Advanced Power Analysis: Into the Weeds

BERDC Special Topics Talk 12

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Biostatistics, Epidemiology, and Research Design Core

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Opening

<u>Goal</u>: Trek out into the weeds to wrangle advanced power analysis

- Fundamentals of power analysis: ‘***tapping into the roots***’
- Overview of basic methods: ‘***if it’s easy, leaf it alone***’
- More difficult experimental designs: ‘***thorny problems in my side***’
- Ways to deal with problems: ‘***from floundering to flowering***’
- Other resources that are out there: ‘***releasing seeds on the wind***’

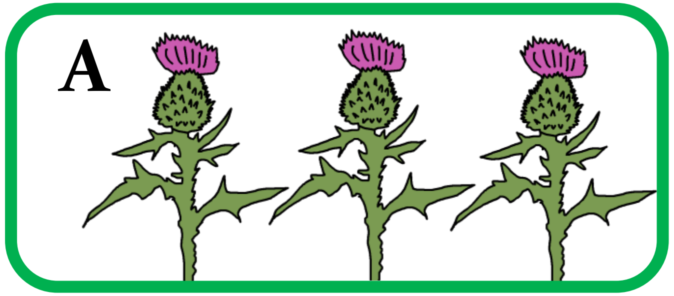
<u>Before Moving On:</u>

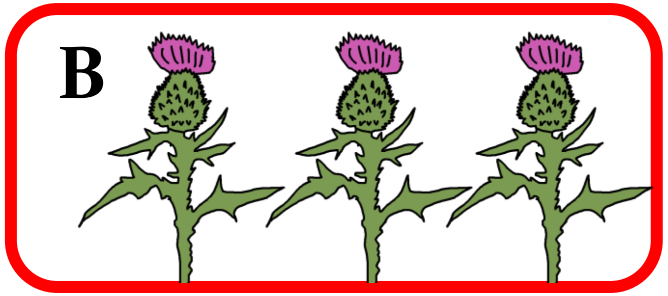
Pre-test: https://und.qualtrics.com/jfe/form/SV_cTMHCNZ2G2MrpPo

R code: https://med.und.edu/daccota/_files/docs/berdc_docs/advanced_power_analysis_rcode.txt

Power Analysis Roots

- Why run power analysis?
- When to do something else





Already generated data

Limited Study Types

Resource Equation Model [1]

"This method is called 'resource equation' method. This method is used when it is not possible to assume about effect size, to get an idea about standard deviation as no previous findings are available or when multiple endpoints are measured or complex statistical procedure is used for analysis."

Sample size formulas for three ANOVA designs

ANOVA design	Application	Minimum n/group	Maximum n/group
One-way ANOVA	Group comparison	$10/k + 1$	$20/k + 1$
One within factor, repeated-measures ANOVA	One group, repeated measurements	$10/(r - 1) + 1^{a,b}$	$20/(r - 1) + 1^{a,b}$
One-between, one within factor, repeated-measures ANOVA	Group comparison, repeated measurements	$10/kr + 1^{b}$	$20/kr + 1^{b}$

Open in a separate window

k = number of groups, n = number of subjects per group, N = total number of subjects, r = number of repeated measurements.

[a] $n = N$, because only one group is involved,

[b] n must be multiplied by r whenever the experiment involves sacrificing the animals at each measurement.

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Power Analysis Roots

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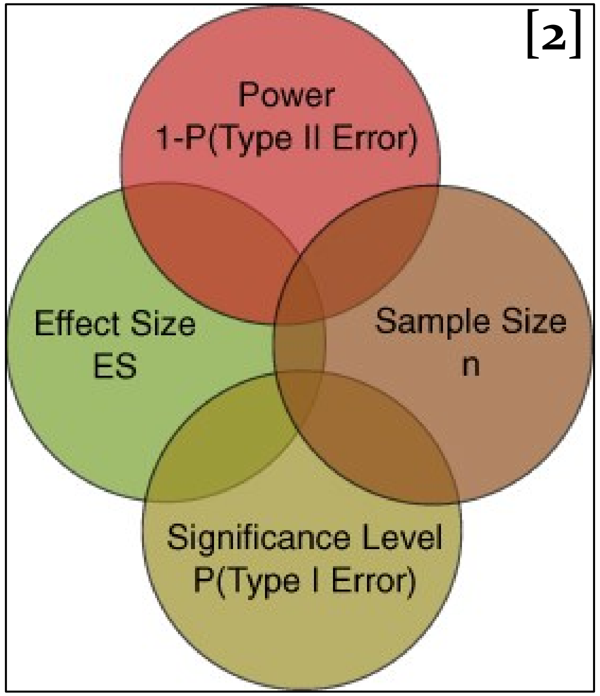
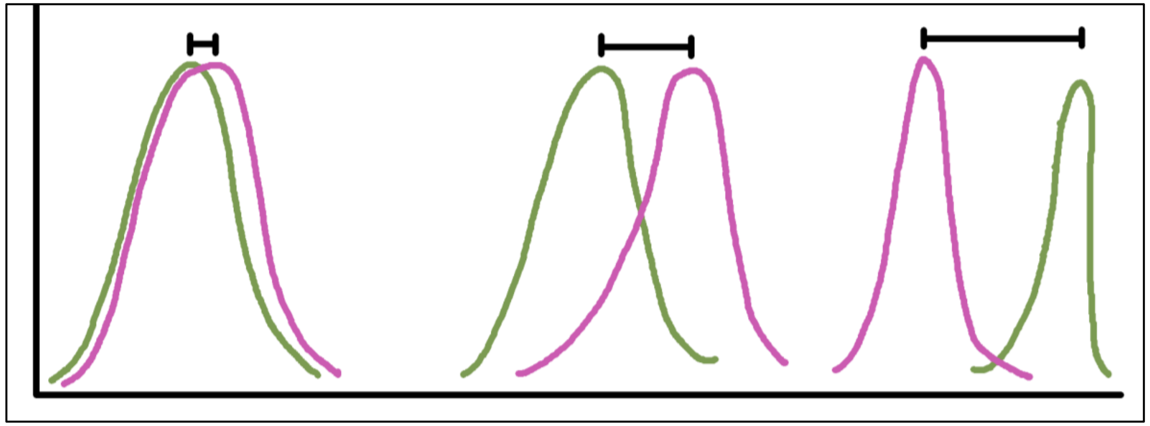
- Core Components
  - Sample Size
  - Effect Size
  - Significance Level
  - Power





[2]

Table 10.3. Cohen's effect size benchmarks

Statistical method	Effect size measures	Suggested guidelines for effect size		
		Small	*Medium*	*Large*
t-test	d	0.20	0.50	0.80
ANOVA	f	0.10	0.25	0.40
Linear models	f2	0.02	0.15	0.35
Test of proportions	h	0.20	0.50	0.80
Chi-square	w	0.10	0.30	0.50

$\alpha = 0.05$

power = 0.80

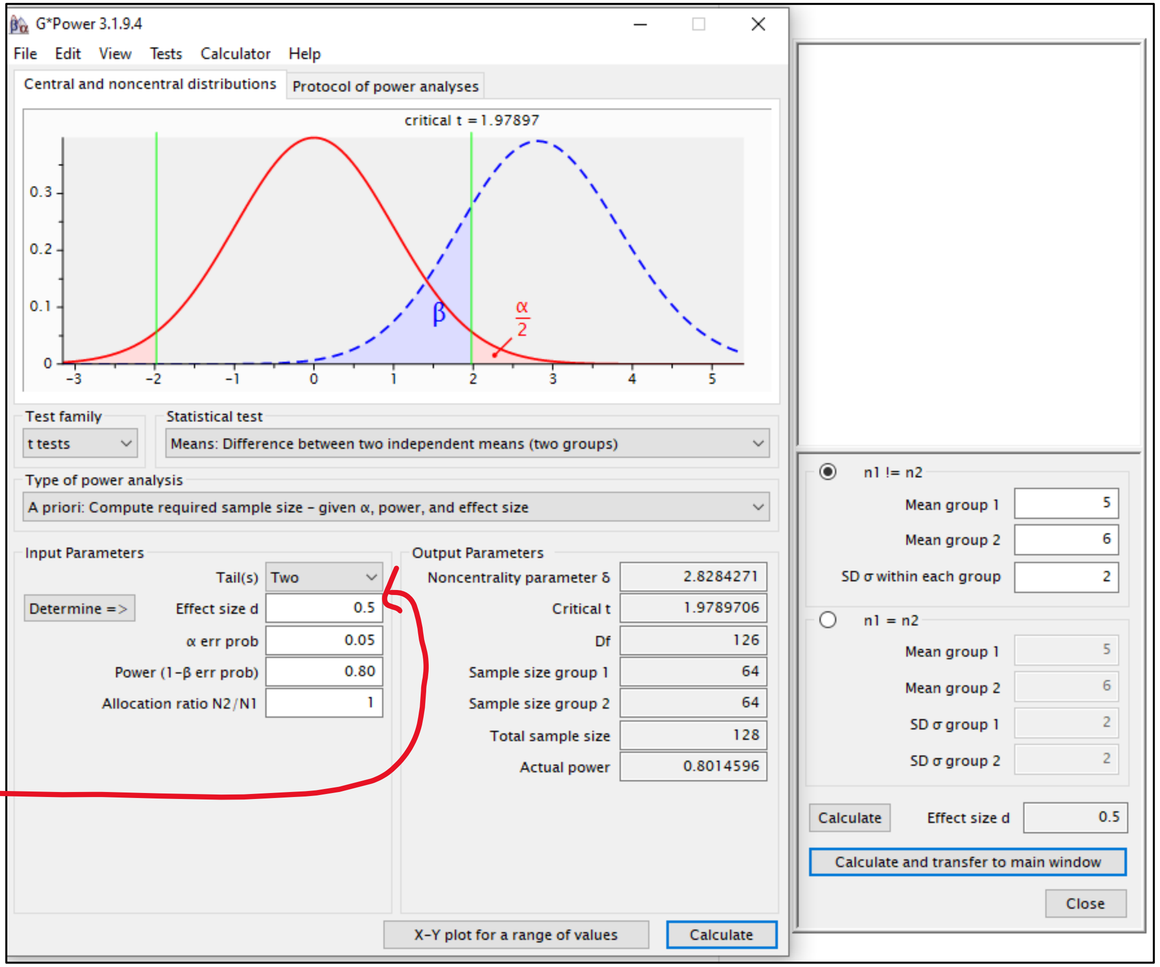
Leafy basics

- T-tests

$$d = \frac{(M_1 - M_2)}{SD}$$

$$= \frac{6 - 5}{2}$$

$$= \frac{1}{2} = 0.5$$



Leafy basics

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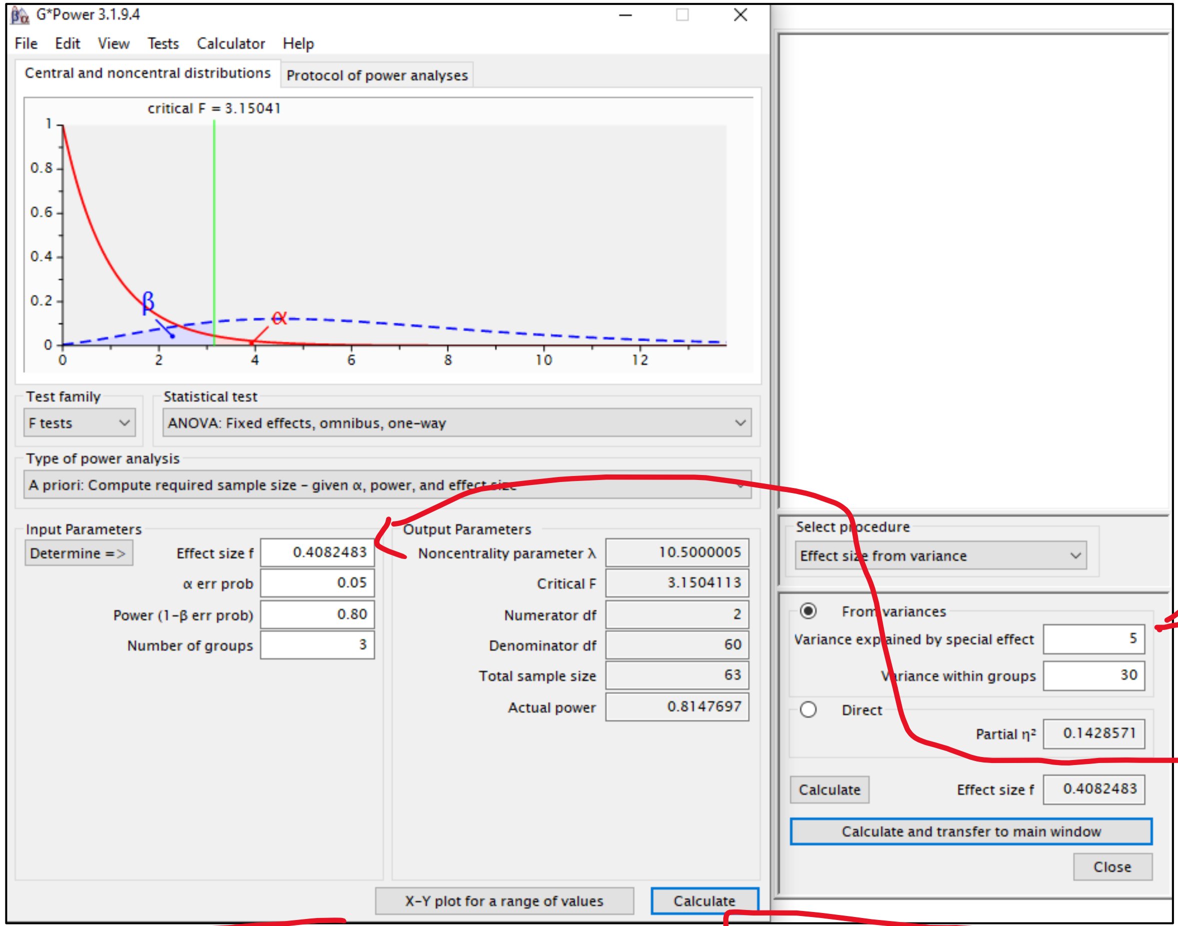
ANOVA

$$f = \sqrt{\frac{\eta^2}{(1-\eta^2)}}$$

$$= \sqrt{\frac{\sigma_e^2/\sigma_t^2}{(1-(\sigma_e^2/\sigma_t^2))}}$$

$$= \sqrt{\frac{SS_e/SS_t}{(1-(SS_e/SS_t))}}$$



$5 = \sigma_e^2$

$5 + 30 = 35 = \sigma_t^2$

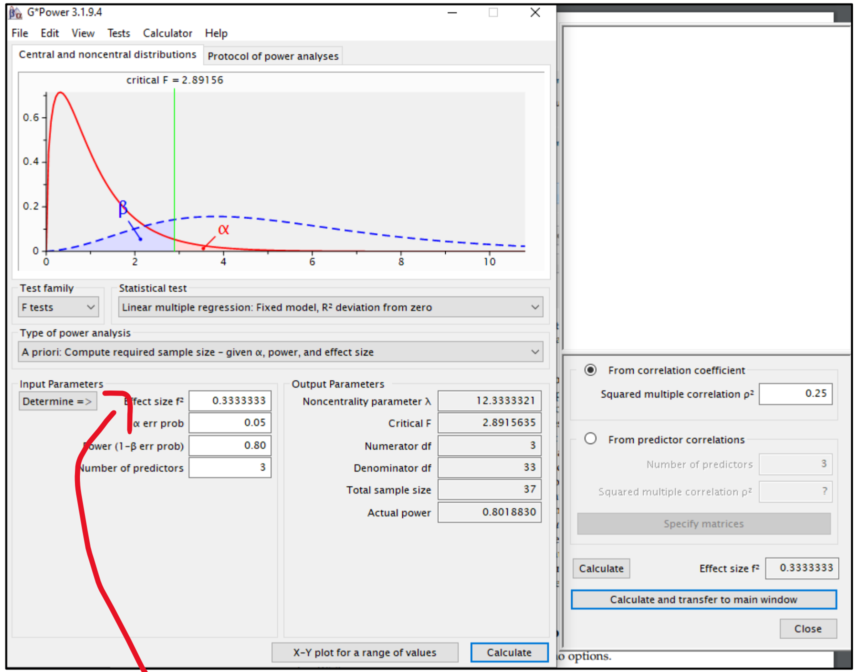
$$= \sqrt{\frac{5/35}{1-(5/35)}} = \sqrt{0.143/0.857} = 0.408$$

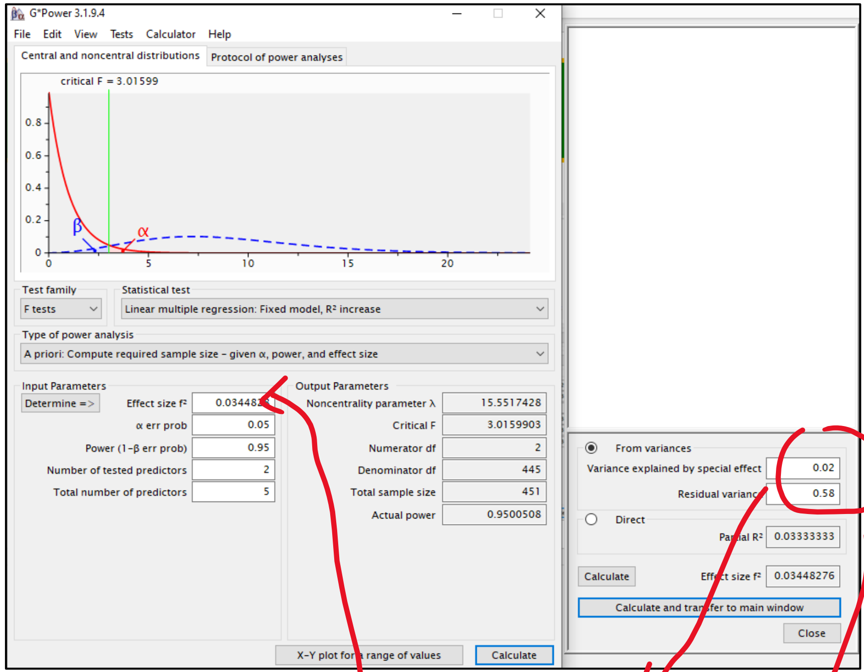
Leafy basics

Regression [3]

$$f2 = \frac{R^2}{(1-R^2)}$$

$$= \frac{R^2_{AB} - R^2_{A}}{(1 - R^2_{AB})}$$



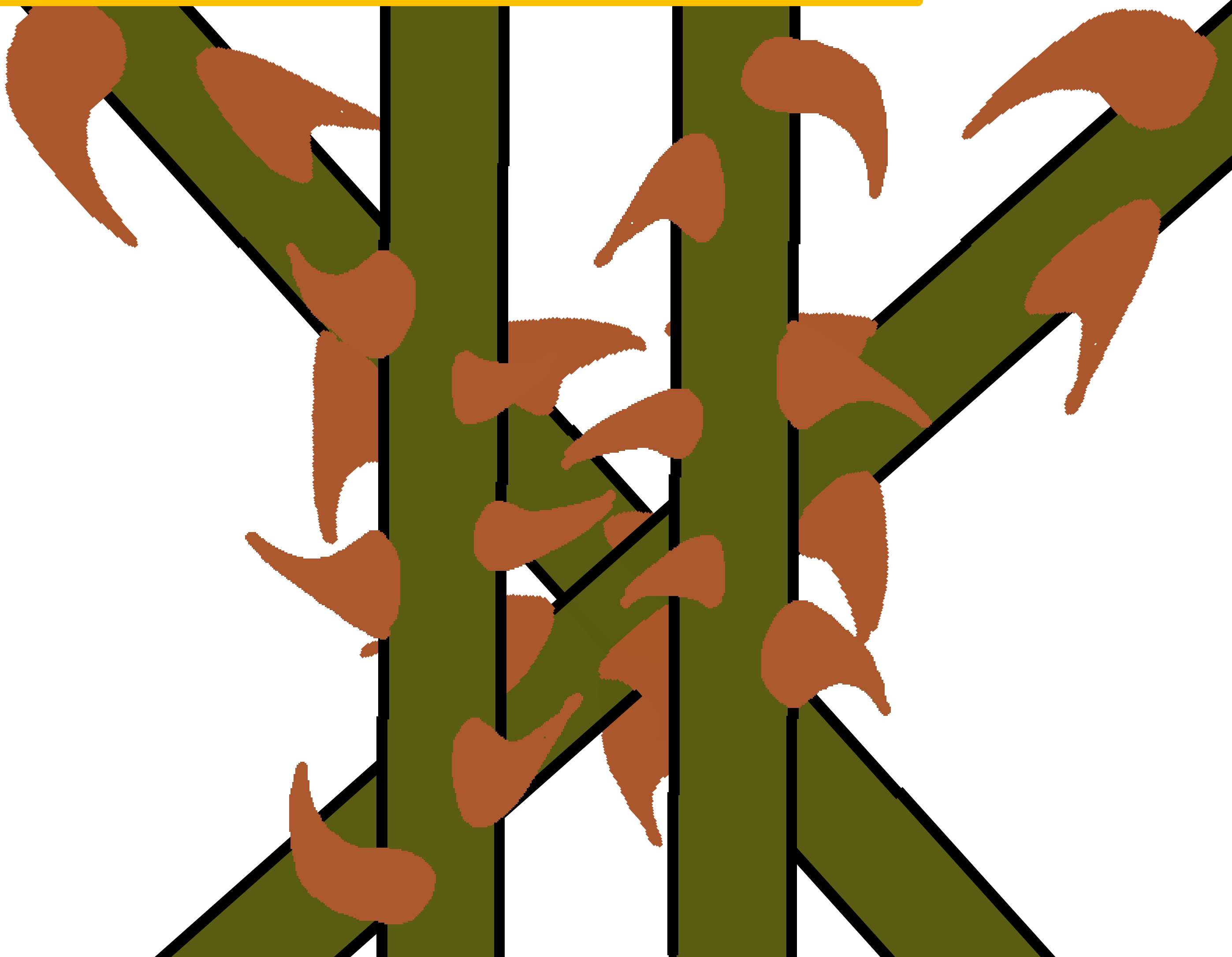


$$\frac{0.25}{1-0.25} = \frac{0.25}{0.75} = 0.33$$

$$\frac{0.42-0.40}{1-0.42} = \frac{0.02}{0.58} = 0.03$$

Thorny issues

- Repeated Measures ANOVA
- Generalized and Mixed Models
- Longitudinal data and Survival Analysis
- Structural Equation and Latent Class Mixed Models



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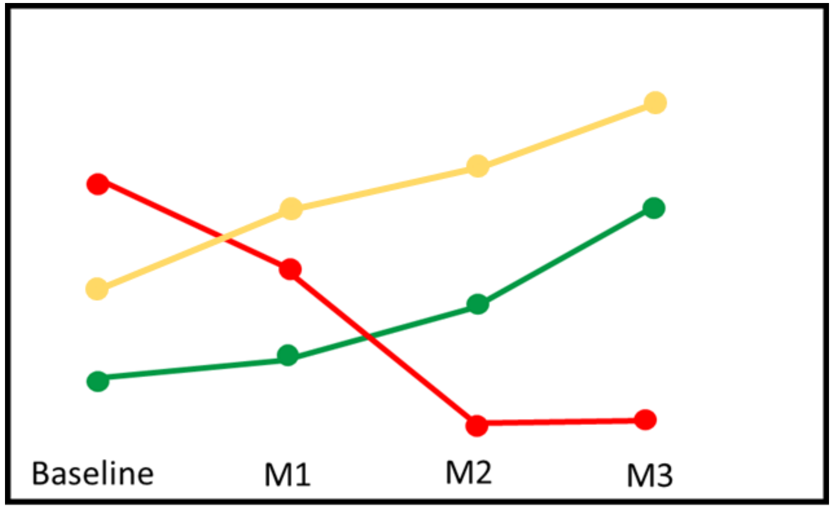
Repeated Measures ANOVA

Settings	G*Power [4]	WebPower [5]
Test	ANOVA: Repeated measures, between-factors	wp.rmanova (type='0') between effects
Alpha	0.05	0.05
Power	0.80	0.80
Group number	3	3
Measurements	4	4
Corr. among rep.	0.5	0.5
Nonsphericity corr.	N/A	N/A
Effect size	**0.25**	**0.25** * 1.264911
Total Sample size	**102**	99.4047 -> 100 -> **102***



$$C = \sqrt{\frac{K}{1 + (K-1)\rho}}, \text{between effect}$$

C = sqrt(4/(1+(4-1)*0.5)) = 1.264911

*need to divide by 3 evenly

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Repeated Measures ANOVA

Settings	G*Power	WebPower
Test	ANOVA: Repeated measures, within-effects	wp.rmanova (type='1') within effects
Alpha	0.05	0.05
Power	0.80	0.80
Group number	3	3
Measurements	4	4
Corr. among rep.	0.5	0.5
Nonsphericity corr.	1	1
Effect size	**0.25**	**0.25** * 2.83
Total Sample size	**24**	23.23 -> **24**

$$C = \sqrt{\frac{K}{1-\rho}},$$ within and between-within effects

c = sqrt (4/(1-0.5) = 2.83

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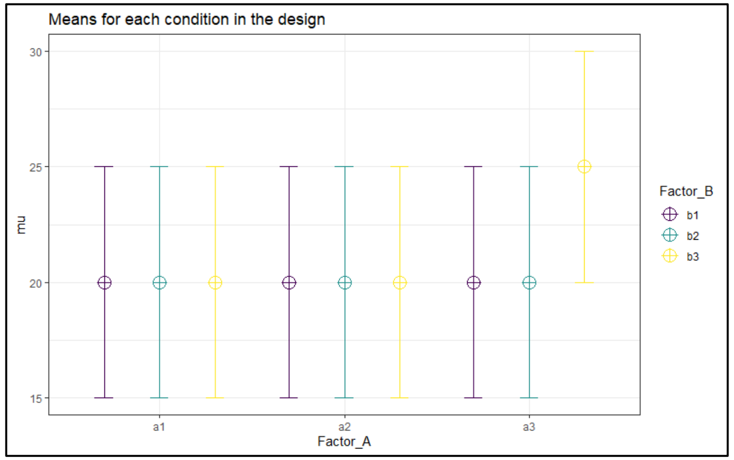
Repeated Measures ANOVA

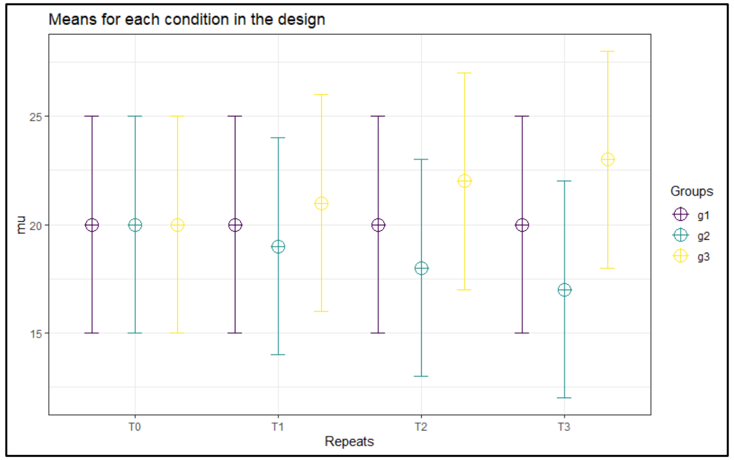
Superpower [6]

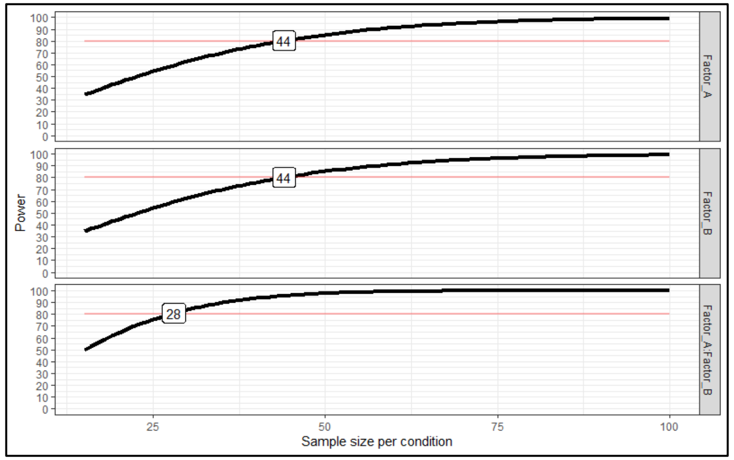
```
design <- "3b*3b"
n <- 20
mu <- c(20, 20, 20, 20, 20, 20, 20, 20, 25)
# Enter means in the order that matches the labels below.
sd <- 5
labelnames <- c("Factor_A", "a1", "a2", "a3",
                "Factor_B", "b1", "b2", "b3") #
# the label names should be in the order of the means specified above.

design_result <- ANOVA_design(design = design,
                   n = n,
                   mu = mu,
                   sd = sd,
                   labelnames = labelnames)
plot(design_result)
```

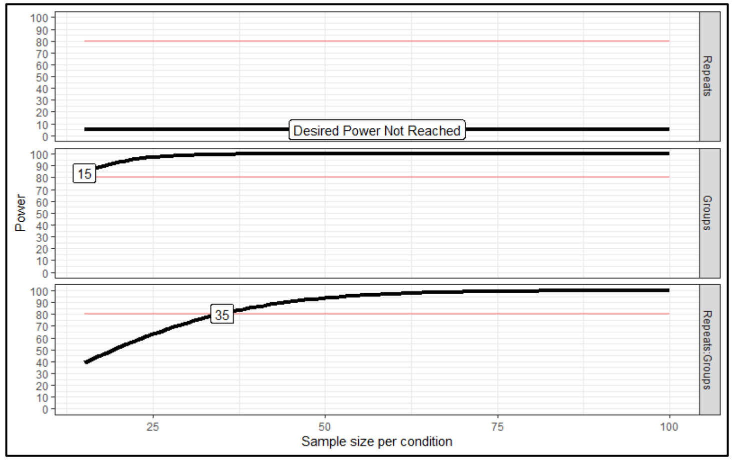
```
plot_power(design_result, min_n = 20, max_n = 100)
```

```
design <- "4b*3b"
n <- 15
mu <- c(20, 20, 20, 20, 19, 21, 20, 18, 22, 20, 17, 23)
sd <- 5
labelnames <- c("Repeats", "T0", "T1", "T2", "T3",
                "Groups", "g1", "g2", "g3")
```









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Generalized and Mixed Models

Model	R tools [7, 8]	SAS tools [9-13]
General linear model (LM)	Package 'pwr'	PROC POWER
Generalized linear model (GLM)	Package 'pwr'	PROC POWER
Linear mixed model (LMM)	Package 'simr'	PROC GLMPOWER/POWER
Generalized linear mixed model (GLMM)	Package 'simr'	PROC GLMPOWER/POWER

will just cover R
in examples

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Generalized and Mixed Models

General linear model (LM) & Generalized linear model (GLM)

```
>pwrglm1 <- pwr.f2.test(u = 1, f2 = 0.02,
            sig.level = 0.05, power=0.80)

>pwrglm1 #power calculation
```

```
Multiple regression power calculation
          u = 1
          v = 392.373
         f2 = 0.02
  sig.level = 0.15
      power = 0.8
```

```
>ssgglm1 <-round((pwrglm1$v+2)/2,0)

>ssgglm1 #sample size per group
```

```
197
```

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Generalized and Mixed Models

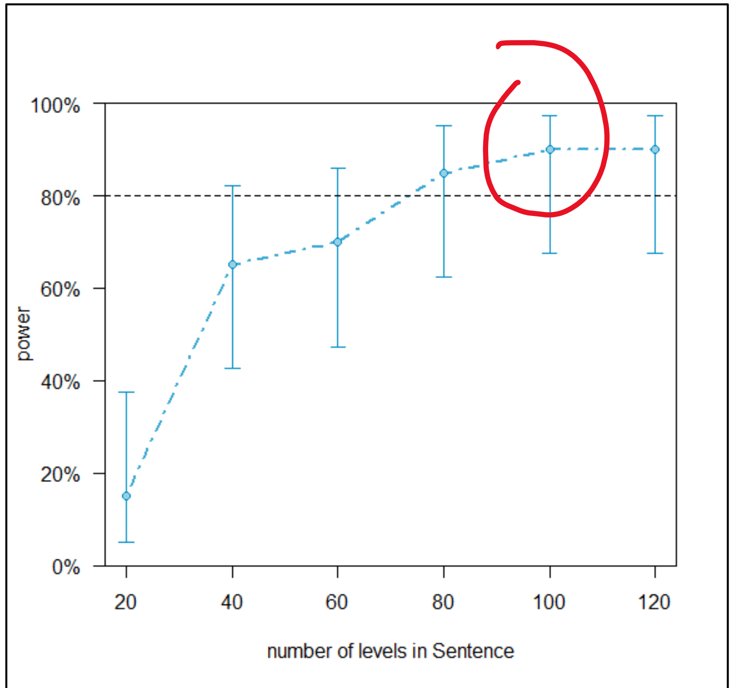
Number of obs: 480, groups: Sentence, 24; ID, 20

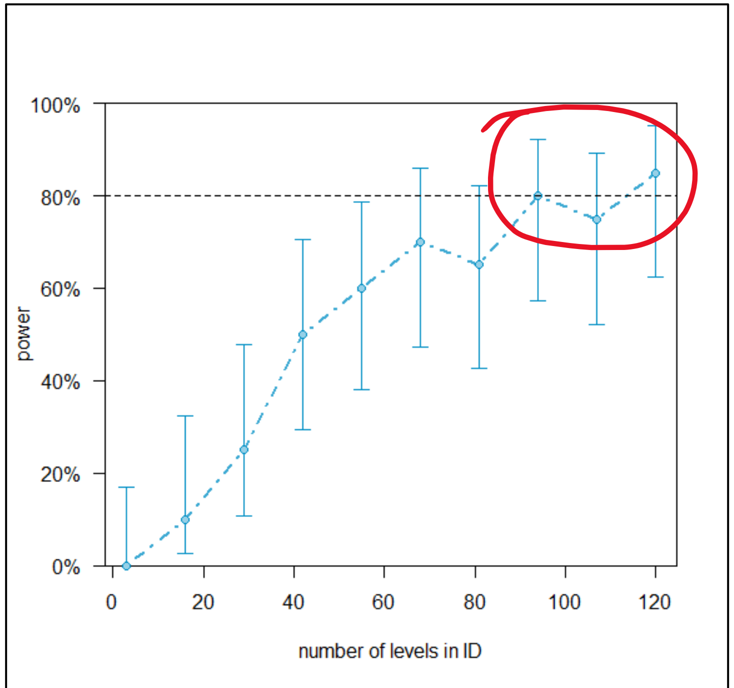
Linear Mixed Model (LMM) [8]

y ~ (1 | Sentence) + (1 | ID) + Group * SentenceType + WordOrder

Power for model comparison, (95% confidence interval):
30.00% (11.89, 54.28)

Power for model comparison, (95% confidence interval):
25.00% (8.66, 49.10)





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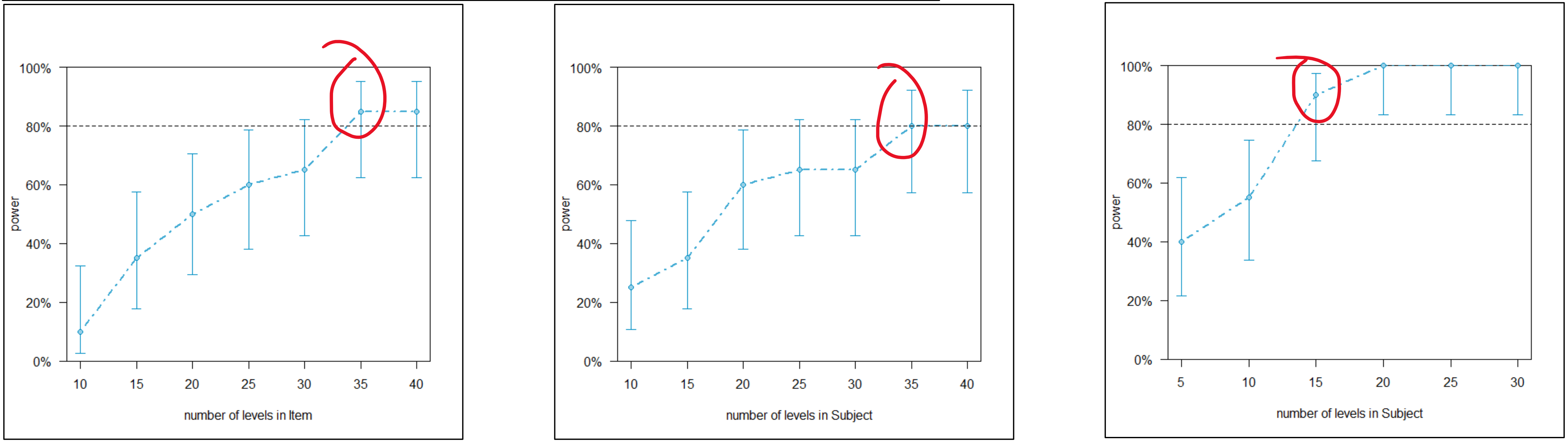
Generalized and Mixed Models

Generalized Linear Mixed Model (GLMM) [8]

Family: binomial (logit)
Formula: y ~ (1 | Subject) + (1 | Item) + Condition
Number of obs: 200, groups: Subject, 10; Item, 10

Power for predictor 'ConditionTest', (95% confidence interval):
40.00% (19.12, 63.95)



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Longitudinal data and Survival Analysis

Longitudinal data (package 'longpower')

```
#General
>lmmpower(delta=1.5, t = seq(0,1.5,0.25),
      sig2.i = 55, sig2.s = 24, sig2.e = 10,
      cov.s.i=0.8*sqrt(55)*sqrt(24), power = 0.80)

>lmmpower(n=208, t = seq(0,1.5,0.25),
      sig2.i = 55, sig2.s = 24, sig2.e = 10,
      cov.s.i=0.8*sqrt(55)*sqrt(24), power = 0.80)

>lmmpower(beta = 5, pct.change = 0.30, t = seq(0,1.5,0.25),
      sig2.i = 55, sig2.s = 24, sig2.e = 10,
      cov.s.i=0.8*sqrt(55)*sqrt(24), power = 0.80)
```

```
N = 414.6202
n = 207.3101, 207.3101
delta = 1.5
sigma2 = 1
sig.level = 0.05
power = 0.8
alternative = two.sided
```

```
N = 416
n = 208, 208
delta = 1.49751
sigma2 = 1
sig.level = 0.05
power = 0.8
alternative = two.sided
```

```
N = 414.6202
n = 207.3101, 207.3101
delta = 1.5
sigma2 = 1
sig.level = 0.05
power = 0.8
alternative = two.sided
beta = 5
```

NOTE: *N is *total* sample size and n is sample size in *each* group*

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Longitudinal data and Survival Analysis

Longitudinal data (package 'longpower')

```
#General Cont.
>fm1 <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy)
>lmmpower(fm1, pct.change = 0.30, t = seq(0,9,1), power = 0.80)
```

N = 136.94
n = 68.46999, 68.46999

```
>fm2 <- lme(Reaction ~ Days, random=~Days|Subject, sleepstudy)
>lmmpower(fm2, pct.change = 0.30, t = seq(0,9,1), power = 0.80)
```

N = 136.9388
n = 68.46938, 68.46938

```
>fm3 <- lme(Reaction ~ Days, random=~1|Subject, sleepstudy)  #random intercept only
>lmmpower(fm3, pct.change = 0.30, t = seq(0,9,1), power = 0.80)
```

N = 37.06643
n = 18.53322, 18.53322

```
>fm4 <- gee(Reaction ~ Days, id = Subject, data = sleepstudy,  corstr = "exchangeable")
>lmmpower(fm4, pct.change = 0.30, t = seq(0,9,1), power = 0.80)
```

N = 37.69
n = 18.845, 18.845

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Longitudinal data and Survival Analysis

Longitudinal data (package ‘longpower’)

```
#An Alzheimer's Disease example using ADAS-cog pilot estimates
>sig2.i <- 55 #var of random intercept
>sig2.s <- 24 #var of random slope
>sig2.e <- 10 #residual var
>cov.s.i <- 0.8*sqrt(sig2.i)*sqrt(sig2.s) #covariance of slope and intercept
>cov.t <- function(t1, t2, sig2.i, sig2.s, cov.s.i){sig2.i + t1*t2*sig2.s + (t1+t2)*cov.s.i}
>t <- seq(0,1.5,0.25) #vector of time points
>n <- length(t)
>R <- outer(t, t, function(x,y){cov.t(x,y, sig2.i, sig2.s, cov.s.i)})
>R <- R + diag(sig2.e, n, n)  #marginal model working correlation matrix

>diggle.linear.power(delta=1.5, t=t, R=R, sig.level=0.05, power=0.80)
>edland.linear.power(delta=1.5, t=t, sig2.s = 24, sig2.e = 10, sig.level=0.05, power = 0.80)
```

N = 414.6202
n = 207.3101, 207.3101

N = 414.6202
n = 207.3101, 207.3101

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Longitudinal data and Survival Analysis

Survival analysis (package ‘powerSurvEpi’)

```
#Deaths required for Cox Propo. Hazards regression w/ 2 covariates
>X1 <- c(rep(1, 39), rep(0, 61))  #generate a mock pilot data set
>set.seed(123456)
>X2 <- sample(c(0, 1), 100, replace = TRUE)
>res <- numDEpi(X1 = X1, X2 = X2,
            power = 0.8, theta = 2, alpha = 0.05)

>print(res)
>psi <- 0.505   #proportion of subjects died of the disease of interest
>ceiling(res$D / psi)   #total number of subjects required to achieve the desired power
```

```
$D
[1] 70
```

```
137
```

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Longitudinal data and Survival Analysis

Survival analysis (package 'powerSurvEpi')

```
  #Power Calc. in Analysis of Survival Data for Clinical Trials
>data(Oph)
>resA <- powerCT(formula=Surv(times, status)~group, dat=Oph,
           nE=200, nC=200, RR=0.70, alpha=0.05)
>resB <- powerCT(formula=Surv(times, status)~group, dat=Oph,
           nE=250, nC=250, RR=0.70, alpha=0.05)
>resC <- powerCT(formula=Surv(times, status)~group, dat=Oph,
           nE=300, nC=300, RR=0.70, alpha=0.05)
>resA; resB; resC
  #Sample size calc. in Analysis of Survival Data for Clinical Trials
>resD <- ssizeCT(formula = Surv(times, status) ~ group, dat = Oph,
           power = 0.8, k = 1, RR = 0.7, alpha = 0.05)
>resD
```

```
$power
[1] 0.638356
```

```
$power
[1] 0.7347367
```

```
$power
[1] 0.8089775
```

```
$ssize
 nE  nC
294 294
```

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Structural Equation and Latent Class Mixed Models

Structural Equation Models (package 'semPower') [14]

>ap <- semPower.aPriori(effect = .10, effect.measure = 'RMSEA', alpha = .05, power = .80, df = 100)

>summary(ap)

Required Num Observations 42

>ap2 <- semPower.aPriori(effect = .10, effect.measure = "F0", alpha = .05, power = .80, df = 100)

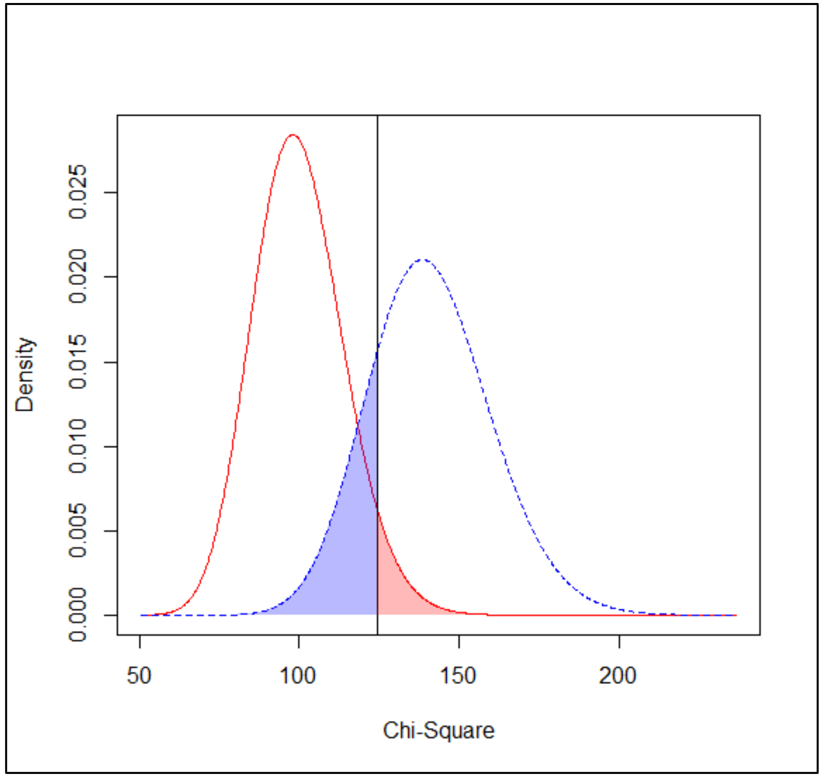
>summary(ap2)

Required Num Observations 407

>ap3 <- semPower.aPriori(effect = 1.0, effect.measure = "F0", alpha = .05, power = .80, df = 100)

>summary(ap3)

Required Num Observations 42



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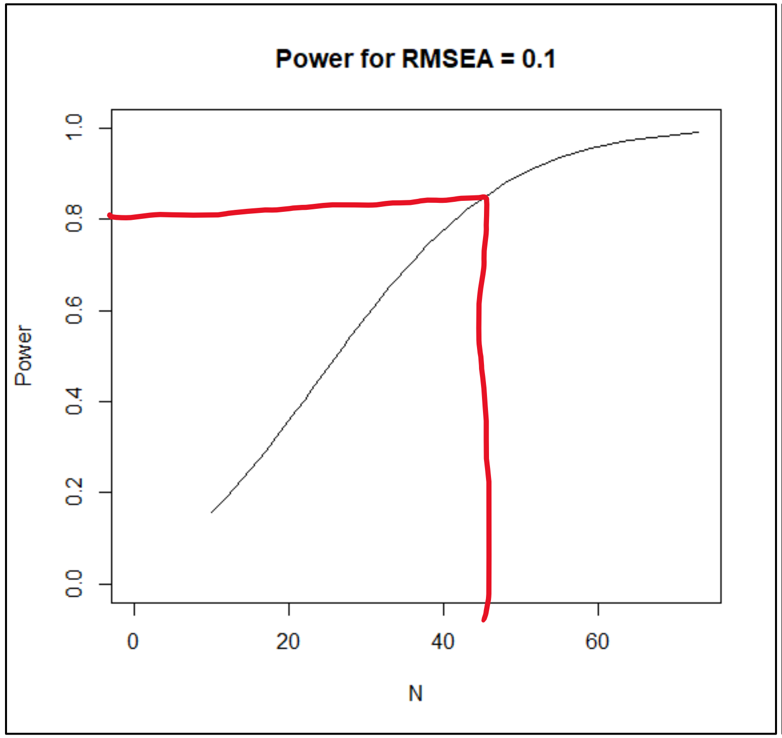
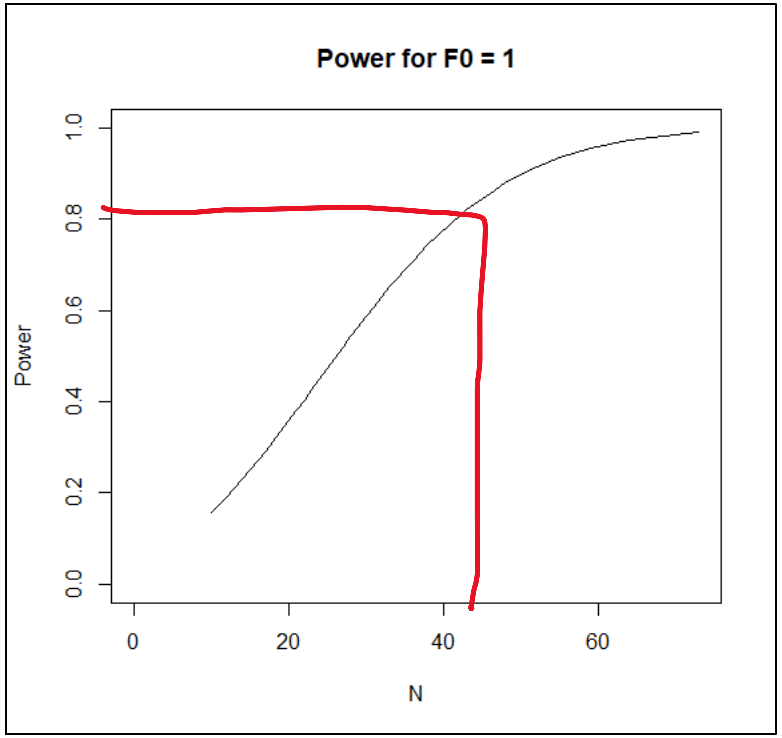
Structural Equation and Latent Class Mixed Models

Structural Equation Models (package 'semPower') [14]

```
>semPower.powerPlot.byN(effect = .10,
          effect.measure = 'RMSEA',
          alpha = .05, df = 100,
          power.min = .05, power.max = .99)

>semPower.powerPlot.byN(effect = 1.0,
          effect.measure = "F0",
          alpha = .05, df = 100,
          power.min = .05, power.max = .99)
```





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Structural Equation and Latent Class Mixed Models

Latent Class Mixed Models [15]

When designing a study, one common question is "What sample size do I need?"
Unfortunately, there is no standard or simple answer to this question.

Ran simulations using models with different group numbers, samples per group, complexity, distinctness, and number of indicators

The design yielded 384 (6 x 8 x 2 x 2 x 2) simulation conditions by crossing the five manipulated factors as previously described

Table 2. Minimum Sample Size Requirements per Group (n_g) Under the Simulation Design.

Distinctness	Indicator	Number of parameters	G	Minimum n_g (C_L)	Minimum n_g (C_H)
D_H	6	15/26	10	40	>100
			20	20	50
			25	20	40
			30	10	40
			50	10	20
			100	10	20
	12	27/44	10	30	>100
			20	20	30
			25	20	30
			30	10	20
			50	5	20
			100	5	10
D_L	6	15/26	10	>100	>100
			20	75	100
			25	75	100
			30	50	100
			50	40	75
			100	30	50
	12	27/44	10	>100	>100
			20	50	75
			25	40	50
			30	40	50
			50	30	40
			100	10	30

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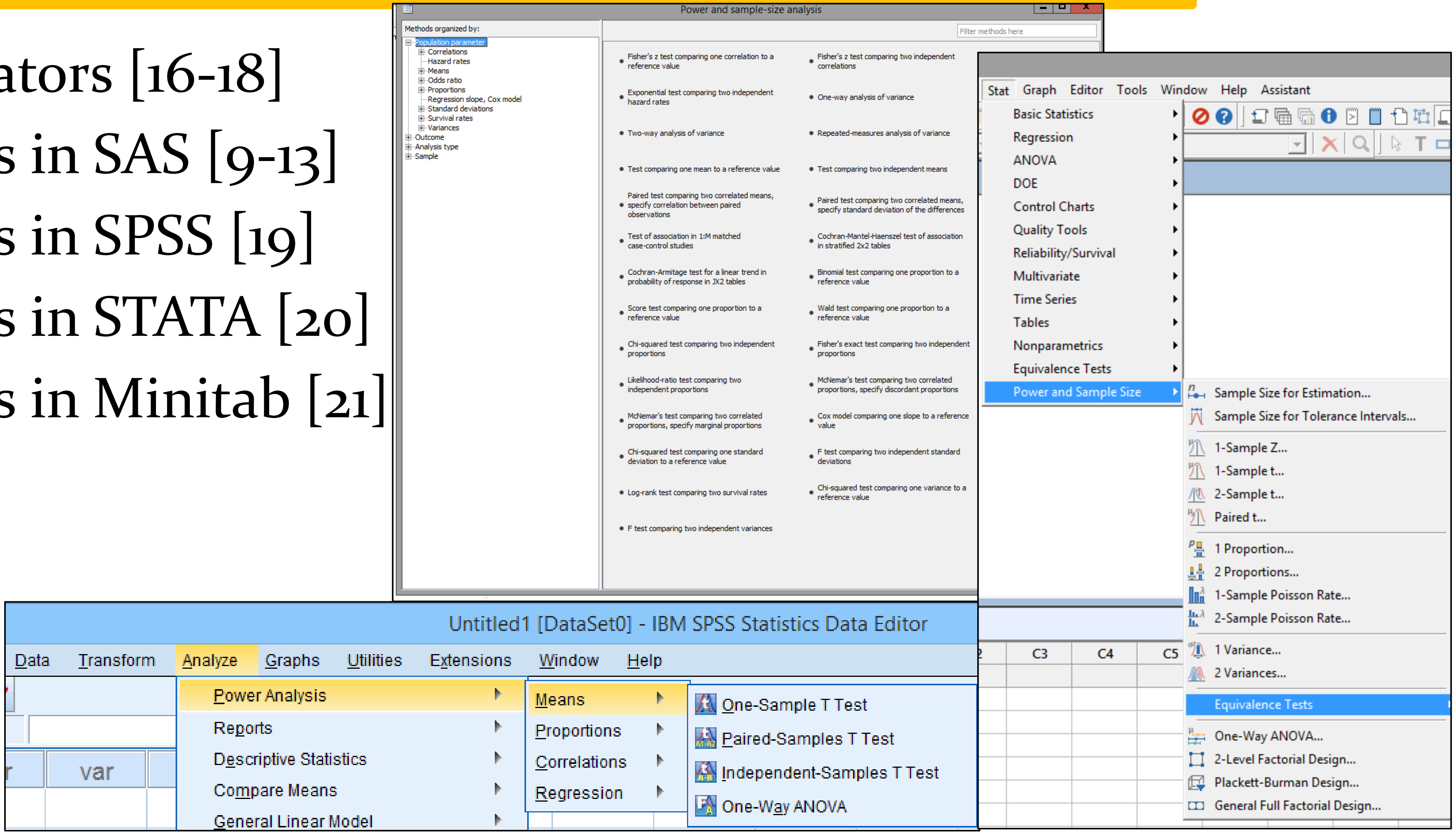
Seeds

- Online Calculators [16-18]
- Power Analysis in SAS [9-13]
- Power Analysis in SPSS [19]
- Power Analysis in STATA [20]
- Power Analysis in Minitab [21]



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Seeds

Other R Packages: Recommendations

[2]

Table 10.4. Specialized power-analysis packages

Package	Purpose
asypow	Power calculations via asymptotic likelihood ratio methods
longpower	Sample-size calculations for longitudinal data
PwrGSD	Power analysis for group sequential designs
pamm	Power analysis for random effects in mixed models
powerSurvEpi	Power and sample-size calculations for survival analysis in epidemiological studies
powerMediation	Power and sample-size calculations for mediation effects in linear, logistic, Poisson, and cox regression
powerpkg	Power analyses for the affected sib pair and the TDT (transmission disequilibrium test) design
powerGWASinteraction	Power calculations for interactions for GWAS
pedantics	Functions to facilitate power analyses for genetic studies of natural populations
gap	Functions for power and sample-size calculations in case-cohort designs
ssize.fdr	Sample-size calculations for microarray experiments

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Other R Packages: ‘Power Analysis’ in name/description

"GRS.test -----> GRS Test for Portfolio Efficiency, Its Statistical Power Analysis, and Optimal Significance Level Calculation"
"metapower -----> Power Analysis for Meta-Analysis"
"MKpower -----> Power Analysis and Sample Size Calculation"
"powerAnalysis -----> Power Analysis in Experimental Design"
"powerCompRisk -----> Power Analysis Tool for Joint Testing Hazards with Competing Risks Data"
"powerLATE -----> Generalized Power Analysis for LATE"
"PowerUpR -----> Power Analysis Tools for Multilevel Randomized Experiments"
"pwrAB -----> Power Analysis for AB Testing"
"smartsizer -----> Power Analysis for a SMART Design"
"sparrpowR -----> Power Analysis to Detect Spatial Relative Risk Clusters"

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Other R Packages: 'Power' in name/description

"bayescount -----> Power Calculations and Bayesian Analysis of Count Distributions and FECRT Data using MCMC"
"BayesianPower -----> Sample Size and Power for Comparing Inequality Constrained Hypotheses"
"BetaPASS -----> Calculate Power and Sample Size with Beta Regression"
"bimetallic -----> Power for SNP analyses using silver standard cases"
"clusterPower -----> Power Calculations for Cluster-Randomized and Cluster-Randomized Crossover Trials"
"CoRpower -----> Power Calculations for Assessing Correlates of Risk in Clinical Efficacy Trials"
"CP -----> Conditional Power Calculations"
"DelayedEffect.Design -----> Sample Size and Power Calculations using the APPLE and SEPPLE Methods"
"FDRsampsize -----> Compute Sample Size that Meets Requirements for Average Power and FDR"
"genpwr -----> Power Calculations Under Genetic Model Misspecification"
"HierO -----> A graphical user interface for calculating power and sample size for hierarchical data"
"HMP -----> Hypothesis Testing and Power Calculations for Comparing Metagenomic Samples from HMP"
"ICC.Sample.Size -----> Calculation of Sample Size and Power for ICC"
"JMdesign -----> Joint Modeling of Longitudinal and Survival Data - Power Calculation"
"LPower -----> Calculates Power, Sample Size, or Detectable Effect for Longitudinal Analyses"
"MIDN -----> Nearly Exact Sample Size Calculation for Exact Powerful Nonrandomized Tests for Differences Between Binomial Proportions"
"MultiRR -----> Bias, Precision, and Power for Multi-Level Random Regressions"
"npsurvSS -----> Sample Size and Power Calculation for Common Non-Parametric Tests in Survival Analysis"
"odr -----> Optimal Design and Statistical Power of Multilevel Randomized Trials"
"pass.lme -----> Power and Sample Size for Linear Mixed Effect Models“
"PASSED -----> Calculate Power and Sample Size for Two Sample Mean Tests"

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Other R Packages: ‘Power’ in name/description cont.

"PharmPow -----> Pharmacometric Power calculations for mixed study designs"
"PoweR -----> Computation of Power and Level Tables for Hypothesis Tests"
"Power2Stage -----> Power and Sample-Size Distribution of 2-Stage Bioequivalence Studies"
"powerbydesign -----> Power Estimates for ANOVA Designs"
"powerCompRisk -----> Power Analysis Tool for Joint Testing Hazards with Competing Risks Data"
"powerEQTL -----> Power and Sample Size Calculation for Bulk Tissue and Single-Cell eQTL Analysis"
"powerMediation -----> Power/Sample Size Calculation for Mediation Analysis"
"PowerNormal -----> Power Normal Distribution"
"PowerTOST -----> Power and Sample Size for (Bio)Equivalence Studies"
"PowerUpR -----> Power Analysis Tools for Multilevel Randomized Experiments"
"precisely -----> Estimate Sample Size Based on Precision Rather than Power"
"PSS.Health -----> Power and Sample Size for Health Researchers via Shiny"
"pwrFDR -----> FDR Power"
"qcapower -----> Estimate Power and Required Sample Size in QCA"
"rdpower -----> Power Calculations for RD Designs"
"samplesizeCMH -----> Power and Sample Size Calculation for the Cochran-Mantel-Haenszel Test"
"SteppedPower -----> Power Calculation for Stepped Wedge Designs"
"survSNP -----> Power Calculations for SNP Studies with Censored Outcomes"
"swdpwr -----> Power Calculation for Stepped Wedge Cluster Randomized Trials"
"TrendInTrend -----> Odds Ratio Estimation and Power Calculation for the Trend in Trend Model"
"wmwpow -----> Precise and Accurate Power of the Wilcoxon-Mann-Whitney Rank-Sum Test for a Continuous Variable"

over 50 R-packages total!

Conclusions

- Power analysis and sample size calculations are fundamental for proper experimental design
- Calculating effect size is a huge part of it
- It can get tricky to understand what to do for advanced experiment designs
- Never fear, there are a bevy of methods to do just that

Please take the post-test and survey:

Post-test: https://und.qualtrics.com/jfe/form/SV_6Fq8AtCtgWoW1hk

Survey: https://und.qualtrics.com/jfe/form/SV_6zkvRdWFlqsm36m

References

[1] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5772820/#!po=62.5000

[2] https://livebook.manning.com/book/r-in-action-second-edition/chapter-10/1

[3] https://www.frontiersin.org/articles/10.3389/fpsyg.2012.00111/full

[4] https://www.psychologie.hhu.de/fileadmin/redaktion/Fakultaeten/Mathematisch-Naturwissenschaftliche_Fakultaet/Psychologie/AAP/gpower/GPowerManual.pdf

[5] https://webpower.psychstat.org/wiki/manual/power_of_Rmanova

[6] https://cran.microsoft.com/snapshot/2021-10-23/web/packages/Superpower/vignettes/more_anova_designs.html#power-in-repeated-measures-anova

[7] https://cran.r-project.org/web/packages/pwr/vignettes/pwr-vignette.html

[8] https://slcladal.github.io/pwr.html#Resources_and_Links

[9] https://www.stat.purdue.edu/~bacraig/notes525/Power%201.pdf

[10] https://support.sas.com/rnd/app/stat/procedures/PowerSampleSize.html

[11] https://www.sas.com/content/dam/SAS/support/en/sas-global-forum-proceedings/2018/1983-2018.pdf

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References

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[12] https://webpages.uidaho.edu/cals-statprog/sas/workshops/power/handout3.pdf

[13] https://stats.oarc.ucla.edu/sas/dae/multiple-regression-power-analysis/

[14] https://cran.r-project.org/web/packages/semPower/vignettes/semPower.pdf

[15] https://journals.sagepub.com/doi/pdf/10.1177/0013164417719111

[16] http://powerandsamplesize.com/Calculators/

[17] https://www.gigacalculator.com/calculators/power-sample-size-calculator.php

[18] https://webpower.psychstat.org/wiki/start

[19] https://www.ibm.com/docs/en/spss-statistics/SaaS?topic=features-power-analysis

[20] https://www.stata.com/features/power-and-sample-size/

[21] https://support.minitab.com/en-us/minitab/18/help-and-how-to/statistics/power-and-sample-size/supporting-topics/power-and-sample-size-analyses-in-minitab/

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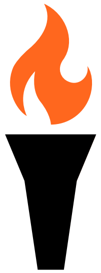
Acknowledgements



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