Reply to PCIRR 2nd revise and resubmit decision letter: Hsee and Kunreuther (2000) replication and extensions

Please note that the editor's and reviewers' comments are in bold with our reply underneath in normal script.

A track-changes comparison of the previous submission and the revised submission can be found on: https://draftable.com/compare/jDDwCcNigASB

Reply to Editor: Dr./Prof. Chris Chambers

> **I have now received two re-reviews. There is just one remaining issue to clarify concerning the distribution of the prior (and whether an informed prior may be more statistically sensitive). Please consider this point in a final revision and response, and we will then be ready to move forward with Stage 1 IPA.**

Thank you for the reviews obtained, your feedback, and the invitation to revise and resubmit.

Please see our reply below. Action wise, we changed the prior of the supplementary Bayesian analyses to 0.33.

Reply to Reviewer #1: Dr./Prof. Rima-Maria Rahal

> **I have read the carefully argued responses of the author team to concerns raised, believe that these concerns are sufficiently addressed, and have no further comments. I'm interested to see the results of the replication, and wish the authors much success with implementing the study.**

Thank you very much for reviewing our revised submission and the positive supportive feedback!

Reply to Reviewer #2: Dr./Prof. Bence Palfi

> **I thank the authors for revising the manuscript and for thoroughly addressing the comments of the reviewers. I only have a minor comment regarding the specification of the prior of the Bayes factor. Otherwise, I`m happy for the project to proceed and I`m looking forward to seeing the Stage 2 submission soon.**

Thank you very much for reviewing our revised submission and the positive supportive feedback!

> **I presume that the Bayesian analysis will use a Cauchy distribution to model the predictions of H1. This is a heavy-tailed distribution which assumes a wide range of effect sizes to be plausible under H1, especially if the mode is large like the chosen value of 0.7. This means that the Bayes factor will have a strong bias towards evidence for the null when the real effect size is small. For this reason, I would recommend reducing the mode of the distribution. For instance, you could use the same effect size that is utilised for the sample size estimation (0.330).**

Our understanding is that the impact of the prior here would be rather minimal given that large sample size, and our experience so far has been that many of the judgment and decision making effects that our team has previously targeted for replication and summarized as successful replications (~67%) had on average comparable effect sizes to those reported in the target articles (sometimes stronger, sometimes weaker).

Given your suggestion, we changed the prior of the supplementary Bayesian analyses to 0.33.