

Yes, YOU can simulate!



<https://openclipart.org/detail/280519/strange-meeting>

**Reproducible, Tidy
Workflows with the
Reimagined simpr
Package**



*Ethan C. Brown, PhD
useR! 2024, Salzburg*

The case for simplr

1. Do you want to understand the models you're using?
2. Are you planning a study, doing a power analysis, or trying to evaluate a statistical method?
3. Do you know that simulation can help but you're **overwhelmed by the complexity** of creating a simulation?

Understanding Your Models

*Looking at the world using data
is like looking through a window with ripples in the glass*

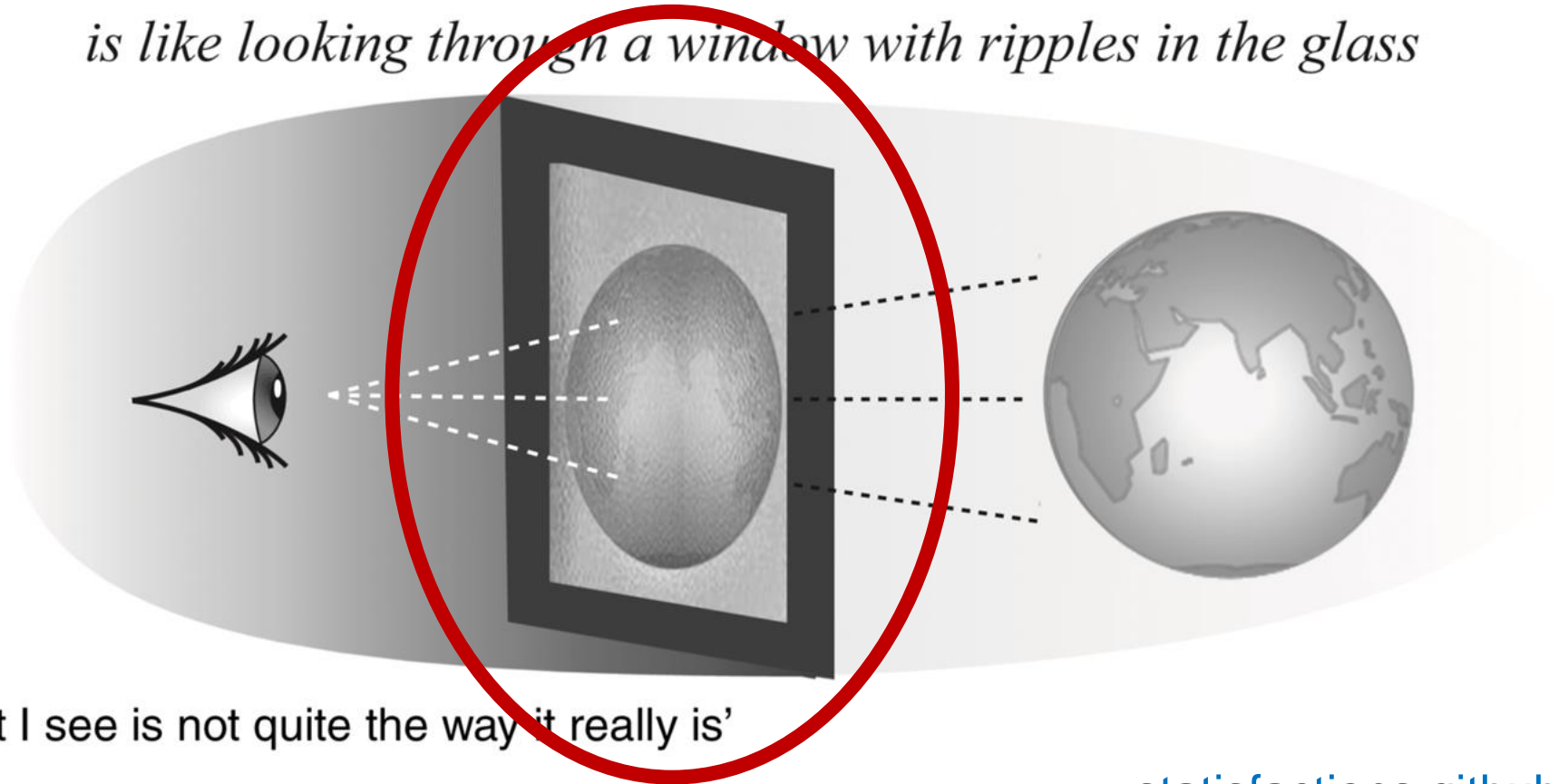
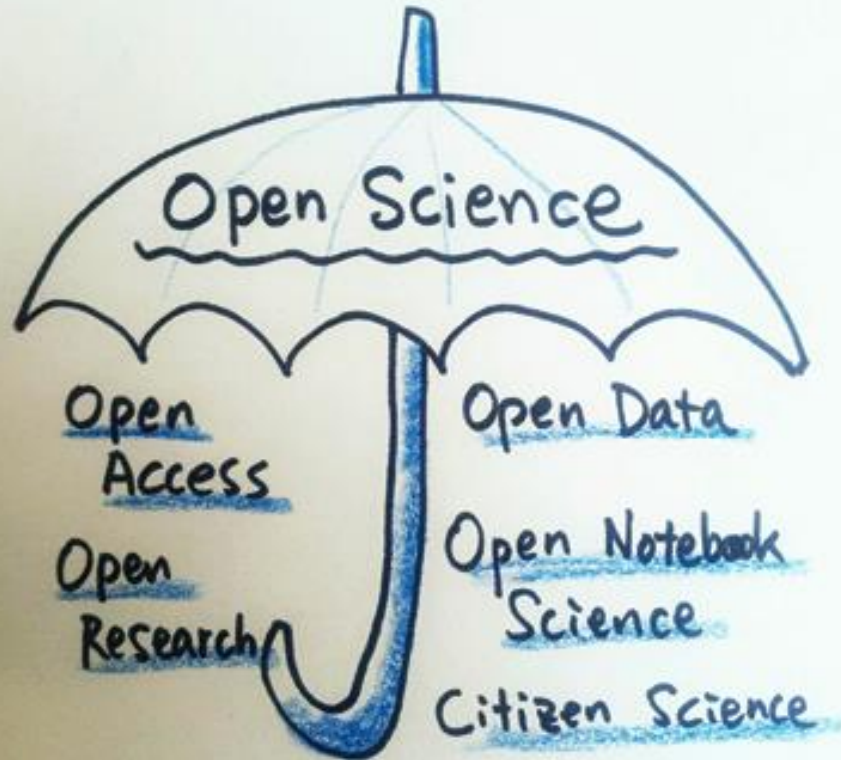


Fig. 2. 'What I see is not quite the way it really is'



OPEN SCIENCE AND “WHAT IFS”

Will this design answer our research questions?

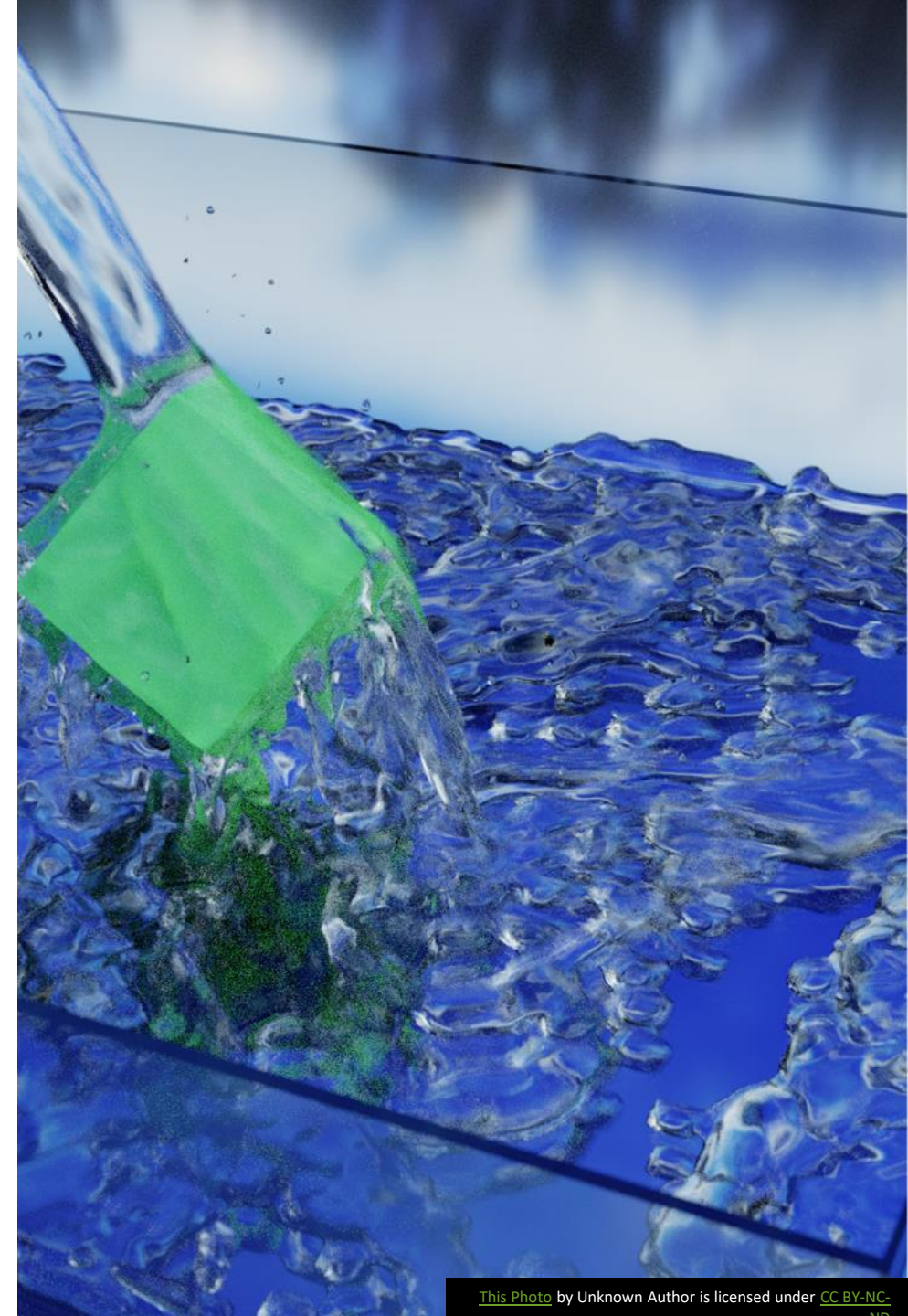
vs

Under what conditions will this design answer our research questions?

- Transparently show the boundaries and assumptions of the design
- Support writing of preregistrations, prospectuses, and registered reports by a disciplined examination of possibilities
- Look at the ranges of possible quality (power, bias) based on what we assume is true about reality

SIMULATION-BASED DESIGN ANALYSIS

- Model the data-generating process, including sampling, assignment, measurement
- Generate simulated data based on the data-generating process
- Fit the proposed model and evaluate whatever outcomes we're interested in (power, bias, convergence...).



Is this your feeling when doing a simulation?

Power Analysis

Some notes from *Greg Snow* (tweaked by Ben Bolker) on power analysis (for a LMM rather than a GLMM, but the general principles are the same). Here is some code to get you started (based on some assumptions that may be way off):

```
library(lme4)

sim1 <- function(bSex=0, bFreq=0, bSF=0, b0=1000, Vsubj=1, Vword=1, Verror=1) {
  Subject <- rep( 1:60, each=50 )
  Word <- rep( 1:50, 60 )
  Sex <- rep(c('M','F'), each=50*30)
  ## or use expand.grid(), although it won't work perfectly for this case:
  ## expand.grid(Word=1:50, Subject=1:30, Sex=c('M','F')) would give
  ## subjects 1 to 30 in EACH sex rather subjects 1 to 60 of which
  ## half are each sex

  # assume frequency is constant across word, random from 1-100
  tmp <- sample( 1:100, 50, replace=TRUE )
  Frequency <- tmp[Word]

  # random effects per subject
  S.re <- rnorm(60, 0, sqrt(Vsubj))

  # random effects per word
  W.re <- rnorm(50, 0, sqrt(Vword))

  # epsilons
  eps <- rnorm(50*60, 0, sqrt(Verror))

  # put it all together
  # or use model.matrix() for more complex problems
  ReactionTime <- b0 + bSex*(Sex=='M') + bFreq*Frequency + bSF*(Sex=='M')*Frequency +
    S.re[Subject] + W.re[Word] + eps

  # put into a data frame
  mydata <- data.frame( Subject = paste('s', Subject, sep=''),
    Word = paste('w', Word, sep=''), Sex=Sex, Frequency=Frequency,
    ReactionTime = ReactionTime)

  # analyze looking at interaction term with LR test
  fit1 <- lmer( ReactionTime ~ (Sex*Frequency) + (1|Subject) + (1|Word), data=mydata)
  fit2 <- lmer( ReactionTime ~ Sex + Frequency + (1|Subject) + (1|Word), data=mydata)
  anova(fit2, fit1)[2, "Pr(>Chisq)"]
}
```

Set random number seed for reproducibility:



Source: <http://glmm.wikidot.com/power-analysis>

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Challenges of simulation

- Require understanding underlying statistical model
- Simulations make just as many assumptions as analytical methods, and may not be reasonable
- Custom simulations often difficult to code
- Simulations easy to mislead by missing fundamental features of the process

IS 100 STUDENTS ENOUGH?

Study: *Pre-post comparison of the “Triglicious” intervention*

Research question: *Did Triglicious improve students’ math scores?*

Method: *Paired t-test*



Simulations in base R

```
## Set up parameters  
ns = c(100, 150, 200)  
mean_diffs = c(10, 20, 30)  
sds = c(50, 100)  
reps = 10
```

Simulations in base R

Set up parameters

```
ns = c(100, 150, 200)
```

```
mean_diffs = c(10, 20, 30)
```

```
sds = c(50, 100)
```

```
reps = 10
```

Bring together into data frame

```
results_template = expand.grid(n = ns,  
                               mean_diff = mean_diffs,  
                               sd = sds, p.value = NA_real_)
```

```
base_r_sim = results_template[rep(1:nrow(results_template), each = reps),]
```

Simulations in base R

Set up parameters

```
ns = c(100, 150, 200)
mean_diffs = c(10, 20, 30)
sds = c(50, 100)
reps = 10
```

Bring together into data frame

```
results_template = expand.grid(n = ns,
                              mean_diff = mean_diffs,
                              sd = sds, p.value = NA_real_)
```

```
base_r_sim = results_template[rep(1:nrow(results_template), each = reps),]
```

Loop over rows of the data frame and calculate the p-value

```
for(i in 1:nrow(results_template)) {
  params = results_rep[i,]
  pre = rnorm(params$n, 0, params$sd)
  post = pre + rnorm(params$n, params$mean_diff, params$sd)

  base_r_sim$p.value[i] = t.test(pre, post)$p.value
}
```

##		n	mean_diff	sd	p.value
##	1	100	10	50	5.977957e-01
##	1.1	100	10	50	2.245753e-01
##	1.2	100	10	50	4.449589e-01
##	1.3	100	10	50	6.099931e-01
##	1.4	100	10	50	3.258414e-01
##	1.5	100	10	50	1.647985e-01
##	1.6	100	10	50	6.690890e-01
##	1.7	100	10	50	1.333951e-02
##	1.8	100	10	50	9.811185e-02
##	1.9	100	10	50	1.576709e-01
...					
##	18	200	30	100	4.655720e-03
##	18.1	200	30	100	9.155604e-03
##	18.2	200	30	100	7.904275e-02
##	18.3	200	30	100	6.980651e-02
##	18.4	200	30	100	4.588371e-02
##	18.5	200	30	100	6.476568e-02
##	18.6	200	30	100	6.849110e-03
##	18.7	200	30	100	3.409384e-03
##	18.8	200	30	100	2.076897e-03
##	18.9	200	30	100	1.731442e-03

Disadvantages of this approach

Already good solutions (DeclareDesign, MonteCarlo, ...)

- Most important pieces (model specification, definitions) are hidden
- What if there's an error?
- What if we want parallel processing?

Not yet implemented...

- **What if we want this to be easier?**

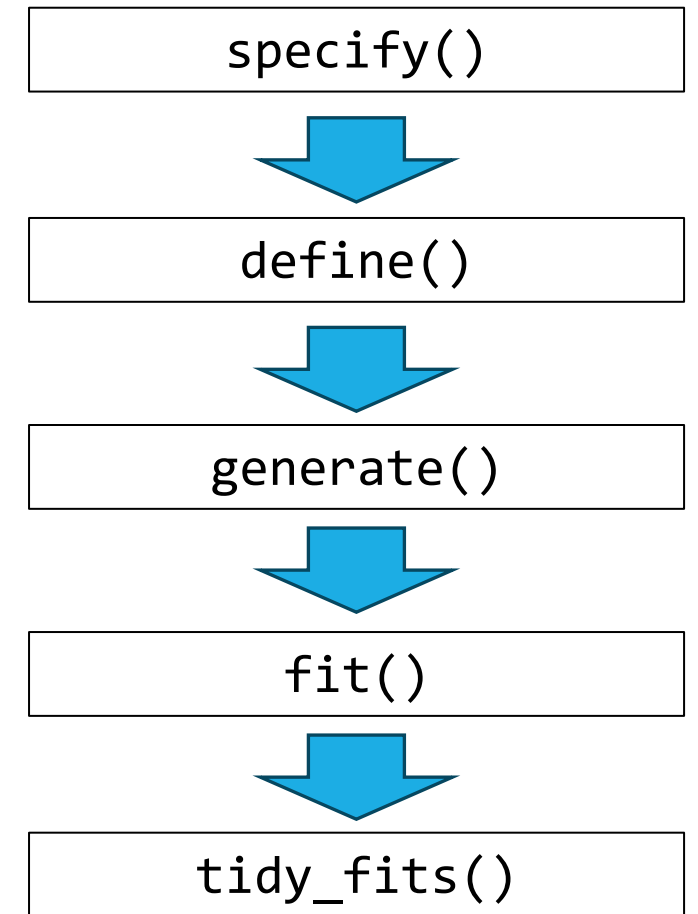
simpr does the housekeeping.
You focus on your model!



INTRODUCING SIMPR

What is simpr?

- provides a grammar and a workflow for simulating data
- Targeted to intermediate R users, especially those who use the 'tidyverse' ecosystem
- Makes simulation code substantially easier



THE SIMPR WORKFLOW

The `simplr` workflow, inspired by the [`infer`](#) package, distills a simulation study into five primary steps:

- [`specify\(\)`](#) your data-generating process
- [`define\(\)`](#) parameters that you want to systematically vary across your simulation design (e.g. n , effect size)
- [`generate\(\)`](#) the simulation data
- [`fit\(\)`](#) models to your data (e.g. [`lm\(\)`](#))
- [`tidy_fits\(\)`](#) for consolidating results using [`broom::tidy\(\)`](#), such as computing power or Type I Error rates

Specify pre and post scores that differ by a given amount

```
specify(pre = ~ rnorm(n, 0, sd),  
        post = ~ pre + rnorm(n, mean_diff, sd)) %>%
```

```
## Specify pre and post scores that differ by a given amount  
specify(pre = ~ rnorm(n, 0, sd),  
        post = ~ pre + rnorm(n, mean_diff, sd)) %>%  
## Define parameters that can be varied  
define(n = 100,  
       mean_diff = 10,  
       sd = 50) %>%
```

```
## Specify pre and post scores that differ by a given amount
specify(pre = ~ rnorm(n, 0, sd),
        post = ~ pre + rnorm(n, mean_diff, sd)) %>%
## Define parameters that can be varied
define(n = 100,
       mean_diff = 10,
       sd = 50) %>%
## Generate datasets
generate(100) %>%
```

```
## Specify pre and post scores that differ by a given amount
specify(pre = ~ rnorm(n, 0, sd),
        post = ~ pre + rnorm(n, mean_diff, sd)) %>%

## Define parameters that can be varied
define(n = 100,
       mean_diff = 10,
       sd = 50) %>%

## Generate datasets
generate(100) %>%

## Fit datasets
fit(t = ~t.test(post, pre, paired = TRUE)) %>%
```



```
## Specify pre and post scores that differ by a given amount
specify(pre = ~ rnorm(n, 0, sd),
        post = ~ pre + rnorm(n, mean_diff, sd)) %>%

## Define parameters that can be varied
define(n = 100,
       mean_diff = 10,
       sd = 50) %>%

## Generate datasets
generate(100) %>%

## Fit datasets
fit(t = ~t.test(post, pre, paired = TRUE)) %>%

## Collect results
tidy_fits()
```

And, that's all!

```
## # A tibble: 100 × 14
##   .sim_id      n mean_diff      sd    rep Source estimate statistic    p.value
##   <int> <dbl>    <dbl> <dbl> <int> <chr>    <dbl>    <dbl>    <dbl>
## 1       1    100        10    50     1 t      12.1      2.26 0.0258
## 2       2    100        10    50     2 t      14.5      3.00 0.00337
## 3       3    100        10    50     3 t      13.5      3.02 0.00326
## 4       4    100        10    50     4 t      11.9      2.18 0.0319
## 5       5    100        10    50     5 t      24.2      4.71 0.00000811
## 6       6    100        10    50     6 t      17.7      3.79 0.000256
## 7       7    100        10    50     7 t      11.7      2.32 0.0222
## 8       8    100        10    50     8 t      11.1      2.35 0.0206
## 9       9    100        10    50     9 t      15.0      2.83 0.00569
## 10      10    100        10    50    10 t       5.11      1.02 0.312
## # i 90 more rows
## # i 5 more variables: parameter <dbl>, conf.low <dbl>, conf.high <dbl>,
## #   method <chr>, alternative <chr>
```

VARYING PARAMETERS

```
## Specify pre and post scores that differ by a given amount
sim_vary = specify(pre = ~ rnorm(n, 0, sd),
                   post = ~ pre + rnorm(n, mean_diff, sd)) %>%

## Define parameters and vary them
define(n = c(100, 150, 200),
       mean_diff = c(10, 20, 30),
       sd = c(50, 100)) %>%

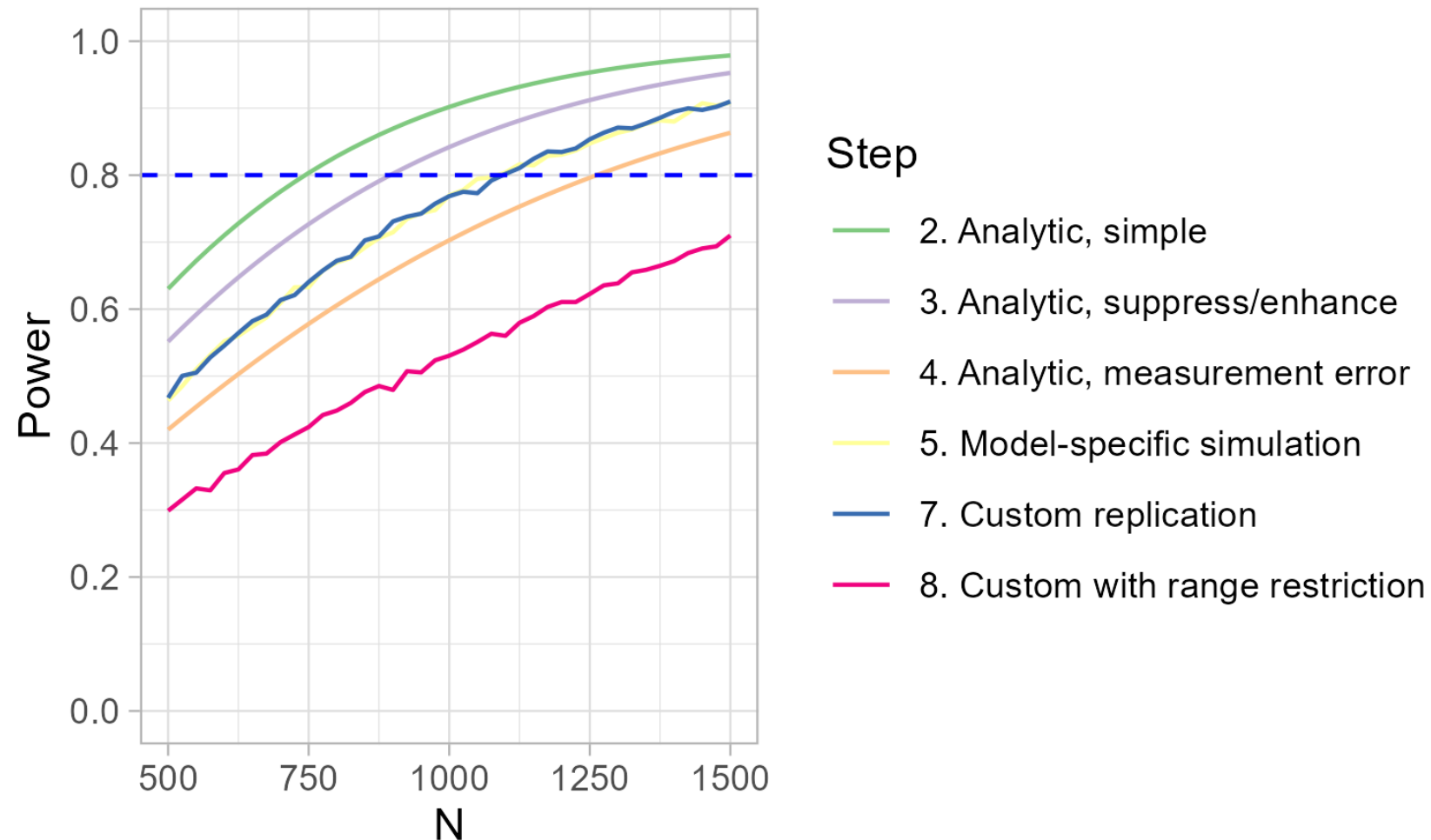
## Generate datasets
generate(1000, .progress = TRUE) %>%
## Fit datasets
fit(t = ~t.test(post, pre, paired = TRUE)) %>%
## Collect results
tidy_fits()
```

SUMMARIZING RESULTS WITH THE TIDYVERSE

```
sim_vary %>%  
  group_by(n, mean_diff, sd) %>%  
  summarize(Power = mean(p.value > 0.05))
```

```
## # A tibble: 18 × 4  
## # Groups:   n, mean_diff [9]  
##      n mean_diff sd Power  
##   <dbl>   <dbl> <dbl> <dbl>  
## 1    100      10   50 0.507  
## 2    100      10  100 0.831  
## 3    100      20   50 0.026  
## 4    100      20  100 0.482  
## 5    100      30   50 0  
## 6    100      30  100 0.16  
## 7    150      10   50 0.336  
## 8    150      10  100 0.791  
## 9    150      20   50 0.002  
## 10   150      20  100 0.303  
## 11   150      30   50 0  
## 12   150      30  100 0.041  
## 13   200      10   50 0.212  
## 14   200      10  100 0.684  
## 15   200      20   50 0.001  
## 16   200      20  100 0.219  
## 17   200      30   50 0  
## 18   200      30  100 0.016
```

EXAMPLE: POWER ANALYSIS OF REGRESSION INTERACTIONS



SIMPR PHILOSOPHY

- Custom functions not required
- Minimize overhead code
- **Get people simulating as fast as possible!**

ADVANCED FEATURES OF SIMPR

- More sophisticated specifications
- Data munging capabilities
- Sensibly handle errors
- Reproducible workflows
- Easy-to-use parallel processing

DATA MUNGING CAPABILITIES

```
range_sim = specify(pre = ~ rnorm(n, 0, sd),  
                    post = ~ pre + rnorm(n, mean_diff, sd)) %>%  
  ## Define parameters and vary them  
  define(n = c(100, 150, 200),  
        mean_diff = c(10, 20, 30),  
        sd = c(50, 100)) %>%  
  ## Generate datasets  
  generate(1000, .progress = TRUE) %>%  
  ## Apply tidyverse functions to every simulation dataset  
  per_sim() %>%  
  ## Mutate to add a range restriction  
  mutate(across(everything(), case_when(  
    pre > 100 ~ 100,  
    pre < -100 ~ -100,  
    .default ~ pre))) %>%  
  ## Fit datasets  
  fit(t = ~t.test(post, pre, paired = TRUE)) %>%  
  ## Collect results  
  tidy_fits()
```

ERROR HANDLING

- Can change error handling to keep going with simulation, stop simulation, or to skip warnings
- Debug and recovery options to enter into simulation during error

REPRODUCIBLE WORKFLOWS

- Same seed, same results
- Can regenerate *just a specific subset* to see what happened in that particular dataset or fit
- Useful in debugging and diagnosing unexpected results, etc.

REPRODUCIBLE WORKFLOWS

Filtering Full Simulation

```
set.seed(500)

specify(a = ~ runif(6)) %>%
  generate(3) %>%
  filter(.sim_id == 3)

## full tibble
## -----
## # A tibble: 1 × 3
##   .sim_id    rep sim
##   <int> <int> <list>
## 1       3     3 <tibble [6 × 1]>
##
## sim[[1]]
## -----
## # A tibble: 6 × 1
##       a
##   <dbl>
## 1 0.371
## 2 0.959
## 3 0.633
## 4 0.177
## 5 0.803
## 6 0.133
```

Simulate Subset Only

```
set.seed(500)

specify(a = ~ runif(6)) %>%
  generate(3, .sim_id == 3)

## full tibble
## -----
## # A tibble: 1 × 3
##   .sim_id    rep sim
##   <int> <int> <list>
## 1       3     3 <tibble [6 × 1]>
##
## sim[[1]]
## -----
## # A tibble: 6 × 1
##       a
##   <dbl>
## 1 0.371
## 2 0.959
## 3 0.633
## 4 0.177
## 5 0.803
## 6 0.133
```

PARALLEL PROCESSING

```
library(simpr)
library(tidyverse)
library(future)

plan(multisession, workers = 6) # or however many cores are reasonable to use

## Specify pre and post scores that differ by a given amount
sim_vary = specify(pre = ~ rnorm(n, 0, sd),
                   post = ~ pre + rnorm(n, mean_diff, sd)) %>%

## Define parameters and vary them
define(n = c(100, 150, 200),
       mean_diff = c(10, 20, 30),
       sd = c(50, 100)) %>%

## Fit datasets
fit(t = ~t.test(post, pre, paired = TRUE)) %>%

## Collect results
tidy_fits() %>%

## Generate datasets (and perform post-processing)
generate(1000, .progress = TRUE)
```


Pros and Cons of simplr vs. other solutions

- ✓ tidyverse friendly
- ✓ Beginner friendly
- ✓ Reproducibility, error handling built in
- ✓ General-purpose, customizable and can handle arbitrary R code
- ✗ Likely not as fast/optimized as some alternatives
- ✗ Not as customizable/powerful as DeclareDesign
- ✗ Not specifically set up for any particular application (no MC errors, plots, reports, specific models...)

Future Directions

- “Chunking”/options for autosaving intermediate results to disk
- Model-specific support for common design analyses (use DesignLibrary?)
- Test coverage! 🐜 🐜 🐜

**WE'LL BEGIN SPECIFYING
TO DEFINE THE WORLD OF YOUR CREATION**

**YOU'LL THEN SEE HOW TO TRY
DATA GENERATION**

specify()



define()



generate()

**IF YOU WANT TO RUN IN PARALLEL
SIMPLY ADD A FUTURED TO IT
ANYTHING TO REPRODUCE, SET.SEED IT,**



**WANT TO TEST YOUR WORLD?
SIMPLY USE FITO**

```
library(simpr)
library(tidyverse)
library(future)
```

```
plan(multisession, workers = 6) # or however  
many cores are reasonable to use
```

```
set.seed(500)
```

```
specify(a = ~ runif(6)) %>%  
generate(3, .sim_id == 3)
```

fit()



tidy_fits()



THERE IS NO WAY, I KNOW TO COMPARE
WITH SIMPR SIMULATION
CODING THERE, YOU'LL BE FREE
IF YOU TRULY WISH TO BE

- **Algorithm Optimization**
 - **CAISER** determines the sample size required for comparing the performance of a set of k algorithms on a given problem instance when power inaccuracy is predefined
- **ANCOVA**
 - **pwr2ppl** computes power for one or two factor ANCOVA with a single covariate
- **ANOVA:**
 - General options include **pwr** (one-way ANOVA), **pwr2** & **pwr2ppl** (up to two-way ANOVA) and **WebPower** (up to two-way and repeated measures). The **easypower** package, based on the **pwr** package, simplifies the user input for factorial ANOVA.
 - **BUCSS** allows any number of factors, using uncertainty and publication bias correction.
 - **powerbydesign** provides functions for bootstrapping the power of ANOVA designs based on estimated means and standard deviations of the conditions
 - **powerAnalysis** only should be used with balanced one-way analysis of variance tests.
 - **powerMediation** performs power calculation for interaction effect in 2x2 two-way ANOVA.
 - **Superpower** uses simulations and analytic power solutions for ANOVA designs of up to three factors to calculate power and average observed effect sizes.
- **Bayesian:**
 - **bayescount** provides analysis and power calculations for count data.
 - **BayesESS** determines effective sample size of a parametric prior distribution in Bayesian conjugate models (beta-binomial, gamma-exponential, gamma-Poisson, dirichlet-multinomial, normal-normal, inverse chi-squared-normal, inverse-gamma-normal), Bayesian linear and logistic regression models, Bayesian continual reassessment method (CBM), and Bayesian time to event model.
 - **BayesianPower** determine the required sample size for a given power and effect size for a given factor
 - **SampleSizeMeans** calculates sample size required for a given power and effect size for a given factor, using three different Bayesian designs: binomial, normal, and Poisson. It also provides sample sizes for the Average Length Criterion (ALC) and the Average Length Criterion (ALC) for both the fully Bayesian and the mixed Bayesian designs.
- **Beta Distribution:**
 - **PASSED** and **BetaPASS** helps find the power of a beta distribution for a given effect size and sample size. It also provides functions to plot power curves demonstrating the effect of sample size on power.
- **Bioequivalence Study**
 - **Power2Stage** contains functions to obtain the power of a two-stage bioequivalence study via simulations.
 - **PowerTOST** calculates power and sample size for a two-stage bioequivalence study.
- **Case-Control study:**
 - **CoRpower** calculates power for assessment of a biomarker in clinical efficacy trials. The methods differ between the two groups, and in biomarker response subgroups, which is a function of efficacy/protection.
 - **epiR** calculates sample size, power, and detection probability for a case-control study.
 - **samplesizelogisticcasecontrol** determines sample size for a logistic case-control study.
- **Chi-squared test:**
 - Options include **powerAnalysis**, **pwr**, **pwr2ppl**, **bimetallic**, **ssd**.
- **Cochran-Mantel-Haenszel Test:**
 - **samplesizeCMH** calculates the power and sample size for Cochran-Mantel-Haenszel tests, with several helper functions for working with probability, odds, relative risk, and odds ratio values.
- **Competing Risks Analysis:**
 - **powerCompRisk** is power analysis tool for jointly testing the cause-1 cause-specific hazard and the any-cause hazard with competing risks data.
- **Complex Surveys**

- **Diagnostic Test**
 - **MKpower** computes sample size, power, delta, or significance level of a diagnostic test for an expected sensitivity or specificity.
- **Dirichlet-Multinomial distribution:**
 - **HMP** uses the Dirichlet-Multinomial distribution to provide several functions for formal hypothesis testing, power and sample size calculations.
- **Factorial Design**
 - **BDEsize** calculates the sample size required to detect a certain standardized effect size, under a significance level (two-level fractional factorial, randomized complete block design, full factorial design, and split-plot design). This package also provides three graphs; detectable standardized effect size vs power, sample size vs detectable standardized effect size, and sample size vs power, which show the mutual relationship between the sample size, power and the detectable standardized effect size.
 - **H2x2Factorial** estimates the required number of clusters or the achieved power level under different types of hypothesis tests in a hierarchical 2x2 factorial trial with unequal cluster sizes and a continuous outcome.
- **Fisher's Test**
 - Power calculations for differences between binomial proportions can be achieved with **Exact** for unconditional exact tests with 2x2 contingency tables. **MIDN** computes the exact sample sizes required based on the Boschloo's technique and Fisher-Boschloo test mid-N estimates.
 - **ssanv** provides a calibrated power calculation by leveraging the uncertainty in either nonadherence or parameter estimation.

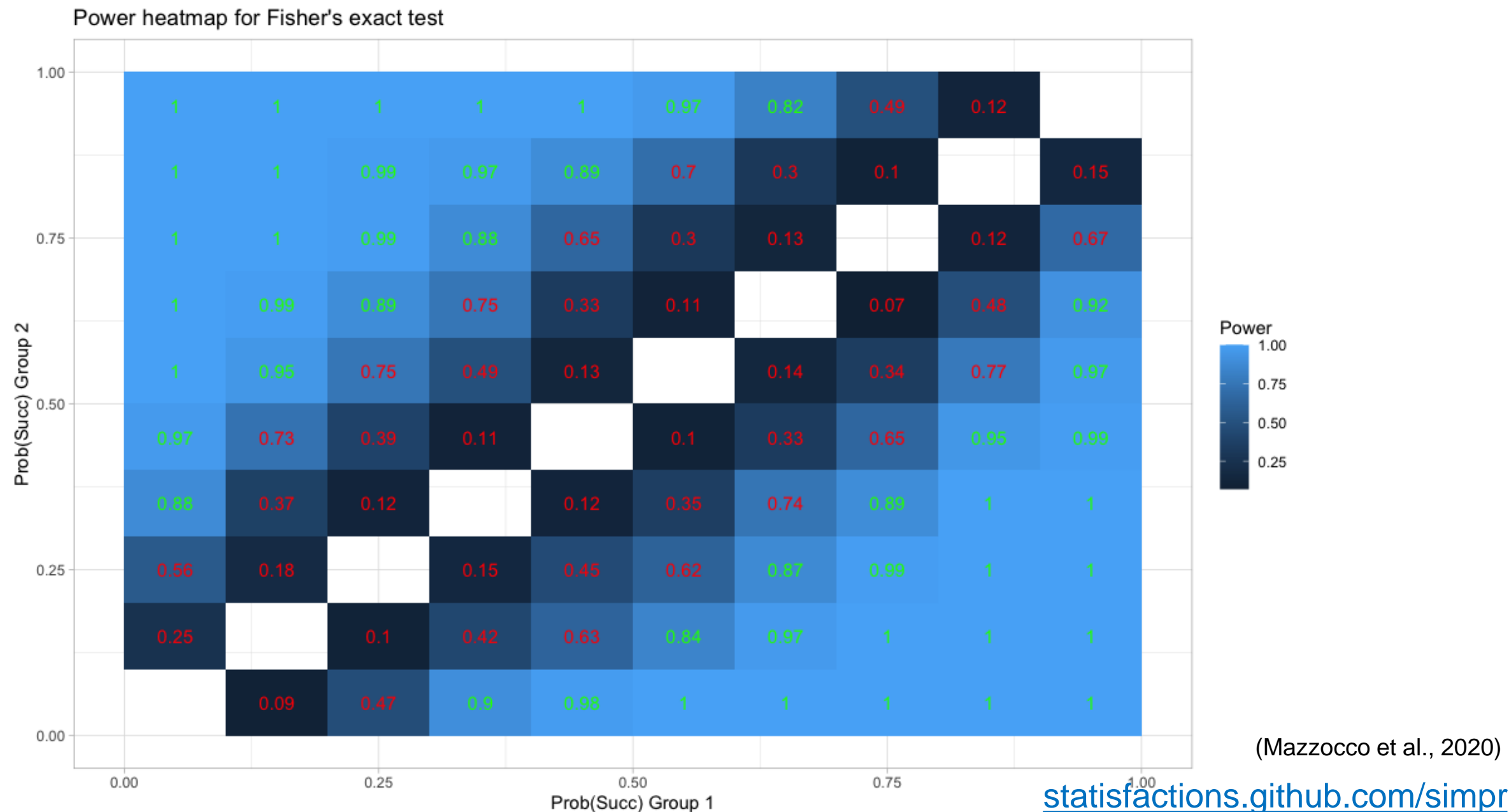
- **Intraclass Correlation**
 - **ICC.Sample.Size** calculates power for given value of p , the null hypothesis p_0 , number of raters (k), number of subjects (N), and alpha. Can also be used to calculate the effect of increasing N at given intervals to a maximum N , or the effect of increasing k at given intervals to a maximum k , or the effect of increasing p at given intervals to a maximum p , or the effect of increasing p_0 at given intervals to a maximum p_0 , or the effect of increasing α at given intervals to a maximum α , or the effect of increasing p at given intervals to a maximum p , or the effect of increasing p_0 at given intervals to a maximum p_0 , or the effect of increasing α at given intervals to a maximum α .
- **Interobserver Agreement Studies**
 - **kappaSize** provides basic tools for sample size estimation in studies of interobserver/interobserver agreement. It provides functions for both the power-based and confidence interval-based methods, with binary or multinomial data, and through six raters.
- **Likelihood Ratio test**
 - **asypow** calculates power utilizing asymptotic likelihood ratio methods
- **Linear Regression**
 - **pwr**, **powerMediation** and **WebPower** provide analytical power calculations.
 - **simr** and **simpr** provided simulated power calculations.
 - **BayesESS** provided simulated power calculations for Bayesian models
- **Local Average Treatment Effect (LATE)**
 - **powerLATE** is an implementation of the generalized power analysis for the local average treatment effect (LATE). It uses standardized effect sizes to place a conservative bound on the power under minimal assumptions. It also allows users to recover power, sample size requirements, or minimum detectable effect sizes. Package also allows users to calculate bounds, and

Relatedly: Message me if you're interested in helping with a Power Analysis Task view! 🙄🙄🙄🙄🙄
Github/X: @statisfactions
<https://github.com/statisfactions/ctv-power>

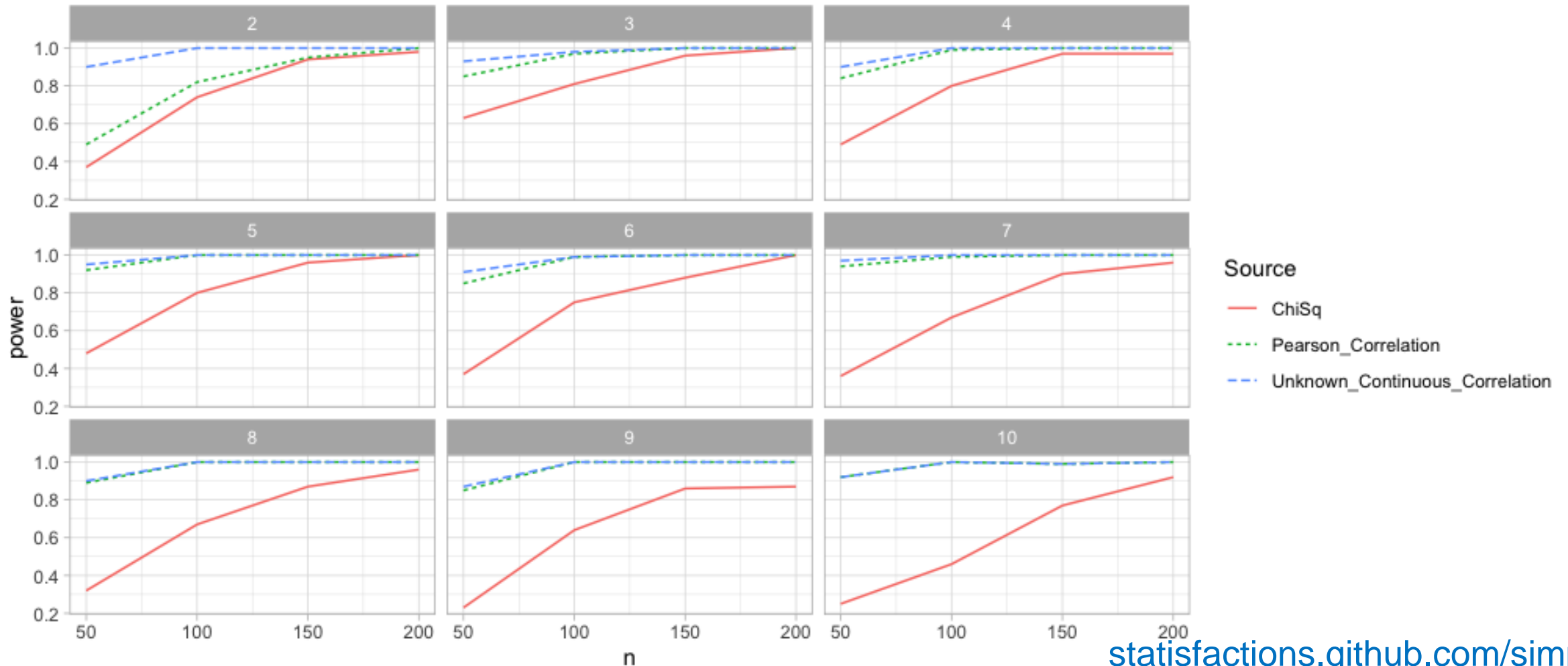
- **Hierarchical Data**
 - **HierO** calculates statistical power for given type I error (alpha), effect size (Delta) and non-centrality parameter (ncpar) of a non-central chi-square distribution.
- **High Dimensional Classification Study**
 - **HDDesign** determines the sample size requirement to achieve the target probability of correct classification (PCC) for studies employing high-dimensional features.
- **Human Microbiome Experiment**
 - **HMP** uses the Dirichlet-Multinomial distribution to provide several functions for formal hypothesis testing, power and sample size calculations for human microbiome experiments.

- **MANOVA**
 - **pwr2ppl** supports power for one factor MANOVA with up to 2 levels and 4 measures.
- **McNemar Test**
 - **MIDN** computes the exact sample sizes required in the randomized UMPU test and its conservative non-randomized counterpart for attaining prespecified power. However, in contrast to the parallel group setting, the midpoint between these two numbers shall now be used as a nearly exact value of the number of pairs to be observed. The test based on the score-statistic corrected for possible exceedances of the nominal significance level.
- **Mediation Analysis (see also Structural Equation Modeling)**
 - **pwr2ppl** and **WebPower** both support power analysis of mediation. WebPower additionally supports statistical power analysis for mediation in structural equation models.

STUDY PLANNING: POWER FOR A FISHER EXACT TEST

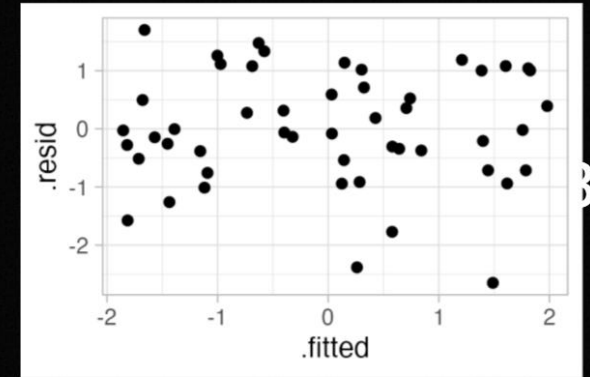
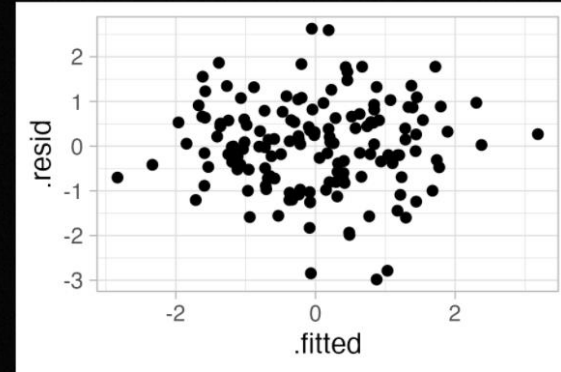
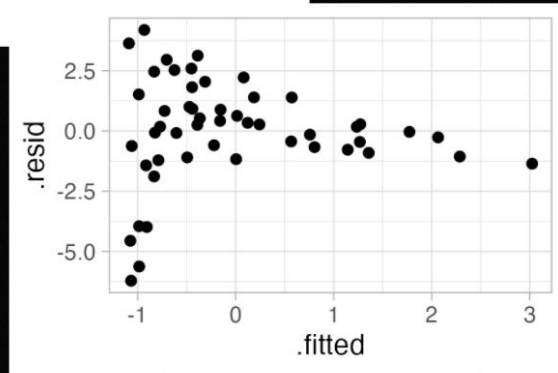
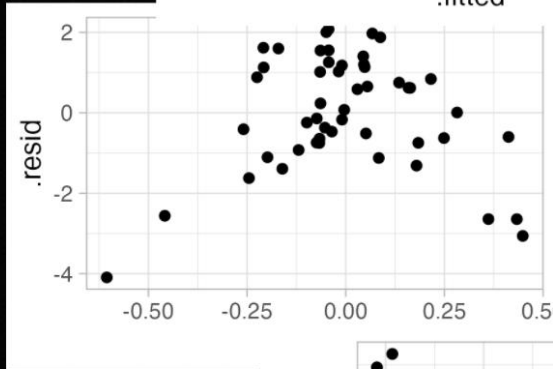
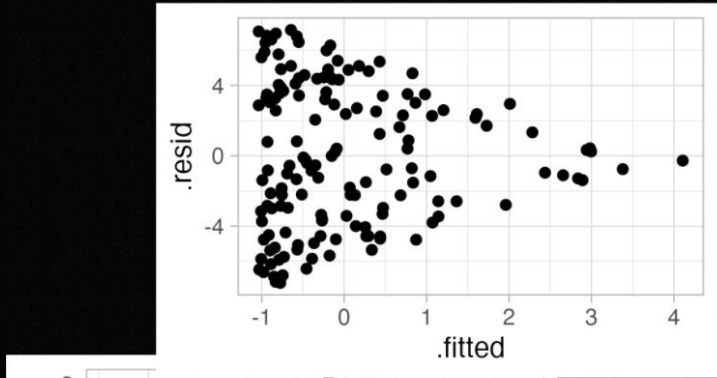


METHODOLOGICAL RESEARCH: EFFECT OF THE NUMBER OF CATEGORIES ON POWER

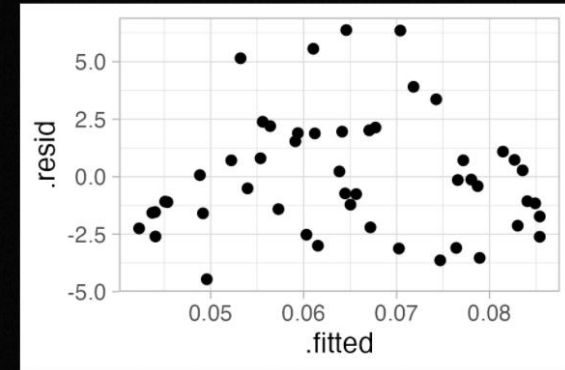


Linearity 🤔

Worst



Best



GENERATING EXAMPLES FOR TEACHING: REGRESSION ASSUMPTIONS

staticfactions.github.io