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R Journal
Editorial Office
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Revision cover letter to manuscript *bayesanova: An R package for Bayesian inference in the analysis of variance via Markov Chain Monte Carlo in Gaussian mixture models*

Dear Editorial Office, dear reviewers,

thanks for the reviews on the above manuscript. The feedback and advice on the submitted paper has now been carefully considered and fully integrated into the revised version. Below, point-by-point responses to the reviews are given. Changes in the revised paper are highlighted in blue.

Point-by-point response to Review 1:

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> General comments

> The bayesanova package provides R users an alternative way of
> conducting ANOVA. This is useful to users who want to focus on
> parameter estimations aspects of ANOVA instead of calculating some
> magical statistical metrics. It is nice to see the author
> advocating for alternative measures instead of getting fixated on p
> -values or Bayes Factor. For general R community, this package will
>  be particularly beneficial to people who want to use Bayesian
> approach to their ANOVA problem but are not familiar (or cannot be
> bothered) with JAGS, Nimble, or Stan. I think the package is a
> useful addition to the statistical toolsets of many people, even if
>  the scientific community is still entrenched with p-values.
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Thanks, this nicely summarizes the goal of the method.

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> I have been able to follow through the article and understand the
> contents well enough. The introduction and examples portion of the
> article is generally well-written. However, it was relatively
> challenging for me to walk through the modeling portion of the
> article. The flow of this part is confusing, and I feel that it can
>  be shortened and rewritten to better convey the message. The
> following two paragraphs detail my main concerns.

> There are four approaches to understanding how and if response
> differ among some grouping (so called ANOVA) discussed here:
> frequentist ''classic'' ANOVA, Bayesian ANOVA using Bayes factor as
>  measure, Bayesian ANOVA focusing on parameter estimations, and
> Bayesian ANOVA using Gaussian mixture approach. I find the
> presentation confusing. Notations across the four approaches are
> inconsistent: e.g., $i = 1,...,I$ and $j = 1,...,J$ in frequentist approach,
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> but i = 1, ..., n and j = 1, ..., p in Bayesian approach, and i = 1, ..., K
> indexing grouping instead of observation in the Gaussian mixture
> approach.
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Agreed. The notation among the four approaches has been unified to improve readability.

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> Moreover, the Gaussian mixture model is not clearly laid out like
> what was done for other approaches, making it difficult to know how
>  the mixture approach differ from others.
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Further details have been added to clarify the difference in particular from Kruschke's model based on JAGS or Stan (see also next comment).

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> As far as I understand, the mixture approach is essentially a more
> sophisticated version of method 3 with varying variance in each
> group.
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Correct. Also, in the mixture approach we assume that the sample we obtain (e.g. n_1 participants in group 1 and n_2 participants in group 2) result from a mixture process, e.g. by flipping a coin, or using any randomization device (as is the case e.g. in clinical trials when assigning patients to groups double-blinded). Thus, the process of data generation is not "one has collected n_j participants for group j" but "the given sample of n_j participants in group j is assumed to be a realization of a mixture process where with probability η_j participants are assigned to group j".

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> In fact, method 2 and method 3 are fundamentally using the same
> model formulation; one circumvents parameter estimation and focus
> on calculating Bayes Factor while another focuses on parameter
> estimation and avoids using any metric. Having completely
> different sets of notations among these methods make it harder to
> read and confusing. I think it helps to note the continuity among
> method 1-4, and present them along that continuum.
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> I appreciate the statistical and mathematical details and I think
> they are important in this manuscript. Nevertheless, R Journal is
> meant for a more general audience. I think it is important to bring
>  across the point about why and how these methods differ. These
> points are currently buried in the details. If it helps, a table
> summarizing the differences among the models can help (purpose:
> calculating metrics or estimating parameters; assumptions etc.)
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True. First, mathematical details have been reduced by referring readers to the appropriate statistical papers instead. Second, I like the idea of a table which can be used for noting the continuity among the four approaches as you mentioned and such a table has now been added at the end of the section about the proposed Gaussian mixture modelling approach. This outlines the big picture instead of distorting readers with too much mathematical subtleties. Also, this hopefully improves readability for a wider audience.

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> In addition, the ''models'' section could be streamlined, e.g.,
> the calculation of F-test statistics can be omitted since you can
> get them in any stats textbook.
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Agreed. The models section has been trimmed as follows now: I created an appendix where I placed parts of the mathematical details. This improves accessibility while still retaining self-containment of the article.

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> Likewise the one-sample approach in the Bayes factor method may not
>  be needed. It helps to go straight into the models that are
> relevant to this paper, and let references (or supplemental
> information) to do the detailed explanations.
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True. The one-sample approach has been removed.

> I think the package is straightforward and seemingly easy to use.
> My specific comments regarding the package are:

> 1. I think the package MCMCpack should be specified as Import
> instead of Suggest. It is required in the bayes.anova function
> which is the core of the package. I get thrown an error message
> because I didn't have MCMCpack installed.

Good suggestion, thanks for noticing. I was not aware of this important difference and the MCMCpack package is now specified as Import.

> 2. I have noticed that there are purple, orange, green, red lines
> in some of the anovaplot output but it is unclear what are they. I
> know from the code that they are marking the bins in calculating
> ROPE, but it helps to at least spell them out in the help file of
> the function.

True. Details are now provided in the help file of the function.

> 3. Minor aesthetic comment here. As demonstrated in. Figure4, post.
> pred.check produces lines that are out of the ylim. This should be
> an easy fix I think.

Thanks, this has been fixed now.

> Specific Comments
> Pg 3. 3rd paragraph
> ''They start with one-sample model, where $y_i \sim \mathcal{N}(0, \sigma^2)$...'' Shouldn't
> this be $y_i \sim \mathcal{N}(\mu, \sigma^2)$?

This is again a misformulation of mine. Here, $y_i \sim \mathcal{N}(0, \sigma^2)$ holds only under $\mathcal{M}_0$, the model corresponding to the null hypothesis of no effect, compare Equation (10). Equation (9) states how data y_i are distributed when reparameterizing $\delta = \mu/\sigma$, and this clearly makes only sense if we start with $y_i \sim \mathcal{N}(0, \sigma^2)$ as you stated. This part has been removed in the revised version because single-group cases are not relevant as you mentioned earlier.

> It is somewhat confusing moving from frequentist ANOVA to Bayesian
> ANOVA and suddenly we moved from multi-group comparison to one-
> sample model. Is it possible to go straight into multi-group
> version of the Bayesian ANOVA?

Agreed. The details on the one-sample design have been removed.

> Pg 4. Paragraph with equation 19-23

> This part is very confusing: the first sentence of the paragraph
> suggests that there are p groups (unclear what is it indexed by),
> and i observations, thus $i = 1, ..., n$. But the following sentence ''the
> mean μ_i of group i ...'' seems to suggest that i indexed for groups
> instead of observations? It would be helpful for the author to
> indicate that i indexes the observation and j indexes the group here
> (as far as I understand).

Thanks and sorry for the mess! You are of course correct, there are only k different means, but Kruschke models these through indicator variables. Notation has been changed to avoid misunderstandings in this paragraph.

> Also, I think $y_i \sim \mathcal{N}(\mu_i, \sigma_y)$ should instead be $y_i \sim \mathcal{N}(\mu_i, \sigma_y^2)$.

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> It helps to explain that β_0 is the grand mean here.

Agreed, the revised version contains a short note on this aspect now.

> It is unclear to me what's the difference between ''deflection
> parameter'' here and ''effects'' used in describing previous model.
> The choice of word suggests they might be different?

This is due to the original formulation of Kruschke, but there is no semantic difference. I unified notation by always using effects in the revised version.

> Also, I don't understand how the choice of prior to β_j which is
> normal with mean zero can lead to ''the deflections sum up to zero
> again.'' It only result in expectation of μ_i equal to the grand
> mean β_0, but the actual deflections for each μ_i are most certainly
> not sum up to zero.

True, this has been fixed now, thanks for noticing.

> Pg 4. Last paragraph

> This should go into available software section? Also, I think the
> advantage of a package (BANOVA in this case) allows inference
> without having to code in JAGS and Stan; the advantage of HMC is
> instead on computational efficiency.

I concur, this should be placed in the available software section. I noted that this is redundant as I mention the same information at the top of page 6, so I removed the section.

Thanks for the time and expertise you invested in reviewing the manuscript, which definitely helped to improve its overall quality.

Kind regards,

Riko Kelter

*References