Statistical Power

Fill In Your Name

01 March, 2022

What is power?

What is power?

- We want to separate signal from noise.
- Power = probability of rejecting null hypothesis, given true effect $\neq 0$.
- In other words, it is the ability to detect an effect given that it exists.
- Formally: (1 - Type II) error rate.
- Thus, power $\in (0, 1)$.
- Standard thresholds: 0.8 or 0.9.

Starting point for power analysis

- Power analysis is something we do *before* we run a study.
  - Helps you figure out the sample you need to detect a given effect size.
  - Or helps you figure out a minimal detectable difference given a set sample size.
  - May help you decide whether to run a study.
- It is hard to learn from an under-powered null finding.
  - Was there an effect, but we were unable to detect it? or was there no effect? We can't say.

Power

- Say there truly is a treatment effect and you run your experiment many times. How often will you get a statistically significant result?
- Some guesswork to answer this question.
  - How big is your treatment effect?
  - How many units are treated, measured?
  - How much noise is there in the measurement of your outcome?

Approaches to power calculation

- Analytical calculations of power
- Simulation

Power calculation tools

- Interactive
  - EGAP Power Calculator
  - rpsychologist
- R Packages
  - pwr
  - DeclareDesign, see also https://declaredesign.org/

Analytical calculations of power

Analytical calculations of power

- Formula:

$$\text{Power} = \Phi\left(\frac{|\tau|\sqrt{N}}{2\sigma} - \Phi^{-1}(1 - \frac{\alpha}{2})\right)$$

- Components:
  - ϕ: standard normal CDF is monotonically increasing
  - τ: the effect size
  - N: the sample size
  - σ: the standard deviation of the outcome
  - α: the significance level (typically 0.05)

Example: Analytical calculations of power

```r
# Power for a study with 80 observations and effect
# size of 0.25
library(pwr)
pwr.t.test(
  n = 40, d = 0.25, sig.level = 0.05,
  power = NULL, type = c(
    "two.sample",
    "one.sample", "paired"
  )
)
```

```
     Two-sample t test power calculation

              n = 40
              d = 0.25
      sig.level = 0.05
          power = 0.1972
    alternative = two.sided

NOTE: n is number in *each* group
```

Limitations to analytical power calculations

- Only derived for some test statistics (differences of means)
- Makes specific assumptions about the data-generating process
- Incompatible with more complex designs

Simulation-based power calculation

Simulation-based power calculation

- Create dataset and simulate research design.
- Assumptions are necessary for simulation studies, but you make your own.
- For the DeclareDesign approach, see https://declaredesign.org/

Steps

- Define the sample and the potential outcomes function.
- Define the treatment assignment procedure.
- Create data.
- Assign treatment, then estimate the effect.
- Do this many times.

Examples

- Complete randomization
- With covariates
- With cluster randomization

Example: Simulation-based power for complete randomization

```r
# install.packages("randomizr")
library(randomizr)
library(estimatr)

## Y0 is fixed in most field experiments.
## So we only generate it once:
make_Y0 <- function(N) {
  rnorm(n = N)
}
repeat_experiment_and_test <- function(N, Y0, tau) {
  Y1 <- Y0 + tau
  Z <- complete_ra(N = N)
  Yobs <- Z * Y1 + (1 - Z) * Y0
  estimator <- lm_robust(Yobs ~ Z)
  pval <- estimator$p.value[2]
  return(pval)
}
```

Example: Simulation-based power for complete randomization

```r
power_sim <- function(N, tau, sims) {
  Y0 <- make_Y0(N)
  pvals <- replicate(
    n = sims,
    repeat_experiment_and_test(N = N, Y0 = Y0, tau = tau)
  )
  pow <- sum(pvals < .05) / sims
  return(pow)
}

set.seed(12345)
power_sim(N = 80, tau = .25, sims = 100)
```

```
[1] 0.15
```

```r
power_sim(N = 80, tau = .25, sims = 100)
```

```
[1] 0.21
```

Example: Using DeclareDesign I

```r
library(DeclareDesign)
library(tidyverse)
P0 <- declare_population(N, u0 = rnorm(N))
# declare Y(Z=1) and Y(Z=0)
O0 <- declare_potential_outcomes(Y_Z_0 = 5 + u0, Y_Z_1 = Y_Z_0 + tau)
# design is to assign m units to treatment
A0 <- declare_assignment(Z = conduct_ra(N = N, m = round(N / 2)))
# estimand is the average difference between Y(Z=1) and Y(Z=0)
estimand_ate <- declare_inquiry(ATE = mean(Y_Z_1 - Y_Z_0))
R0 <- declare_reveal(Y, Z)
design0_base <- P0 + A0 + O0 + R0

## For example:
design0_N100_tau25 <- redesign(design0_base, N = 100, tau = .25)
dat0_N100_tau25 <- draw_data(design0_N100_tau25)
head(dat0_N100_tau25)
```

Example: Using DeclareDesign II

```
   ID      u0 Z Y_Z_0 Y_Z_1     Y
1 001 -0.2060 0 4.794 5.044 4.794
2 002 -0.5875 0 4.413 4.663 4.413
3 003 -0.2908 1 4.709 4.959 4.959
4 004 -2.5649 0 2.435 2.685 2.435
5 005 -1.8967 0 3.103 3.353 3.103
6 006 -1.6401 1 3.360 3.610 3.610
```

```r
with(dat0_N100_tau25, mean(Y_Z_1 - Y_Z_0)) # true ATE
```

```
[1] 0.25
```

```r
with(dat0_N100_tau25, mean(Y[Z == 1]) - mean(Y[Z == 0])) # estimate
```

```
[1] 0.5569
```

```r
lm_robust(Y ~ Z, data = dat0_N100_tau25)$coef # estimate
```

```
(Intercept)           Z
     4.8458      0.5569
```

Example: Using DeclareDesign III

```
E0 <- declare_estimator(Y ~ Z,
  model = lm_robust, label = "t test 1",
  inquiry = "ATE"
)
t_test <- function(data) {
  test <- with(data, t.test(x = Y[Z == 1], y = Y[Z == 0]))
  data.frame(statistic = test$statistic, p.value = test$p.value)
}
T0 <- declare_test(handler = label_test(t_test), label = "t test 2")
design0_plus_tests <- design0_base + E0 + T0

design0_N100_tau25_plus <- redesign(design0_plus_tests, N = 100, tau = .25)

## Only repeat the random assignment, not the creation of Y0. Ignore warning
names(design0_N100_tau25_plus)
```

```
[1] "P0"        "A0"        "O0"        "R0"        "t test 1" "t test 2"
```

```
design0_N100_tau25_sims <- simulate_design(design0_N100_tau25_plus,
  sims = c(1, 100, 1, 1, 1, 1)
) # only repeat the random assignment
```

```
Warning: We recommend you choose a higher number of simulations than 1 for the
```

Example: Using DeclareDesign IV

```
# design0_N100_tau25_sims has 200 rows (2 tests * 100 random assignments)
# just look at the first 6 rows
head(design0_N100_tau25_sims)
```

```
                     design   N  tau sim_ID estimator term estimate std.error sta
1 design0_N100_tau25_plus 100 0.25      1  t test 1    Z   0.1108    0.2150
2 design0_N100_tau25_plus 100 0.25      1  t test 2 <NA>       NA        NA
3 design0_N100_tau25_plus 100 0.25      2  t test 1    Z   0.2458    0.2154
4 design0_N100_tau25_plus 100 0.25      2  t test 2 <NA>       NA        NA
5 design0_N100_tau25_plus 100 0.25      3  t test 1    Z   0.5463    0.2133
6 design0_N100_tau25_plus 100 0.25      3  t test 2 <NA>       NA        NA
  step_1_draw step_2_draw
1           1           1
2           1           1
3           1           2
4           1           2
5           1           3
6           1           3
```

```
# for each estimator, power = proportion of simulations with p.value < 0.5
design0_N100_tau25_sims %>%
  group_by(estimator) %>%
  summarize(pow = mean(p.value < .05), .groups = "drop")
```

Example: Using DeclareDesign V

```
# A tibble: 2 x 2
  estimator   pow
  <chr>     <dbl>
1 t test 1    0.2
2 t test 2    0.2
```

Power with covariate adjustment

Covariate adjustment and power

- Covariate adjustment can improve power because it mops up variation in the outcome variable.
  - If prognostic, covariate adjustment can reduce variance dramatically. Lower variance means higher power.
  - If non-prognostic, power gains are minimal.
- All covariates must be pre-treatment. Do not drop observations on account of missingness.
  - See the module on threats to internal validity and the 10 things to know about covariate adjustment.
- Freedman's bias as n of observations decreases and K covariates increases.

Blocking

- Blocking: randomly assign treatment within blocks
  - "Ex-ante" covariate adjustment
  - Higher precision/efficiency implies more power
  - Reduce "conditional bias": association between treatment assignment and potential outcomes
  - Benefits of blocking over covariate adjustment clearest in small experiments

Example: Simulation-based power with a covariate I

```r
## Y0 is fixed in most field experiments. So we only generate it once
make_Y0_cov <- function(N) {
  u0 <- rnorm(n = N)
  x <- rpois(n = N, lambda = 2)
  Y0 <- .5 * sd(u0) * x + u0
  return(data.frame(Y0 = Y0, x = x))
}
##  X is moderarely predictive of Y0.
test_dat <- make_Y0_cov(100)
test_lm <- lm_robust(Y0 ~ x, data = test_dat)
summary(test_lm)
```

```
Call:
lm_robust(formula = Y0 ~ x, data = test_dat)

Standard error type:  HC2

Coefficients:
            Estimate Std. Error t value    Pr(>|t|) CI Lower CI Upper DF
(Intercept)     0.11     0.1880   0.585 0.559753653   -0.263    0.483 98
x               0.44     0.0814   5.413 0.000000441    0.279    0.602 98

Multiple R-squared:  0.231 ,    Adjusted R-squared:  0.223
```

Example: Simulation-based power with a covariate II

```
F-statistic: 29.3 on 1 and 98 DF,  p-value: 0.000000441
```

```
## now set up the simulation
repeat_experiment_and_test_cov <- function(N, tau, Y0, x) {
  Y1 <- Y0 + tau
  Z <- complete_ra(N = N)
  Yobs <- Z * Y1 + (1 - Z) * Y0
  estimator <- lm_robust(Yobs ~ Z + x, data = data.frame(Y0, Z, x))
  pval <- estimator$p.value[2]
  return(pval)
}
## create the data once, randomly assign treatment sims times
## report what proportion return p-value < 0.05
power_sim_cov <- function(N, tau, sims) {
  dat <- make_Y0_cov(N)
  pvals <- replicate(n = sims, repeat_experiment_and_test_cov(
    N = N,
    tau = tau, Y0 = dat$Y0, x = dat$x
  ))
  pow <- sum(pvals < .05) / sims
  return(pow)
}
```

Example: Simulation-based power with a covariate III

```
set.seed(12345)
power_sim_cov(N = 80, tau = .25, sims = 100)
```

```
[1] 0.13
```

```
power_sim_cov(N = 80, tau = .25, sims = 100)
```

```
[1] 0.19
```

Power for cluster randomization

Power and clustered designs

- Recall the randomization module.
- Given a fixed N, a clustered design is weakly less powered than a non-clustered design.
  - The difference is often substantial.
- We have to estimate variance correctly:
  - Clustering standard errors (the usual)
  - Randomization inference
- To increase power:
  - Better to increase number of clusters than number of units per cluster.
  - How much clusters reduce power depends critically on the intra-cluster correlation (the ratio of variance within clusters to total variance).

A note on clustering in observational research

- Often overlooked, leading to (possibly) wildly understated uncertainty.
  - Frequentist inference based on ratio $\hat{\beta}/\hat{se}$
  - If we underestimate $\hat{se}$, we are much more likely to reject H_0. (Type-I error rate is too high.)
- Many observational designs much less powered than we think they are.

Example: Simulation-based power for cluster randomization I

```r
## Y0 is fixed in most field experiments. So we only generate it once
make_Y0_clus <- function(n_indivs, n_clus) {
  # n_indivs is number of people per cluster
  # n_clus is number of clusters
  clus_id <- gl(n_clus, n_indivs)
  N <- n_clus * n_indivs
  u0 <- fabricatr::draw_normal_icc(N = N, clusters = clus_id, ICC = .1)
  Y0 <- u0
  return(data.frame(Y0 = Y0, clus_id = clus_id))
}

test_dat <- make_Y0_clus(n_indivs = 10, n_clus = 100)
# confirm that this produces data with 10 in each of 100 clusters
table(test_dat$clus_id)
```

Example: Simulation-based power for cluster randomization II

```
  1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20
 10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10
 34  35  36  37  38  39  40  41  42  43  44  45  46  47  48  49  50  51  52  53
 10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10
 67  68  69  70  71  72  73  74  75  76  77  78  79  80  81  82  83  84  85  86
 10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10  10
100
 10
```

```r
# confirm ICC
ICC::ICCbare(y = Y0, x = clus_id, data = test_dat)
```

```
[1] 0.09655
```

Example: Simulation-based power for cluster randomization III

```
repeat_experiment_and_test_clus <- function(N, tau, Y0, clus_id) {
  Y1 <- Y0 + tau
  # here we randomize Z at the cluster level
  Z <- cluster_ra(clusters = clus_id)
  Yobs <- Z * Y1 + (1 - Z) * Y0
  estimator <- lm_robust(Yobs ~ Z,
    clusters = clus_id,
    data = data.frame(Y0, Z, clus_id), se_type = "CR2"
  )
  pval <- estimator$p.value[2]
  return(pval)
}
power_sim_clus <- function(n_indivs, n_clus, tau, sims) {
  dat <- make_Y0_clus(n_indivs, n_clus)
  N <- n_indivs * n_clus
  # randomize treatment sims times
  pvals <- replicate(
    n = sims,
    repeat_experiment_and_test_clus(
      N = N, tau = tau,
      Y0 = dat$Y0, clus_id = dat$clus_id
    )
  )
        <- sum(pvals < .05) / sims
```

Example: Simulation-based power for cluster randomization (DeclareDesign) I

```
P1 <- declare_population(
  N = n_clus * n_indivs,
  clusters = gl(n_clus, n_indivs),
  u0 = draw_normal_icc(N = N, clusters = clusters, ICC = .2)
)
O1 <- declare_potential_outcomes(Y_Z_0 = 5 + u0, Y_Z_1 = Y_Z_0 + tau)
A1 <- declare_assignment(Z = conduct_ra(N = N, clusters = clusters))
estimand_ate <- declare_inquiry(ATE = mean(Y_Z_1 - Y_Z_0))
R1 <- declare_reveal(Y, Z)
design1_base <- P1 + A1 + O1 + R1 + estimand_ate

## For example:
design1_test <- redesign(design1_base, n_clus = 10, n_indivs = 100, tau = .25)
test_d1 <- draw_data(design1_test)
# confirm all individuals in a cluster have the same treatment assignment
with(test_d1, table(Z, clusters))
```

```
   clusters
Z     1   2   3   4   5   6   7   8   9  10
  0 100   0 100 100 100   0   0 100   0   0
  1   0 100   0   0   0 100 100   0 100 100
```

Example: Simulation-based power for cluster randomization (DeclareDesign) II

```
# three estimators, differ in se_type:
E1a <- declare_estimator(Y ~ Z,
  model = lm_robust, clusters = clusters,
  se_type = "CR2", label = "CR2 cluster t test",
  inquiry = "ATE"
)
E1b <- declare_estimator(Y ~ Z,
  model = lm_robust, clusters = clusters,
  se_type = "CR0", label = "CR0 cluster t test",
  inquiry = "ATE"
)
E1c <- declare_estimator(Y ~ Z,
  model = lm_robust, clusters = clusters,
  se_type = "stata", label = "stata RCSE t test",
  inquiry = "ATE"
)

design1_plus <- design1_base + E1a + E1b + E1c

design1_plus_tosim <- redesign(design1_plus, n_clus = 10, n_indivs = 100, tau =
```

Example: Simulation-based power for cluster randomization (DeclareDesign) III

```
## Only repeat the random assignment, not the creation of Y0. Ignore warning
## We would want more simulations in practice.
set.seed(12355)
design1_sims <- simulate_design(design1_plus_tosim,
  sims = c(1, 1000, rep(1, length(design1_plus_tosim) - 2))
)
```

```
Warning: We recommend you choose a higher number of simulations than 1 for the
```

```
design1_sims %>%
  group_by(estimator) %>%
  summarize(
    pow = mean(p.value < .05),
    coverage = mean(estimand <= conf.high & estimand >= conf.low),
    .groups = "drop"
  )
```

Example: Simulation-based power for cluster randomization (DeclareDesign) IV

```
# A tibble: 3 x 3
  estimator               pow coverage
  <chr>                 <dbl>    <dbl>
1 CR0 cluster t test 0.155    0.911
2 CR2 cluster t test 0.105    0.936
3 stata RCSE t test  0.131    0.918
```

```
library(DesignLibrary)
## This may be simpler than the above:
d1 <- block_cluster_two_arm_designer(
  N_blocks = 1,
  N_clusters_in_block = 10,
  N_i_in_cluster = 100,
  sd_block = 0,
  sd_cluster = .3,
  ate = .25
)
d1_plus <- d1 + E1b + E1c
d1_sims <- simulate_design(d1_plus, sims = c(1, 1, 1000, 1, 1, 1, 1, 1))
```

Example: Simulation-based power for cluster randomization (DeclareDesign) V

```
d1_sims %>%
  group_by(estimator) %>%
  summarize(
    pow = mean(p.value < .05),
    coverage = mean(estimand <= conf.high & estimand >= conf.low),
    .groups = "drop"
  )
```

```
# A tibble: 3 x 3
  estimator              pow coverage
  <chr>                <dbl>    <dbl>
1 CR0 cluster t test 0.209    0.914
2 estimator          0.143    0.941
3 stata RCSE t test  0.194    0.925
```

Comparative statics

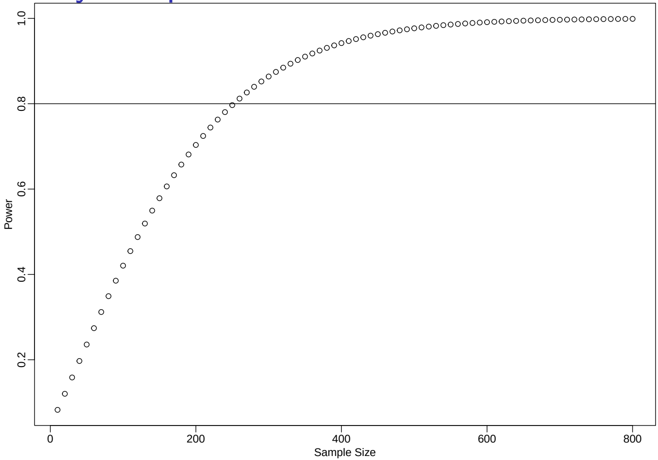
Comparative Statics

- Power is:
  - Increasing in N
  - Increasing in $|\tau|$
  - Decreasing in σ

Power by sample size I

```
some_ns <- seq(10, 800, by = 10)
pow_by_n <- sapply(some_ns, function(then) {
  pwr.t.test(n = then, d = 0.25, sig.level = 0.05)$power
})
plot(some_ns, pow_by_n,
  xlab = "Sample Size",
  ylab = "Power"
)
abline(h = .8)
```

Power by sample size II

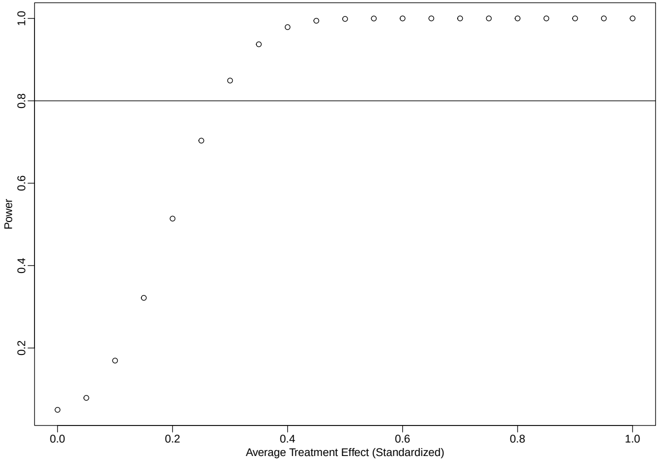



```
## See https://cran.r-project.org/web/packages/pwr/vignettes/pwr-vignette.html
## for fancier plots
## ptest <-  pwr.t.test(n = NULL, d = 0.25, sig.level = 0.05, power = .8)
## plot(ptest)
```

Power by treatment effect size I

```
some_taus <- seq(0, 1, by = .05)
pow_by_tau <- sapply(some_taus, function(thetau) {
  pwr.t.test(n = 200, d = thetau, sig.level = 0.05)$power
})
plot(some_taus, pow_by_tau,
  xlab = "Average Treatment Effect (Standardized)",
  ylab = "Power"
)
abline(h = .8)
```

Power by treatment effect size II



EGAP Power Calculator

- Try the calculator at: https://egap.shinyapps.io/power-app/
- For cluster randomization designs, try adjusting:
  - Number of clusters
  - Number of units per clusters
  - Intra-cluster correlation
  - Treatment effect

Comments

- Know your outcome variable.
- What effects can you realistically expect from your treatment?
- What is the plausible range of variation of the outcome variable?
    - A design with limited possible movement in the outcome variable may not be well-powered.

Conclusion: How to improve your power

1. Increase the N
   - If clustered, increase the number of clusters if at all possible
2. Strengthen the treatment
3. Improve precision
   - Covariate adjustment
   - Blocking
4. Better measurement of the outcome variable