The correlation structure of mixed effects models with crossed random effects in controlled experiments

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Abstract

The design of experiments in psychology can often be summarized to participants reacting to stimuli. For such an experiment, the mixed effects model with crossed random effects is usually the appropriate tool to analyse the data because it considers the sampling of both participants and stimuli. However, these models let to users several choices when analysing data and this practice may be disruptive for researchers trained to a set of standardized analysis such as ANOVA. In the present article, we are focusing on the choice of the correlation structure of the data, because it is both subtle and influential on the results of the analysis. We provide an overview of several correlation structures used in the literature and we propose a new one that is the natural extension of the repeated measures ANOVA. A large simulation study shows that correlation structures that are either too simple or too complex fail to deliver credible results, even for designs with only three variables. We also show how the design of the experiment influences the correlation structure of the data. Moreover, we provide R code to estimate all the correlation structures presented in this article, as well as functions implemented in an R package to compute our new proposal.

1 Introduction

The statistical practice in psychology is dominated by the ANOVA. It has been a standardize tool to analyse various experiments or randomized control trails. ANOVA and particularly repeated measures ANOVA (rANOVA) are useful to consider the variability induced by the sampling of participants in the experiment. The complexity of the experiment tends to increase and there is a need for more complex statistical tools. The experiments often are designed by crossing a sample of participants and a sample of stimuli (e.g. images or words). To take into account the induced variability of both the sampling of participants and stimuli, the methodologists suggest using crossed random effects mixed effects models (CRE-MEM). These models are part of the family of mixed effects models (MEM) and sometimes called crossed random effects models. They have been introduced by Baayen (2008), Lachaud and Renaud (2011) or Judd et al. (2012) to psychologists, discussed by Barr et al. (2013) and Bates et al. (2015a), and efficiently implemented by Bates et al. (2015b) in the R programming language.

The CRE-MEM are used to test factors or fixed effects in experiments but need a correlation structure of the response variable as a set of parameters specified by users. The correlation structure is a set of assumptions on the distribution of the response variable, more specifically its covariance matrix. It models the full consequences that the variability induced by the sampling of participants and stimuli have on the response variables. For instance, if the responses of the same participant are correlated seems reasonable, or if the responses to the same stimuli are correlated seems also reasonable. This correlation structure is complexified by assuming that the responses of the same subject in the same condition are even more correlated, etc. In the literature, CRE-MEM are used assuming very simple correlation structures to very complex ones. In this paper, we discuss the effect of the choice of correlation structure on the tests of fixed effects. We will see that this discussion was already relevant in the rANOVA framework and that some of its conclusion should be transposed to CRE-MEM.

In Section 2, we explain the main differences and similarities between the CRE-MEM and rANOVA. We discuss the default choices that are made the rANOVA framework and open choices in CRE-MEM, and we focus on the correlation structure of the data. In Section 3, we present the statistical models of rANOVA and CRE-MEM with published examples. In Section 4, we discuss how the design of the experiment influences the correlation structure and propose a classification of variables that is general for any experiment using both participants and stimuli. In Section 5, we present the main correlation structures used in the literature,
discuss their properties and propose a new one that is the natural candidate to generalize the rANOVA. In Section 6, we present a simulation study that shows consequences of the choice of the correlation structure on the type I error of test of fixed effects. This simulation study allows us to advise again some correlation structures that may the inflate type I error. In Appendix, readers will find ready to use R codes for all correlation structures presented in this article as well as many extensions designed to understand CRE-MEM and their correlation structures.

2 "All models are wrong, ...", but why?

When analysing an experiment, we are mostly interested in testing a few hypotheses. However, this cannot be achieved without (explicitly or implicitly) building a statistical model, choosing a test statistic and computing its associated $p$ value or other decision rule. All those steps require to choose settings among several options. For classical analyses, those options are often hidden to users (e.g. the model underlying rANOVA cannot be changed in many software although several models are conceivable) and even the distinction between model and test is fuzzy. For instance, the ANOVA refers both to tests statistics (test of the differences of means with a $F$ statistics), or to a model (linear model with factors and all their interactions) (Gelman, 2005). We can hypothesis that this framework was created both intentionally by methodologists, by tradition and by the use of default settings in software. By contrast, for CRE-MEM, no consensus exists for the choice of the statistic of the tests of fixed effects, neither for the choice of the model (and its correlation structure) and software usually let users tune each setting. Coming from the rANOVA framework, users must make choices that they are not used to, and, each of them will have consequences on the results of the data analysis (in particular on the $p$-value). The most influential choice is the statistical model which is a set of assumptions on the mathematical relationship between the response variable and the design and the measurements of an experiment. It is mathematically summarized by probability distributions with unknown parameters. Hence, to perform a good data analysis, researchers must choose a reasonably good model. But there is no unique answer to what a good data analysis is, hence, no unique choice for the statistical model.

Many interesting thoughts have already been written about the relationship between the statistical model and the real phenomena we are interesting in. And as Box and Draper (1987) warn, “Essentially, all models are wrong, but some are useful”. Indeed, even for the simplest experiment that compares two groups, nobody can guarantee that the data are Gaussian, with the same variance for the two groups, independent (and randomly sampled from the population), which are necessary assumptions of the $t$ test or one-way ANOVA. If these assumptions are not met, one cannot know how misleading the $p$-value obtained by a $t$-test will be. There is no “right model” for this simplest experiment, and therefore no sure answer to the research question. For complex experiments with many variables, participants and stimuli, there is no “right model” either. However, some models will be more useful in the sense that they will deliver an answer to the research hypotheses that is more valuable. And we can measure the value of a model depending on the goal of the data analysis: it can be the prediction power, or the replicability of the findings or finding a model close to the real phenomena. So, the model and consequently the correlation structure in case of a CRE-MEM should be assumed in order to best fulfil the goal of the data analysis.

In this article, we concentrate on frequentist approach and evaluate the effect of the model on the $p$-value. However, all the argument developed here are also relevant in a Bayesian framework, as the choice of the model influences the results equally.

In the following sections, we recall the choices user faces when analysing data with a CRE-MEM, and establish parallels with more usual models like regression and ANOVA.

2.1 The predictors in a linear model

Regression, 2 samples $t$ test and factorial ANOVA (without repeated measures) are subsets of the same model: the linear model which is sometimes called general lineal model. The main feature of linear models is to assume a linear relationship between one or several predictor(s) (continuous variables, factors or interactions)
and the mean of the response variable (also called dependent variable or outcome). Those 3 methods are mainly different in the choice of the predictors in model. The 2 samples t test refers to a linear model with one factor with only two levels, the choice of the predictor in this model is entirely defined by the hypothesis. A factorial ANOVA refers to a linear model with several factors (with possibly more than 2 levels) and all their interactions. In that case, users have more options, as they may include more predictors than constraints by their research hypothesis. More importantly, the ANOVA tradition imposes to select all interactions although this might not be necessary. In contrast, for regression, we do not assume a model with constraints on the choice of the predictors, and usually users have to choose themselves the appropriate predictors and do not add interactions except if it represents a hypothesis.

It is noteworthy that the regression and ANOVA traditions are so different although they are based on the same (general) model. However, none of these approaches guarantees that the “right model” is used as, once again, all models are wrong.

In CRE-MEM, software let users choose which predictors and which interactions to include in the model, as in the regression tradition. However, to analyse data from experiments, the ANOVA tradition is still influential, and researchers tend to include all interactions of the selected factors.

Although very important as these choices will have an impact on the inference (p-value) of one’s hypothesis (e.g. the main effect of a precise predictor) in regression, ANOVA and in CRE-MEM, they will not be discussed further as we will concentrate on the correlation structure.

2.2 The error terms and the correlation structure

Concerning classical models, ANOVA (without repeated measures), regression and 2 samples t-test assume an error term which is (1) normally distributed, (2) independent, and (3) homoscedastic. When one or several of those assumptions is/are not true, users should perform other statistical analysis. The first strategy is to use other tests statistics and perform, for instance, quantile regression for skewed residuals (Koenker and Bassett, 1978), robust regression for heavy tails distribution of the errors (Heritier et al. 2009), Wilcoxon test (Wilcoxon, 1945) or Kruskal-Wallis test (Kruskal and Wallis, 1952) when the errors are not normally distributed. Moreover when the errors are heteroscedastic, we can also change the statistics and use Welch’s statistics (Welch, 1951, 1947) or Satterthwaite’s approximation (Brown and Forsythe, 1974). A second strategy is to use resampling methods like bootstrap (Efron and Tibshirani, 1994) or permutation tests which allow to compute distribution of statistics when the errors do not satisfy the default assumptions.

When some responses are linked, correlated with others, it implies that the errors may not be independent and homoscedastic, and it violates the assumption of the linear model. In that case, we must use a more complex model as we need to include the correlation structure of the data in its assumptions. This question arises as soon as several measures are made on the same sampling unit (e.g. a participant). This is the case when performing a one-way rANOVA. Its underlying model may be represented as a mixed-effects model (MEM) and it decomposes the error term into an error term per observation and a random effect (unique for each participant). We call the latter a random intercept and it considers that some participants are better/worst (have higher/lower response values) on average over all experimental conditions than others. For the MEM underlying a rANOVA, we must make assumptions on the distribution of both the error term (independent and homoscedastic), and the random effects (here also independent and homoscedastic) to fully define the model with its correlation structure.

In less complex models with only one measure per participant (like a 2 samples t tests or an ANOVA), the assumption of random intercepts per participant may be relevant in the sense that, in the true phenomena we are observing, some participants are likely to be better than others. But, with only one measure per participant, this random effect (its variability) will not be estimable because it will be included/confounded with the error term. Hence, a less complex design allows less random effects to be estimable. The corollary is that a more complex design allows more random effects to be estimable. And, with a complex experimental design, we may be able to estimate not only random intercepts per participant but also random slopes. By analogy to the regression, the literature defines a random slope as a random effect that describes the variation of a subject given the value of a covariate or a factor and represents the change of slope of this subject with
respect to one of the population; and we can generalize this concept to random interactions which represents the change of interaction effect with respect to the population for each subject.

In a complex MEM, the choice of the correlation structure not only includes which random effects we assume in the model (random intercepts, slopes and interactions) but also their full (joint) distribution. If each participant has more than one random effect, all those random effects create together a multivariate random effect and we have to make assumptions on its full multivariate distribution. For instance, we can assume correlation between random effects or constraints like the equality of variance of several random effects. This correlation is for example relevant in learning processes, where it seems natural to assume that someone with a lower score at the beginning will learn more than someone with a higher starting score. This feature can be implemented in the model by assuming that the random intercept (for a participant, his score’s difference with respect to the average) is correlated with the random slope (for a participant, the learning’s difference with respect to the average learning); in this example, we therefore expect a negative correlation between the random intercept and the random slope. As a second example, the equality of some variances is used to implement spherical random effects and it is mainly used for factors. We could specify a different variability for each level of a factor, but this assumption is often neither useful nor rooted with strong information on the correlation structure. As a result, it is reasonable to assume spherical random effects which means that, in each level, random effects will have the same variability. Here, the sphericity assumption reduces the number of free parameters and increases the parsimony of the model.

rANOVA is said to control the type I error rate at its nominal level. However, this good property is mathematically derived assuming a specific model with its specific correlation structure. Specifically, the correlation structure underlying the rANOVA is assumed to be saturated which means that the random intercepts, random slopes and random interactions are all included (up to the last interaction which is confounded with the error term). Moreover, all effects are independent and spherical within each factor or interaction. The model underlying the rANOVA is a special case of MEM and researchers could use the MEM framework to analyse this type of data. It is however appropriate only if its assumptions are tenable.

When the response variable is the result of the crossing between the samples of 2 units (typically participants and stimuli/pictures), we model the response using a CRE-MEM. The correlation structure becomes much more complex because random effects can be associated with the participants and the stimuli but also with their interactions. To define the correlation of a CRE-MEM, we need to select which random intercepts, slopes or interactions and which multivariate distributions we assume for the participants and the stimuli. Moreover, if it is relevant to assume that some participants may be better/worst with some stimuli, we specify this feature by including in the correlation structure random effects associated to the interaction between the participants and stimuli. As for any MEM, the estimable random effects are also constraint by the design, and by which fixed variable is included in the model. And, the set of random effects estimable which depends on the design becomes more complex with two sampling units rather than only one. To have the full picture of the estimable effects, we develop a classification of variables in Section 4.

2.3 The test statistics

The model is specified in the Section 2.1 and Section 2.2 and for the sake of completeness, the testing procedure, which includes the test statistic, its distribution and the associated p value, have to be specified. For the regression or ANOVA model, the common solution is to use t or F statistics. If the model is well specified and the assumptions of independence, homoscedasticity and normality of the errors are met, they provide tests that are exact and powerful (low type II error rate). As we saw in Section 2.2 for those simple models, there exists alternative solutions when the model is not well specified.

However, for CRE-MEM, no exact solution exists even if the assumptions of the model are met. Methodologists still debate the advantages of 4 test statistics: the quasi-F statistic (Raaijmakers et al., 1999), the likelihood ratio statistics (and its chi-square asymptotic distribution), the Satterthwaite’s approximation (Schaalje et al., 2002) and the Kenward-Roger approximation (Kenward and Roger, 1997). The quasi-F statistic is limited to balanced design using only factors and simulation studies tend to show that likelihood ratio statistics does not control type I error rate very well. By contrast, the Satterthwaite and the Kenward-Roger approximations
seem to be closer to the nominal level when the model is well specified and its assumptions are met \cite{Luke2017}. Simulations show that the latter seems to perform slightly better but at a higher computation cost. Only the quasi-$F$ statistics imposes condition on the correlation structure. As for rANOVA, the statistic is based on sum of squares and the distribution on the quasi-$F$ statistic approximates a $F$ distribution only by assuming spherical and uncorrelated random effects.

2.4 The design-driven vs data-driven approach

In Section 2.1, 2.2 and 2.3 we described the main choices a researcher have to do when analysing data. Once again, no choice can guarantee that the right model is used, but there are two “families” of strategies that are often implemented to attempt to obtain this useful model. The two approaches are well described by \cite{Barr2013}. Here we recall and enhance their descriptions.

The first approach is called design-driven and is prominent in the ANOVA setting. It is usually performed to analyse data issued from experiments in which all variables are carefully chosen in advanced, and where we expect to find a causal relationship between variables. The creation of the model is instrumental to reporting a test of hypothesis and all the choices of the analysis could be made before even collecting the data. The main worry of the analyst is to control the type I error rate and the replicability of the findings.

The second approach, called data-driven, plays a prominent role in regression, which has many extensions in model selection like the Lasso \cite{Tibshirani1996}. The focus of the analysis is not to test hypotheses, but to find a good model in the specific sense that it provides good prediction capacity and is parsimonious. The chosen model should be the closest to the true underlying model or, at least, should produce similar predictions. In this context, external assumptions are kept minimal and ideally all the choices are merely based on the data. The main worry of the analyst is over-fitting.

This typology is clearly a caricature and real data analyses always lie somewhere between these two extremes. For experimental designs, the first approach seems more relevant. This is the case for the ANOVA/rANOVA framework which has standardized the data analysis. Regardless of the scientific domain, researchers perform tests of main effects, interactions, contrasts, simple effects or post-hoc analyses using the same construction of fixed effects and, for rANOVA, the same correlation structure. By contrast, no standard solution is as well established to analyse CRE-MEM: if researchers tend to include all fixed effects in the linear predictor, the random structure that should be assumed is still debated. Data-driven \cite{Bates2015} or design-driven \cite{Barr2013} solutions have been proposed, and our solution (referred latter to gANOVA in Section 5.5) is a parsimonious design-driven approach which generalizes the correlation structure of rANOVA to several random units.

3 rANOVA and CRE-MEM

In order to understand the (sometimes hidden) correlation structure of the models behind usual analyses, we first investigate the model of rANOVA, highlight some of its properties and show how this model can be extended to CRE-MEM. To illustrate with a research example, \cite{Erickson2011} use a rANOVA to analyse their experiment. They are interested in the effect of exercise on the volume of the brain of elderly participants. They split the sample into an aerobic training group (AT) and a stretching control group (SC) and measured their brain volume using magnetic resonance images at the baseline (BL), after 6 months (6M) and after one year (1Y) of training. This experiment is analysed using a generic rANOVA with one between-participant variable (the group with two levels: AT and SC), and one within-participant variable (the time with 3 levels: BL, 6M and 1Y). We note that the between-participant variable is a feature of the participants because the participants are not allowed a change of levels during the experiment. And the within-participant variable indicates a feature of the experimental manipulation: the time of data collection, which is defined by the experimenter. As for many models, each response, is decomposed into fixed effects and random effects. Following the notation of e.g. \cite{Howell2012}, we write the underlying model using the equation:
The model represented by the Equation 1, should only be used when we assume only one sampling unit, the
$k^{th}$ occasion of measure. The fixed part of the equation is decomposed into the between-participants effects
and within-participants effects. The between-participant effects are $\alpha_j$ for $j \in \{1, \ldots, n_j\}$, which corresponds
to the main effect of the groups. The within effects are $\psi_k$ for $k \in \{1, \ldots, n_k\}$, which correspond to the effect
of the time and all interactions that contain it. Here $(\alpha\psi)_{jk}$ is the effect of the interaction group:time in
our example. The random part is composed of random intercepts $\pi_i$ for $i \in \{1, \ldots, n_i\}$ which correspond
to the participant’s average brain volume relative to the overall mean brain volume, and random slopes,
$(\pi\psi)_{ik}$, which is interpreted as the difference of the time’s effect of each participant to the population time’s
effect on brain volume. Finally, the error term $\epsilon_{ijk} \sim \mathcal{N}(0, \sigma^2)$ capture everything that cannot be captured
by the previous terms. The correlation structure used in the rANOVA model is implied by the assumed
distribution of the $\pi_i$’s and $(\pi\psi)_{ik}$’s. To have an exact test for the fixed effect in rANOVA, we must assume
that the random effects $\psi_k$, $(\pi\psi)_{ik}$, follows each a normal homoscedastic distribution. Therefore, the assumed
correlation structure needs 2 variance parameters in addition to the error term.² Except for this last random
effect, each term in Equation 1 is associated to a sum of squares as produced by many statistical software.
This model is today’s standard in statistical software and in published researches, but it is the results a
debate dating from the 70’s. We provide in Appendix[A] a small summary of the discussion and arguments
that lead to what we now today as a rANOVA.

The model represented by the Equation 1 should only be used when we assume only one sampling unit, the
participants. In many studies, in addition to the sampling of participants, researchers sample stimuli, and
the value of the responses will depend on the crossing of a sample of participants and a sample of stimuli. In
that setting, we also must consider the variability induced by this second sampling, which means have to use
a CRE-MEM. To illustrate with a research example, Wilson et al. [2017] perform several experiments that
highlight racial biases in judgement of physical size and weight and analyse them with a CRE-MEM. They
showed to a sample of male participants a sample of stimuli (images of Black men) and asked the participants
to evaluate the size of the people shown in the stimuli. As each participant viewed each stimulus, we say
that the estimation of size was made by crossing participants and stimuli. [Wilson et al. (2017)] recorded also
features of the participants, their race: Black (B) or White (W), and features of the stimuli, the actual size of
the people in the images. Note that each stimulus is evaluated in each level of the factor race, which means
they are evaluated by Black and by White participants. And each participant sees stimuli of different actual
sizes. It may have been interesting to also change the presentation of the stimuli, where stimuli are shown
in a neutral environment (N) or with a context (C) where the size is easier to evaluate.² We will assume
that each participant sees each stimuli two times: in the neutral environment and with a context. This third
factor is then a feature of the experimental manipulation each pair participant-stimuli are recorded in both
contexts. To analyse this experiment, we use a CRE-MEM which equation is written:

\[
y_{imk} = \mu + \alpha_j + \psi_k + (\alpha\psi)_{jk} + (\alpha\psi)_{jk} + (\psi\phi)_{kl} + (\alpha\psi\phi)_{jkl} \\
+ \pi_i + (\pi\psi)_{ik} + (\pi\phi)_{il} + (\pi\psi\phi)_{ijkl} \\
+ \omega_{im} + (\omega\psi)_{mik} + (\omega\alpha)_{mjk} + (\omega\psi\alpha)_{mkj} \\
+ (\pi\omega)_{im} + (\pi\omega\psi)_{imk} + \epsilon_{imk},
\]

with the response $y_{imk}$ (here the estimated size) and with a fixed part written in the first line of Equation 2
composed of $\alpha_j$ (features of participants: here the race), $\psi_k$ (features of stimuli: here the actual size), $\phi_l$

1 Actually, rANOVA models are always overparametrized as the highest interaction, here $(\pi\psi)_{ik}$, and the errors $\epsilon_{ik}$ are
confounded. This has no harmful consequence as we do not estimate each parameter

2 We add this third factor (presentation of stimuli) which was not in the original study not as a criticism but to highlight the
effect of the design on the correlation structure of a CRE-MEM.
Table 1: Link between random units and the type of variables. A cross means that a random interaction (i.e. an interaction between the random effect define by the row and the fixed effect defined by the column) is estimable or allowed in a CRE-MEM with a fully balanced design.

|                | intercept | $V_P$ | $V_S$ | $V_{PS}$ | $V_M$ | $V_O$ |
|----------------|-----------|-------|-------|----------|-------|-------|
| Participants   |           | X     |       | X        | X     | X     |
| Stimuli        |           |       | X     | X        | X     | X     |
| Participants:Stimuli |       | X     |       | X        | X     |       |

(features of experimental manipulation: here the presentation of stimuli), and their interactions, $(\alpha\psi)_{jk}$, $(\alpha\psi)_{jk}$, $(\psi\phi)_{kl}$ and $(\alpha\psi\phi)_{jkl}$. The decomposition of the random part has then effects associated to the participants and their interactions with some factors (second line of Equation 2), $\pi_i$, $(\pi\psi)_{ik}$, $(\pi\phi)_{il}$ and $(\pi\psi\phi)_{ikl}$; effects associated to the stimuli and their interactions with some factors (third line), $\omega_m$, $(\omega\psi)_{mk}$, $(\omega\alpha)_{mj}$ and $(\omega\psi\alpha)_{mkj}$; and effects associated to the participants-stimuli interactions and to the error term (fourth line), $(\pi\omega)_{im}$ and $(\pi\omega\psi)_{imj}$. Note that the interaction between sampling units and a fixed effect is only feasible if the sampling units are evaluated in several levels of the fixed effect. The correlation structure of this CRE-MEM is implied by the multivariate distribution of the random effects (defined in the three last lines of Equation 2). The correlation structure is de facto more complex than the one for rANOVA and the different choices and assumptions are discussed in Section 5.

Note that the effects on the fourth line are seldom if ever presented or used in the context of CRE-MEM and correspond to the random effect associated to the interaction participant-stimuli and model the assumption that some participant will have a better response with some particular stimuli (or vice versa). With CRE-MEM, the dichotomy of “between-participant” variables and “within-participant” variables used in rANOVA is insufficient and, in Section 4, we present a classification of 5 types of variables for the CRE-MEM.

4 Classification of variables for the CRE-MEM

In the ANOVA framework, explanatory variables are split into “within-participant” variables and “between-participant” variables. Often between-participant variables (that we will call $V_P$) represent a feature of the participants, like their sex, and the participants can be or is measured in only one level of the between-participant variables. The within-participant variables often represent the feature of the experimental manipulations ($V_M$) which means that the participants can be measured in multiple levels of a within-participant variables. This classification is feasible since there is only one sampling unit, the participants. Based on this dichotomy, we know that only within-participant variables may interact with the sampling unit to create random effects.

As viewed in previous Section, many experiments in psychology are more complex as they cross of a random sample of participants and a random sample of stimuli (and therefore must be analysed with CRE-MEM). In that setting, 3 random units are actually present: the participants, the stimuli, and their interactions. In order to know which models are at least feasible (or more precisely, which random effects can be included in the model), we have to know which explanatory variables may interact with which random units. The aim of this section is to provide a classification of variables that replies to this question and to illustrate it with a few examples.

In summary, for CRE-MEM, as in rANOVA, some variables are either $V_P$ or $V_M$ as they specify a feature of the participants or of the manipulation. By symmetry with $V_P$, there might be variables that specify a feature of the stimuli, called $V_S$, and variables that specify a feature of the interaction of participants and stimuli, that will be called $V_{PS}$. Finally, some variables designate a feature of the specific occurrence, or observation, and will be called $V_O$. In more detail, here is the list of potential types of variables:

1. $V_P$: variables that specify a feature of the participants. The typical example is the sex of the participants. It can also happen that for experimental reasons, participants are (randomly) assigned to a single experimental condition, like a learning method in education or given a specific instruction.
in social psychology. Experimentally, this condition becomes a feature of the participant and thus the corresponding variable is also classified as $V_P$. In Equation 2, the effects $\alpha_j$ come from a $V_P$ variable and is the race in the experiment of Wilson et al. (2017). This type of variables reduces to a between-participant variable in the rANOVA setting.

2. $V_S$: variables that specify a feature of stimuli, in the same way as $V_P$ specify features of participants. The typical example is the valence of an image or the characteristic (frequency, type, ...) of a word. In Equation 2, the effects $\phi_l$ come from a $V_S$ variable and correspond to the actual size of stimuli.

3. $V_M$: variables that specify a feature of the experimental manipulation. The experimenter has usually the ability to manipulate it independently of the participants and of the stimuli, showing several different conditions to the same pair participants-stimuli. Examples are the hemifield of presentation of a target, the lightning or surrounding sound conditions. In Equation 2, the effects $\psi_k$ come from a $V_M$ variable and correspond to the presentation of the stimuli. This type of variable reduces to the within-participant variables in the rANOVA.

4. $V_{PS}$: variables that specify a feature of the interaction between a participant and a stimulus, and therefore that cannot vary for a given pair participant-stimulus. Often, this type of variables is the results of constraints on the experimental design: if the same participant cannot see the same stimulus in several conditions, this factor is then specific for each pair of participant and stimulus and become a variable $V_{PS}$. For example, if only the high-frequency or only the low-frequency of an image is shown, for a given image, half of the participants will see its high-frequency version and the other half its low-frequency version, and conversely for another image. As an additional example in linguistics, in a novel word experiment design half the participants learn half the words with spelling and the other half with only the spoken input, and the association between one word and a level is balanced across participants. In the experiment of Wilson et al. (2017), if the participants were asked, afterward, to evaluate a characteristic of the stimuli, like the level of masculinity, and use this measure as a predictor, this variable would be of type $V_{PS}$.

5. $V_O$: variables that specify a feature of the specific occurrence or observation. It may be a physiological or physical measure taken at the precise time of the measures of the response (for a given participant subject to a given stimulus). The position of the trial in the experiment, or the RT to the previous stimulus fall also in this category.

As a rule, for any factors or variables, if the random unit is measured in several of its levels, then a random interaction between this variable and the random unit is estimable, i.e. it can be included in the CRE-MEM. This random interaction is interpreted as a random slope. As a result, the random slope of a $V_P$ variable is only estimable for the stimuli, the random slope of a $V_M$ variable is estimable for the participants, the stimuli and their interaction, etc. Table 1 gives a summary of the estimable random slopes for the 5 types of variables. In this section, we discussed the cases where the variables are factors. When dealing with one or more continuous variables, the classification of variables and its consequences on the correlation structure of the data are the same. However, especially in the presence of interaction, a special care is needed in the interpretation of the results (e.g. depending if the variables are centred or not). Moreover, we believe that this classification and the approach described above can be extended for cases with more than 2 random units.

Finally, note that in rANOVA, the “wide” format of the data makes a clear distinction between the representation of the within-participant and between-participant variables. In Appendix B, we extend this representation for the 5 types of variables of the CRE-MEM.

5 Several families of correlation structures

In this section, we describe the correlation structures that are discussed in the literature and propose a new one in Section 5.5. Several goals are pursued. First, to list the major models and to give them a name, second to link them with R code of the lme4 package (Bates et al., 2015b), third to explain their assumptions and
Table 2: List of 5 typical experimental designs involving participants and stimuli that will be exemplified in this article (column Use: 'Formu' meaning that its R formulas are given in the Appendix E for all correlation structures, and "Simul" means that it is used in the simulation study of Section 6). The five different types of variables ($V_P$, $V_S$, $V_M$, $V_{PS}$, and $V_O$) are defined in Section 4 and the number of levels are given within parentheses.

| Model | Variables                      | Use      |
|-------|-------------------------------|----------|
| M1    | $V_P$(2), $V_S$(2), $V_M$(2)  | Formu/Simul |
| M2    | $V_P$(3), $V_S$(3), $V_M$(3)  | Simul    |
| M3    | $V_P$(3), $V_S$(3), $V_M$(3), $V_M$(2) | Formu    |
| M4    | $V_P$(3), $V_S$(3), $V_M$(3), $V_{PS}$(2) | Simul    |
| M5    | $V_P$(3), $V_S$(3), $V_M$(3), $V_M$(2), $V_{PS}$(2), $V_O$(2) | Formu    |

Table 3: Number of parameters for the correlation structure for the five models described in Table 2 and for all the random structures defined in Section 5. A plus sign describe a random structure that includes the interaction participants:stimuli.

|                      | M1 | M2  | M3  | M4  | M5  |
|----------------------|----|-----|-----|-----|-----|
| **without interaction participants:stimuli** |    |     |     |     |     |
| RI                   | 2  | 2   | 2   | 2   | 2   |
| RI-L                 | 8  | 8   | 16  | 16  | 64  |
| MAX                  | 20 | 90  | 342 | 342 | 5256|
| ZCP                  | 8  | 18  | 36  | 36  | 144 |
| gANOVA               | 8  | 8   | 16  | 16  | 64  |
| **with interaction participants:stimuli**    |    |     |     |     |     |
| RI+                  | 3  | 3   | 3   | 3   | 3   |
| RI-L+                | 9  | 9   | 19  | 17  | 71  |
| MAX+                 | 21 | 91  | 352 | 343 | 5311|
| ZCP+                 | 9  | 19  | 40  | 37  | 154 |
| gANOVA+              | 9  | 9   | 19  | 17  | 71  |

fourth to compare them theoretically. In Section 6, we will compare them based on simulations so that some guidelines can be learned.

Note first that all correlation structures discussed in the literature assume independence between the random effects associated with (a) participants, (b) stimuli and (c) their interactions. For the model of Equation (2), it implies that for all following proposals, the random effects on the second line are independent with the random effects on the third line and the fourth line. This is a minor assumption if the interaction between participants and stimuli is included but might be questionable if not.

Second, each of the proposal may include effects coming from the interaction participants:stimuli even if the authors who originally described these correlation structures did not include them. Those interactions terms model if some participants are especially good/bad with a particular stimulus. Below, a “+” sign in the name of a correlation structure indicates its inclusion.

In CRE-MEM, the optimization process is defined for parameters which are function of the elements of the correlation structure \cite{Bates2015}. So, having more free parameters in the correlation structure imply a more difficult optimization process and more convergence errors of the algorithm. And, as for any statistical model, including additional parameters makes the model “less wrong” (in the sense of the goodness of fit) at the price of reducing its parsimony. In practice, for CRE-MEM, the usual trade-off between parsimony and goodness of fit is disturbed by the convergence error of the algorithm. For the five models presented in Table 2, we show in Table 3 the number of parameters for each correlation structure presented next. It clarifies the huge difference between the proposed correlation structures.
Moreover, the replicability of the findings has become a major worry in many fields. The choices carried out when using CRE-MEM should reflect this tendency. For that purpose, the correlation structure should have good properties: specially to have the expected results of the analysis reproducible through experiments, be robust to some misspecification of the model and have a high rate of convergence. If the model is used for testing in a frequentist approach, a good choice will exhibit a type I error rate close to the nominal level under the null hypothesis and, at the same time, a high power under the alternative.

5.1 The correlation structure with random intercepts (RI)

In this simplest case, the correlation structure has only a random intercept for the participants and a random intercept for stimuli. These intercepts are not correlated, which means that only 1 variance parameter per random unit is estimated regardless of the number of fixed effects, hence the value of 2 in the first line and 3 in the sixth line of Table 3. All the interaction terms in the second, third and fourth lines of Equation (2) are removed, or equivalently, their variances are set to zero.

For two factors f1 and f2 and the participant and stimulus identifier PT and ST, the typical formula of RI using the lme4 package is:

\[
\text{lmer}(y \sim f1*f2 + (1|PT) + (1|SM), \text{ data = mydata})
\]

and for th RI+ structure:

\[
\text{lmer}(y \sim f1*f2 + (1|PT) + (1|SM) + (1|PT:SM), \text{ data = mydata})
\]

Full examples are provided in Appendix E. For space reason and in order to focus on the part of interest, in the main text we will summarize the formulas. For the RI and the RI+, it becomes:

\[
\text{lmer}(y \sim [...]) + (1|PT) [...]
\]

In lay language, this correlation structure just suppose that some participants are better than others on each measurement, and that some stimuli are more difficult than others for all participants alike. Although this correlation structure is used in the literature, in most cases, the true correlation structure will most probably be more complex that only random intercepts and more random effects are estimable. Choosing this correlation structure will reduce the reproducibility of the results with a gain in parsimony we do not really need. RI is probably too simple for most applications and does not provide credible inference (Barr et al., 2013).

5.2 The correlation structure with random intercepts at each level (RI-L)

One way to view the rANOVA model (as in Equation (1)) is to think that it incorporates all interactions between the random effect of the participant (\(\pi_i\)) and the within-participant fixed effects (only \(\mu\) and \(\alpha_j\) here), to produce all possible random effects (here \(\pi_i\) and \(\pi\psi_{ik}\)). Bates et al. (2015b) suggest following the same idea for CRE-MEM, starting with the random effect of both participants (\(\pi_i\)) and stimuli (\(\omega_m\)). This random structure corresponds to random intercepts and slopes that are IID and spherical (\(\pi_i \sim N(0, \sigma^2_{\pi})\), \(\pi\psi_{ik} \sim N(0, \sigma^2_{\pi\psi})\), \(\alpha_j \sim N(0, \sigma^2_{\alpha})\) and so on), and independence between them, for all the elements in the 2nd, 3rd and 4th lines of Equation (2). The typical formula of RI-L using the lme4 package is:

\[
\text{lmer}(y \sim [...]) + (1 | PT) + (1 | PT:f1) + (1 | PT:f2) + (1 | PT:f1:f2) [...]
\]

The RI-L correlation structure keeps a relatively low number of parameters which does not increase with respect to the number of levels of the factors (see Table 3).

This may seem the natural extension of rANOVA, however with the same number of parameters, gANOVA includes all the correlation structures that can be obtained with RI-L and strictly more. Therefore, the likelihood (and criteria like AIC and BIC) will always be better or equal when using gANOVA instead of RI-L. More details on the difference between the two correlation structures are given in Section 5.5. The numerical optimisation is also easier for gANOVA compared to RI-L, as exemplified in Appendix D.
5.3 The "maximal" correlation structure (MAX)

The “maximal” correlation structure is suggested by Barr et al. (2013) and it is defined by including all possible random effects associated with the participants on one side and all possible random effects associated with the stimuli on the other side. Moreover, Barr et al. (2013) let also a maximal correlation structure between random effects, which means that all random effects can correlate with each other (within the same random unit), or said differently, the covariance matrix of the random effects is full and unstructured. The typical formula of MAX using the lme4 package is:

\[
\text{lmer}(y - [...]) + (f1*f2 | PT) [\ldots] 
\]

This correlation structure may seem the appropriate choice without prior information on the correlation structure, but the problem is that it is not parsimonious enough except for the smallest models, see Table 3. Note that the authors did not specified explicitly how to handle factors with more than two levels. Moreover, the actual optimization algorithms often do not converge even for small models (see Table 4). It might therefore be used when the design has only one IV but is probably not suited for experiments with two variables or more.

5.4 The zero-correlation parameter correlation structure (ZCP)

The ZCP (Bates et al., 2015a) also includes all the random effects associated with stimuli and with participants. Unlike the MAX model, the ZCP model does not include correlations between the random effects. This means that one variance parameter is estimated for each effect, but no correlation is assumed. When one or more factors have 3 or more levels, there is a twist and the number of variance parameters that are estimated for each random part will be equal to the number of degree-of-freedom of the corresponding fixed factor (or interaction of factors). Said differently, variance parameters are attached to contrasts of the factor or interaction of factors and not to the factors themselves.

For two factors \( f1 \) and \( f2 \) and the participant identifier \( PT \), one first transforms the factors \( f1 \) (e.g. with 4 levels) and \( f2 \) (e.g. with 3 levels) into coding variables \( x1a, x1b \) and \( x1c \), respectively \( x2a \) and \( x2b \) (more information about the necessity of transformation into coding variables is in the Appendix E). Then the typical formula using the lme4 package is, for ZCP:

\[
\text{lmer}(y - [...]) + ((x1a + x1b + x1c)*(x2a + x2b) | | PT) [\ldots] 
\]

This correlation structure is relatively parsimonious when all factors have exactly two levels, but the number of parameters will increase with respect to the number of levels of the factors (see Table 3). It has the drawback to be dependent on the choice of the coding of the factors. This correlation structure can be viewed as a workaround to force lme4 not to add correlations between random effects, but that this workaround does not give the expected results with factors that have 3 or more levels. Although, we do not expect a huge difference in practice, the maximum likelihood and the inference will depend on the choice of the coding variables (or contrasts), even when they are forced to be orthonormal. In many applications, the choice of the coding variable does not correspond to any hypothesis and is therefore arbitrary. Moreover, this may be an obstacle for the repeatability of the data analysis because it will be challenging to report the all coding variables of the factors and their interactions.

5.5 The random structure of the generalized ANOVA (gANOVA)

In order to generalize rANOVA to CRE-MEM, gANOVA first assumes a saturated model with all random effects, the one associated to participants, with stimuli and with their interaction. As in the experimental design literature, the covariance structure of random effects is assumed to be minimal, i.e. each random effect is independent from the others, and spherical. A correlation structure with spherical random effects will have random effects that share the same variance for each level of the same factor; which means that the number of parameters will not increase with respect to the number of levels (see the lines gANOVA in Table 3 for models M1 vs M2). The model behind gANOVA is the same as RI-L suggested in Bates et al. (2015b),
1973). These assumptions are identical to the one made in rANOVA (independence and homoscedasticity of 
the variance-covariance of the response and the same deviance. The fit is exactly the same. However,
the random effects put restrictions on the variance of the random effects of lower interaction. Perhaps surprisingly,
gANOVA in Table 3). The difference with RI-L is that some constraints are assumed on the random effects.
In Equation 2, those constraints are written: \( \sum_i (\pi\psi\phi)_{ikl} = 0 \; \forall \; i,k \) and \( \sum_l (\pi\psi\phi)_{ikl} = 0 \; \forall \; i, l \). For the algorithm, those constraints are simply implemented by transforming the
factors into orthonormal coding variables and forcing them to share the same variance parameter (within each factor).

It is not possible to use lme4 to estimate the gANOVA model, as it needs to satisfy both the constraints of
equality of variances for each level and to use coding variables for the random interactions. However, a simple modification of the lmer function implemented in the gANOVA package (https://github.com/jaromilfrossard/gANOVA) allows to perform this optimization. For two factors \( f_1 \) and \( f_2 \) and the participant identifier \( PT \), the gANOVA is perform using the gANOVA package and the formula:

\[
gANOVA(y \sim \ldots + (1 | PT | f1*f2) \ldots )
\]

The justification for this correlation structure is that it is much more in line with the tradition of experimental
design. Indeed, it is exactly as defined by Cornfield and Tukey (1956) for ANOVA including one or several random
effects (see Appendix A). Moreover, one of the first tools to obtain \( p \)-values for balanced experiments
where there is crossing of random samples of participants and stimuli was the quasi-\( F \) statistic (Winer, 1962).
This statistic is based on sums of squares which are easy to compute after averaging over the participants and over the stimuli. The quasi-\( F \) statistic follows an approximative \( F \) distribution under some assumptions (Clark, 1973). These assumptions are identical to the one made in rANOVA (independence and homoscedasticity of the random effects). For balanced data, the model and the implied correlation structure are the same for
quasi-\( F \) and CRE-MEM based on gANOVA (but the statistic, \( t \)-value and \( p \)-value are computed differently) and we expect to obtain quite similar results (very close \( p \)-values). However, gANOVA generalizes naturally to non-balanced designs since it is a mixed effect model.

Secondly, as mentioned in Section 5.2, the possible correlations between all responses assumed by RI-L are only a (strict) subset of the ones with gANOVA. For some data, both methods lead to the same variance-covariance matrix of the response, but its decomposition into variances of random effects are different. Which is similar
to say that, in the Equation 2 all the variances and covariances of the responses \( y_{imk} \) are the same for
ANOVA and RI-L, but its decomposition into variances of random effects \( \pi_i, \ldots, (\pi\omega\psi)_{lmk} \) is different, due
to the sum-to-zero constraints in gANOVA. In lay terms, without these constraints, higher order interaction random effects put restrictions on the variance of the random effects of lower interaction. Perhaps surprisingly,
this imply that the possible variances and covariances of the responses are reduced in RI-L (compared to
gANOVA), and for some data the variance-covariance matrix of the response will be different between the two
methods. It often implies a solution at the boundary of the domain of definition (one or several variances set to zero) in RI-L during the optimization. In those cases, RI-L and gANOVA do not share the same solution and gANOVA has always a smaller deviance (and AIC, BIC, ...) which suggests a better fit.

The equations below show the relationship between the variance parameters of both parametrization for a
model with one variable:

\[
\sigma_{RIL;i}^2 = \sigma_{gANOVA;i}^2 - a\sigma_{gANOVA:F}^2 \\
\sigma_{RIL:F}^2 = \sigma_{gANOVA:F}^2 \\
\sigma_{RIL;e}^2 = \sigma_{gANOVA;e}^2
\]

where \( \sigma_{RIL;i} \) and \( \sigma_{gANOVA;i} \) are the standard deviation of the random intercepts for both parametrizations,
\( \sigma_{RIL:F} \) and \( \sigma_{gANOVA:F} \) are the standard of the random slopes (participant:F), and \( \sigma_{RIL;e} \) is the standard
deviation of the error term. \( a \) is positive constant that depends on the number of levels of the factor F:
\( a = 1 - 1/(\# \text{ levels}) \). See Appendix D for the full derivation of this example.

Several comments can be made. First, one has to be aware that the interpretation is different between the
two covariance structures. Second, if \( \sigma_{gANOVA;i}^2 - a\sigma_{gANOVA:F}^2 \) is positive, RI-L and gANOVA will produce
the same variance-covariance of the response and the same deviance. The fit is exactly the same. However,
there will cases where this term is negative. In that case, RI-L cannot attain the optimum and is forced to set a variance to zero (and to adjust the two other ones), leading to a poorer fit compared to the solution of gANOVA. This leads to the conclusion than gANOVA is strictly better than RI-L.

Concerning now the comparison between gANOVA and ZCP, they are the same model for designs that have factors with exactly two levels. But it is not the case when at least one factor has 3 levels or more. For this type of factors and when they interact with random effects, gANOVA has the assumption of sphericity which imposes the same variance parameters for each coding variables of the factors. On the other hand, ZCP will have a new variance parameter for each new coding variable and adding these new parameters has two drawbacks. First, the number of parameters to estimate increases which implies more variable estimations (see Table 3). Moreover, these new parameters are usually not dictated by theoretical ground but more by the convenience of an existing R formula. Secondly, the random structure, the maximum likelihood and the inference depend on this arbitrary choice of the coding variable, even when they are forced to be orthonormal. There are infinitely many groups of coding variables that may be used for a single dataset and for each of which ZCP will give a different $p$-value. This arbitrariness in a model that is precisely design-driven is not desirable. On the other hand, the sphericity assumption in gANOVA keeps one variance parameter for all coding variables of a given factor (or interaction). This will reduce the number of parameters and the arbitrariness of the coding of factors by being independent to the choice of the coding of the factors.

Finally, the constraints used in gANOVA (almost) orthogonalize the random effects (they would be orthogonal if fixed) such that the parameters have a small mutual influence in comparison with RI-L. Figure 7 shows an example of the likelihood within the space of the parameters. For the same data (one sampling unit, one $V_M$ variable and replications), and fitting random intercepts and random slopes, we see that the two ridges defining the two profile likelihoods cross almost at 90° at the optimum in the gANOVA case but is far more inclined for RI-L. This suggests less dependency between the parameters and a better optimization process for gANOVA. In higher dimension, it is known that all optimization suffers from the curse of dimensionality, and the better independence of gANOVA parameters is clearly an asset.

### 5.6 The correlation structure based on PCA (CS-PCA)

[Bates et al. (2015a)] proposed a heuristic to find the appropriate correlation structure. This correlation structure has a data-driven approach and therefore change even between two experiments sharing the same design. To compare it to the previous methods, we summarize the proposition of [Bates et al. (2015a)] by a fully defined algorithm in Algorithm 1. The idea behind this method is to use PCA on the estimated maximal correlation structure (from the MAX model) to estimate the dimensionality of the random effects; by assuming that the true correlation structure is of lower dimension than the one defined by the MAX model, we restrict to a subspace in which it is hoped that most of the variability of the random effect lives. Then by deleting random effects of the model (suppressing the higher-level interaction first), we match the correlation structure to the estimated dimensionality. Then based on the new maximal dimensionality, [Bates et al. (2015a)] proposed to reduce the number of parameters based on test or goodness of fit; first we decide whether to drop the covariances between random effects and select the random structure based on test, then we decide whether to drop random effects one by one beginning with the higher interaction levels. We stop this procedure when it does not improve the model anymore. The selected random structure is then compared to a last one by adding or subtracting the covariance between random effects.
Algorithm 1 Correlation structure based on PCA

1: Choose a model selection procedure $\mathcal{P}$.
2: Estimate the model based on $\text{MAX}$ $\mathcal{I}_{\text{max}}$.
3: for participants and stimuli do
4: Perform PCA to find the dimensionality $r_{\mathcal{I}_{\text{max}}}$ of the random effects.
5: Drop random effects with higher interaction levels to match $r_{\mathcal{I}_{\text{max}}}$.
6: Define the new random structure $\mathcal{I}^+_{\text{PCA}}$.
7: Drop covariance between random effects and define this random structure $\mathcal{I}^-_{\text{PCA}}$.
8: Choose between $\mathcal{I}^+_{\text{PCA}}$ and $\mathcal{I}^-_{\text{PCA}}$ using $\mathcal{P}$. The chosen random structure is called $\mathcal{I}_{\text{reduced}}$.
9: while $\mathcal{P}$ suggests the smaller correlation structure do
10: $\mathcal{I}^0_{\text{reduced}}$ is defined by dropping from $\mathcal{I}_{\text{reduced}}$ the random effect of the higher interaction levels.
11: Choose between $\mathcal{I}_{\text{reduced}}$ and $\mathcal{I}^0_{\text{reduced}}$ using $\mathcal{P}$.
12: Update $\mathcal{I}_{\text{reduced}}$ by the previous choice.
13: Given the choice made in 8, add or drop covariance to $\mathcal{I}_{\text{reduced}}$ to create $\mathcal{I}^1_{\text{reduced}}$.
14: Choose between $\mathcal{I}_{\text{reduced}}$ and $\mathcal{I}^1_{\text{reduced}}$ using $\mathcal{P}$.

This algorithm will choose a correlation structure that is a subset of the correlation structure defined by $\text{MAX}$. However, it is possible to imagine new algorithms that chooses a correlation structure that is a subset of $\text{ZCP}$, $\text{RI-L}$ or $\text{gANOVA}$ correlation structure. Moreover, being based on a $\text{MAX}$ correlation structure, $\text{CS-PCA}$ will have problems in complex designs.

Note that even if the goal of the algorithm is to match the data, some design-driven components persist, like reducing the higher interaction levels first or, keeping the dimension of the random effects based on the design even after a PCA.

It is not possible to produce meaningful theoretical comparison with the other correlation structures discussed above and we will compare it through simulations in Section 6. However, the correlation structure $\text{CS-PCA}$, being mainly data-driven, may seem to come from a different family than the design-driven random structure $\text{RI-L}$, $\text{ZCP}$, $\text{MAX}$ or $\text{gANOVA}$. However, all correlation structures can be summarized as a function or algorithm of the design and of the data. The main difference is that the procedures $\text{RI-L}$, $\text{ZCP}$, $\text{MAX}$ and $\text{gANOVA}$ will mostly use information about the design to select the correlation structure and $\text{CS-PCA}$ will also use information from the data. And, again, they will all be false, and the goal is to select the most useful one.

6 Simulation study

This simulation study is designed to compare the above correlation structures when performing tests on the fixed effects, which is the principal interest of researchers. Our focus are the type I error rate and the convergence rate of the methods. The type I error rate is the average number of rejected null hypotheses per simulation settings. It should be close to the nominal level, that is set here to $\alpha = 5\%$; a lower value indicates a conservative method and a higher value indicates a liberal one. Moreover, to evaluate the power of the tests, we recorded, under the alternative hypothesis, the average number of true positive (the empirical power). A higher number of true positive indicates a more powerful method.

6.1 Simulating the datasets

We choose several simulation settings in order to match likely experimental designs and 4000 samples were simulated in order to have smaller confidence interval of our metrics. The settings vary according to 3 different designs, 2 different sample sizes, 2 different correlations of random effects, and the fact that random effects for the interaction participants:stimuli are included or not.
Table 4: Percentage of convergence error for all simulations ($N_{sim} = 4000$) under the null hypothesis. Results are split by rows according to the simulation settings based on (1) the sample size for stimuli, (2) the true correlation between random effects, (3) the presence/absence of random effects associated with the participants:stimuli interaction and (4) the size of the design. The columns represent the type of estimation: all 7 correlation structures are assumed with (+) and without (-) the interaction participants:stimuli. The dash "-" indicates settings without simulations. MAX and to a lesser extent CS-PCA present problems of convergence.

|                  | RI | RI-L | MAX | ZCP-sum | ZCP-poly | gANOVA | CS-PCA |
|------------------|----|------|-----|---------|----------|--------|--------|
|                  | -  | +    | -   | +       | -        |        |        |
| no PT:SM         | M1 | 0.0  | 0.0 | 0.0     | 0.0      | 0.0    | 0.0    |
|                  | M2 | 0.0  | 0.0 | 0.0     | 0.0      | 0.0    | 0.0    |
|                  | M4 | 0.0  | 0.0 | 0.0     | 0.0      | 0.0    | 0.0    |
| spheric.         |    |      |      |         |          |        |        |
| PT:SM            | M1 | 0.0  | 0.0 | 0.0     | 0.0      | 0.0    | 0.0    |
|                  | M2 | 0.0  | 0.0 | 0.0     | 0.0      | 0.0    | 0.0    |
|                  | M4 | 0.0  | 0.0 | 0.0     | 0.0      | 0.0    | 0.0    |
| corr.            |    |      |      |         |          |        |        |
| no PT:SM         | M1 | 0.0  | 0.0 | 0.0     | 0.0      | 0.0    | 0.0    |
|                  | M2 | 0.0  | 0.0 | 0.0     | 0.0      | 0.0    | 0.0    |
|                  | M4 | 0.0  | 0.0 | 0.0     | 0.0      | 0.0    | 0.0    |
| PT:SM            | M1 | 0.0  | 0.0 | 0.0     | 0.0      | 0.0    | 0.0    |
|                  | M2 | 0.0  | 0.0 | 0.0     | 0.0      | 0.0    | 0.0    |
|                  | M4 | 0.0  | 0.0 | 0.0     | 0.0      | 0.0    | 0.0    |

The 3 experimental designs are: a small design with only 2 levels per factor (M1 in Table 3), a rather common design with 3 levels per factor (M2 in Table 3) and a larger design with more variables (M4 in Table 3). The designs M1 and M2 have variables of type $V_P$, $V_S$, $V_M$ and M4 has an additional variable of type $V_{PS}$.

Two correlations between random effects are used for the generation of the data. In the first case, the random effects are spherical (spheric.) and in the second case, the random effects are fully correlated (corr.); the fully correlated covariance matrix is such that random effects spanned a space of half of the dimension of the random effects (but not in the canonical directions). In order to give more importance to the main effects, the standard deviations of random effects are halved when increasing an order (or degree) of interaction. Moreover, all standard deviations of the random effects associated to stimulus and interaction participants:stimuli are shrunken by 0.9, respectively 0.8. Each design is simulated with random effects associated to the interaction participants:stimuli (PT:SM) and without (no PT:SM). Moreover, the small (M1) and common (M2) designs are simulated with 2 different sample sizes: 18 participants and 18 stimuli, and 18 participants and 36 stimuli. The large model (M4) was only simulated using 18 participants and 18 stimuli to reduce computation time.

Because decreasing variability as the interaction level increases favours RI-L correlation structure, we also produce another simulation based on design M1. We change the variance of random effects to highlight the difference of gANOVA and RI-L on the type I error rate. In that case, we simulate data without random intercepts while all others standard deviations of random effects are kept the same.

Finally, we produce a power analysis by increasing the fixed effect parameters. We first estimated a maximum value for the parameter such that the empirical power exceed 90% for each effect. Then, each effect is
Table 5: Type I error rate for three variables of the common model (M2 of in Table 3). Correct methods should be close the the nominal level $\alpha = .050$. The first column indicates the true correlation between random effects (homoscedastic or correlated). The second one indicates if the true model is generated with the interaction participants-stimuli. The third column indicates if model is estimated assuming the interaction participants-stimuli (+) or not (-). The RI and CS-PCA correlation structures show huge deviations from the nominal level.

|                   | RI         | RI-L       | MAX        | ZCP-sum     | ZCP-poly    | gANOVA     | CS-PCA     |
|-------------------|------------|------------|------------|-------------|-------------|------------|------------|
| **Vs**            |            |            |            |             |             |            |            |
| no PT:SM          | .136       | .051       | .051       | .049        | .052        | .050       | .052       |
| -                  | [.126; .148]| [.044; .058]| [.044; .059]| [.043; .056]| [.045; .059]| [.044; .058]| [.045; .059]|  
| +                  | .139       | .054       | .059       | .053        | .054        | .053       | .055       |
| -.                 | [.129; .150]| [.047; .061]| [.046; .061]| [.046; .060]| [.048; .062]| [.047; .061]| [.048; .062]|  
| PT:SM             | .139       | .054       | .059       | .053        | .054        | .054       | .058       |
| -                  | [.129; .150]| [.047; .061]| [.051; .067]| [.047; .060]| [.051; .065]| [.047; .061]| [.051; .066]|  
| +                  | .134       | .050       | .056       | .046        | .050        | .050       | .050       |
| -.                 | [.124; .145]| [.044; .058]| [.048; .065]| [.040; .053]| [.043; .057]| [.044; .058]| [.043; .057]|  
| **Vp:Vm**         |            |            |            |             |             |            |            |
| no PT:SM          | .723       | .059       | .065       | .077        | .069        | .058       | .077       |
| -                  | [.709; .737]| [.052; .066]| [.057; .074]| [.069; .086]| [.081; .077]| [.062; .066]| [.069; .085]|  
| +                  | .809       | .055       | .064       | .075        | .063        | .054       | .068       |
| -.                 | [.782; .824]| [.048; .062]| [.056; .073]| [.067; .083]| [.056; .071]| [.048; .062]| [.060; .076]|  
| PT:SM             | .824       | .054       | .059       | .072        | .064        | .054       | .066       |
| -                  | [.812; .836]| [.048; .062]| [.052; .068]| [.064; .081]| [.057; .072]| [.048; .062]| [.059; .074]|  
| +                  | .698       | .059       | .055       | .075        | .067        | .059       | .077       |
| -.                 | [.684; .712]| [.052; .067]| [.047; .064]| [.063; .074]| [.068; .084]| [.060; .075]| [.052; .067]|  
| **Vp:Vs:Vm**      |            |            |            |             |             |            |            |
| no PT:SM          | .250       | .075       | .036       | .103        | .087        | .075       | .409       |
| -                  | [.237; .264]| [.067; .083]| [.036; .043]| [.094; 112]| [.079; .096]| [.067; .083]| [.394; .425]|  
| +                  | .446       | .051       | .040       | .092        | .070        | .051       | .249       |
| -.                 | [.431; .462]| [.045; .059]| [.034; .047]| [.083; .101]| [.063; .079]| [.045; .059]| [.235; .263]|  
| PT:SM             | .436       | .049       | .039       | .085        | .060        | .049       | .195       |
| -                  | [.425; .475]| [.043; .056]| [.033; .046]| [.077; .094]| [.053; .068]| [.043; .056]| [.183; .208]|  
| +                  | .463       | .049       | .040       | .085        | .059        | .049       | .189       |
| -.                 | [.448; .479]| [.042; .056]| [.034; .047]| [.076; .094]| [.052; .067]| [.042; .056]| [.177; .202]|  

tested by multiplying this value by .2, .4, .6, .8 and 1. For factors with more than 3 levels, we let all fixed parameters increase simultaneously. Moreover, to reduce the computation time, we increased all fixed effects.
Table 6: Type I error rate for three variables of the common model (M1 of in Table 3) with 36 stimuli. Correct methods should be close the the nominal level \( \alpha = .050 \). The data are generated without random intercepts. In this setting, the type I error rates of RI-L deviate strongly from the nominal level, whereas gANOVA stay close to it.

|        | RI-L | RI-L+ | gANOVA | gANOVA+ |
|--------|------|-------|--------|---------|
| Vp     | corr. no PT:SM | .005 [.003; .008] | .005 [.003; .008] | .046 [.040; .054] | .046 [.040; .054] |
|        | PT:SM | .006 [.004; .008] | .006 [.004; .008] | .049 [.043; .056] | .049 [.043; .056] |
|        | no PT:SM | .006 [.004; .008] | .006 [.004; .008] | .051 [.045; .058] | .051 [.045; .058] |
|        | PT:SM | .005 [.003; .008] | .005 [.003; .008] | .039 [.033; .045] | .039 [.033; .045] |
| Vm     | corr. no PT:SM | .119 [.109; .129] | .119 [.109; .129] | .047 [.041; .054] | .047 [.041; .054] |
|        | PT:SM | .118 [.108; .128] | .118 [.108; .128] | .050 [.043; .057] | .050 [.043; .057] |
|        | no PT:SM | .117 [.107; .127] | .117 [.107; .127] | .046 [.040; .054] | .046 [.040; .054] |
|        | PT:SM | .107 [.098; .117] | .107 [.098; .117] | .051 [.044; .058] | .051 [.044; .058] |
| Vp:Vs  | corr. no PT:SM | .114 [.105; .125] | .114 [.105; .125] | .052 [.045; .059] | .052 [.045; .059] |
|        | PT:SM | .114 [.104; .124] | .113 [.104; .123] | .050 [.044; .058] | .050 [.044; .058] |
|        | no PT:SM | .113 [.103; .123] | .113 [.103; .123] | .047 [.041; .054] | .047 [.041; .054] |
|        | PT:SM | .111 [.101; .121] | .110 [.101; .121] | .050 [.044; .058] | .050 [.044; .058] |

6.2 Fitting of the data

The randomly generated data are fitted using the correlation structures presented in Section 5: the random intercepts (RI), the random intercepts at each level (RI-L), the maximal (MAX), the zero-correlation parameter (ZCP), the generalized ANOVA (gANOVA) and correlation structure based on PCA (CS-PCA). ZCP is computed once with the default (non-orthonormal) “sum” coding (ZCP-sum) and once with a “polynomial” (and orthonormal) coding (ZCP-poly) on the random effects. Each model is estimated with (+) and without (-) assuming the random effects associated to the interaction participant-stimulus. Moreover, the significance is evaluated using the type III test with Satterthwaite’s approximation of the degrees of freedom using the \texttt{lmerTest} package (Kuznetsova et al., 2017) and the restricted maximum likelihood (REML) estimation (Bates et al., 2015b). The larger model (M4) was only estimated using RI, ZCP and gANOVA to reduce computation time.

To reduce the convergence error, each model is first optimized using the default \texttt{BOBYQA} optimizer (Powell, 2009), then the Nelder-Mead optimizer (Nelder and Mead, 1965), then from the \texttt{optimx} package (Nash and Varadhan, 2011) the \texttt{nlminb} optimizer and the \texttt{L-BFGS-B} optimizer. We stop the procedure when a solution is found without convergence error. If all optimizers fail, we declare a failure of convergence for that sample.

6.3 Evaluation of simulation

Table 4 shows the percentage of samples with convergence error based on 4000 simulated samples for all simulation settings (designs M1, M2 and M4 in Table 3). We deduce that MAX is not scalable to even moderately sized designs because with only 3 levels per factor we recorded up to 40% of convergence error. Moreover, our implementation of the CS-PCA by Algorithm 5.6 did not reach a low number of convergence error. For the other correlation structure, we achieve a high convergence rate. This means that using several optimizers seems a good practice to reduce convergence error.

Table 5 shows estimated type I error rates with their confidence intervals (Agresti and Coull, 1998) for the common model (M2). The liberal type I error rates are shown in red and the conservative ones in italic. The rates are computed using only the samples without convergence error which might bias the results for MAX. One sees that RI and CS-PCA are globally too liberal as their type I error rates show huge deviations from the nominal level. The second observation is that including the interaction participant-stimuli does not

simultaneously (all main effects and all interactions).
The difference between gANOVA and RI-L is visible in Table 6 which shows simulations with data from model M2 with a null standard deviation for the random intercepts. For these datasets, gANOVA stay close to the nominal level but RI-L shows large deviations (liberal or conservative). In addition to the theoretical remarks on the difference between RI-L and gANOVA given in Section 5 and Appendix D these simulations show that gANOVA is strictly better than RI-L for reporting tests of fixed effects.

Moreover, the parsimony of gANOVA seems to endow it an advantage for the power of the test. All the power results are provided in the supplementary material. Figure 3 summarizes the findings by computing
Figure 2: Display of type I error rates of the model M2 split given the simulations settings. The vertical lines indicate the range of all simulations within the condition. RI-L and gANOVA are the closest to the nominal level $\alpha = .050$ represented by a red dashed line. The variable $V_M$ and its interaction produce higher deviation from the nominal level across all correlation structures. No other simulation setting tends to have an effect on the type I error rate.

the ratio of uncorrected average observed powers of RI-L, ZCP-sum and ZCP-poly compared to the one of gANOVA. A method has larger power than gANOVA if the ratio is bigger than one and smaller power if $< 1$. One sees that ZCP-poly and gANOVA perform clearly better than ZCP-sum and that RI-L is close to gANOVA due to the choice of the variance parameters of the random effects. As seen in Figure 1, ZCP-poly has a higher type I error rate for most of the simulation settings under the null hypothesis. However, by increasing the effect size, this deviation decreases. This means that the better control of the type I error rate of gANOVA is not achieved at the expense of the power of the test. Moreover, when the power is corrected by using a critical value set at the nominal level (Figure 1), gANOVA performs better than ZCP-poly. No other simulation settings have a big influence on the average difference of power between the methods.

7 Conclusion

Using CRE-MEM in psychology is a growing practice and there is a diversity of correlation structures that are available and that are used. These correlation structures directly depend on the design of experiment and we develop a classification of variables in order to help users in the planning of the experiment and its analysis. All correlation structures do not share the same advantages and there is no predefined tools to help researchers select the appropriate correlation structure given the experiment. Depending on the goal of the analysis some properties are more important to control than others.

In the case of hypothesis testing, we have shown that the gANOVA correlation structure has many desirable
Figure 3: Ratio of uncorrected average observed powers of RI-L, ZCP-sum and ZCP-poly compared to the one of gANOVA. A method has larger power than gANOVA if the ratio is bigger than one. The vertical lines indicate the range of all simulations within the condition. ZCP-poly is liberal which explains that for lower effects size, gANOVA has a slightly lower power than ZCP-poly, but the deviation reduces for higher effect sizes.

properties. Simulations show that it controls the type I error rate without a loss in power even with misspecifications of the model. It also provides a high rate of convergence and is scalable to complex datasets. Moreover, it is in line with the experimental design tradition represented by the ANOVA/rANOVA framework, which is helpful for the interpretation of the results for researchers familiar with the ANOVA.

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A Correlation structure of the rANOVA

In the earlier times when the repeated measures ANOVA model was first discussed, an abundant literature on the choice of the model and especially on the choice of the correlation structure was written. At that time, the necessity to compute everything by hand gave constraints on the analysis and all the available test statistics were based on sum of squares. Under specific assumptions, these statistics possess an exact \( F \) distribution. Let’s first mention that \cite{huynh1970} showed that the sphericity (or circularity) of
Figure 4: Ratio of corrected average observed powers of RI-L, ZCP-sum and ZCP-poly compared to the one of gANOVA. A method has larger power than gANOVA if the ratio is bigger than one. The vertical lines indicate the range of all simulations within the condition. In all simulation settings, no correlation structure performs better than gANOVA.

the covariance structure was a necessary and sufficient condition for an exact test. Box (1954) and Huynh and Feldt (1976) proposed modifications in the degrees of freedom – called \( \epsilon \)-correction – when this condition is not fulfilled. Note that even earlier, a discussion was engaged whether to include in the correlation structure the interactions between the participant and the fixed effects (\( \pi \psi_{ik} \) in Equation 1), which are now called the random slopes. Rouanet and Lepine (1970), for example, compare the models with and without them. Ultimately, the model that includes all random slopes became the reference and statistical software, like SPSS or Statistica, use it as if it was the only possible random structure.

On a more technical side, for the fixed effects, some constraints have to be chosen since the model is otherwise overparametrized and no estimation or test can be obtained (Cardinal and Aitken, 2013). In order to keep the interpretation of main effects as in the ANOVA tradition, we use the sigma-restricted parametrizations, which corresponds in Equation 1 to the following constraints: \( \sum_j \alpha_j = 0 \), \( \sum_j (\alpha \psi)_{jk} = 0 \) \( \forall k \) and \( \sum_k (\alpha \psi)_{jk} = 0 \) \( \forall j \), and so on. Concerning random slopes, which are technically interactions between a fixed and a random unit, it is worth asking if this type of constraints should also be also applied. In a very influential paper, Cornfield and Tukey (1956), with a construction called “pigeonhole” that includes both fixed and random factors as special cases, show that the distributional behaviour for factorial designs lead to constraints only for one margin: \( \sum_k (\pi \psi)_{ik} = 0 \) \( \forall i \), see e.g. Montgomery (2017). If these constraints are not included e.g. when simulating data, some variances will be inflated.

The discussion in the previous paragraphs shows that there was a debate over several decades on the best model for rANOVA, both for the fixed part and for the correlation structure. It is therefore not surprising that concerning the more recently proposed CRE-MEM, a similar debate is ongoing. It is noteworthy that it concerns exactly the same questions on the best correlation structure and the correlation structures for
Figure 5: Representation of the variables and the responses of a rANOVA in the 'wide' format. The responses are stored in a 2D array that stem from the crossing of 2 tables. Table $P$ stores the participants and their features $V_P$ (or between-participant variables) and Table $M$ stores the features of the experimental manipulations $V_M$ (or within-participant variables).

As a complement to Section 4, we propose here a generalisation of the “wide” format for the 5 types of variables. In the rANOVA framework, software like SPSS or Statistica use data in the “wide” format. This format makes explicit the difference between within-participant variables ($V_P$) and between-participant variables ($V_M$), see Figure 5. Each line of the data represents one participant and the “data” column are split into between-participant variables, and columns which values are the response recorded in one level of the within-participant variables. So, the responses are stored in a two-dimensional (2D) array which entries, by rows, correspond to the participants and by column to the within-participants levels. This 2D array is the results of the crossing of one table storing the participant and $V_P$ variables and one table storing the experimental manipulations and the $V_M$ variables.

The “wide” format shows clearly the fundamental difference between within-participant and between-participant variables. This representation can be extended to CRE-MEM. In that setting, we cross 3 tables (instead of 2): one for the participants and the variables $V_P$ (Table $P$), one for the stimuli and the variables $V_S$ (Table $S$) and one for the experimental manipulations and the variables $V_M$ (Table $M$). The crossing of those 3 tables creates a 3D array (like a building, of dimension $[n_P, n_S, n_M]$) in which the responses can be stored. This construction is represented in the Figure 6. In this example, each participant is represented by one row of the Table $P$ and each stimulus is represented by one row (here rotated by 90°) of the Table $S$. Then, the responses of one participant are a stored in one “floor” (of dimension $[1, n_S, n_M]$), the responses of one stimulus are stored in one “vertical slide” from forefront to back (of dimension $[n_P, 1, n_M]$) and the responses in one experimental manipulation is one “slice” (of dimension $[n_P, n_S, 1]$) of the 3D array. The responses associated to one pair participant-stimulus is consequently a “pile” (of dimension $[1, 1, n_M]$) of the 3D array. Note that to simplify the representation the variables $V_{PS}$ and $V_O$ are not represented in Figure 6. However, they could be associated both to their own table (Table $PS$ and Table $O$) and each entry of the...
Figure 6: Representation of the variables and the responses of CRE-MEM. The responses are stored in a 3D array that is the result of the crossing of Table P, Table S and Table M. Participants are associated with the Table P and the levels of variable \( V_P \) will be identical for each "floor". Stimuli are associated with the Table S and variables \( V_S \) will take the same value for each "vertical slide". And the experimental manipulations are associated with the Table M and each "slice" of the 3D array.

Table \( PS \) would be associated with one “pile” of the 3D array. Finally, each entry of the Table \( O \) would be associated with one cell of the 3D array.

This representation is a tool to understand which interactions between fixed effects and random units are allowed in a model. Each “floor” (the responses by participants) crosses all levels of the \( V_S \) and \( V_M \) variables, which implies that participants are measured in all levels of \( V_S \) and \( V_M \). Moreover each “floor” is composed of multiple “piles” and multiple “cells” which means that a participant will be measured in multiple levels of the variables \( V_{PS} \) and \( V_O \). All the random interactions participant: \( V_S \), participant: \( V_M \), participant: \( V_{PS} \), participant: \( V_O \) are then allowed for CRE-MEM. The same rational is applied for stimuli: each stimulus is represented in by one “vertical slide” and will be measured in all levels of the \( V_P \) and \( V_M \), then the random interaction stimuli: \( V_P \), stimuli: \( V_M \), stimuli: \( V_{PS} \), stimuli: \( V_O \) are feasible. To understand which random slopes associated to the interaction participants:stimuli can be included in the model we apply the same strategy for the “pile” and each interaction crosses all levels of the variables \( V_M \). And each “pile” is composed of multiple cells (which are associated to variables \( V_O \)). Which means that the random interactions between participants:stimuli: \( V_M \) and participants:stimuli: \( V_O \) are feasible. These findings are summarized in Table 1.
C Matrix formulation of the CRE-MEM

C.1 General Notation for mixed models

Following Bates et al. (2015b), we define the mixed linear model:

\[ y = X\beta + Z\gamma + \epsilon \]

where \( y \) is the response, the fixed part of the design is \( X \) and the random part is \( Z \). The fixed parameters are \( \beta \), the random effects are \( \gamma \sim (0, \Sigma) \) and the error terms are \( \epsilon \sim (0, \sigma^2 I) \). For a CRE-MEM, we split the random effects into \( G \) independent components \( \gamma = [\gamma_1^T | ... | \gamma_g^T | ... | \gamma_G^T]^T \) and their associated design matrices \( Z = [Z_1 | ... | Z_g | ... | Z_G] \) which led to the decomposition of the covariance matrix of the random effects into \( \Sigma = \text{diag}(\Sigma_1, ..., \Sigma_g, ..., \Sigma_G) \). The covariance matrix of the response variable \( y \) can then be written as \( \Omega = Z\Sigma Z^T + I\sigma^2 = Z\Sigma_1 Z_1^T + ... + Z_g \Sigma_g Z_g^T + ... + Z_G \Sigma_G Z_G^T + I\sigma^2 \).

C.2 Generalized ANOVA and RI-L for the CRE-MEM

The gANOVA is written following the Equation 3 with specific constraints on the random effects. Independence between random components is specified using \( \gamma = [\gamma_P^T | \gamma_S^T | \gamma_P^S]^T \) and by defining a covariance matrix of observations split into the parts relative to participants, stimuli and their interactions:

\[ \Omega = Z\Sigma Z^T + I\sigma^2 = Z_P \Sigma_P Z_P^T + Z_S \Sigma_S Z_S^T + Z_P S \Sigma_P S Z_P^T + I\sigma^2, \]

where \( Z_P = (X_{\text{parti}}^T * [1 | X_S | X_P S | X_M | X_O] X_{\text{stimulus}}^T)^T \), \( Z_S = (X_{\text{stimulus}}^T * [1 | X_P | X_P S | X_M | X_O] X_{\text{stimulus}}^T)^T \), \( Z_P S = ((X_{\text{parti}}^T * X_{\text{stimulus}}^T) * [1 | X_M | X_O] X_{\text{stimulus}}^T)^T \) and the Khatri-Rao product (Khatri and Rao, 1968) is written using *. \( X_{\text{parti}} \) and \( X_{\text{stimulus}} \) are matrices dummy coding xxoli est ce bien des 0/1 for the participants and stimuli, and \( \Sigma_P \), \( \Sigma_S \), \( \Sigma_P S \) are covariance matrices.

If the dataset has no missing value and after the appropriate permutation \( (P_P, P_S \text{ and } P_P S) \), the covariance matrices are written as block diagonal matrices of the individual covariance structure: \( \Sigma_P = P_P (I_P \otimes \Sigma_P^0) P_P^T \), \( \Sigma_S = P_S (I_S \otimes \Sigma_S^0) P_S^T \) and \( \Sigma_P S = P_P S (I_P S \otimes \Sigma_P S^0) P_P S^T \). gANOVA assumes that the matrices \( \Sigma_P^0 \), \( \Sigma_S^0 \) and \( \Sigma_P S^0 \) are diagonal matrices with the same value for the random effects (i.e. contrasts) associated to the same factor.

For gANOVA, the \( X \) matrices \( X_S \), \( X_P \), \( X_P S \), \( X_M \) and \( X_O \) are written using orthonormal contrasts \( C \) (e.g.: contr.poly) and overparametrized dummy-coded design matrices \( X^0 \) such that \( X = X^0 C^- \) where \( C^- \) is the generalized inverse of \( C \). If \( C \) is orthonormal gives the properties \( C C^- = I \) and \( C^- C^- = I - a I \) where \( a \) is a positive value that depends on the dimension of \( C \).

Concerning the RI-L model, the only difference with gANOVA is that there is no constraints on the random effects. Its matrix formulation is therefore the same as gANOVA except that the contrasts \( C \) are not used (or are replaced by an identity matrix \( I \)). Note that the \( X^0 \) matrices are used to construct the fixed part of the design and are usually associated with contrasts. Depending on the hypothesis, these contrasts may be represented by non-orthonormal matrices (e.g.: using contr.sum).

D Comparison of the gANOVA and RI-L model

In this appendix, we provide evidence that gANOVA has a better decomposition of the correlation structure than RI-L. For the sake of the argument, we focus the comparison to a model with only one sampling unit (the participants), balanced design and replications (one variable \( V_M \)), which means that there will be 3 variances parameters: one for random intercepts, one for the random slopes and one for the residuals. The
Fig. 7: Likelihood of RI-L and gANOVA for a model with one sampling units and 1 variable $V_M$ with replications and assuming random intercepts and random slopes. The two top figures represent the likelihood in the $\sigma$ parameters space (standard deviation of random effects), and two bottom one represents the $\theta$ parameters space (space of optimization parameters; see Equation (4) in Bates et al. (2015b) for an exact definition of the $\theta$’s.). The dotted lines are the two ridges defining the profile likelihoods. We see in this example that the gANOVA tends to orthogonalize the profile likelihoods as they cross almost at a $90^\circ$ angle, which suggest less dependency of the two parameters and an easier optimization process.

replications will make the variance of the random slopes estimable. The gANOVA and RI-L correlation structure differ by the constraints on the random effects and those constraints are represented by contrast matrices. We will call constraint (c) the design of gANOVA and unconstraint (uc) the one of RI-L.

In that setting, the RI-L model is written:
\[ y = X \beta + Z_{uc} \gamma_{uc} + \epsilon, \]

where \( \gamma_{uc} \sim (0, I_{Np} \otimes \Sigma_{uc}) \), \( \epsilon \sim (0, \sigma^2_{uc\epsilon}) \) for \( Np \) the number of participants. \( \Sigma_{uc} \) is a diagonal covariance matrix of dimension \( N_M + 1: \Sigma_{uc} = \text{diag}(\sigma^2_{uc,i}, I_{N_M} \sigma^2_{uc,T}). \)

The design matrix of the random effects is written \( Z_{uc} = \left(Z^\top [1 \ X_{uc}]\right)^\top \) and \( * \) denotes the column-wise Khatri-Rao product [Khatri and Rao 1968]. Assuming a balanced design, we write:

\[
Z_{uc} = \left((I_{Np} \otimes [I_{N_M + 1}]^\top) \right. \\
\left. \left. (1_{Np} \otimes [I_{N_M} X_{ucp}]^\top)\right) = (I_{Np} \otimes [1_{N_M} X_{ucp}]),\right.
\]

where \( X_{ucp} \) is a \( N_M N_R \times N_M \) matrix representing the overparametrized design of one participant for a \( V_M \) factor of \( N_M \) levels and assuming \( N_R \) replications in each cell. The covariance matrix of the response \( y \) is:

\[
Z_{uc}(I_{Np} \otimes \Sigma_{uc})Z_{uc}^\top + I\sigma^2_{uc\epsilon} = (I_{Np} \otimes [1_{N_M} X_{ucp}]) (I_{Np} \otimes \Sigma_{uc}) (1_{Np} \otimes 1_{N_M} X_{ucp}) + I\sigma^2_{uc\epsilon} \\
= (I_{Np} \otimes 1_{N_M} X_{ucp}) (I_{Np} \otimes \Sigma_{uc} 1_{N_M} X_{ucp}) + I\sigma^2_{uc\epsilon} \\
= I_{Np} \otimes (1_{N_M} X_{ucp} \Sigma_{uc} 1_{N_M} X_{ucp}) + I\sigma^2_{uc\epsilon} \\
= I_{Np} \otimes (1_{N_M} X_{ucp} \Sigma_{uc} 1_{N_M} X_{ucp}) + I\sigma^2_{uc\epsilon}.
\]

The covariance matrix of the response is a block diagonal matrix with block-elements of the form:

\[
[1_{N_M} \ X_{ucp}] \Sigma_{uc} [1_{N_M} \ X_{ucp}]^\top + I_{N_M} \sigma^2_{uc\epsilon} = 1_{N_M} 1_{N_M} \sigma^2_{uc\epsilon} + X_{ucp} X_{ucp}^\top + I_{N_M} \sigma^2_{uc\epsilon}.
\]

Similarly, gANOVA is written:

\[
y = X \beta + Zc \gamma_{c} + \epsilon,
\]

where \( \gamma_{c} \sim (0, I_{Np} \otimes \Sigma_{c}) \), \( \epsilon = (0, \sigma^2_{c\epsilon}) \). \( \Sigma_{c} \) is a diagonal matrix covariance matrix of dimension \( N_M : \Sigma_{c} = \text{diag}(\sigma^2_{c,i}, I_{N_M} \sigma^2_{c,T}). \)

The design matrix of the random effects is written using the orthonormal contrast \( C_{c} = \left(Z^\top [1 \ X_{ucc}]\right)^\top \) and assuming that it is balanced, it becomes: \( C_{c} = (I_{Np} \otimes 1_{N_M} X_{ucp} X_{ucp}^\top). \)

The covariance matrix of the response is then:

\[
Z_{c}(I_{Np} \otimes \Sigma_{c})Z_{c}^\top + I\sigma^2_{c\epsilon} = I_{Np} \otimes (1_{N_M} X_{ucp} X_{ucp}) + I\sigma^2_{c\epsilon} \\
= I_{Np} \otimes (1_{N_M} X_{ucp} X_{ucp} C^{-}) + I\sigma^2_{c\epsilon}.
\]

Using the properties of the orthonormal contrasts, the block-elements of the covariance matrix simplify:

\[
[1_{N_M} \ X_{ucp} C^{-}] \Sigma_{c} [1_{N_M} \ X_{ucp} C^{-}]^\top + I_{N_M} \sigma^2_{c\epsilon} = 1_{N_M} 1_{N_M} \sigma^2_{c\epsilon} + X_{ucp} C^{-} X_{ucp}^\top + I\sigma^2_{c\epsilon} \\
= 1_{N_M} 1_{N_M} \sigma^2_{c\epsilon} + X_{ucp} (I - 11^\top a) X_{ucp}^\top + I\sigma^2_{c\epsilon} \\
= 1_{N_M} 1_{N_M} \sigma^2_{c\epsilon} + X_{ucp} X_{ucp}^\top + I\sigma^2_{c\epsilon}.
\]
with positive value $a$ defined by the number of levels of $V_M$: $a = 1 - 1/N_M$. The covariance matrices of the 2 models are equal if and only if:

$$
\begin{align*}
\sigma_{uc;i}^2 &= \sigma_{c;i}^2 - a\sigma_{c;i,F}^2 \\
\sigma_{uc:F}^2 &= \sigma_{c;i,F}^2 \\
\sigma_{uc;\epsilon}^2 &= \sigma_{c;i,\epsilon}^2.
\end{align*}
$$

These equalities show us that the 2 models are equal for values of the variances of random effects. But, the first equality tells us that the 2 models are not equal when $\sigma_{c;i}^2 < a\sigma_{c;i,F}^2$. Which means that adding the constraint of the contrasts $C$ increases the parameters space. With more factors in the model, higher level interactions put similar conditions on lower level interactions. The RI-L model will produce more estimates equal to 0 with maximal values of the optimal function at the boundary of the parameter space. And, when RI-L and gANOVA are not equal, gANOVA will always have a better likelihood which suggests a better fit of the model.

### E Examples of lme4 formulas for CRE-MEM with different correlation structures

In this appendix, some examples of R formula from simple to more complex designs (see Table 2 for the selected designs). The type of variable is explained in the Section 4. We use the notation PT and SM for the identifier variables of the participants and stimuli respectively and $y$ for the response variable. All those variables and the design will be variables of the mydata dataframe. To interpret correctly main effects as in the ANOVA framework, it is extremely important to use contrasts that sum to zero (like contr.sum or contr.poly) and not the contr.treat default in R). The fixed part will be assumed to be a full factorial design in each case. For saturated design, we drop the last interaction term because we assume no replication of the same observations (multiple observations associated to the same cell in the design) and the last interaction terms would not be estimable because it is confounded with the error terms.

Using factors in the formula will not produce always the model that the users expect. R assigns to factors the maximum degree of freedom (some sort of contrasts) available which means that, for the factors A and B with 2 levels, using the formula `~A*B` and `~A:B` will assign respectively 1 and 3 degrees of freedom for the interaction A:B; one other example is `~A` and `~0 + A` which assign 1 and 2 degrees of freedom for the effect of A. In lme4, this feature happens when R compute separately the effects; for instance, `~(1|PT) + (A|PT)` will assign 2 variances (+1 covariance) for the levels of A and `~(A*B||PT)` will assign 4 variances (+6 covariances) for the interaction A:B. In order to produce the correlation structures described in the Section 5 the solution is to convert factors into numeric variables, we use the model.matrix() function for that purpose.

#### E.1 A simple case, variables $V_P(2)$, $V_S(2)$ and $V_M(2)$

This design corresponds to model M1 in Table 3. In that simple case, the saturated correlation structure will not have the last term of interaction between the variable $V_M$ and the random units participant:stimulus. With only 2 levels per factor, the “sum” coding will produce similar results to the polynomial coding variable.

**RI and RI+**

```r
lmer(y ~ Vp*Vs*Vm + (1|PT) + (1|SM) + (1|PT:SM), data = mydata)
```
RI-L and RI-L+

\[
\text{lmer}(y \sim V_p \times V_s \times V_m + (1|PT) + (1|PT:V_s) + (1|PT:V_m) + (1|PT:V_s:V_m) \\
+ (1|SM) + (1|SM:V_p) + (1|SM:V_m) + (1|SM:V_s:V_m) \\
+ (1|PT:SM), \text{ data} = \text{mydata})
\]

MAX and MAX+

\[
\text{lmer}(y \sim V_p \times V_s \times V_m + (V_s:V_m|PT) + (V_p:V_m|SM) + (1|PT:SM), \text{ data} = \text{mydata})
\]

ZCP and ZCP+

\[
\text{mydata}$X_s < - \text{model.matrix}(\sim V_s, \text{ data} = \text{mydata})[, -1]
\]
\[
\text{mydata}$X_p < - \text{model.matrix}(\sim V_p, \text{ data} = \text{mydata})[, -1]
\]
\[
\text{mydata}$X_m < - \text{model.matrix}(\sim V_m, \text{ data} = \text{mydata})[, -1]
\]
\[
\text{lmer}(y \sim V_p \times V_s \times V_m + (X_s:V_m||PT) + (X_p:V_m||SM) + (1|PT:SM), \text{ data} = \text{mydata})
\]

gANOVA and gANOVA+

The gANOVA package use the same notation as the RI-L formula

\[
( + (1|PT) + (1|PT:f_1) + (1|PT:f_2) \\
+ (1|PT:f_1:f_2)) \text{ and puts orthonormal coding from the second factors of the right part of the random effect. Doing so, the order of the factors matters and the first variable to the right of the bar must be the random unit. Note that it implies that the interaction participant-stimulus should be written as only one variable. Moreover, the multiple terms in the notation can be reduced to the formula } + (1|PT|f_1*f_2). \text{ Then gANOVA is specified using:}
\]
\[
\text{mydata}$PTSM < - \text{interaction(mydata}$PT, \text{ mydata}$SM)
\]
\[
\text{gANOVA}(y \sim V_p \times V_s \times V_m + (1|PT) + (1|PT:V_s) + (1|PT:V_m) + (1|PT:V_s:V_m) \\
+ (1|SM) + (1|SM:V_p) + (1|SM:V_m) + (1|SM:V_s:V_m) \\
+ (1|PTSM), \text{ data} = \text{mydata})
\]

or equivalently:

\[
\text{mydata}$PTSM < - \text{interaction(mydata}$PT, \text{ mydata}$SM)
\]
\[
\text{gANOVA}(y \sim V_p \times V_s \times V_m + (1|PT:V_s:V_m) + (1|SM:V_p:V_m) + (1|PTSM), \\
\text{ data} = \text{mydata})
\]

E.2 A common case, variables \(V_P(3), V_S(3), V_M(3)\) and \(V_M(2)\)

This design corresponds to model M3 in Table 3. The last interaction terms is confounded with the error term is the interaction between the 2 variables \(V_{M1}, V_{M2}\) and the participant:stimulus random unit.

RI and RI+

\[
\text{lmer}(y \sim V_p \times V_s \times V_{m1} \times V_{m2} + (1|PT) + (1|SM) + (1|PT:SM), \text{ data} = \text{mydata})
\]
RI-L and RI-L+

\[ \text{lmer}(y \sim Vp*Vs*Vm1*Vm2 + (1|PT) + (1|PT:Vs) + (1|PT:Vm1) + (1|PT:Vm2) \\
   + (1|PT:Vs:Vm1) + (1|PT:Vs:Vm2) + (1|PT:Vm1:Vm2) + (1|PT:Vs:Vm1:Vm2) \\
   + (1|SM) + (1|SM:Vp) + (1|SM:Vm1) + (1|SM:Vm2) + (1|SM:Vp:Vm1) \\
   + (1|SM:Vp:Vm2) + (1|SM:Vm1:Vm2) + (1|SM:Vp:Vm1:Vm2) \\
   + (1|PT:SM) + (1|PT:SM:Vm1) + (1|PT:SM:Vm2), \text{data = mydata}) \]

MAX and MAX+

With more than two levels, it is not advisable to use the sum coding for the random part and we must create new factors with the appropriate coding variable. Moreover, \text{lmer} does not handle different type of coding for the fixed part and the random part. We suggest creating new variables with the appropriate coding. Here we choose the orthonormal \text{contr.poly} coding:

```r
mydata$VpPoly <- mydata$Vp; contrasts(mydata$VpPoly) <- contr.poly
mydata$VsPoly <- mydata$Vs; contrasts(mydata$VsPoly) <- contr.poly
mydata$Vm1Poly <- mydata$Vm1; contrasts(mydata$Vm1Poly) <- contr.poly
mydata$Vm2Poly <- mydata$Vm2; contrasts(mydata$Vm2Poly) <- contr.poly
```

\[ \text{lmer}(y \sim Vp*Vs*Vm1*Vm2 + (VsPoly*Vm1Poly*Vm2Poly|PT) \\
   + (VpPoly*Vm1Poly*Vm2Poly|SM) \\
   + (Vm1Poly + Vm2Poly|PT:SM), \text{data = mydata}) \]

ZCP and ZCP+

For ZCP, we transform the factors into orthonormal coding variable. We first need to set the coding using the procedure described in the previous section. Then, we transform the factors into numeric variables using the \text{model.matrix()} function.

```r
dataVp <- \text{data.frame}(\text{model.matrix}( ~ VpPoly, \text{data = mydata})[,-1])
colnames(dataVp) <- c("Xpa", "Xpb")
```

```r
dataVs <- \text{data.frame}(\text{model.matrix}( ~ VsPoly, \text{data = mydata})[,-1])
colnames(dataVs) <- c("Xsa", "Xsb")
```

```r
dataVm1 <- \text{data.frame}(\text{model.matrix}( ~ Vm1Poly, \text{data = mydata})[,-1])
colnames(dataVm1) <- c("Xm1a", "Xm1b")
```

```r
dataVm2 <- \text{data.frame}(\text{model.matrix}( ~ Vm2Poly, \text{data = mydata})[,-1])
colnames(dataVm2) <- c("Xm2a")
```

```r
mydata <- \text{cbind}(mydata, dataVp, dataVs, dataVm1, dataVm2)
```

\[ \text{lmer}(y \sim Vp*Vs*Vm1*Vm2 + ((Xsa + Xsb)*(Xm1a + Xm1b)*Xm2a||PT) \\
   + ((Xpa + Xpb)*(Xm1a + Xm1b)*Xm2a||SM) \\
   + (Xm1a + Xm1b + Xm2a||PT:SM), \text{data = mydata}) \]

gANOVA and gANOVA+

As explained previously, the interaction participant:stimuli should be written as only one variable when we can run the gANOVA function:
mydata$PTSM <- interaction(mydata$PT, mydata$SM)

gANOVA(y ~ Vp*Vs*Vm1*Vm2 + (1|PT|Vs*Vm1*Vm2) + (1|SM|Vp*Vm1*Vm2)
  + (1|PTSM|Vm1+Vm2), data = mydata)

E.3 A complex case, variables $V_P(3)$, $V_S(3)$, $V_{M_1}(3)$, $V_{M_2}(2)$, $V_{PS}(2)$, $V_O(2)$

This design corresponds to model M5 of Table 3. The last interaction term confounded with the error term is the interaction between the 3 variables $V_{M_1}$, $V_{M_2}$, $V_O$ and the participant:stimulus random unit.

RI and RI+

\[
\text{lmer}(y \sim V_P*V_S*V_{M_1}*V_{M_2}*V_{PS}*V_O + (1|PT) + (1|SM) + (1|PT:SM), data = \text{mydata})
\]

RI-L and RI-L+

\[
\text{lmer}(y \sim V_P*V_S*V_{M_1}*V_{M_2}*V_{PS}*V_O + (1|PT) + (1|PT:V_P) + (1|PT:V_{M_1}) + (1|PT:V_{M_2})
  + (1|PT:V_S) + (1|PT:V_{M_1}:V_{M_2}) + (1|PT:V_S:V_{M_1}:V_{M_2}) + (1|PT:V_{PS}) + (1|PT:V_S:V_{PS}) + (1|PT:V_{M_1}:V_{PS})
  + (1|PT:V_{M_2}:V_{PS}) + (1|PT:V_O) + (1|PT:V_{M_1}:V_O) + (1|PT:V_{M_2}:V_O) + (1|PT:V_{PS}:V_O) + (1|PT:V_S:V_{PS}:V_O)
  + (1|PT:V_{M_1}:V_{PS}:V_O) + (1|PT:V_{M_2}:V_{PS}:V_O) + (1|PT:V_S:V_{M_1}:V_{PS}:V_O) + (1|PT:V_{M_1}:V_{M_2}:V_{PS}:V_O)
  + (1|PT:V_S:V_{M_1}:V_{M_2}:V_{PS}:V_O), data = \text{mydata})
\]

MAX and MAX+

We set the orthonormal coding using the following functions. Note that the variables with 2 levels do not need to change from coding of type “sum” to coding of type “polynomial”.

\[
\text{mydata$V_PPoly} \leftarrow \text{mydata$V_P}; \text{contrasts(mydata$V_PPoly)} \leftarrow \text{contr.poly}
\]
\[
\text{mydata$V_SPoly} \leftarrow \text{mydata$V_S}; \text{contrasts(mydata$V_SPoly)} \leftarrow \text{contr.poly}
\]
\[
\text{mydata$V_{M_1}Poly} \leftarrow \text{mydata$V_{M_1}}; \text{contrasts(mydata$V_{M_1Poly})} \leftarrow \text{contr.poly}
\]
\[
\text{mydata$V_{M_2}Poly} \leftarrow \text{mydata$V_{M_2}}; \text{contrasts(mydata$V_{M_2Poly})} \leftarrow \text{contr.poly}
\]
\[
\text{mydata$V_{PSPoly} Poly} \leftarrow \text{mydata$V_{PS}}; \text{contrasts(mydata$V_{PSPoly})} \leftarrow \text{contr.poly}
\]
\[
\text{mydata$V_{OPoly} Poly} \leftarrow \text{mydata$V_O}; \text{contrasts(mydata$V_{OPoly})} \leftarrow \text{contr.poly}
\]

\[
\text{lmer}(y \sim V_P*V_S*V_{M_1}*V_{M_2}*V_{PS}*V_O + (V_SPoly*V_{M_1}Poly*V_{M_2}Poly*V_PPoly*V_OPoly|PT)
  + (V_PPoly*V_{M_1}Poly*V_{M_2}Poly*V_PPoly*V_OPoly|SM)
  + (V_{M_1}Poly + V_{M_2}Poly + V_{OPoly} + V_{M_1}Poly:V_{M_2}Poly + V_{M_1}Poly:V_{OPoly} + V_{M_2}Poly:V_{OPoly}|PT:SM),
  data = \text{mydata})
\]

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ZCP and ZCP+

See the MAX model to change the coding of the factors.

dataVp <- data.frame(model.matrix(~ VpPoly, data = mydata)[-1])
colnames(dataVp) <- c("Xpa", "Xpb")

dataVs <- data.frame(model.matrix(~ VsPoly, data = mydata)[-1])
colnames(dataVs) <- c("Xsa", "Xsb")

dataVm1 <- data.frame(model.matrix(~ Vm1Poly, data = mydata)[-1])
colnames(dataVm1) <- c("Xm1a", "Xm1b")

mydata$Xm2 <- model.matrix(~ Vm2Poly, data = mydata)[-1]
mydata$Xps <- model.matrix(~ VpsPoly, data = mydata)[-1]
mydata$Xo <- model.matrix(~ VoPoly, data = mydata)[-1]

mydata <- cbind(mydata, dataVp, dataVs, dataVm1)

lmer(y ~ Vp*Vs*Vm1*Vm2*Vps*Vo + ((Xsa+Xsb)*(Xm1a+Xm1b)*Xm2*Xps*Xo||PT) + ((Xpa+Xpb)*(Xm1a+Xm1b)*Xm2*Xps*Xo||SM) + ((Xm1a+Xm1b) + Xm2 + Xo + (Xm1a+Xm1b):Xm2 + (Xm1a+Xm1b):Xo + Xm2:Xo||PT:SM), data = mydata)

gANOVA and gANOVA+

mydata$PTSM <- interaction(mydata$PT, mydata$SM)

gANOVA(y ~ Vp*Vs*Vm1*Vm2*Vps*Vo + (1|PT|Vs*Vm1*Vm2*Vps*Vo) + (1|SM|Vp*Vm1*Vm2*Vps*Vo) + (1|PTSM|Vm1 + Vm2 + Vo + Vm1:Vm2 + Vm1:Vo + Vm2:Vo), data = mydata)

References

Agresti, A. and Coull, B. A. (1998). Approximate Is Better than "Exact" for Interval Estimation of Binomial Proportions. The American Statistician, 52(2):119–126.

Baayen, R. H. (2008). Analyzing Linguistic Data: A Practical Introduction to Statistics Using R. Cambridge University Press.

Barr, D. J., Levy, R., Scheepers, C., and Tily, H. J. (2013). Random effects structure for confirmatory hypothesis testing: Keep it maximal. Journal of memory and language, 68(3).

Bates, D., Kliegl, R., Vasishth, S., and Baayen, H. (2015a). Parsimonious mixed models. arXiv preprint arXiv:1506.04967.

Bates, D., Mächler, M., Bolker, B., and Walker, S. (2015b). Fitting Linear Mixed-Effects Models Using lme4. Journal of Statistical Software, 67(1).

Box, G. E. P. (1954). Some Theorems on Quadratic Forms Applied in the Study of Analysis of Variance Problems, I. Effect of Inequality of Variance in the One-Way Classification. The Annals of Mathematical Statistics, 25(2):290–302.

Box, G. E. P. and Draper, N. R. (1987). Empirical Model-Building and Response Surfaces. Wiley.
Brown, M. B. and Forsythe, A. B. (1974). The Anova and Multiple Comparisons for Data with Heterogeneous Variances. *Biometrics*, 30(4):719–724.

Cardinal, R. N. and Aitken, M. R. (2013). *ANOVA for the Behavioral Sciences Researcher*. Psychology Press.

Clark, H. H. (1973). The language-as-fixed-effect fallacy: A critique of language statistics in psychological research. *Journal of verbal learning and verbal behavior*, 12(4):335–359.

Cornfield, J. and Tukey, J. (1956). Average Values of Mean Squares in Factorials. *The Annals of Mathematical Statistics*, 27(4):42.

Efron, B. and Tibshirani, R. J. (1994). *An Introduction to the Bootstrap*. CRC Press.

Erickson, K. I., Voss, M. W., Prakash, R. S., Basak, C., Szabo, A., Chaddock, L., Kim, J. S., Heo, S., Alves, H., White, S. M., Wojcicki, T. R., Maley, E., Vieira, V. J., Martin, S. A., Pence, B. D., Woods, J. A., McAuley, E., and Kramer, A. F. (2011). Exercise training increases size of hippocampus and improves memory. *Proceedings of the National Academy of Sciences*, 108(7):3017–3022.

Gelman, A. (2005). Analysis of variance--why it is more important than ever. *The Annals of Statistics*, 33(1):1–53.

Heritier, S., Cantoni, E., Copt, S., and Victoria-Feser, M.-P. (2009). *Robust Methods in Biostatistics*. Wiley.

Howell, D. C. (2012). *Statistical Methods for Psychology*. Cengage Learning.

Huynh, H. and Feldt, L. S. (1970). Conditions Under Which Mean Square Ratios in Repeated Measurements Designs Have Exact F-Distributions. *Journal of the American Statistical Association*, 65(332):1582–1589.

Huynh, H. and Feldt, L. S. (1976). Estimation of the Box Correction for Degrees of Freedom from Sample Data in Randomized Block and Split-Plot Designs. *Journal of Educational Statistics*, 1(1):69–82.

Judd, C. M., Westfall, J., and Kenny, D. A. (2012). Treating stimuli as a random factor in social psychology: A new and comprehensive solution to a pervasive but largely ignored problem. *Journal of Personality and Social Psychology*, 103(1):54–69.

Kenward, M. G. and Roger, J. H. (1997). Small Sample Inference for Fixed Effects from Restricted Maximum Likelihood. *Biometrics*, 53(3):983.

Khatri, C. G. and Rao, C. R. (1968). Solutions to some functional equations and their applications to characterization of probability distributions. *Sankhyā: The Indian Journal of Statistics, Series A*, pages 167–180.

Koenker, R. and Bassett, G. (1978). Regression Quantiles. *Econometrica*, 46(1):33–50.

Kruskal, W. H. and Wallis, W. A. (1952). Use of Ranks in One-Criterion Variance Analysis. *Journal of the American Statistical Association*, 47(260):583–621.

Kuznetsova, A., Brockhoff, P. B., and Christensen, R. H. (2017). lmerTest package: Tests in linear mixed effects models. *Journal of Statistical Software*, 82(13):1–26.

Lachaud, C. M. and Renaud, O. (2011). A tutorial for analyzing human reaction times: How to filter data, manage missing values, and choose a statistical model. *Applied Psycholinguistics*, 32(2):389–416.

Luke, S. G. (2017). Evaluating significance in linear mixed-effects models in R. *Behavior Research Methods*, 49(4):1494–1502.

Montgomery, D. C. (2017). *Design and Analysis of Experiments*. Wiley.

Nash, J. C. and Varadhan, R. (2011). Unifying optimization algorithms to aid software system users: Optimx for R. *Journal of Statistical Software*, 43(9):1–14.

Nelder, J. A. and Mead, R. (1965). A Simplex Method for Function Minimization. *The Computer Journal*, 7(4):308–313.
Powell, M. J. (2009). The BOBYQA algorithm for bound constrained optimization without derivatives. *Cambridge NA Report NA2009/06, University of Cambridge, Cambridge.*

Raaijmakers, J. G. W., Schrijnemakers, J. M. C., and Gremmen, F. (1999). How to Deal with “The Language-as-Fixed-Effect Fallacy”: Common Misconceptions and Alternative Solutions. *Journal of Memory and Language, 41*(3):416–426.

Rouanet, H. and Lepine, D. (1970). Comparison between treatments in a repeated-measurement design: ANOVA and multivariate methods. *British Journal of Mathematical and Statistical Psychology, 23*(2):147–163.

Schaalje, G. B., McBride, J. B., and Fellingham, G. W. (2002). Adequacy of Approximations to Distributions of Test Statistics in Complex Mixed Linear Models. *Journal of Agricultural, Biological, and Environmental Statistics, 7*(4):512–524.

Tibshirani, R. (1996). Regression Shrinkage and Selection via the Lasso. *Journal of the Royal Statistical Society. Series B (Methodological), 58*(1):267–288.

Welch, B. L. (1947). The generalization of 'student’s’ problem when several different population variances are involved. *Biometrika, 34*(1-2):28–35.

Welch, B. L. (1951). On the Comparison of Several Mean Values: An Alternative Approach. *Biometrika, 38*(3/4):330–336.

Wilcoxon, F. (1945). Individual Comparisons by Ranking Methods. *Biometrics Bulletin, 1*(6):80–83.

Wilson, J. P., Hugenberg, K., and Rule, N. O. (2017). Racial bias in judgments of physical size and formidability: From size to threat. *Journal of Personality and Social Psychology, 113*(1):59–80.

Winer, B. J. (1962). *Statistical Principles in Experimental Design.* McGraw-Hill Book Company.