

Keeping Data Analysis Simple – Or Why I Love the emmeans R Package

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Two Parts

Contrasts for Factors With
More Than 2 Levels

A General Approach for Testing
Omnibus Tests

“Two Statistics”

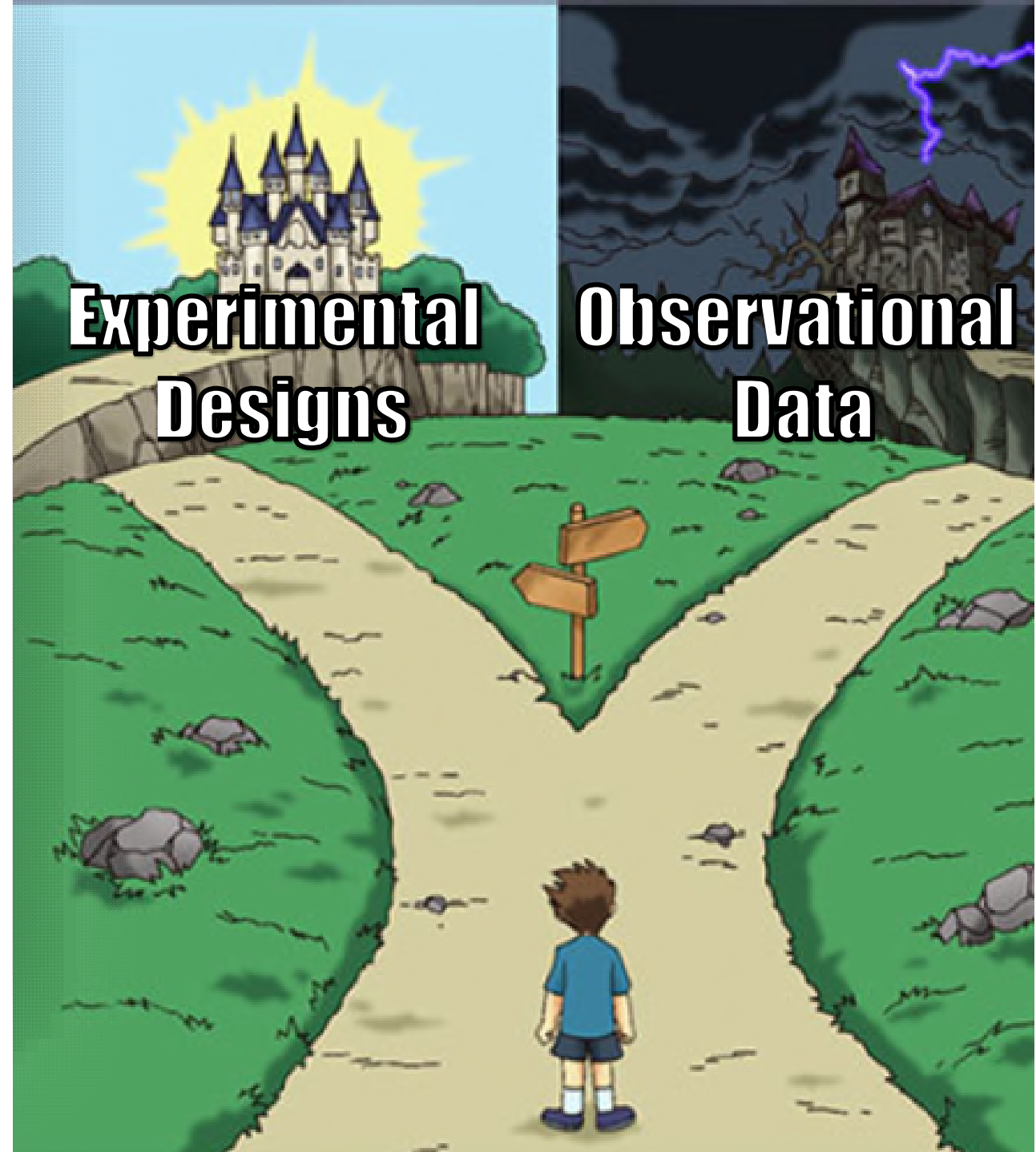
Statistics is tool that helps us answer substantive questions!

Talk applies to experimental designs:

- IVs are **categorical** (factors)
- IV is **randomly assigned** (i.e., manipulated) and DV is measured
- Inferential and substantial goal is **hypothesis test**: Is there effect of IV on DV?
- Random assignment allows **causal interpretation**: IV is cause of change in DV

Different considerations can apply for **observational data**

- IV is **measured** (and not manipulated) and **graded/continuous**
- Inferential goal is **estimation**: What is size and magnitude of effect of IV on DV?
- Substantive goal is **interpretation of effect** (causal or non-causal): What does effect of IV on DV mean?




Contrasts for Factors With More Than 2 Levels

My Provocative Take

The Contrast-First Approach

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How to capitalize on a priori contrasts in linear (mixed) models: A tutorial

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ABSTRACT

Factorial experiments in research on memory, language, and in other areas are often analyzed using analysis of variance (ANOVA). However, for effects with more than one numerator degrees of freedom, e.g., for experimental factors with more than two levels, the ANOVA omnibus F-test is not informative about the source of a main effect or interaction. Because researchers typically have specific hypotheses about which condition means differ from each other, a priori contrasts (i.e., comparisons planned before the sample means are known) between specific conditions or combinations of conditions are the appropriate way to represent such hypotheses in the statistical model. Many researchers have pointed out that contrasts should be “tested instead of, rather than as a supplement to, the ordinary ‘omnibus’ F test” (Hays, 1973, p. 601). In this tutorial, we explain the mathematics underlying different kinds of contrasts (i.e., treatment, sum, repeated, polynomial, custom, nested, interaction contrasts), discuss their properties, and demonstrate how they are applied in the R System for Statistical Computing (R Core Team, 2018). In this context, we explain the generalized inverse which is needed to compute the coefficients for contrasts that test hypotheses that are not covered by the default set of contrasts. A detailed understanding of contrast coding is crucial for successful and correct specification in linear models (including linear mixed models). Contrasts defined a priori yield far more useful confirmatory tests of experimental hypotheses than standard omnibus F-tests. Reproducible code is available from <https://osf.io/7ukf6/>.

PSYCHOLOGICAL SCIENCE

General Article

**“SOME THINGS YOU LEARN
AREN’T SO”:
Cohen’s Paradox, Asch’s
Paradigm, and the Interpretation
of Interaction**

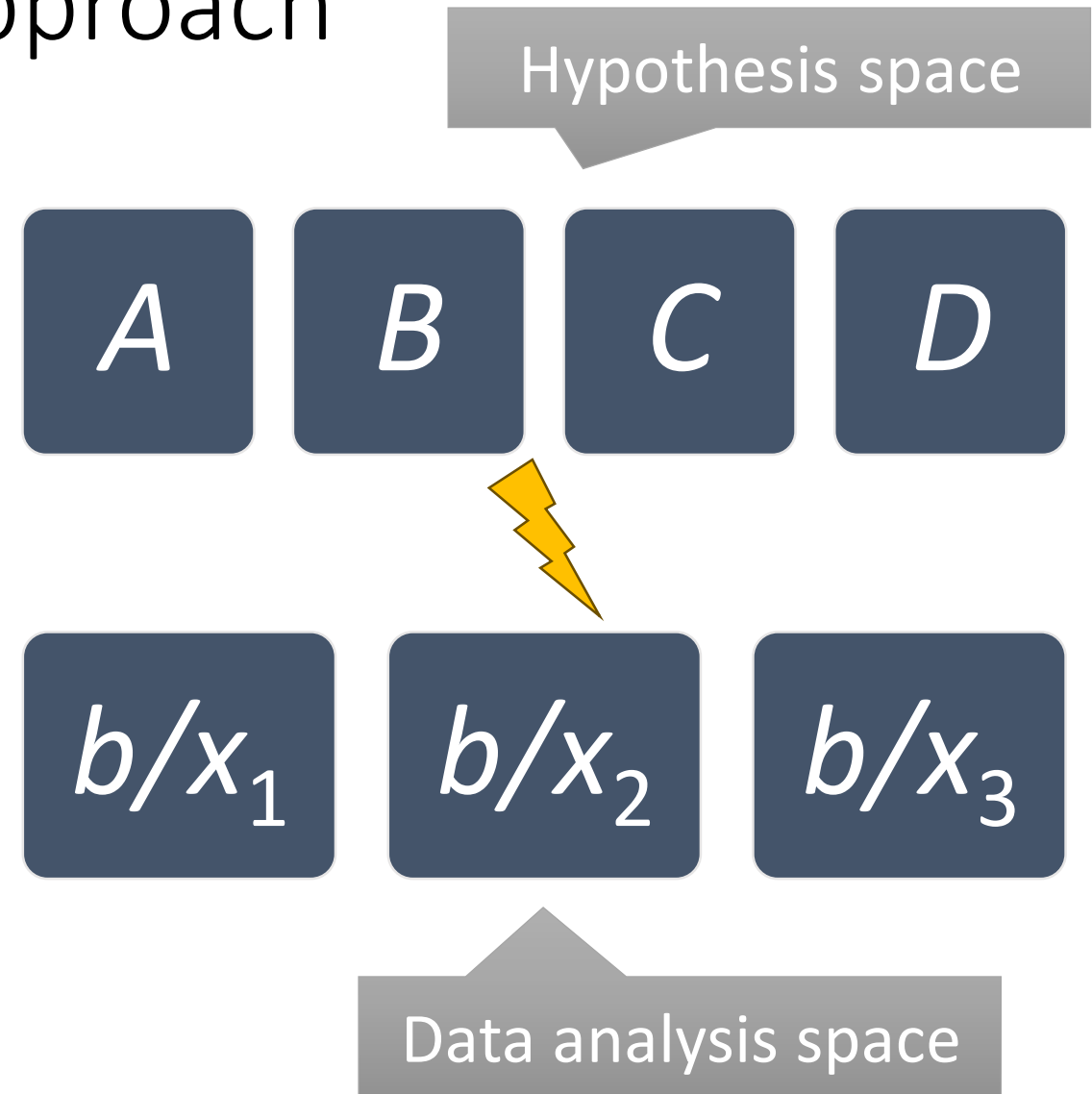
By Ralph L. Rosnow¹ and Robert Rosenthal²

¹Temple University and ²Harvard University

Steps of Contrast-First Approach

1. For factor with k levels, specify k hypotheses among cell means (based on theory/EDA)
2. Transform k hypothesis into set of $k - 1$ non-redundant contrasts
3. Estimate model with specified contrasts and inspect estimates
4. For testing additional hypotheses, set up new contrasts and refit model

May require several model fits,
which can be expensive

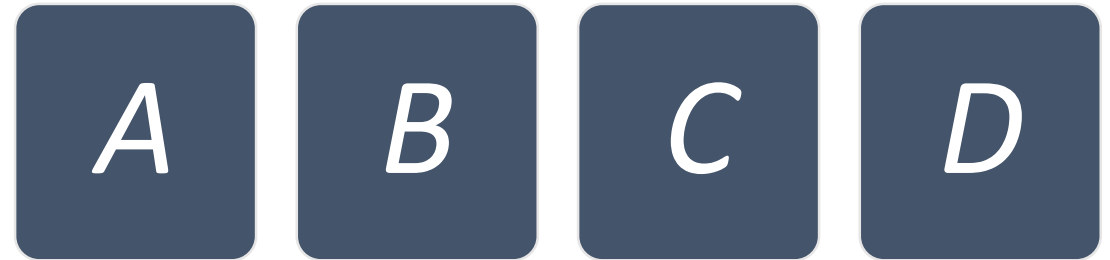


The Model-First Approach

1. Set up statistical model using sum-to-zero contrasts
2. Check ANOVA table with omnibus tests
 - Don't look at fixed-effect coefficients!
3. Inspect estimated means for model terms (main effects and interactions) of interest
4. Follow-up analysis: specify and tests contrasts on means using emmeans
 - consider use of multiple comparison procedure (e.g. "holm")

Only requires single fit of model

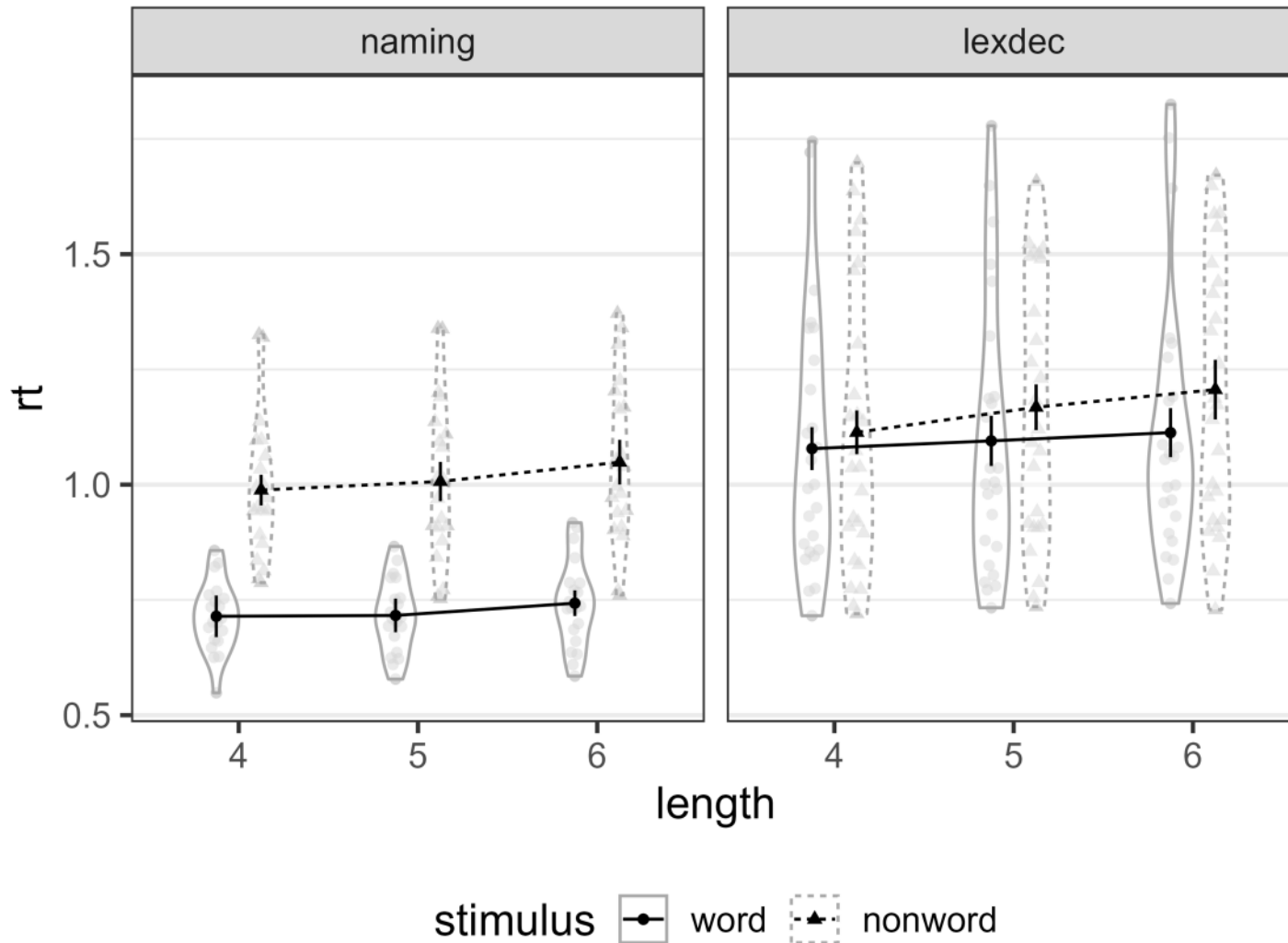
Hypothesis space



Data analysis space

Leverage *abstraction* through emmeans: hide contrast details behind software interface

Example Data



- Freeman et al. (2010, *JML*):
 - Cognitive task: 1 letter string per trial, 300 trials per participant
 - IV_1 (between-subjects) task: Naming task vs. lexical decision task
 - IV_2 stimulus (within-subjects): word vs. nonwords
 - IV_3 length (within-subjects): 4, 5, or 6 letters length
 - *DV*: response time
 - Crossed random-effect design
 - 45 participants (20 in naming task, 25 in lexical decision task)
 - 600 items (300 words, 300 nonwords)

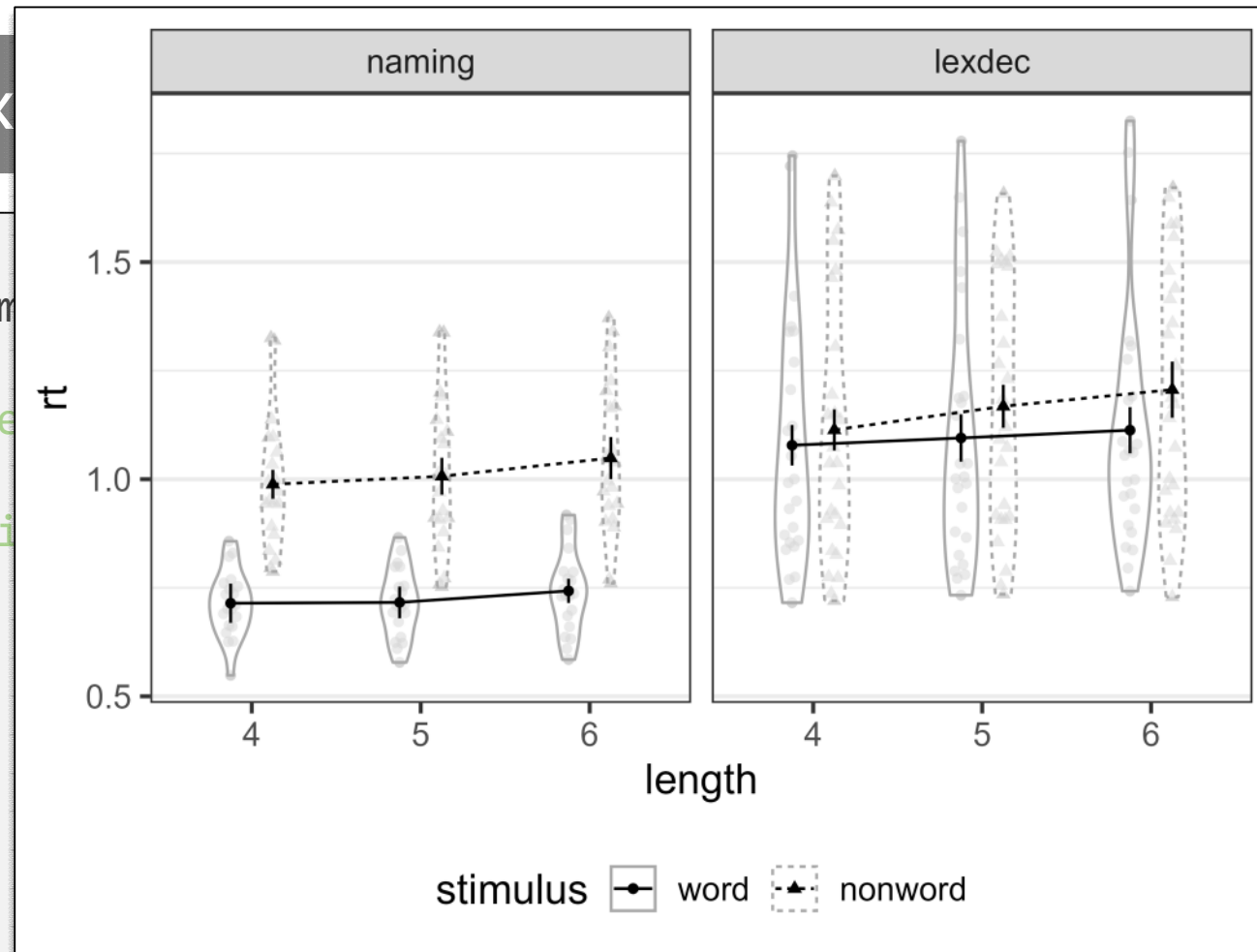
Steps 1 & 2: Fit model using `afex::mixed()` and inspect ANOVA table

```
library("afex")
m3 <- mixed(rt ~ task*stimulus*length + (stimulus||id) + (task||item), fhch, expand_re=TRUE)
m3
# Mixed Model Anova Table (Type 3 tests, S-method)
#
# Model: rt ~ task * stimulus * length + (stimulus || id) + (task || item)
# Data: fhch
#
#           Effect           df           F p.value
# 1           task    1, 44.23 15.17 ***    <.001
# 2      stimulus    1, 50.36 80.37 ***    <.001
# 3        length    2, 590.04 11.88 ***    <.001
# 4  task:stimulus    1, 58.29 29.01 ***    <.001
# 5  task:length    2, 578.59      0.52    .596
# 6 stimulus:length    2, 590.07      2.07    .127
# 7 task:stimulus:length    2, 578.60      0.14    .871
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1
```

Steps 1 & 2: Fit model using afex

```
library("afex")
m3 <- mixed(rt ~ task*stimulus*length + (stimulus|id), data = fhch)
# Mixed Model Anova Table (Type 3 tests, S-measures)
#
# Model: rt ~ task * stimulus * length + (stimulus|id)
# Data: fhch
#
#          Effect          df          F
# 1          task      1, 44.23  15.17 ***
# 2      stimulus      1, 50.36  80.37 ***
# 3          length      2, 590.04  11.88 ***
# 4  task:stimulus      1, 58.29  29.01 ***
# 5  task:length      2, 578.59    0.52
# 6  stimulus:length      2, 590.07    2.07 .127
# 7  task:stimulus:length      2, 578.59    0.52
# ---
# Signif. codes:  0. '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 '.' 1
```

```
afex_plot(m3_nc, "length", "stimulus", "task", id = "id", error = "within",
          data_geom = list(geom_quasirandom, geom_violin),
          data_arg = list(list(width = 0.05, dodge.width = 0.5),
                          list(width = 0.5)))
```

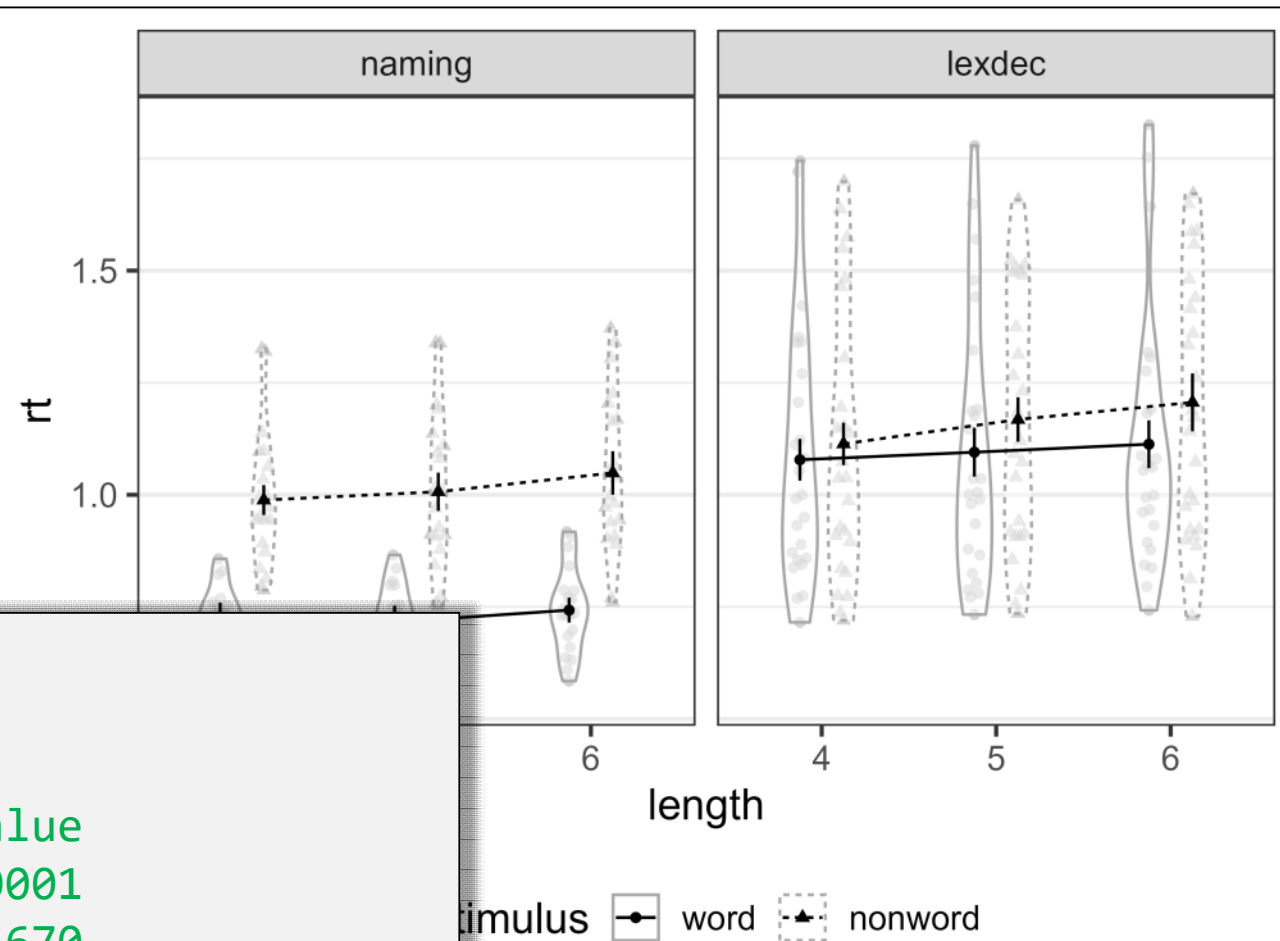


Step 3: Inspect estimated means

Steps 1 & 2: Fit model using afex

```
library("afex")
m3 <- mixed(rt ~ task*stimulus*length + (stimulus|length)
m3
# Mixed Model Anova Table (Type 3 tests, S-me
#
# Model: rt ~ task * stimulus * length + (sti
# Data: fbcb

library("emmeans")
emmeans(m3_nc, "length") %>%
  contrast("poly")
# contrast estimate SE df z.ratio p.value
# linear 0.05405 0.0111 Inf 4.856 <.0001
# quadratic 0.00827 0.0192 Inf 0.430 0.6670
#
# Results are averaged over the levels of: task, stimulus
# Degrees-of-freedom method: asymptotic
```



Step 4(a): Follow-up analysis

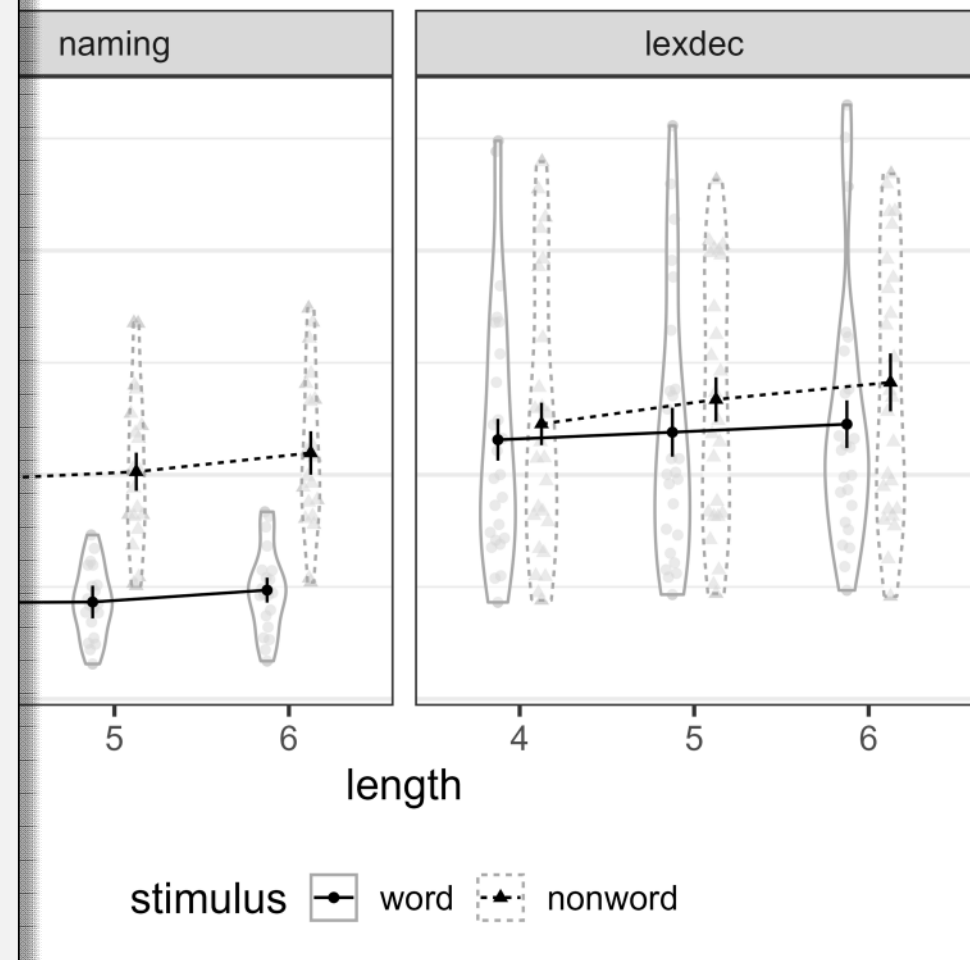
```

em1 <- emmeans(m3_nc, c("stimulus", "task"))
em1
# stimulus task emmean SE df asymp.LCL asymp.UCL
# word naming 0.725 0.0517 Inf 0.623 0.826
# nonword naming 1.015 0.0518 Inf 0.913 1.116
# word lexdec 1.095 0.0464 Inf 1.004 1.186
# nonword lexdec 1.163 0.0464 Inf 1.072 1.254
#
# Results are averaged over the levels of: length

## let's test: is there effect of stimulus per task?
con1 <- list(
  stim_naming = c(-1, 1, 0, 0),
  stim_lexdec = c(0, 0, -1, 1)
)

contrast(em1, con1, adjust = "holm")
# contrast estimate SE df z.ratio p.value
# stim_naming 0.2901 0.0301 Inf 9.646 <.0001
# stim_lexdec 0.0672 0.0273 Inf 2.460 0.0139
#
# Results are averaged over the levels of: length

```



1 ' ' 1

Step 4(b): Follow-up analysis

FAQ on Model-First Approach

- What is ultimately benefit of model-first approach?
 - Less cumbersome and mentally taxing, all tests are performed on design-cell space. In case you want to test more than one set of contrasts, avoids refitting model.
- What if I have a specific hypothesis or am interested in the random-effect estimates?
 - If you have very specific hypothesis and no real uncertainty of how the means will order or hypotheses regarding the random-effect estimates, the contrast-first approach is probably better, even if more cumbersome.
- Can you only test contrasts for model term if corresponding omnibus test is significant?
 - No. Whether you want to look at omnibus tests depends on hypothesis. If strong hypothesis exists, omnibus test not necessary (and can hide effects). Consult omnibus test if results can surprise you.
- Do you always have to correct for multiple testing when calculating contrasts?
 - It depends. If you only conduct $k - 1$ pre-planned contrasts (for factor with k levels), multiple comparison correction probably not necessary. For not planned contrasts or more than $k - 1$ contrasts, Holm-correct probably a good idea.
- Why should I not look at model coefficients for factors with more than 2 levels?
 - For a factor with k levels there are only $k - 1$ coefficients so there exist no 1 to 1 mapping. Especially for popular canned contrasts (especially `contr.sum` or `contr.equalprior`), coefficients cannot be interpreted.

Henrik's List of Things to Remember About Contrasts

- Appropriate contrasts for models with interactions need to sum to zero (in balanced designs): `contr.sum()`, `contr.helmert()`, `contr.sdif()`
 - Intercept needs to correspond to (unweighted) grand mean
 - For treatment contrasts and other contrasts that do not sum to zero, lower order effects correspond to simple effects and not main effects
- For Bayesian models, contrasts should have same marginal effect on all factor levels: `bayestestR::contr.equalprior()`
- For factors with more than 2 levels, avoid looking at model estimates unless contrasts were specifically chosen for this purpose

A General Approach for Testing Omnibus Tests

Wald Tests + More emmeans Magic

Estimation and Testing can be Easy in Frequentist Approach

- `lme4` and `MixedModels.jl`
 - LMMs (normal distribution) and GLMMs (with response distribution in the “exponential family”: binomial, Poisson, Gamma, etc.)
 - Allows estimating only conditional mean of response distribution
- `glmmTMB` (or `gamlss`)
 - Supports wider set of selected response distributions, e.g. beta, Student t , beta-binomial, negative binomial, Tweedie
 - Allows distributional models: can model both location and scale (with fixed-effects) or other distributional parameters (supports e.g. zero-one-inflated models)
 - Supports flexible correlation structures (compound-symmetric, autoregressive, etc.)
- Statistical testing “easy”
 - Wald tests of simple or compound hypotheses require only fitted model
 - For LMMs, some methods even allow estimating denominator df for small samples

Problems for Frequentist Approach

1. Convergence Issues:

- Every additional parameter increases dimensionality of search space by one
- If data is sparse for given model, difficult to estimate variance/covariance parameters (“singular fit”): Eager & Roy (2017) - Mixed Effects Models are Sometimes Terrible
- Dale Barr: “Reducing random-effects structure of model introduces unknown risk of anti-conservativity, and should be done with caution”

2. Extension to other response distributions **very** difficult for models involving random effects

- Evaluating likelihood equation requires integrating likelihood of data with respect to random effects:

$$Pr(y | \beta, \theta, \sigma^2) = \int f(y | b, \beta, \theta, \sigma^2) f(b | \theta, \sigma^2) db$$

- Simple only for normal response distribution (random effects can be integrated out)
- Generally requires numerical methods (Gauss-Hermite method) or approximations (Laplace Approximation of integral) and model-specific approach
- In psych/cognitive science, often interested in cognitive models with complicated likelihoods: Diffusion model, multinomial processing tree (MPT) models





Bayesian Alternatives Make Estimation Easy

- Can use MCMC integration for integrating likelihood of data with respect to random effects (i.e., no further numerical methods necessary)
- `brms`
 - Supports wide range of response distributions including 4-parameter diffusion model (Wiener model)
 - Allows extension to new response distribution via `custom_family()`
 - Fully supports estimation of distributional models with arbitrarily complex formula for each parameter of response distribution
 - Supports various advanced features: multivariate responses, monotonic effects, meta-analyses, certain mixture models, etc.
 - Estimation much more robust due to regularisation provided by priors and MCMC sampling (e.g., Bates et al., 2015, arXiv)

Bayesian Testing Generally Not Trivial

- Simplest method for testing (inspection of whether 95%-CI includes 0) only possible for simple hypothesis
- Principled testing in Bayesian framework of simple and compound hypotheses is *Bayes factor*
 - Bayes factor can be highly sensitive to parameter priors
 - For compound hypotheses computationally expensive:
 - Requires estimating two models, full and restricted model, for each test
 - `bridgesampling` package requires at least an order of magnitude more samples for testing than for estimation; see also Schad et al., 2022)
- Misleading propaganda on philosophical issues surrounding Bayes factors
 - Bayes factor only provides relative comparison of two parameterised models (which allows providing evidence for null model/hypothesis)
 - Does not control false positives (type I errors): does not provide adequate control of fooling oneself
 - Type I error control of p -values provides some connection to external world outside of model

Easiness and Flexibility for Mixed-Effects Models

	Frequentist	Bayesian
Estimation	 Fast, brittle, & difficult to extend	 Slower, robust, & easy to extend
Testing	 Fast, specification simple, control errors, prone to misunderstanding	 Very slow, cumbersome model setup, prior dependence

Combining Bayesian Estimation with Frequentist Testing?



```
library("bayestestR") # for contr.equalprior_deviations
library("brms")       # for model estimation
library("emmeans")   # for calculating p-values using joint_tests()

options(contrasts = c('contr.equalprior_deviations', 'contr.poly')) # set contrasts

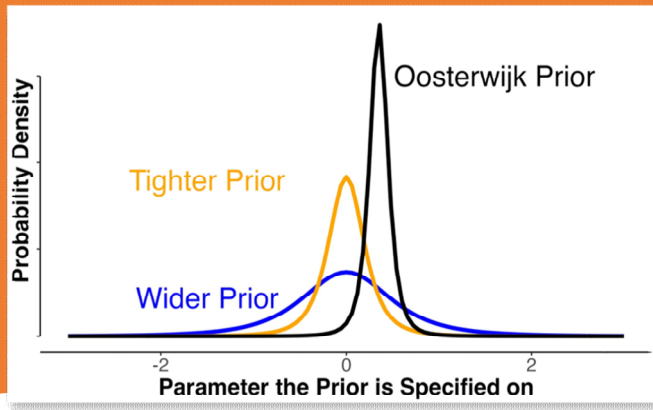
mbayes <- brm(rt ~ task*stimulus*length + (stimulus*length|id) + (task|item), fhch)
```

```
joint_tests(mbayes)
```

# model term	df1	df2	F.ratio	Chisq	p.value
# task	1	Inf	13.806	13.806	0.0002
# stimulus	1	Inf	73.654	73.654	<.0001
# length	2	Inf	10.220	20.440	<.0001
# task:stimulus	1	Inf	26.615	26.615	<.0001
# task:length	2	Inf	0.437	0.874	0.6463
# stimulus:length	2	Inf	1.908	3.816	0.1484
# task:stimulus:length	2	Inf	0.128	0.256	0.8796

Can we use Bayesian-Frequentist p -Values?

A Simulation Study



on Setup

Repeat 1000 times

01

Simulate Data

- Null hypothesis is true
- 2 and 3 groups
- Sample size: 20 to 100
- 3 models:
 - ANOVA ($\sigma^2_\epsilon = 1$)
 - Logistic $\beta(a = 2, b = 2)$
 - Logistic GLMM ($\sigma^2 = .5$ or 1)

02

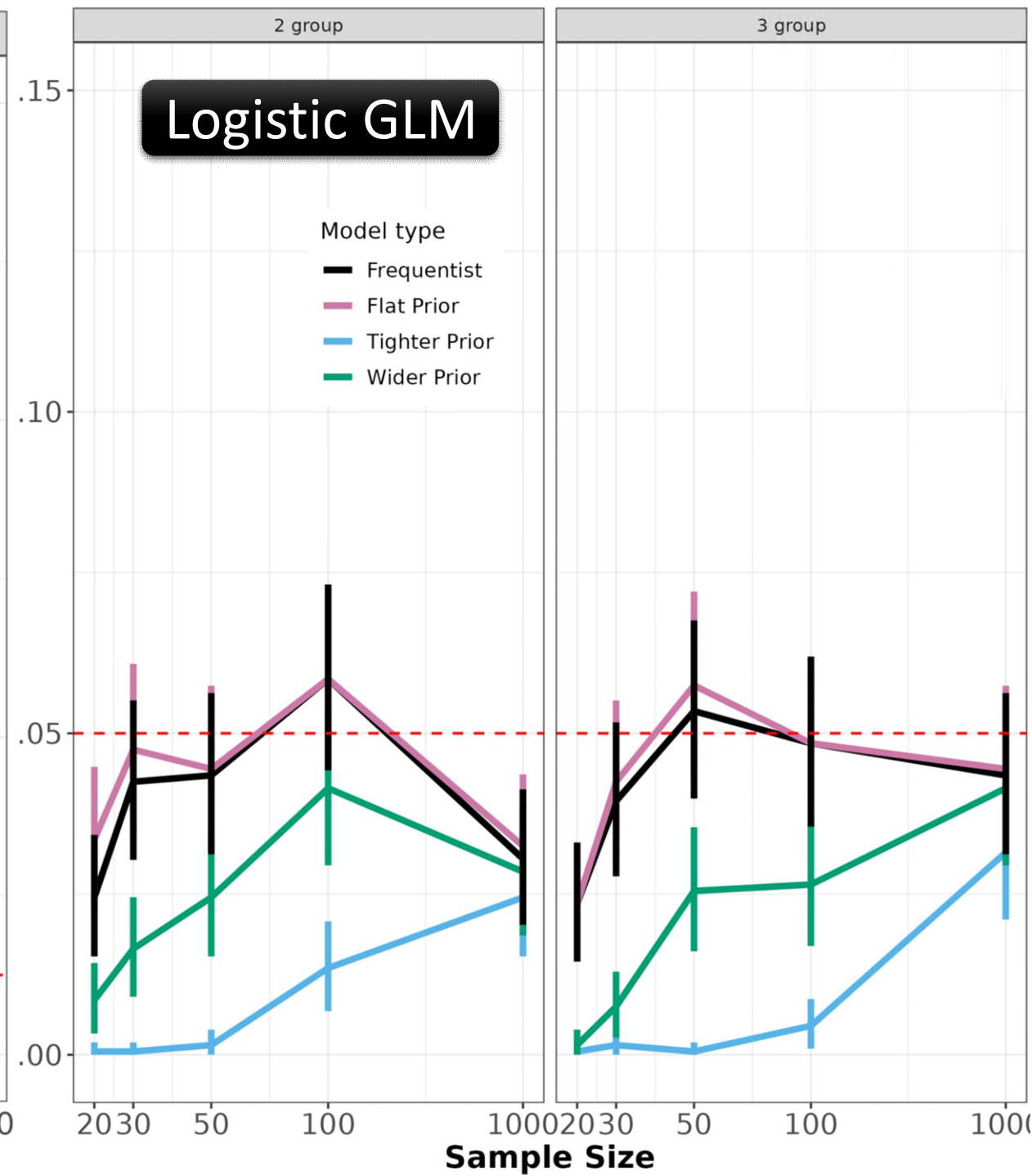
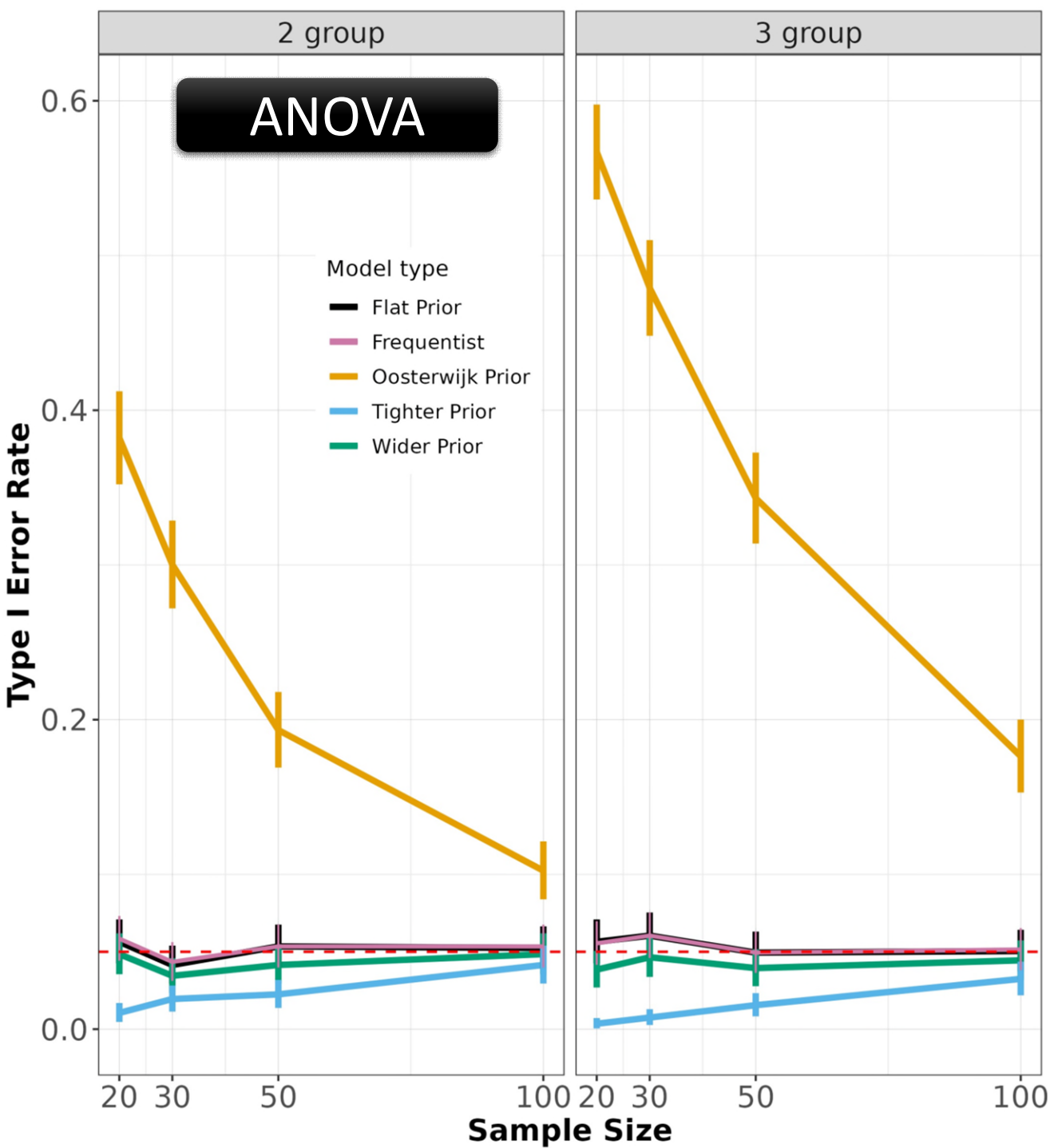
Estimate Model

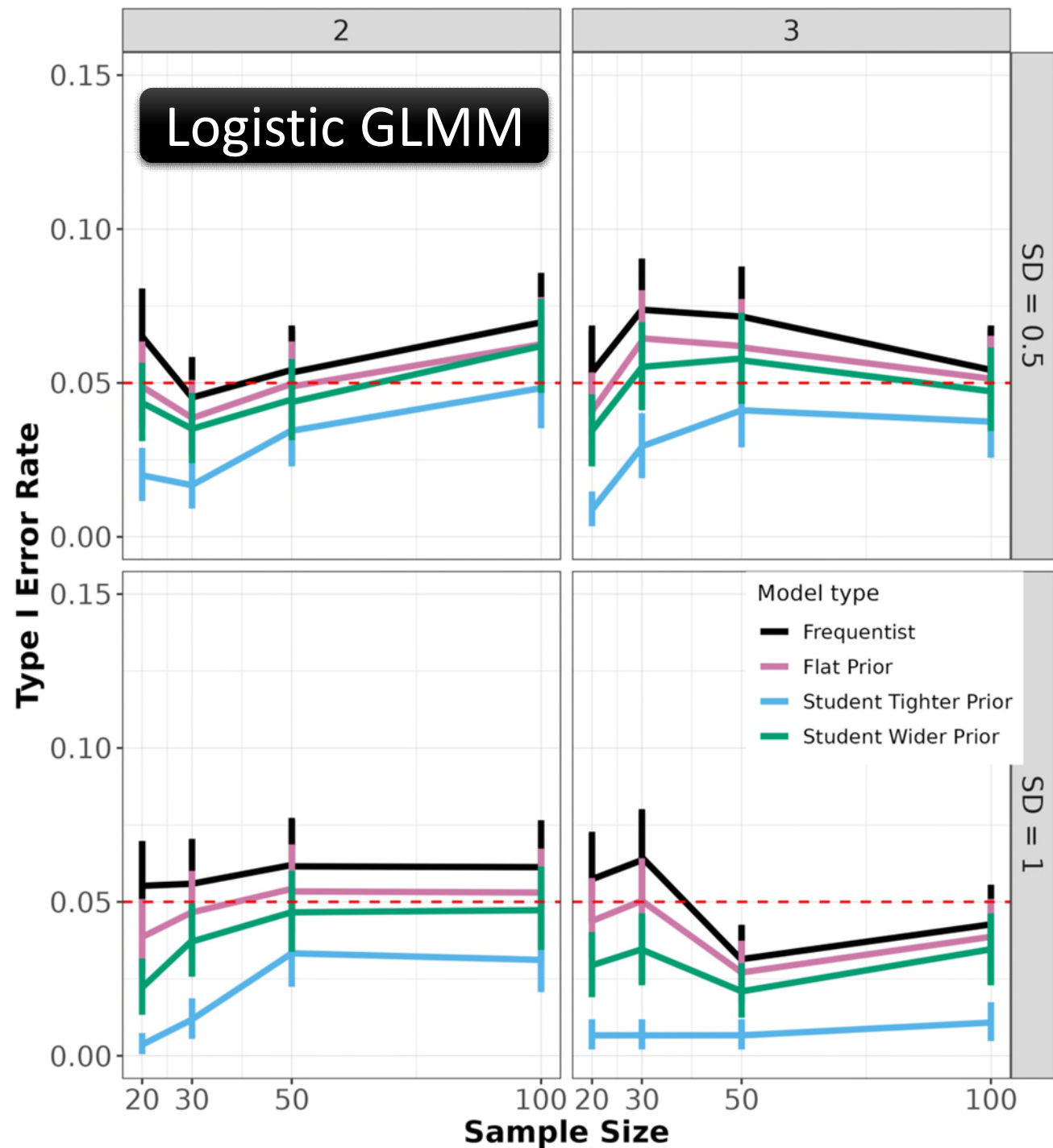
- Frequentist model
- Bayesian models:
 - Improper flat prior
 - Wide prior: $t(3, 0, 0.5)$
 - Tight prior: $t(3, 0, 0.2)$
 - [ANOVA only] Non-centred Oosterwijk prior: $t(3, 0.35, 0.102)$

03

Calculate p -value

- Using `emmeans::joint_tests()`
- Record p -value of main effect of group





Simulation Results Summary

- Type I error rates of flat prior very similar to frequentist model
- Type I error rates of zero-centred priors conservative
 - wider (i.e., weakly informative) priors only slightly conservative
 - tighter priors noticeable conservative, especially for small N s
- Non-centred priors have highly anti-conservative Type I error rates and are unsuitable for calculation p -values
- We should probably run more than 1000 replicates per simulation!
- brms default – improper flat priors on fixed-effects – seems to provide performance like frequentist approach so is probably OK!

Henrik's Simple Statistics

Learn emmeans

p -values are OK

Model-First + Follow-Up Analysis Approach

1. Set up statistical model using sum-to-zero contrasts
2. Check ANOVA table with omnibus tests
 - Don't look at fixed-effect coefficients!
3. Inspect estimated means for model terms (main effects and interactions) of interest
 - Ideally graphically (e.g., `afex_plot()`)
4. Follow-up analysis: specify and tests contrasts on means using emmeans
 - consider use of multiple comparison procedure (e.g. "holm")

Bayesian-frequentist p -values

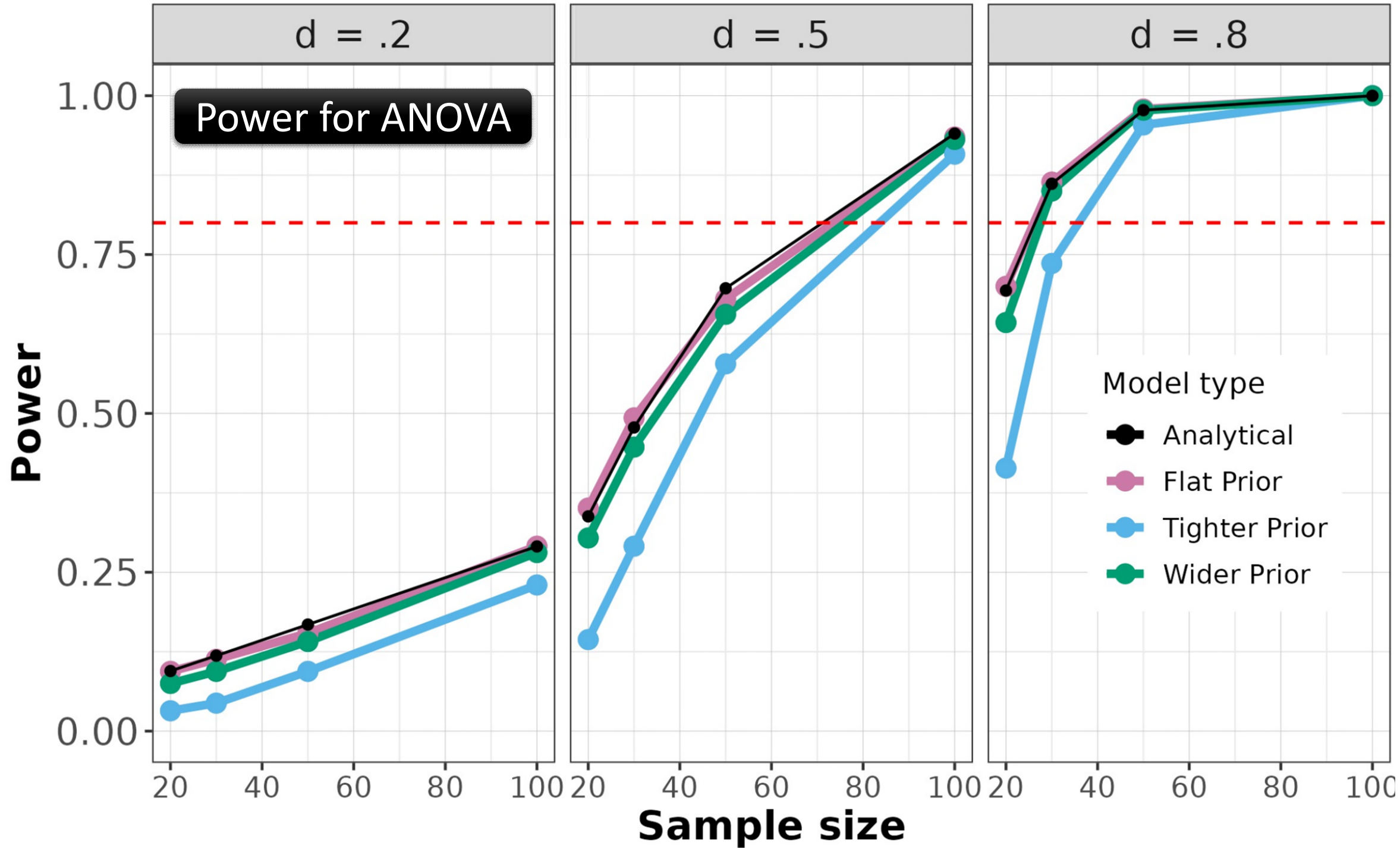
- Nominal type I errors with flat/wide priors

```
library("bayestestR")
library("brms")
library("emmeans")

options(contrasts = c('contr.equalprior',
'contr.poly'))

bayesian_model <- brm(formula, data)
joint_tests(bayesian_model)

afex::afex_plot(bayesian_model, ...)
emmeans(bayesian_model, ...)
```



My Take on Specifying Random Effects

Specifying Random-Effects Structure

- Omitting random-effect parameters for model terms that vary within levels of a random-effect grouping factor and for which random variability exists leads to non-iid residuals (i.e., σ_ϵ) and potentially anti-conservative results (e.g., Barr, Levy, Scheepers, & Tily, 2013, *JML*).
- Safeguard is **maximal model justified by the design** (Barr et al., 2013).
 - Which factors/terms vary within levels of (i.e. are crossed with) each random-effect grouping factor?
 - Are there replicates within factor levels (or parameters/coefficients) for levels of random-effects grouping factor?
- If maximal model is overparameterized and/or contains degenerate estimates or **singular fits**, power of maximal model can be reduced and a reduced model should be used (Bates et al., 2015; Matuschek et al., 2017).
 - Start by removing correlation among random-effect parameters
 - Remove random-effect parameters with variance of 0 and/or for highest-order effects with lowest variance
 - Compare p -values/fixed-effect estimates across models (p -values from degenerate/minimal models are potentially not reliable)
 - Warning: Reducing model introduces unknown risk of anti-conservativity and should be done with caution!