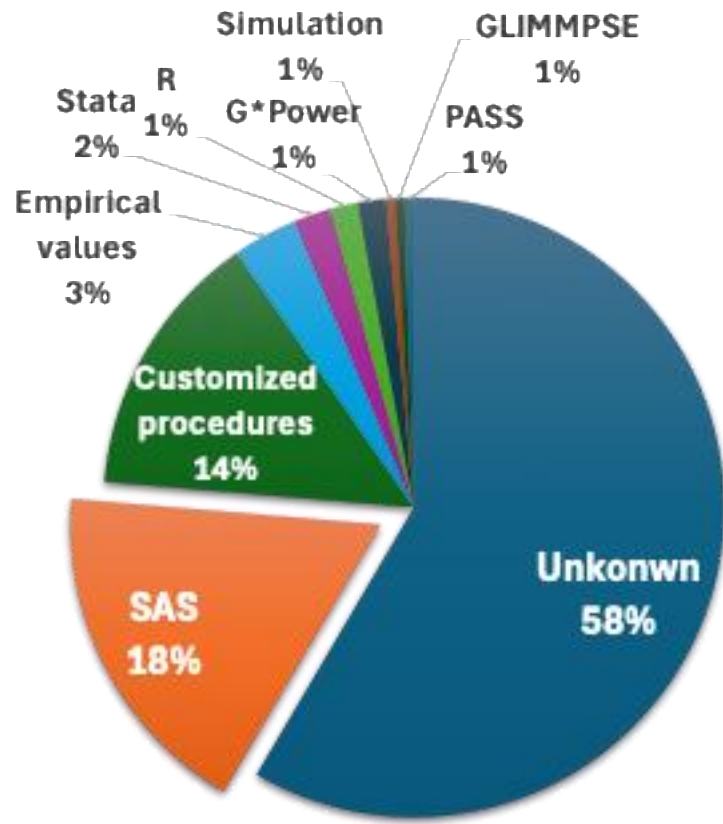


Power analysis was rarely reported in animal nutrition papers



- Literature review of 4,376 papers on JDS – Production: Animal Nutrition section
- **4.72%** reported power analysis

Challenges in conducting standardized power analysis



- **SAS** is most widely used
 - The **Stroup procedure** (1999, 2002) is versatile for many designs
 - No built-in **degrees-of-freedom approximation**
- Most tools have limitations in:
 - 🧩 **Complex designs**: e.g., multiple blocking factors
 - ⚙️ **Treatment interactions**: e.g., higher-order effects
 - 📈 **Contrasts**: e.g., linear or polynomial contrasts
 - 📊 **Correlation structures**: e.g., repeated measures

Objective: to develop a comprehensive open-source power analysis tool

Theory background of the *pwr4exp* R Package



Model: $y = X\beta + Zu + \varepsilon \quad u \sim N(\mathbf{0}, G), \varepsilon \sim N(\mathbf{0}, R)$

$$V := \text{var}(y) = ZGZ^T + R$$

$$C := \text{var}(\beta) = (X^T V^{-1} X)^{-1}$$

Test statistic

$$F = \frac{(K\hat{\beta})^T [K\hat{C}K^T]^{-1} (K\hat{\beta})}{ndf}$$

$$ndf = \text{rank}(K)$$

ddf: Satterthwaite approximation

Distributions

$$H_0: F \sim F(ndf, ddf)$$

$$H_A: F \sim F(ndf, ddf, ncp)$$

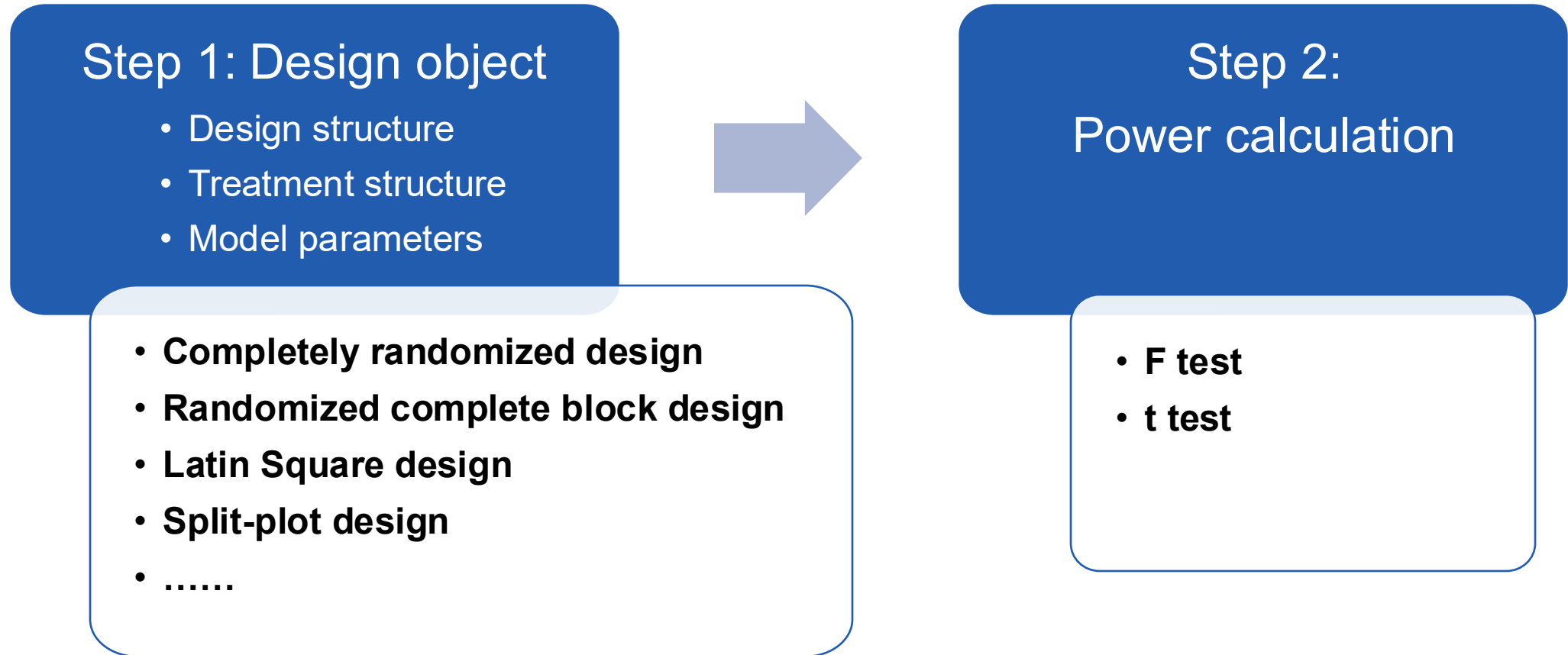
$$ncp = (K\beta)^T [KCK^T]^{-1} (K\beta)$$

Power calculation

$$F_c: P[F > F_c | H_0: F \sim F(ndf, ddf)] = \alpha$$

$$\text{power} = P[F > F_c | H_A: F \sim F(ndf, ddf, ncp)]$$

Key steps in conducting power analysis using *pwr4exp*



Start by creating a design object

What are the inputs?

- Know your data structure and model

$$y = X\beta + Zu + \varepsilon$$

$$u \sim N(0, G), \varepsilon \sim N(0, R)$$

● ● ●

mkdesign()

```
mkdesign(  
  formula,  
  data,  
  beta = NULL,  
  means = NULL,  
  vcomp = NULL,  
  sigma2 = NULL,  
  correlation = NULL,  
  template = FALSE,  
  REML = TRUE  
)
```

▪ The universal function for any design

- Model formula
- Data frame

Design matrices: X, Z

- Fixed effects or means (β)
- (Co-)variances components (G)
- Residual variance (R),
(optional) correlation structure (R)
(imported from *nlme* package)

Model parameters under H_A
Educated assumptions

- Input templates for fixed and random effects parameters

Built-in designs available in *pwr4exp*

- **Completely randomized design (CRD)**

[designCRD](#)(*treatments*, label, *replicates*, formula, beta, means, sigma2, template = **FALSE**)

- **Randomized complete block design (RCBD)**

[designRCBD](#)(*treatments*, label, *blocks*, formula, beta, means, vcomp, sigma2, template = **FALSE**)

- **Latin Square design (LSD)**

[designLSD](#)(*treatments*, label, *squares*, *reuse*, formula, beta, means, vcomp, sigma2, template = **FALSE**)

- **Split-plot design (SPD)**

[designSPD](#)(*trt.main*, *trt.sub*, label, *replicates*, formula, beta, means, vcomp, sigma2, template = **FALSE**)



A default model is set, but can be modified.

Power calculation with F - or t -test

● ● ● Power of F -test

```
pwr.anova(  
  object,  
  sig.level, # significance level  
  type      # The type of SS  
)
```

● ● ● Power of t -test

```
pwr.contrast(  
  object,  
  which,    # The factor of interest  
  by,       # The variable to condition on  
  contrast, # e.g., "pairwise", "poly", "trt.vs.ctrl", or a vector  
  sig.level, # significance level  
  p.adj,     # whether or not using the Bonferroni method  
  alternative, # "two.sided" or "one.sided"  
  strict  
)
```

Demo time!

Example – Latin Square design

■ 4 × 4 Latin Square design with 2 × 2 factorial arrangement

- 16 cows (C), 4 periods (P), 4 squares
- Temperature (Temp): T1 vs. T2
- Dose: D1 vs. D2

	P1	P2	P3	P4
Cow 1	a	b	c	d
Cow 2	b	d	a	c
Cow 3	c	a	d	b
Cow 4	d	c	b	a

Expected means		
Temp \ Dose	D1	D2
	35	38
T1		
T2	40	41

Treatments:

- a: T1D1
- b: T1D2
- c: T2D1
- d: T2D2

$$y_{ijkl} = \mu + \text{Temp}_i + \text{Dose}_j + (T \times D)_{ij} + C_k + P_l + e_{ijkl}$$

$$C_k \sim N(0, \sigma_c^2), P_l \sim N(0, \sigma_p^2), e_{ijkl} \sim N(0, \sigma_e^2)$$

Variance components

$$\sigma_c^2 = 11, \sigma_p^2 = 2$$

Residual variance

$$\sigma_e^2 = 2$$

Define the design and generate input templates

```
designLSD(  
  treatments = c(2, 2),  
  label = list(  
    temp = c("T1", "T2"),  
    dose = c("D1", "D2")),  
  squares = 4,  
  reuse = "col",  
  template = TRUE  
)
```

Two treatment factors each with 2 levels
(Optional) Labels of factor and factor levels
Four squares
Column blocks (periods) are identical across 4 squares
Generate the input templates for fixed and random effects

The default model: $\sim temp*dose + (1|row) + (1|col)$

Define the design and generate input templates

```
## $fixeff Fixed effects
## $fixeff$beta
## (Intercept) tempT2 doseD2 tempT2:doseD2
## 1 2 3 4
##
## $fixeff$means
## tempT1:doseD1 tempT2:doseD1 tempT1:doseD2 tempT2:doseD2
## 1 2 3 4
##
##
## $varcov Variance component
## $varcov$row
## (Intercept)
## (Intercept) 1  $\leftarrow \sigma_c^2 = 11$ 
##
## $varcov$col
## (Intercept)  $\leftarrow \sigma_p^2 = 2$ 
## (Intercept) 2
```

Input order of means

	D1	D2
T1	(1) 35	(3) 38
T2	(2) 40	(4) 14

Create the design object

```
lsd <- designLSD(  
  treatments = c(2, 2),  
  label = list(  
    temp = c("T1", "T2"),  
    dose = c("D1", "D2")),  
  squares = 4,  
  reuse = "col",  
  means = c(35, 40, 38, 41),  
  vcomp = c(11, 2),  
  sigma2 = 2  
)
```

Design characteristics

Means

Variance components of random effects

Residual variance

Calculate power of F -test

```
pwr.anova(lsd)
```

```
## Power of type III F-test  
##           NumDF DenDF sig.level  power  
## temp           1    42      0.05 1.00000  
## dose           1    42      0.05 0.99982  
## temp:dose      1    42      0.05 0.78909
```

Calculate power of t -test

- Compare T1 vs. T2 at each dose level

```
pwr.contrast(lsd, which = "temp", by = "dose")
```

```
## $`dose = D1`  
##               effect df sig.level power alternative  
## tempT1 - tempT2    -5 42    0.05    1 two.sided  
##  
## $`dose = D2`  
##               effect df sig.level    power alternative  
## tempT1 - tempT2     -3 42    0.05 0.9999516 two.sided
```

- Compare each treatment with control (T1D1)

```
pwr.contrast(lsd, which = "temp:dose", contrast = "trt.vs.ctrl")
```

```
##               effect df sig.level    power alternative  
## tempT2:doseD1 - tempT1:doseD1    5 42    0.05 1.0000000 two.sided  
## tempT1:doseD2 - tempT1:doseD1    3 42    0.05 0.9999516 two.sided  
## tempT2:doseD2 - tempT1:doseD1    6 42    0.05 1.0000000 two.sided
```

Some practical aspects

- **Plan the analysis up front**

- Define the hypothesis and study objective
- Select the appropriate statistical model

- **Collect prior information or conduct a pilot study**

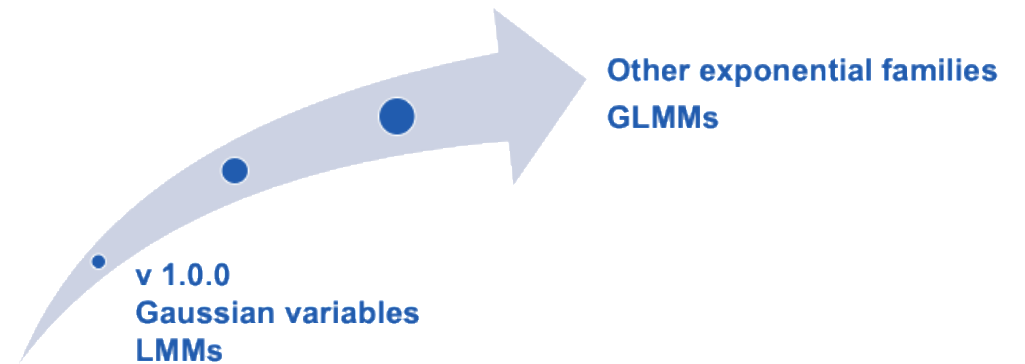
- Estimate treatment effects and variance components for the key response

- **Perform a sensitivity analysis**

- Use confidence intervals instead of point estimates
- Identify the parameter that most influences power (e.g., effect, variances, sample size)

- **Choose an adequate sample size to avoid under- and over-powering**

- e.g., use smallest effect size or largest variance within the plausible regions (confidence interval)



Find out more



pwr4exp package page
Documentation & Bug report



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***Invited review: Enhancing quality of dairy cattle research
through adequate power analysis***

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