Power & Sample Size in R

Design around the primary estimand, plausible nuisance parameters and attrition

Rverse Analytics

Power belongs to a design, not a test name. Specify the primary outcome, estimand, effect scale, allocation, alpha, target power and analysis model before calculating *n*.

Minimum inputs

Element	Example	Source
Primary estimand	adjusted mean difference at week 12	protocol
Clinically important effect	4 points	clinical judgment
Nuisance parameter	SD = 10, control risk = .25	prior data / pilot CI
Error rates	two-sided α = .05, power = .90	design choice
Allocation	1:1 or 2:1	feasibility and efficiency
Attrition / nonadherence	15% loss	operational evidence

Common designs

```r
# Two independent means: solve for n per group
power.t.test(delta = 4, sd = 10, sig.level = 0.05,
             power = 0.90, type = "two.sample",
             alternative = "two.sided")

# Paired mean change: SD must be the SD of paired differences
power.t.test(delta = 3, sd = 8, power = 0.90,
             type = "paired")

# Two proportions
power.prop.test(p1 = 0.25, p2 = 0.15,
                sig.level = 0.05, power = 0.90)

# Correlation and one-way ANOVA
pwr::pwr.r.test(r = 0.30, power = 0.90, sig.level = 0.05)
pwr::pwr.anova.test(k = 3, f = 0.25, power = 0.90, sig.level = 0.05)
```

`pwr` standardized effects: Cohen's *d* for means, *h* for proportions and *f* for ANOVA. Convert from clinically meaningful raw values and plausible variability; do not pick conventional labels without context.

Inflate transparently

```r
n_analyzable <- 172

# Individual attrition
n_recruit <- ceiling(n_analyzable / (1 - 0.15))

# Unequal allocation: round each arm separately
n_control <- ceiling(n_recruit / 3)
n_treat   <- ceiling(2 * n_recruit / 3)

# Cluster-randomized design effect
m_bar <- 20; icc <- 0.04; cv <- 0.30
de_equal <- 1 + (m_bar - 1) * icc
de_cv    <- 1 + ((1 + cv^2) * m_bar - 1) * icc
n_clustered <- ceiling(n_analyzable * de_cv)
```

Attrition inflation preserves analyzable sample size; it does not correct bias from informative dropout. Cluster inflation must be followed by feasible whole-cluster rounding and allowance for cluster loss.

ANCOVA and repeated outcomes

```r
# Approximate ANCOVA gain from baseline-outcome correlation rho
n_unadjusted <- 200
rho <- 0.60
n_ancova <- ceiling(n_unadjusted * (1 - rho^2))
```

```r
# Explore uncertainty rather than trusting one SD/effect assumption
grid <- expand.grid(delta = c(3, 4, 5), sd = c(8, 10, 12))
grid$n_per_arm <- mapply(function(delta, sd) {
  ceiling(power.t.test(delta = delta, sd = sd,
    power = 0.90, sig.level = 0.05, type = "two.sample")$n)
}, grid$delta, grid$sd)
```

For longitudinal mixed models, non-inferiority, survival, adaptive or complex clustered designs, simulate the planned analysis rather than forcing a simple closed-form test.

Simulation pattern

```r
one_trial <- function(n, beta = 4, sd_subject = 6, sd_error = 7) {
  id <- rep(seq_len(n), each = 3)
  group <- rep(rbinom(n, 1, 0.5), each = 3)
  time <- rep(c(0, 6, 12), n)
  b0 <- rep(rnorm(n, 0, sd_subject), each = 3)
  y <- 50 + b0 + 0.2 * time + beta * group * (time == 12) +
    rnorm(3 * n, 0, sd_error)
  d <- data.frame(id, group, time = factor(time), y)
  fit <- lme4::lmer(y ~ group * time + (1 | id), data = d)
  coef(summary(fit))["group:time12", "t value"] > 1.96
}

set.seed(20260711)
mean(replicate(1000, one_trial(n = 160)))
```

Simulation must reproduce randomization, missingness, clustering, analysis code and the exact decision rule. Record seeds and Monte Carlo error.

Non-inferiority / equivalence

- Define the margin on a clinically interpretable scale before seeing results.
- Align effect direction, null hypothesis and CI rule.
- Power for the planned CI/test; do not reuse a superiority calculation.
- Consider both intention-to-treat and per-protocol estimands.

Protocol checklist

- Name the primary outcome, time point, contrast and analysis population.
- Document every input and its evidence; show sensitivity across plausible values.
- State one-/two-sided alpha, multiplicity strategy, allocation and rounding.
- Separate analyzable *n*, recruitment *n* and number of clusters.
- Archive executable code and simulation diagnostics with the protocol.

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