Conjugate distributions in hierarchical Bayesian ANOVA for computational efficiency and assessments of both practical and statistical significance

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Abstract Assessing variability according to distinct factors in data is a fundamental technique of statistics. The method commonly regarded to as analysis of variance (ANOVA) is, however, typically confined to the case where all levels of a factor are present in the data (i.e. the population of factor levels has been exhausted). Random and mixed effects models are used for more elaborate cases, but require distinct nomenclature, concepts and theory, as well as distinct inferential procedures. Following a hierarchical Bayesian approach, a comprehensive ANOVA framework is shown, which unifies the above statistical models, emphasizes practical rather than statistical significance, addresses issues of parameter identifiability for random effects, and provides straightforward computational procedures for inferential steps. Although this is done in a rigorous manner the contents herein can be seen as ideological in supporting a shift in the approach taken towards analysis of variance.

Keywords: ANOVA; fixed effects; random effects; variance components; hierarchical Bayes; multilevel model; constraints

1 Introduction

As an independent field of study Statistics is rather young. Many of the methods, techniques, and philosophies can be attributed to a handful of statisticians during the first
half of the twentieth century. Among these, R.A. Fisher is often recognized as having had a profound influence on the field. It has been said that Fisher single-handedly created the foundations of modern statistical science (Hald, 1998). For statisticians the first contribution that comes to mind is his work in development of likelihood theory. However, for the greater scientific community, one might consider his formulation of analysis of variance as the most significant contribution.

As much of Fisher’s work was in agriculture, an apt example to consider is the one-way ANOVA, $Y_{ij} = \mu + \alpha_i + \epsilon_{ij}$, in which observations are on crop yield, with $i$, $j$ representing the $j^{th}$ plant receiving fertilizer treatment $i$. An appropriate decomposition of the data should then reveal the variability due to different fertilizers while accounting for variability within plant groups that receive the same type of fertilizer treatment. Thus, analysis of variance is essentially a pragmatic decomposition of the data. In correspondence Fisher has been cited (Searle et al., 1992) to have said,

“The analysis of variance is (not a mathematical theorem but) a simple method of arranging arithmetical facts so as to isolate and display the essential features of a body of data with the utmost simplicity.”

The elegance and power of this methodology is perhaps what has caused ANOVA to become so popular in nearly all areas of scientific research. However, along with the ubiquitous support of the methodology has come a pervasive reliance on its conclusory result, the $p$-value. Recognition of this problem is not new. It has been long noted by researchers in other fields that the hypothesis-based point of view, which relies on statistical significance, should be amended. (Yoccoz, 1991; Fidler et al., 2004; Ioannidis, 2005). The statistical community has also long acknowledged the need to provide methodologies that are first and foremost, “of use to scientists in making quantitative inferences,” (Nelder, 1999). The problem is that the standard methods that continue to be imparted on students focus on statistical significance. As stated by Savage (1957), a method that does so “simply reflects the size of the sample and the power of the test, and is not a contribution to science.” Thus, any standard, or default methodology that aims to decompose variation present in a set of observations according to factors of interest,
should be able to address practical significance as well.

In addition to the base objective of analysis of variance, to decompose variation in observations according to distinct sources of variability, a default method used in initial/exploratory work should accomplish the following.

- Allow for each factor to simultaneously consider variability due to the observed set of effects (finite population variance), as well as the variability from unobserved effects (superpopulation variance), thereby permitting greater flexibility in model choice with regards to fixed or random effects.

- Facilitate comparison of magnitude of variability across all factors in the model, including errors, so that attention may be given to practical significance as well as statistical significance of a factor.

- Provide ability to consider both magnitude and uncertainty of variance parameters in the model, by providing confidence, or uncertainty intervals in a default analysis summary.

These are precisely the goals of the analysis of variance framework proposed in this paper. While the primary contribution may be seen as ideological in nature, there are technical issues that are addressed to allow for a shift in the standard approach taken towards the basic method of analysis of variance. By standard approach one may assume the tabular analysis of variance summary and its accompanying test of statistical significance.

The organization of the paper is as follows. Section 2 covers basic concepts of standard methods that are both widely taught and employed, as well as recent shifts in the practice of ANOVA. Section 3 presents an alternative framework of ANOVA along with modifications to the standard ANOVA table summary. Section 4 illustrates our method and compares it to the classical approaches. In particular, we present an example in which classical ANOVA yields identical p-values for two cases; one in which the factor under investigation has low practical significance, and one with high practical significance.
2 Background

Following Fisher’s analysis of variance overall uncertainty is attributed to distinct factors of an experiment through the use of a sum of squares decomposition. This is now shown with the balanced one-way analysis of variance model

$$Y_{ij} = \mu + \alpha_i + \epsilon_{ij}, \quad i = 1, \ldots, n_I, \quad j = 1, \ldots, n_J.$$  \hspace{1cm} (1)

As a seminal example consider observations that are on crop yield with $i, j$ representing the $j^{th}$ plant receiving fertilizer treatment $i$. More generally the indices represent a factor level $i$ and replicate $j$. The appropriate decomposition of the data, which reveals variability due to different fertilizers while accounting for variability within plant groups that receive the same type of fertilizer treatment, is done with the arithmetical arrangement that summarizes yield for each type, $\bar{Y}_i = n_J^{-1} \sum_j Y_{ij}$, and for overall yield, $\bar{Y}_.. = n^{-1} \sum_i \sum_j Y_{ij} = n_I^{-1} \sum_i \bar{Y}_i$, where $n = n_I \cdot n_J$. Observations $Y_{ij}$ are decomposed with the identity

$$Y_{ij} - \bar{Y}_.. = (Y_{ij} - \bar{Y}_i) + (\bar{Y}_i - \bar{Y}_..).$$  \hspace{1cm} (2)

Terms are then squared and summed, noting that the cross term on the right hand side equals zero, so that a decomposition of the mean-adjusted sums of squares is

$$\sum_{i,j} (Y_{ij} - \bar{Y}_..)^2 = \sum_{i,j} (Y_{ij} - \bar{Y}_i)^2 + n_J \sum_i (\bar{Y}_i - \bar{Y}_..)^2,$$  \hspace{1cm} (3)

where $\bar{Y}_i$ is the mean within group $i$ and $\bar{Y}_..$ is the mean of all observations. The terms SST, SSA, and SSE denote total (adjusted) sum of squares, sum of squares among groups, and sum of squared errors, respectively. Note that each of these terms is itself a sum of squares that is analogous to a sample variance $s^2 = k^{-1} \sum_{i=1}^k (x_i - \bar{x})^2$, for a set of independent observations $x_1, \ldots, x_k$, and is thus proportional to a $\chi^2$ distribution with appropriate degrees of freedom. Fisher showed that SSA and SSE are both proportional to $\chi^2$ distributions, with $n_I - 1$ and $n - n_I$ degrees of freedom, respectively, and that they are independent, the general result of which is due to Cochran [1934].

While this classical methodology provides a means to examine statistical significance, it does not provide any formal assessment of practical significance. Loosely speaking,
practical significance can be considered as a contextual basis that allows data-specific conclusions to be drawn, i.e. evidence that SSA is substantial compared, not only to zero, but to SSE as well. Practical significance in the example above implies that the variability due to the fertilizer treatment is not only significantly different than no treatment, but that when compared to plant-to-plant variability it is still significant. One contribution of this paper is in attempting to formalize a statistical methodology that rigorously provides a method of assessing practical significance.

2.1 Conventional Methods

A fixed effects model generally refers to the case when the observations have exhausted the population of factor levels (e.g. treatments), or when interest lies only with the factor levels that have been observed. Alternatively, random effects models are employed when it is assumed that the factor levels are a subset of a greater population of possible levels. This definition provided by Hoaglin et al. (1991, p.195) is somewhat more explicit than that given by Eisenhart (1947), in which the effects of a model are considered to be fixed when they are all nonrandom, and considered to be random when they are all random. There exist many other definitions in the literature, some of which are not compatible. See Gelman (2005) for a summary.

2.1.1 Fixed Effects

Consider the model given by (1) such that $i = 1, \ldots, n_I$ denotes the factor level or treatment, and $j = 1, \ldots, n_J$ denotes replications or errors. Observations are assumed to be independent across replicates as well as across factor levels. Additionally, it is generally assumed that

$$
\epsilon_{ij} \sim N(0, \sigma^2). \quad (4)
$$

Analysis of variance generally aims to test the hypothesis that there is no difference among the treatments,

$$
H_0 : \alpha_1 = \cdots = \alpha_{n_I} = 0, \quad (5)
$$
against the alternative hypothesis that at least one treatment level differs. The test is a result of the sums of squares decomposition in [3], since \( \frac{\text{SSE}}{\sigma^2} \sim \chi^2_{n-n_I} \), where \( n = n_I \cdot n_J \). The expectation of these two terms is \( \frac{n_J}{n_I-1} \sum_i \alpha_i^2 + \sigma^2_\epsilon \) and \( \sigma^2_\epsilon \), respectively. The test of \( H_0 \) is then carried out using the \( F \) distributed ratio \( \frac{\text{MSA}}{\text{MSE}} \), where \( \text{MSA} = \frac{\text{SSA}}{n_I-1} \) and \( \text{MSE} = \frac{\text{SSE}}{n-n_I} \). The term MSA is central \( \chi^2_{n_I-1} \) distributed when (5) is true, and non-central with shift of \( \frac{n_J}{n_I-1} \sum_i \alpha_i^2 + \sigma^2_\epsilon \) when false.

The results described are concisely displayed in a tabular format (Fisher, 1925), as seen in Table 1. The table culminates with (5) being tested based on the \( p \)-value of \( p = \Pr(F_{n_I-1,n-n_I} > F) \), which does not give any indication of the practical significance. And despite recognition of the need to focus on effect sizes and confidence intervals (Gardner and Altman, 1986; Nakagawa and Cuthill, 2007) rather than testing, the table remains a staple among statistical methodologies.

Table 1: One-way analysis of variance.

| Source    | Df  | Sum Sq | Mean Sq | F value | Pr(>F)     |
|-----------|-----|--------|---------|---------|------------|
| Factor A  | \( n_I - 1 \) | SSA    | MSA     | \( F = \frac{\text{MSA}}{\text{MSE}} \) | \( \Pr(F_{n_I-1,n-n_I} > F) \) |
| Errors    | \( n - n_I \) | SSE    | MSE     |         |            |

### 2.1.2 Random Effects

In addition to the statistical model (1) and distributional assumption (4), there is an additional assumption on the factor levels,

\[
\alpha_i \sim N(0, \sigma^2_\alpha), \quad i = 1, \ldots n_I, \tag{6}
\]

with \( \alpha_i \) and \( \epsilon_{ij} \) independent. Observations are then normally distributed with mean and variance

\[
\begin{align*}
\text{E}[Y_{ij}] &= \mu, \\
\text{Cov}(Y_{ij}, Y_{i'j'}) &= \begin{cases} 
\sigma^2_\alpha + \sigma^2_\epsilon & i = i', j = j', \\
\sigma^2_\alpha & i = i', j \neq j', \\
0 & i \neq i'.
\end{cases}
\end{align*}
\]
This parameterization has the added benefit that the parameter space for the factor levels is reduced from \(n_I\) to 1, since only \(\sigma_\alpha^2\) is estimated. Although individual levels, \(\alpha_i\), may be predicted if necessary. Averaging over replications at factor level \(i\) yields the mean \(\bar{Y}_i\), which are independently distributed \(N(\mu, \sigma_\alpha^2)\), where \(\sigma_\alpha^2 = \sigma_\alpha^2 + \sigma_\epsilon^2/n_J\). Thus, the likelihood is a function of the three parameters \(\mu, \sigma_\epsilon^2\), and \(\sigma_\alpha^2\).

Analogous to (5), the initial inquiry of interest is generally concerned with whether greater population variance \(\sigma_\alpha^2\) is significantly different from zero. This corresponds to the null hypothesis

\[
H_0 : \sigma_\alpha^2 = 0,
\]

and is tested using the same F-statistic as for (5) (Searle et al. 1992; Rao 1997; Cox and Solomon 2003). Aside from its unintuitive nature, in that despite being random vs. fixed the same test statistic is used, this hypothesis test does little to remark on the practical significance of the variation due to factor \(\alpha\). Namely, the hypothesis may be rejected even when variation due to the errors is substantially greater, as seen in the example of Section 4.2.

Further inferential procedures on the variance components themselves are typically based on method of moments estimators, or explicitly use the likelihood. In the latter case, variability of the variance components are estimated with the Hessian of the likelihood, as with the widely used R packages nlme (Pinheiro et al. 2006) and lme4 (Bates and DebRoy 2004). Wald-type confidence intervals can be then used to obtain confidence regions for the parameters. Similarly, the asymptotic properties of the log likelihood can be utilized to obtain confidence intervals using the \(\chi^2\) distribution, as seen in Figure 2 of Section 4.1.

### 2.1.3 Issues and Concerns

The choice to use a fixed or random effects model is not always immediately clear. The terminology alone may be seen as ambiguous since the distinction between fixed effects, random effects, and mixed effects is somewhat malleable. The simple fixed effects model of Section 2.1.1 can be seen as having a random component in the errors, \(\epsilon_{ij}\). Similarly, the random effects model of Section 2.1.2 can be seen as having a fixed component, \(\mu\). In
both cases implying a mixed effects model. In practice a mixed effects model is employed when there are two or more factors, other than overall mean and errors, and they are not all fixed (random).

More difficult perhaps is determining when which of these methods should be used. If interest lies in the distribution of the random effects, i.e. the variance component $\sigma^2_\alpha$, then a random effects model should be chosen. If interest lies in the realized/observed levels of the factor, then a fixed effects model is used. If both are of interest, then the random effects should be chosen and levels are then predicted, rather than estimated. Searle et al. (1992, p18) take a pragmatic approach to this by recommending that in any case in which it is reasonable to assume that the levels of the factor come from a probability distribution, i.e. that $\sigma^2_\alpha$ may be assumed, then a random effects model should be chosen. The usage of a random effects model, however, typically precludes the estimation of the finite population variance.

An additional problem that arises in analysis of variance with several factors is the so-called ‘mixed models controversy’ (Voss, 1999; Lencina et al., 2005; Nelder, 2008). The problem essentially comes down to how a hypothesis test of a random effect is carried out when an interaction is also present in the model.

To resolve the issues above we support the notion of Gelman (2005), in that all factors in the model are treated as random. The procedural steps are then carried out equivalently. If interest is in the observed (unobserved) levels of a factor, then the greater focus is given to the finite (super) population variance. However, because of parameter dependencies involved in the unconstrained factor levels, Gelman recommends using MCMC, in which redundant parameterization is used in order to reduce dependencies and to speed up posterior sampling. Alternatively, we recommend using constraints to define an improper joint prior distribution on the factor levels, thereby eliminating the need for complex MCMC procedures, as in Geinitz et al. (2012).

2.2 Multilevel Models

Often times the results of an analysis should allow for simultaneous consideration of both group level and individual level variability, e.g. variability according to schools and
to students within schools. Applications of such scenarios initially arose in the social sciences (Goldstein, 1995; Kreft et al., 1998; Snijders and Bosker, 2011), but have also included the health sciences (Von Korff et al., 1992; Greenland, 2000), and have provided the basis for much of the work in multilevel models.

A multilevel model can be seen as a linear model with coefficients, i.e. factor levels, that are themselves modeled (Gelman and Hill, 2006). More generally, this can be considered as a type of hierarchical Bayesian approach. However, while not explicit, the multilevel point of view is useful in considering a generalized approach towards analysis of variance. Because the simultaneous consideration of group and individual level variability entails the decomposition of variation according to each of these sources, “ANOVA is fundamentally about multilevel modeling” (Gelman, 2005). That is to say, analysis of variance from the viewpoint of multilevel models allows for both finite population and superpopulation variance components to be considered, which can be seen as a unification of fixed and random effects. This comprehensive approach to analysis of variance yields useful results and has been used in other fields such as ecology (Qian and Shen, 2007), genetics (Leinonen et al., 2008), and climate (Sain et al., 2011).

In practice there have been some hindrances in the adoption of this more general approach to ANOVA. Computational procedures to carry out such an analysis typically rely on either mixed effects models (e.g. lme4 package in R) or on MCMC methods (e.g. WinBUGS). However, while mixed effects models can be used to obtain initial estimates of the parameters in a multilevel model, inferential steps, e.g. confidence intervals, for variance parameters are often done through likelihood approximation. For more explicit inferential procedures it is necessary to use MCMC methods (Gelman and Hill, 2006, p.566). Although the added complexity and computation of MCMC, particularly when the use is as an exploratory analysis step, can be a deterrent to this approach. A method that is both precise in its inferential statements while being straightforward to implement is not widely known.
2.3 Bayesian Results

The hierarchical approach towards analysis of variance can be explained most readily in a Bayesian framework. In an effort to explain this approach in a classical inference framework Gelman (2005) recommends a simulation approach, which is reminiscent of posterior sampling. Because we prefer to adopt an explicit Bayesian approach, we now review some results on distributions for variance components that facilitate the procedure.

2.3.1 Prior Distributions

For the normally distributed random variable $Y \sim N(\mu, \sigma^2)$, prior specification of the parameters can be done in many different ways. Initially, consider $\mu, \sigma^2$ to be either known or unknown, each in turn. Following the invariance principle (Jeffreys, 1946), prior distributions in univariate cases are then

$$
\mu \text{ known, } \sigma^2 \text{ unknown: } p(\mu) \propto \text{const},
$$

$$
\mu \text{ unknown, } \sigma^2 \text{ known: } p(\sigma^2) \propto (\sigma^2)^{-1}.
$$

Box and Tiao (1992, p.43) derive same priors using the concept of location and scale parameters. These identical priors are also found using the reference approach of Bernardo and Smith (2000, p314), due to asymptotic normality of the posterior distributions.

Note that the density of $p(\sigma^2) = (\sigma^2)^{-1}$ corresponds to an inverse-gamma distribution, $\Gamma^{-1}(u,v)$, with $u = v = 0$. Common values of hyperparameters have thus been limiting forms thereof, such as $u = v = \varepsilon$, with $\varepsilon$ small (Lunn et al., 2000). If prior independence between $\mu$ and $\sigma^2$ is assumed, then the two univariate priors are combined for

$$
p(\mu, \sigma^2) = p(\mu)p(\sigma^2) \propto (\sigma^2)^{-1}.
$$

(8)

Alternatively, Jeffreys’ prior for multivariate parameters $\theta = (\mu, \sigma^2)^T$ without independence leads to

$$
p(\mu, \sigma^2) \propto (\sigma^2)^{-3/2}.
$$

(9)

These correspond to $\sigma^2 \sim \Gamma^{-1}(u,v)$, with $u = v = 0$ for the prior given by (8), and $u = \frac{1}{2}, v = 0$ for the prior given by (9).
Box and Tiao (1992, p. 251) decompose the likelihood by group means, e.g. \( Y_i \), to place a prior directly on \( \sigma^2_{\alpha} \). The joint prior distribution for \( \mu, \sigma^2, \sigma^2_{\alpha} \) is then

\[
p(\mu, \sigma^2, \sigma^2_{\alpha}) \propto (\sigma^2_{\alpha})^{-1}.
\]

Additionally, Jeffreys’ independence prior of the original variance parameters \( (\sigma^2_{\epsilon}, \sigma^2_{\alpha}) \) also leads to (10) (Box and Tiao, 1992). The multivariate analog of this has been used as well by Everson and Morris (2000). Naturally, a prior may also be placed directly on the parameter \( \sigma^2_{\alpha} \), although the posterior may no longer be as simple to work with.

### 2.3.2 Conjugacy

For observations, \( Y_i \sim N(\mu, \sigma^2), i = 1, \ldots, n \), a multivariate conjugate prior for the parameter \( \theta = (\mu, \sigma^2)^T \) is a normal-inverse-gamma distribution, denoted as \( \text{NIG}(\mu_0, \tau, u, v) \) with \( \tau > 0 \). More specifically,

\[
\mu | \sigma^2 \sim N(\mu_0, \frac{\sigma^2}{\tau}),
\]

\[
\sigma^2 \sim \Gamma^{-1}(u, v),
\]

with joint density,

\[
p(\mu, \sigma^2) = p(\mu | \sigma^2) \cdot p(\sigma^2) = (2\pi \tau)^{-1/2} \exp \left( -\frac{\tau}{2\sigma^2} (\mu - \mu_0)^2 \right) \cdot \frac{v^u}{\Gamma(u)} (\sigma^2)^{-u-1} \exp \left( -\frac{v}{\sigma^2} \right).
\]

Priors corresponding to (8) and (9) are then denoted by \( \text{NIG}(0, 0, 0, 0) \) and by \( \text{NIG}(0, 0, 0, 0) \), respectively. Conjugate priors of this form have been used extensively, although often with precision, \( \tau = (\sigma^2)^{-1} \), resulting in a normal-gamma distribution (Bernardo and Smith, 2000, p.136). The utility of this general parameterization is in being able to conform to different prior specifications while maintaining conjugacy. The full model with likelihood and prior is posterior is

\[
Y | \mu, \sigma^2 \sim N(\mu, \sigma^2),
\]

\[
(\mu, \sigma^2) \sim \text{NIG}(\mu_0, \tau, u, v),
\]
with posterior distribution given by

\[
(\mu, \sigma^2) \mid Y \sim \mathcal{N}(\tau \mu_0 + n\bar{y}, \tau + n, u + \frac{n}{2}, v + \frac{1}{2} \left[ \sum_i (y_i - \bar{y})^2 + \frac{(\bar{y} - \mu_0)^2}{n^{-1} + \tau^{-1}} \right])
\]

(16)

3 Comprehensive ANOVA

Following the view of Gelman (2005) we see the hierarchical Bayesian approach towards ANOVA (Section 2.2) as a means to unify the two distinct fixed and random effects models. In addition to the hierarchical model structure a Bayesian model specification is intuitive and practical. By following this approach the challenges discussed in Section 2.1.3 are resolved.

Hierarchical Bayesian models are typically considered simply as mixed effects models within the statistical community. However, because mixed effects models do not typically provide assessments of uncertainty of the variance component estimates, nor is variability of the observed set of factor levels examined by default, we do not see this as truly providing a comprehensive approach towards ANOVA. As stated, multilevel modeling seems to be a more natural strategy. As a result much of the work with multilevel models, including analysis of variance according to various factors, has largely taken place in other domains, primarily the social sciences (Goldstein 1995, Gelman and Hill 2006, Snijders and Bosker 2011). This can be seen as a failure of the statisticians, as Huber (2011) states, “the consequences of not being able to adequately summarize and disseminate common methodologies may be a divergence of statistics, that each field develops its own version of statistics.” By presenting ANOVA in a more general hierarchical framework we are also, “unifying the philosophies, concepts, statistical methods, and computational tools” (Lindsay et al., 2004).

The unification of fixed and random effect models is clearly seen in the graphical model of Figure 1. The successive layers of distributional assumptions is shown clearly here. The inner-most box represents the fixed effects model, while the middle box represents the random effects model. The hierarchical Bayesian ANOVA model, or simply comprehensive ANOVA, is then represented by the outer-most box. The diagram explicitly shows the
Figure 1: Graphical model representing successive assumptions for the fixed effect (inner box), random effect (middle box), and fully Bayesian (outer box) specifications.

unification of the models and immediately conveys a general view of ANOVA to students and researchers not familiar with variance analyses. The notation created by Eisenhart (1947) is here, where ANOVA\textsubscript{1} corresponds to M\textsubscript{1}, the fixed effects model; and M\textsubscript{2} to ANOVA\textsubscript{2}, the random effects model. Instead of M\textsubscript{3}, which refers to a mixed effects model, we have chosen to allow ANOVA\textsubscript{3} to refer to a fully Bayesian parameterization. This can be confusing though, as Cox and Solomon (2003) have pointed out, “Occasionally the word Bayesian is used for any analysis involving more than one level of random variation.” We agree with them, in that this can seem quite confusing, but nonetheless consider ANOVA\textsubscript{3} as a Bayesian analysis of variance procedure.

Analysis of variance in this framework allows the questions discussed in the Introduction to be addressed, and also resolves many of the issues discussed in Section 2.1.3. Gelman (2005) presents graphical summaries of this ANOVA approach that allow for visual comparison of confidence intervals for the variance components, which is possible for both finite and superpopulation variance parameters. In Table 2, a proposed alternative to the traditional ANOVA table is shown. Commonly significance in the classical ANOVA table is merely a function of power. That is, given enough observations, nearly any effect will be deemed as statistically significant. Alternatively, Table 2 provides estimates of the variance parameters, both finite and superpopulation, as well as a probabilistic
assessment of practical significance. This is done with a direct comparison of posterior distributions of all variance components against the error variance $\sigma^2$. A probability regarding hypothesis (1), i.e. that the superpopulation variance $\sigma^2_\alpha$ is equal to zero, can be given as well. This probability, $\Pr(\sigma^2_\alpha = 0|Y)$, thus provides an assessment of statistical significance.

3.1 One-way Model

In the case of a single source of variation, as in model (1), the model can be stated as $Y_{ij} = \alpha_i + \epsilon_{ij}$. To illustrate the basic point of view of our ANOVA approach we first focus on this problem.

3.1.1 Model Specification

A particularly useful parameterization in the one-way configuration, that allows different variance parameterizations while maintaining conjugacy, is an extension of the normal-inverse-gamma distribution. This involves an additional inverse-gamma distribution for the added variance component. The resulting distribution is given by

$$\alpha_i \mid \alpha_0, \tau_\alpha, \tau_\epsilon, \sigma^2_\alpha, \sigma^2_\epsilon \sim \mathcal{N}\left(\alpha_0, \left[\frac{\tau_\alpha}{\sigma^2_\alpha} + \frac{\tau_\epsilon}{\sigma^2_\epsilon}\right]^{-1}\right),$$

$$\sigma^2_\alpha \mid \sigma^2_\epsilon \sim \Gamma^{-1}(u_\alpha, v_\alpha),$$

$$\sigma^2_\epsilon \sim \Gamma^{-1}(u_\epsilon, v_\epsilon).$$

Table 2: Comprehensive ANOVA summary utilizing posterior distributions to obtain a summary of variance parameters (in units of standard deviation). Quantiles are used to provide a type of confidence interval. The probability $\Pr(\sigma_\alpha > \sigma_\epsilon|Y)$ provides an assessment on practical significance for the parameter.

| Parameter | Mean | Median | Uncertainty Interval | Sig. Rel. to Errors |
|-----------|------|--------|----------------------|--------------------|
| $\alpha$ (finite) $s_\alpha$ | $E[s_\alpha|Y]$ | $Q_{0.5}[s_\alpha|Y]$ | $(Q_{0.025}[s_\alpha|Y], Q_{0.975}[s_\alpha|Y])$ | $\Pr(s_\alpha > \sigma_\epsilon|Y)$ |
| (super) $\sigma_\alpha$ | $E[\sigma_\alpha|Y]$ | $Q_{0.5}[\sigma_\alpha|Y]$ | $(Q_{0.025}[\sigma_\alpha|Y], Q_{0.975}[\sigma_\alpha|Y])$ | $\Pr(\sigma_\alpha > \sigma_\epsilon|Y)$ |
| $\epsilon$ $\sigma_\epsilon$ | $E[\sigma_\epsilon|Y]$ | $Q_{0.5}[\sigma_\epsilon|Y]$ | $(Q_{0.025}[\sigma_\epsilon|Y], Q_{0.975}[\sigma_\epsilon|Y])$ | $-$ |
with $i = 1, \ldots, n_I$ corresponding to the number of groups, and additional parameter $\kappa_\epsilon$ such that $\sigma^2_{ae} = \sigma^2_a + \kappa_\epsilon \sigma^2_\epsilon$. Noting that $\sigma^2_{ae}$ is analogous to the variance of mean of the observations at an individual factor level, as in Section 2.1.2.

The variance parameters and factor levels can then be jointly specified as a combination of normal and inverse gamma distributions, i.e. $\text{N}^{\Gamma^{-1}}(\alpha_0, \tau_\alpha, \tau_\epsilon, \kappa_\epsilon, v_\alpha, u_\alpha, u_\epsilon, v_\epsilon)$, with certain values of hyperparameters, or limits thereof, yielding different prior specifications such as those discussed earlier.

This is in general, however, not a conjugate model specification, i.e. the posterior distribution will not be of the same family as the prior distribution. Although the posterior $\sigma^2_\epsilon$ continues to follow an inverse-gamma distribution, with density

$$
p(\sigma^2_\epsilon \mid Y) \propto (\sigma^2_\epsilon)^{-u_\epsilon - n - n_I/2} \exp \left( -1 \frac{1}{\sigma^2_\epsilon} \left[ v_\epsilon + \frac{1}{2} \sum_{ij} (y_{ij} - \hat{\alpha}_i)^2 \right] \right),$$

the posterior distribution of $\sigma^2_a + \kappa_\epsilon \sigma^2_\epsilon$ will not be the same type as its prior for arbitrary values of hyperparameters $\tau_\epsilon, \kappa_\epsilon$. More specifically, the posterior density of $\sigma^2_a$ is

$$
p(\sigma^2_a \mid Y, \sigma^2_\epsilon) \propto (\sigma^2_a + \kappa_\epsilon \sigma^2_\epsilon)^{-u_a - 1} \left( \frac{\sigma^2}{n_J} \right)^{-n_I/2} \times \exp \left( -1 \frac{1}{\sigma^2_a + \kappa_\epsilon \sigma^2_\epsilon} \left[ v_a + \frac{1}{2} \sum_i (\hat{\alpha}_i - \alpha_0)^2 \right] \right),$$

where $\varsigma^2_{ae} = \left( \frac{v_\alpha}{\sigma^2_a} + \frac{v_\epsilon}{\sigma^2_\epsilon} \right)^{-1}$, which can be seen as a type of shifted inverse-gamma distribution. However, rather than normalizing the posterior density so that it is proper when constrained to non-negative values, it is often more informative to consider a mass point at zero; allowing for the hypothesis (7) to be tested (see Section 4).

Each individual $\alpha_i$ is however normally distributed, with posterior density

$$
p(\alpha_i \mid Y, \sigma^2_\epsilon, \sigma^2_a) \propto Q^{1/2} \exp \left( -\frac{Q}{2} \left[ \alpha_i - Q^{-1} \left( \frac{1}{\varsigma^2_{ae}} \alpha_0 + \frac{n_J}{\sigma^2_a} \hat{\alpha}_i \right) \right]^2 \right),$$

where $Q = \frac{1}{\varsigma^2_{ae}} + \frac{n_J}{\sigma^2_a} = \frac{v_\alpha}{\sigma^2_a} + \frac{v_a n_J}{\sigma^2_a}.$

### 3.1.2 Conjugate Prior

Setting $\tau_\epsilon = 0, \kappa_\epsilon = \frac{v_\epsilon}{n_J}$, for the prior and likelihood

$$
(\alpha_i, \sigma^2_a, \sigma^2_\epsilon) \sim \text{N}^{\Gamma^{-1}}(\alpha_0, \tau_\alpha, \tau_\epsilon = 0, \kappa_\epsilon = \frac{\tau_\alpha}{n_J}, u_\alpha, v_\alpha, u_\epsilon, v_\epsilon), \quad (20)
$$

$$
Y_{ij} \mid \alpha_i, \sigma^2_\epsilon \sim \text{N}(\alpha_i, \sigma^2_\epsilon), \quad (21)
$$
gives way to the posterior distribution
\[
(\alpha_i, \sigma^2_{\alpha}, \sigma^2_{\epsilon}) \mid Y \sim N \Gamma^{-1} \Gamma^{-1} \left( \left[ \frac{\tau_{\alpha}}{\sigma^2_{\alpha}} + \frac{n_J}{\sigma^2_{\epsilon}} \right]^{-1} \left[ \frac{\tau_{\alpha}}{\sigma^2_{\alpha}} \alpha_0 + \frac{n_J}{\sigma^2_{\epsilon}} \hat{\alpha}_i \right], \tau_{\alpha}, n_J, \frac{\tau_{\alpha}}{n_J}, u_{\alpha} + \frac{n_J}{2}, \right.
\]
\[
v_{\alpha} + \frac{\tau_{\alpha}}{2} \sum_i (\hat{\alpha}_i - \alpha_0)^2, \ u_{\epsilon} + \frac{n - n_J}{2}, \ v_{\epsilon} + \frac{1}{2} \sum_{ij} (y_{ij} - \hat{\alpha}_i)^2, \]
(22)
thus maintaining conjugacy. Particularly beneficial is that with this factorization there is no need for MCMC sampling. Rather, posterior draws can be taken immediately without burn-in nor thinning. A single realization from the joint posterior is found by sampling from \(p(\sigma^2_{\epsilon} \mid Y), p(\sigma^2_{\alpha} \mid Y, \sigma^2_{\epsilon}), \) and then \(p(\alpha_i \mid Y, \sigma^2_{\epsilon}, \sigma^2_{\alpha})\) using (19), (18), (17) with the parameters updated using the observations.

Selecting appropriate values hyperparameters can then be done as follows. For invariant priors of variance parameters \(u_{\alpha} = v_{\alpha} = u_{\epsilon} = v_{\epsilon} = 0\) is used. To maintain conjugacy \(\tau_{\epsilon} = 0, \kappa_{\epsilon} = \frac{\tau_{\alpha}}{n_J}\) is used. Practical values of \(\tau_{\alpha}\) and \(\alpha_0\) may then be found using an empirical Bayes approach and yield \(\tau_{\alpha} = 1\) and \(\alpha_0 = n_J^{-1} \sum_i \hat{\alpha}_i, \) i.e. the overall mean.

For more general models, with a mean term, additional factors, interactions, etc., it is possible to consider several such normal–inverse-gamma–inverse-gamma distributions, where the single inverse-gamma distribution of the errors, \(\sigma^2_{\epsilon},\) is common to all. One may then use a prior distribution for the factor levels under a linear constraint so that the posterior distributions can also be factored similarly. This allows not only for conjugacy, but also facilitates computation in a way that even for models with many factors, samples from the posterior can efficiently be drawn without the need for MCMC. This is seen in Geinitz et al. (2012).

4 Examples

4.1 Rails Data

For illustration of the various analysis variance methods consider the balanced one-way design for data consisting of six railway rails (Devore, 2000; Pinheiro and Bates, 2000). Each rail has been measured three times for the amount of time that it takes a certain
type of ultrasonic wave to travel the length of the rail. The objective of any initial analysis is most likely to investigate the (a) variation due to measurement error and (b) variation due to the rails themselves in terms of both statistical and practical significance. Additionally, one may be interested predicting travel time for a future measurement. This can be considered for either (c) one of these rails as well as (d) a future rail that has not yet been seen. For this one-way analysis we consider the simple cell-means model

$$Y_{ij} = \alpha_i + \epsilon_{ij}, \quad i = 1, \ldots, 6, \quad j = 1, 2, 3.$$  

\(23\)

4.1.1 Conventional Methods

For this one-way model error terms \(\epsilon_{ij}\) are assumed to be iid \(N(0, \sigma^2_\epsilon)\), and group terms \(\alpha_i\) as unknown constants, so that the observations are

$$Y_{ij} | \alpha_i, \sigma^2_\epsilon \sim N(\alpha_i, \sigma^2_\epsilon).$$  

\(24\)

The model assumes that the six rails that have been observed are the only rails that are of interest. This is a fixed effects model, which is to say that the population of rails has been exhausted by the sample.

Questions (a) and (b) can be reasonably addressed using this model, although purely from a statistically significant point of view. Results (see Table 3) indicate that the hypothesis (5) should be rejected, but are not able to say anything explicitly about the practical significance of the rails.

|        | Df | Sum Sq | Mean Sq | F value | Pr(>F)   |
|--------|----|--------|---------|---------|----------|
| Rail   | 5  | 9310.50| 1862.10 | 115.18  | 0.000000 |
| Residuals | 12 | 194.00 | 16.17   |         |          |

Table 3: One-way ANOVA of Railway Rails

Question (c) could be answered by looking at the standard error for the estimate \(\hat{\alpha}_i\), to obtain an estimate of the expected travel time. Question (d) can, however, not be answered because of the assumed fixed effect. To address this question the rails must be considered as a random effect, i.e. assumed to come from a greater population of rails.
Alternatively a random effects model may be used, in which the between-rail variability for a large, potentially infinite (super) population of rails is of interest. The hypothesis to be tested is then \( H_0 \) and, as discussed in Section 2.1.2, uses the same F-statistic as for the fixed effects model. A more informative summary is often to identify a confidence region of the variance components, \( \sigma^2_\alpha, \sigma^2_\epsilon \), as seen in Figure 2.

### 4.1.2 Comprehensive ANOVA

Analogous to the ANOVA summary provided by Table 3, but including both finite and superpopulation variances, Table 4 presents a clearer view on the practical significance of the rails. Figure 3 similarly summarizes the analysis. From the graphical plot statistical significance is suggested by the fact that the intervals do not extend to cover 0. Because variance parameter must be nonnegative, it is preferable to assemble a mass point at 0 when the posterior has negative support. This allows for the probability \( p(\sigma^2_\alpha = 0 | Y) \) to be used to test the hypothesis of \( H_0 \), which for this dataset has probability zero.

### 4.2 Simulated Data

In the following example a comparison of practical and statistical significance is illustrated using both classical ANOVA as well as the more comprehensive Bayesian ANOVA. Data

![Figure 2: Comparison of confidence regions for superpopulation standard deviations based on \( \chi^2 \) approximation of relative log-likelihood (solid) and using the highest-posterior-density (dotted). Contours correspond to confidence levels 0.50, 0.75, and 0.95 (small to large).]
Table 4: Bayesian ANOVA Table: Posterior distributions are used to obtain two estimates of the variability. Quantiles provide an assessment of the uncertainty in these estimates. The probability, e.g. \( \text{Pr}(\sigma_\alpha > \sigma_\epsilon) \), provide a relative comparison of each variance parameter to the measurement variability.

| Parameter     | Mean | \( Q_{0.5} \) | \( (Q_{0.025}, Q_{0.975}) \) | \( \text{Pr}(> \sigma_\epsilon) \) |
|---------------|------|---------------|-----------------------------|-------------------------------|
| Rails (finite) \( s_\alpha \) | 24.69 | 24.71 | (22.46, 26.83) | 1.000 |
| (super) \( \sigma_\alpha \) | 25.96 | 23.89 | (14.55, 49.20) | 1.000 |
| Errors \( \sigma_\epsilon \) | 4.27 | 4.10 | (2.87, 6.58) | -- |

Figure 3: Graphical summary of posterior quantiles for variance component (super and finite population) parameters.

of the form \( Y_{ij} = \alpha_i + \epsilon_{ij} \) is generated where \( \alpha_i \sim N(0, \sigma_\alpha^2) \) and \( \epsilon_{ij} \sim N(0, \sigma_\epsilon^2 = 1) \), for \( i = 1, \ldots, n_I \), \( j = 1, \ldots, n_J \) for a total of \( n = n_I \cdot n_J \) observed values. This is done under two distinct cases

Case A: \( \sigma_\alpha^2 = \frac{1}{2} \), \( n_J = 6 \),
Case B: \( \sigma_\alpha^2 = 2 \), \( n_J = 2 \),

and with \( n_I = 5 \) for both. Using the conventional ANOVA method (Table 5) there is not any discernible differences between the two datasets. Statistical significance is approximately equivalent because of the balance of statistical power and the difference in the variance components \( \sigma_\alpha^2 \) and \( \sigma_\epsilon^2 \).

By assembling a mass point at zero whenever the posterior has support for negative values it possible to use the probability \( p(\sigma_\alpha^2 = 0 | Y) \) to test the hypothesis of (7). Interestingly, this posterior probability is 0.0263 for case A and 0.0258 for case B, values
which are comparable to their corresponding $p$-values in Table 5. This is also noted by the end-points corresponding to the 0.025 level of uncertainty for the intervals shown in Figure 4.

A more informative and comprehensive summary of the data is provided by the Bayesian ANOVA table (Table 6). This provides not only estimates of the variance components, but also an indication of the practical significance of the factor $\alpha$ when observed with error $\epsilon$.

Table 5: Classical ANOVA table to summarize the decomposition of variance. Case A (left), with $n_I = 5, n_J = 6, \sigma_\alpha^2 = \frac{1}{2}$, represents low practical significance of factor $\alpha$. Case B (right), with $n_I = 5, n_J = 2, \sigma_\alpha^2 = 2$, represents strong practical significance. Despite practical differences between the two cases, $p$-values are nearly equal.

| Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|----|--------|---------|---------|--------|
| $\alpha$ | 5 | 9.70 | 1.94 | 3.08 | 0.0267 |
| $\epsilon$ | 25 | 15.75 | 0.63 | |
| Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|----|--------|---------|---------|--------|
| $\alpha$ | 5 | 27.69 | 5.54 | 7.31 | 0.0239 |
| $\epsilon$ | 5 | 3.79 | 0.76 | |

Table 6: Bayesian ANOVA tables to summarize the variance decomposition. Case A (left) and Case B (right) illustrate a situation in which factor $\alpha$ has low, or high practical significance.

| Parm | Mean | $Q_{0.5}$ | ($Q_{0.025}, Q_{0.975}$) | Pr($\sigma_\epsilon$) |
|------|------|-----------|--------------------------|------------------|
| $\alpha$ | $s_\alpha$ | 0.48 | 0.49 | (0.02, 0.84) | 0.07 |
| | $\sigma_\alpha$ | 0.57 | 0.51 | (0.02, 1.34) | 0.19 |
| $\epsilon$ | $\sigma_\epsilon$ | 0.81 | 0.80 | (0.62, 1.07) | |

| Parm | Mean | $Q_{0.5}$ | ($Q_{0.025}, Q_{0.975}$) | Pr($\sigma_\epsilon$) |
|------|------|-----------|--------------------------|------------------|
| $\alpha$ | $s_\alpha$ | 1.59 | 1.66 | (0.12, 2.30) | 0.84 |
| | $\sigma_\alpha$ | 1.74 | 1.61 | (0.11, 3.84) | 0.82 |
| $\epsilon$ | $\sigma_\epsilon$ | 1.04 | 0.92 | (0.52, 2.30) | |

5 Discussion

The major contribution of this paper can be seen as ideological in nature, in that the standard method of analysis of variance is treated as a useful procedure to practitioners. As a result, although rigorous treatment is given, the discussion has been restricted to relatively simple designs. Extending from a one-way balanced ANOVA to many factors
Figure 4: Posterior uncertainty intervals of variance parameters shown graphically for both cases. Thick line segments correspond to 50% uncertainty and thin line segments to 95%. Vertical marks denote the posterior median. A point at the end of an interval denotes evidence that the variance component is zero and can be compared to the corresponding hypothesis test.

can be considered as a trivial step from here. However, much more work is needed in order for the method to be able to be widely accepted. Issues of unbalanced designs, non-orthogonal predictors, and generalized linear models are all necessary for the widespread usage of any statistical method. Therefore these are all issues that are to be examined in greater detail in the future.

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