Supplementary Materials: Cognitive and cultural models in psychological science

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Overview

In Appendix A, we implement an alternative likelihood to the zero-one inflated beta, namely the *ordered beta* distribution. For technical details and background, see Kubinec (2020) and for practical implementation, see https://github.com/saudiwin/ordbetareg and source code for present supplementary document.

In Appendix B, we illustrate and implement alternative likelihood models that do not require transforming free-list data to salience scores, as discussed briefly in the main manuscript. We integrate key code chunks in the text but refer to the source code for full reproducible code. For simplicity, we restrict the examples to the Model 1 data and exclude field-site specific 'random effects' in all models.

In Appendix C, we first present plots for Models 3-8 (Figures 10 and 11). Then, we present results for the reduced models, where only non-zero free-list responses are retained (Figures 12–14). Finally, we present results from leave-one-group-out cross-validation (Table 2), an alternative model comparison to the approximate leave-one-out cross-validation as presented in the main manuscript.

In Appendix D, we list `R` packages, their dependencies, and version number used for this project.

Table 1
Focal parameter estimates for all ordered beta models and model comparison metrics.

	Intercept	β^{Scale}	Akaike Weights	ELPD difference [SE]
`m1_ordbeta`	0.16 [-0.33, 0.64]	0.07 [-0.49, 0.67]	0.10	-1.68 [0.74]
`m1_ordbeta_null`	0.21 [-0.20, 0.62]	–	0.90	*
`m2_ordbeta`	-0.85 [-1.75, 0.11]	1.49 [0.50, 2.49]	0.70	*
`m2_ordbeta_null`	-0.24 [-1.34, 0.82]	–	0.30	-3.61 [4.03]
`m3_ordbeta`	-0.16 [-0.70, 0.34]	0.08 [-0.05, 0.19]	0.01	*
`m3_ordbeta_null`	0.08 [-0.36, 0.45]	–	0.99	-0.45 [1.78]
`m4_ordbeta`	-0.03 [-0.72, 0.59]	0.04 [-0.12, 0.19]	0.01	-0.78 [0.93]
`m4_ordbeta_null`	0.10 [-0.32, 0.47]	–	0.99	*
`m5_ordbeta`	-0.30 [-0.83, 0.18]	0.04 [-0.11, 0.19]	1.00	*
`m5_ordbeta_null`	-0.16 [-0.71, 0.36]	–	0.00	-0.25 [1.62]
`m6_ordbeta`	-0.46 [-1.47, 0.40]	0.05 [-0.16, 0.26]	0.08	-0.15 [1.25]
`m6_ordbeta_null`	-0.21 [-1.13, 0.48]	–	0.92	*
`m7_ordbeta`	-0.67 [-1.88, 0.46]	0.07 [-0.16, 0.28]	0.15	-0.52 [0.74]
`m7_ordbeta_null`	-0.30 [-1.37, 0.56]	–	0.85	*
`m8_ordbeta`	-1.09 [-2.15, -0.16]	0.02 [-0.18, 0.23]	0.02	-1.42 [0.78]
`m8_ordbeta_null`	-0.90 [-1.82, -0.22]	–	0.98	*

Note. Point estimates of the β coefficients are posterior means with 95% credible intervals in brackets. The best performing model of the eight pairs is denoted by an asterisk.

Appendix A: The ordered beta distribution

Here's an excerpt from Kubinec (2020) outlining the gist of the ordered beta:

> [the ordered beta] employ[s] ordered cutpoints, similar in spirit to an ordered logit model, to estimate the joint probability of 0s (the lower bound), continuous proportions, and 1s (the upper bound) in bounded continuous data. As only one predictive model is used for all of the outcomes, the effect of covariates is identified across discrete and continuous observations without resulting in over-fitting. The use of cutpoints permits the model to fit distributions with mostly discrete observations or no discrete observations at all, which makes it a general solution to this problem. (p. 2)

The two cutpoints represent the points (including an uncertainty interval) at which there's a 50% change that a response is 0 and 1, respectively. In the context of our case study, the ZOIB and the ordered beta yield similar inferences and posterior predictions (Figures 1 – 3 and Table 1).

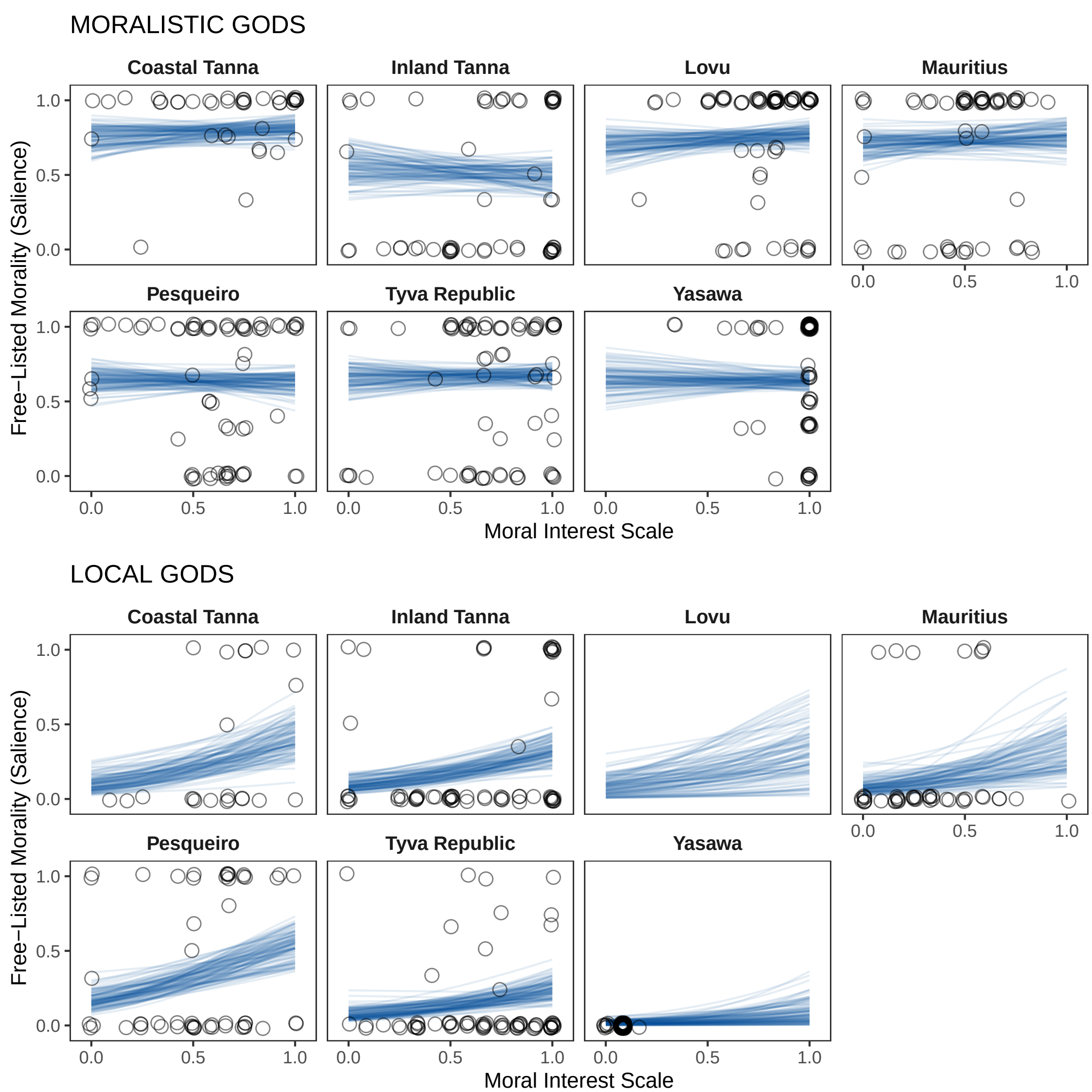


Figure 1. **Ordered beta models**. Posterior predictions for each field site and each deity from the ordered beta Model 1 and 2 on the relationship between the moral interest scale (x-axis) and salience of the free-listed general Morality code (y-axis). Lines are draws of expected values from the posterior predictive distribution. Raw data points are slightly jittered.

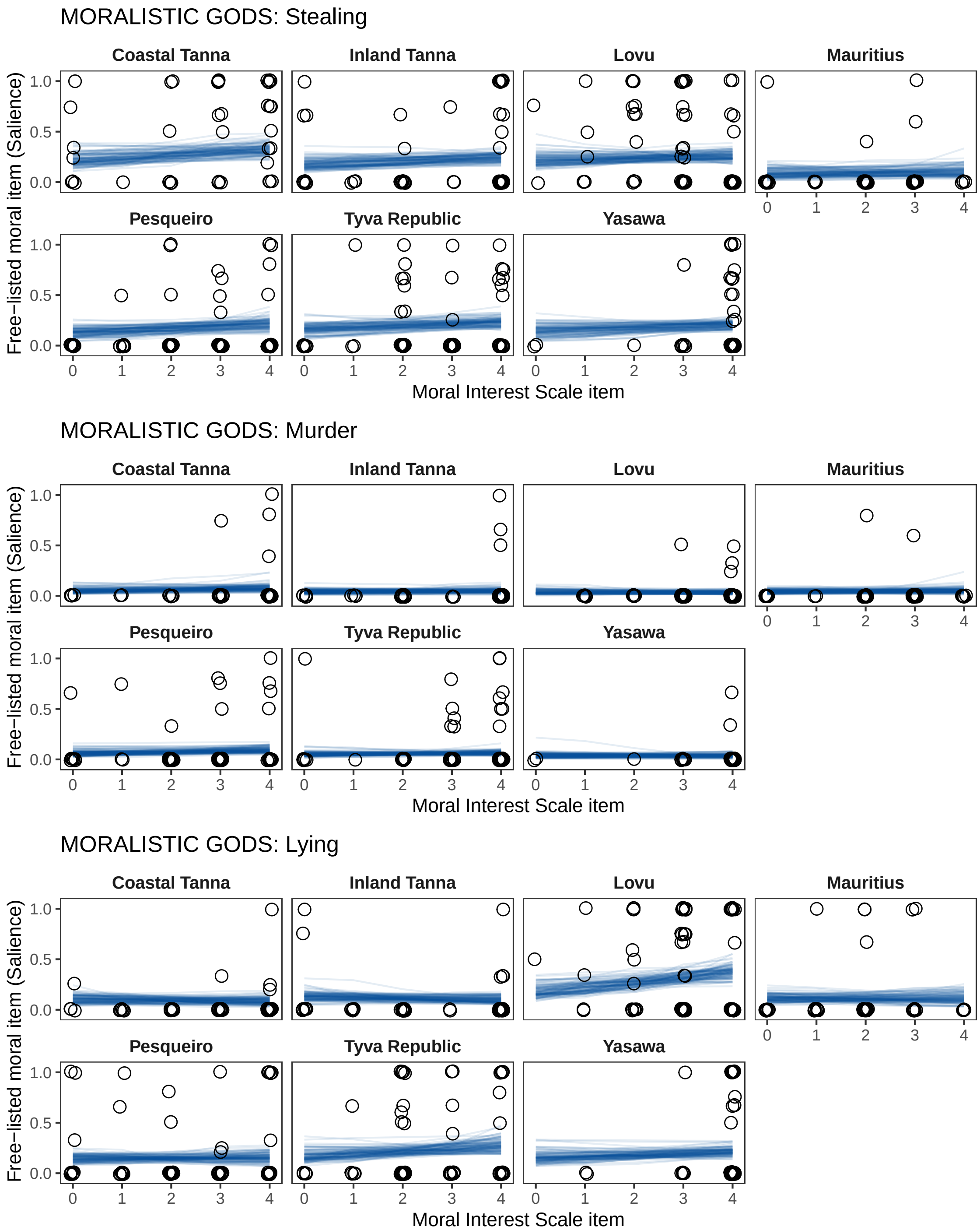


Figure 2. **Ordered beta models.** Posterior predictions for each field site from the ordered beta Model 3 through 5 on the relationship between the moral interest scale items (x-axis) and salience of the corresponding free-listed code (y-axis). Lines are draws of expected values from the posterior predictive distributions. Raw data points are slightly jittered.

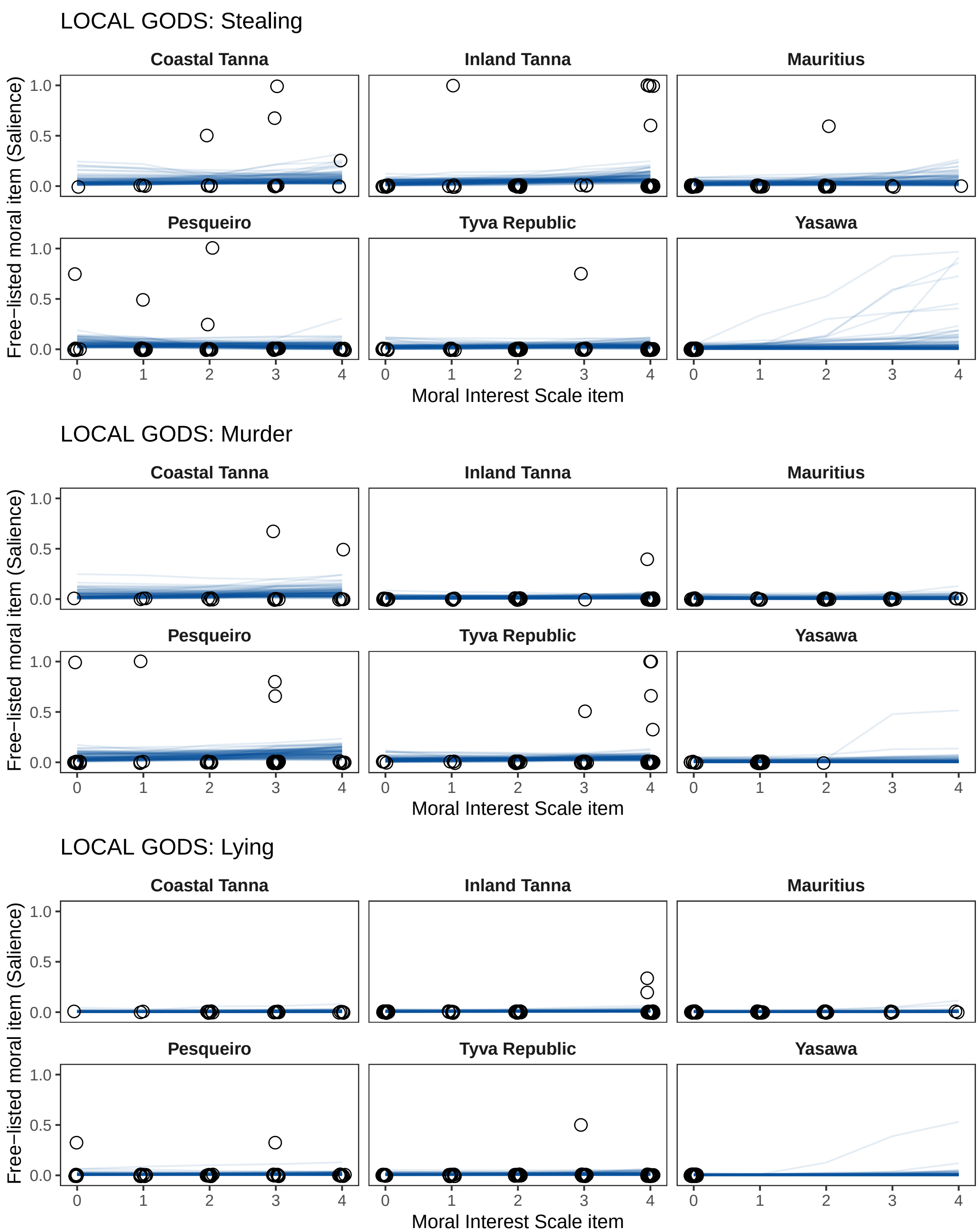


Figure 3. **Ordered beta models**. Posterior predictions for each field site from ordered beta Model 6 through 8 on the relationship between the moral interest scale items (x-axis) and salience of the corresponding free-listed code (y-axis). Lines are draws of expected values from the posterior predictive distributions. Raw data points are slightly jittered.

Appendix B: Alternative likelihood models for free-list data

Presence/absence

An analyst could be interested in simply modeling the presence and absence of some target item using a logistic (Bernoulli) regression. With `tableType = 'PRESENCE'` in `AnthroTools::FreeListTable()` we get a data frame with the presence (= 1) and absence (= 0) of all items listed across participants in our free-list data. We then extract the general 'Morality' code, combine this data with the scale responses, store it in the object `bgd_gen_data_bern`, and then fit a logistic regression with `brms`. A higher coefficient for `scale` is interpreted as a higher probability of listing 'Morality' as predicted by the moral interest scale. For practical applications, see e.g. Purzycki and Bendixen (2020) and Purzycki, Stagnaro, and Sasaki (2020).

```
m1_bern <- brm(
  y ~ 1 + scale,
  data = bgd_gen_data_bern,
  family = bernoulli(),
  cores = 4, chains = 4,
  iter = 1000, control = list(adapt_delta = 0.99),
  seed = 2021)
```

Number of ‘successes’

With a binomial model, we can instead model the number of mentions of a target item given the total number of items listed per participant. With `tableType = 'FREQUENCY'` in `AnthroTools::FreeListTable()` we get a data frame with the number of times each item was listed across participants in our free-list data. Using the `rowSums()` command on this data frame, we can get the total number of items listed per participant; this number will serve as the number of ‘trials’ `n` in our binomial model. We extract the general ‘Morality’ code (i.e., the number of times each participant listed ‘Morality’), which is the ‘successes’ `y` in the binomial model, combine the successes and trials with the scale response, store the resulting data in `bgd_gen_data_bin`, and fit a binomial model to this data.

```
m1_bin <- brm(bf(
  y | trials(n) ~ 1 + scale),
  data = bgd_gen_data_bin,
  family = binomial(),
  cores = 4, chains = 4,
  iter = 1000, control = list(adapt_delta = 0.99),
  seed = 2021)
```

We can check the fit of the model with a convenient posterior predictive check of the marginal distribution of outcome values plotted against model predictions across total number of items listed (Figure 4). The fit is decent but not perfect; the model seems to consistently over-shoot the number of ones and twos, for instance. In an applied case, we would likely work on achieving a closer fit or, failing to do so, abandon this particular likelihood model.

We can then plot the expected number of times that ‘Morality’ was listed as a function of the moral interest scale and the total number of items listed per participant (Figure 5). For instance, the model predicts that a participant that lists only one item (panel 1) lists ‘Morality’ as that one item regardless of their score on the moral interest scale. Generally, the moral interest scale does not appear to predict an increased probability of listing more ‘Morality’ items across various number of trials. A possible exception is for those who lists five items (panel 5), where the model’s best guesses trend upwards from two ‘Morality’ items at the lowest end of the scale to three ‘Morality’ items at the higher end of the scale.

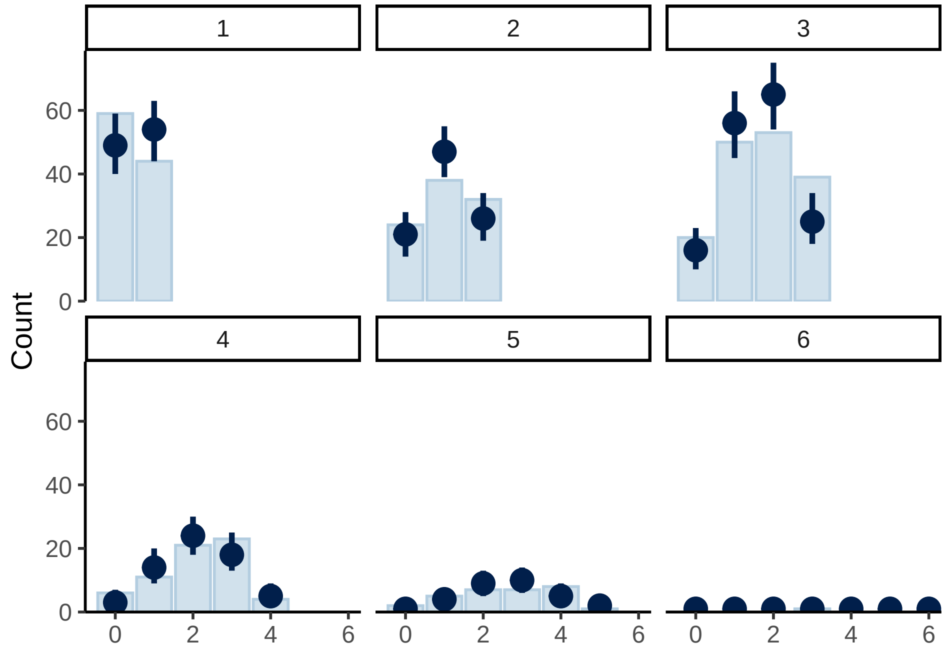


Figure 4. Posterior predictive check for the binomial model. Light blue bars are frequency of each observed outcome while points and intervals are posterior predictions. Panel numbers refer to number of 'trials' n, i.e. total number of items listed per participant.

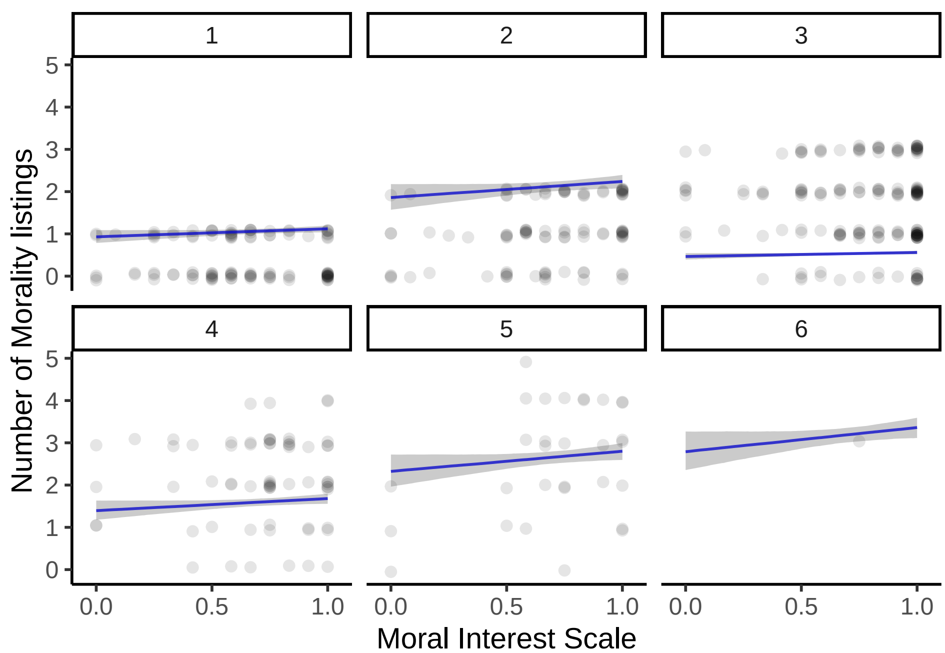


Figure 5. Binomial model. Lines are posterior medians of expected values with 95% interval bands. Raw data points are slightly jittered vertically. Panel numbers refer to number of 'trials' n, i.e. total number of items listed per participant.

Average list position

We can also model the expected list position and how this expectation change as a function of some predictor(s), using a zero-inflated negative binomial. Using `tableType = 'HIGHEST_RANK'` in `AnthroTools::FreeListTable()`, we get the highest rank (i.e., list position) for all items listed across participants. As above, we extract the general ‘Morality’ code, combine this data with the scale responses, and store it in the object `bgd_gen_data_rank`. Now, `y` is the order at which ‘Morality’ was listed, i.e. 1 means first, 2 means second, etc., while 0 means that ‘Morality’ was not listed.

```
str(bgd_gen_data_rank)
```

```
## 'data.frame':    455 obs. of  4 variables:
##  $ id     : chr  "CERC1" "CERC10" "CERC11" "CERC113" ...
##  $ y      : num  1 1 1 0 1 0 2 0 1 0 ...
##  $ culture: chr  "Coastal Tanna" "Coastal Tanna" "Coastal Tanna" "Inland Tanna" ...
##  $ scale  : num  0.167 0.333 0.417 0.25 0.333 ...
```

We then fit a zero-inflated negative binomial model to this data, using scale as a predictor for both the zero-inflation `zi ~ ...` and the negative binomial `y ~ ...`. The implementation is straightforward as this likelihood model is native to `brms`, specified as `family = zero_inflated_negbinomial()`. Note that a larger regression coefficient in the negative binomial part means that the target item moves *down* on participants free-lists (i.e., becomes less salient) as a function of the predictor.

```
m1_zinb <- brm(bf(
  y ~ 1 + scale,
  zi ~ 1 + scale),
  data = bgd_gen_data_rank,
  family = zero_inflated_negbinomial(),
  cores = 4, chains = 4,
  iter = 1000, control = list(adapt_delta = 0.99),
  seed = 2021)
```

We can again assess the fit of model with a quick posterior predictive check (Figure 6). The fit looks far from perfect, as the model fails to capture key aspects of the observed marginal outcome. In an applied case, we would have to look further into this mis-fit, perhaps resulting in the inference that the zero-inflated negative binomial is, after all, not a good model for these particular data. One possible reason for this is that the negative binomial is an uncapped count model, and so it is not prevented from returning predictions that are substantially outside the range of observed values, which in this case means predicting a target item appearing in much later list positions than observed.

For illustrative purposes, however, let’s assess the expected list position of ‘Morality’ as predicted by the moral interest scale (Figure 7). There is not a lot of change, although if anything it seems that the expected position at which ‘Morality’ is listed trends upwards (e.g., becomes less salient) with higher scores on the moral interest scale.

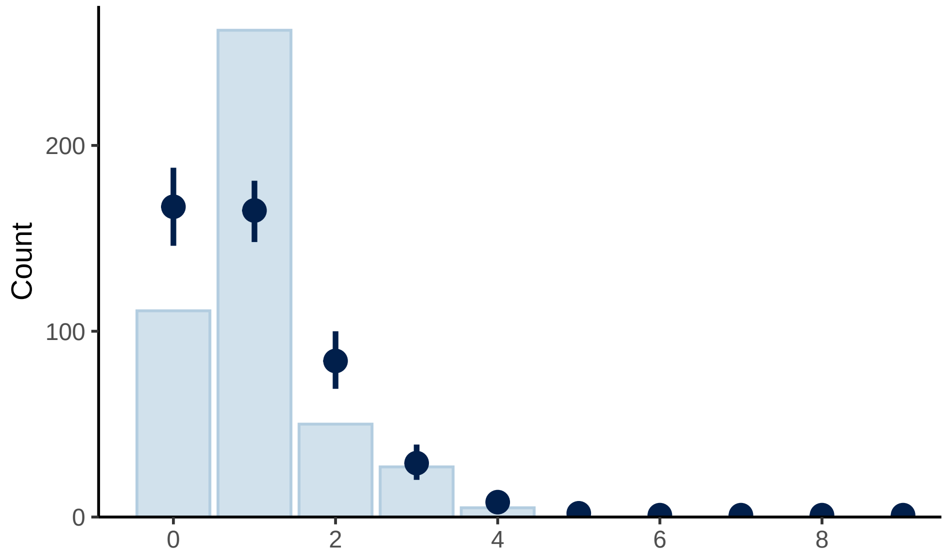


Figure 6. Posterior predictive check for zero-inflated negative binomial. Light blue bars are frequency of each observed outcome while points and intervals are posterior predictions.

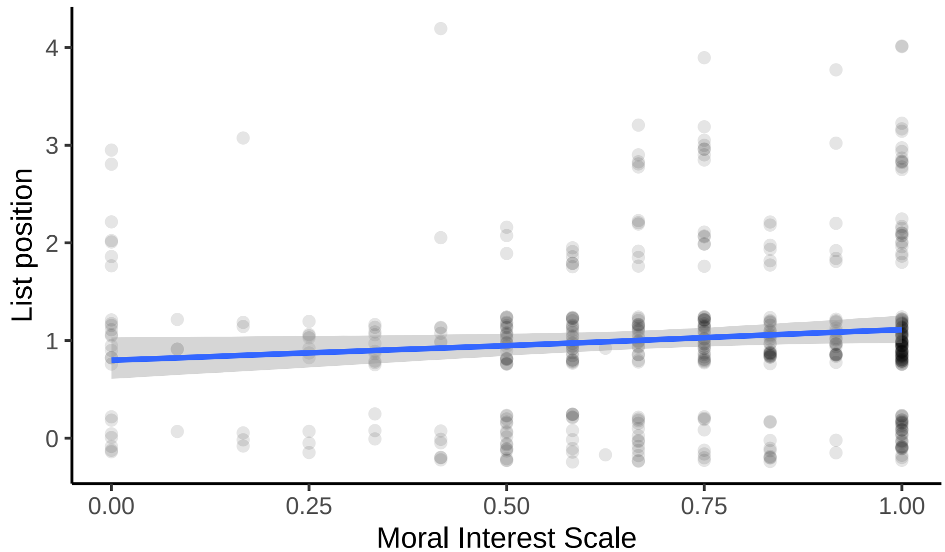


Figure 7. Expected list position according to the zero-inflated negative binomial model. Raw data points are slightly jittered vertically.

Cumulative probability of list positions

Finally, we could model the cumulative probabilities of a target item appearing in each of the positions in which the item appears across the sample using zero-inflated ordinal regression. This likelihood model is not native to `brms`, and hence requires some custom code (stored in `stanvars` in the model code chunk). See the source code, which adopts and modifies code after https://github.com/octmedina/zi-ordinal. We also set some weakly regularizing priors.

The `y ~ 1 + scale` part models the zero-inflation (i.e., the probability of not listing the target item), while `eta ~ 0 + scale` is the ordinal regression of the non-zero outcomes. Note that as with the zero-inflated negative binomial, a larger regression coefficient in the ordinal part means that the target item moves down on participants' free-lists (i.e., becomes less salient) as a function of the predictor. We again use the data frame `bgd_gen_data_rank`

```
ziord_priors <- set_prior("normal(0,1)", class = "b", dpar = "eta") +
                set_prior("normal(0,1)", class = "b") +
                set_prior("normal(0,2)", class = "Intercept")

m1_zi_ord <- brm(bf(
      y ~ 1 + scale,
      eta ~ 0 + scale),
  data = bgd_gen_data_rank,
  prior = ziord_priors,
  family = zi_ordinal, stanvars = stanvars,
  chains = 4, cores = 4, control = list(adapt_delta = 0.99),
```

```
  seed = 2021, iter = 10000)
```

With this data and model, we experienced convergence issues, which would have to be fixed in an actual applied case. We get reasonable convergence diagnostics with a relatively high number of iterations (10,000); however, increasing computational costs is not the ideal strategy for alleviating problematic chain behavior. In the source code, we illustrate an implementation in raw `Stan` that samples much more efficiently.

We can run a posterior predictive check to assess the fit of the model against observed data (Figure 8). The fit looks very reasonable, in that the observed data are well inside the intervals of the posterior predictions. Lastly, we can plot the cumulative probabilities of each list position as predicted by the moral interest scale. That is, how does the probability of listing 'Morality' change as a function of higher or lower scores on the three-item scale? This is Figure 9; lines are medians of posterior predictive draws and bands are 80% intervals to make the trends stand out more clearly. Note that the probability of not listing the target item (0; red line/band) goes down as participants score higher on the scale, whereas the probability of listing 'Morality' as the first item (1; yellow line/band) seems stable across scale responses. Conversely, the probability of 'Morality' appearing at list position two (green) and three (turqoise) seem to increase slightly with higher scores on the scale. The probability of listing ''Morality' as the fourth (blue) and fifth (purple) item is practically zero across the span of the scale.

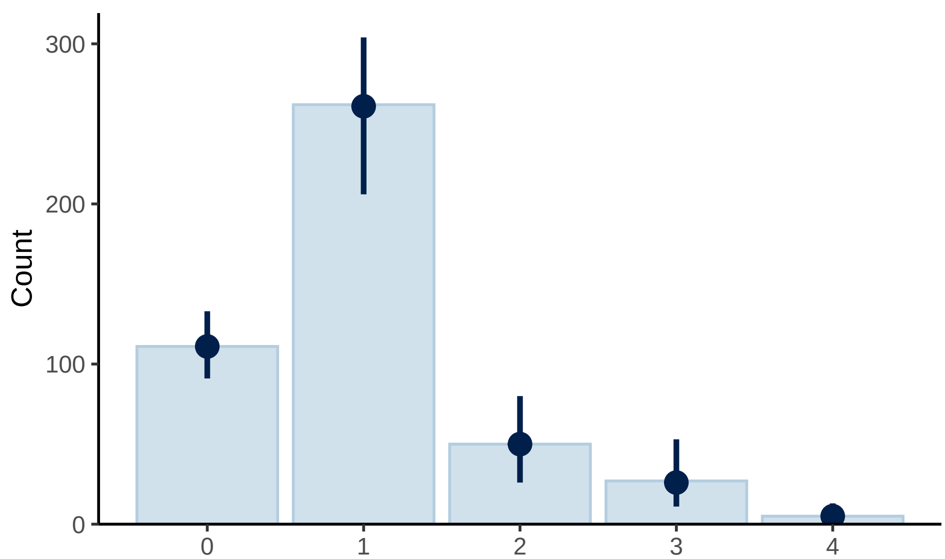


Figure 8. Posterior predictive check for zero-inflated ordinal regression. Light blue bars are frequency of each observed outcome while points and intervals are posterior predictions.

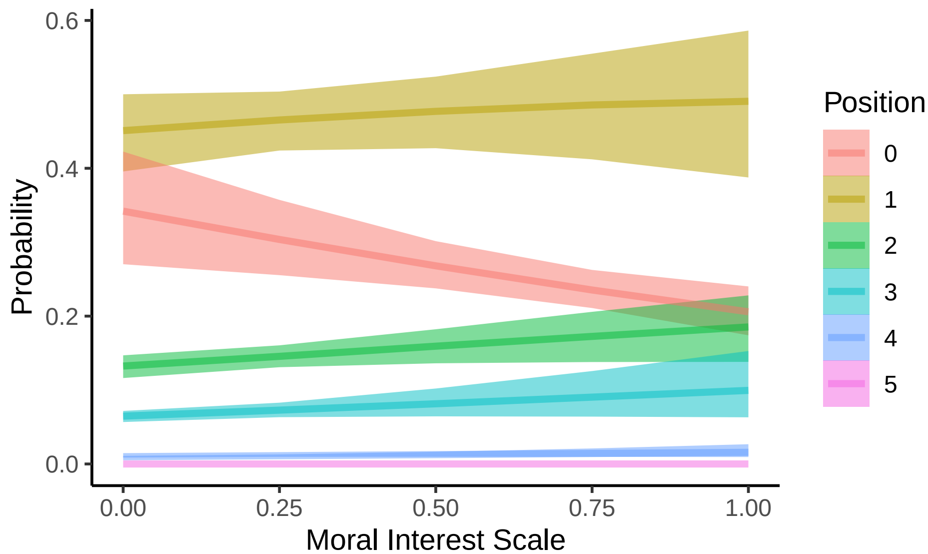


Figure 9. Cumulative probabilities of each list position. 0 = item not listed. Lines are posterior medians and bands are 80% credible intervals.

132 **Appendix C: Supplementary plots and tables**

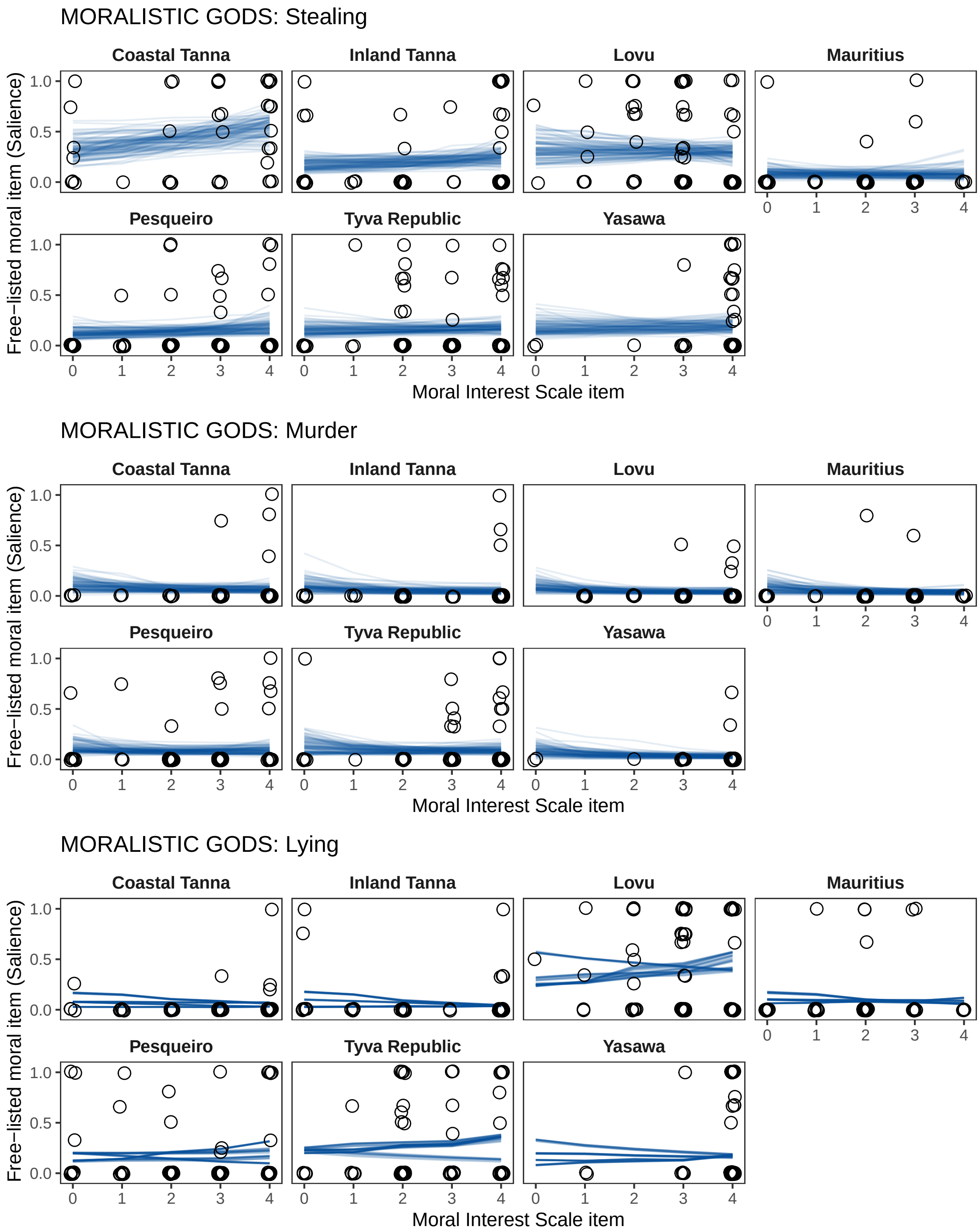


Figure 10. Posterior predictions for each field site from Model 3 through 5 on the relationship between the moral interest scale items (x-axis) and salience of the corresponding free-listed code (y-axis). Lines are draws of expected values from the posterior predictive distributions. Raw data points are slightly jittered.

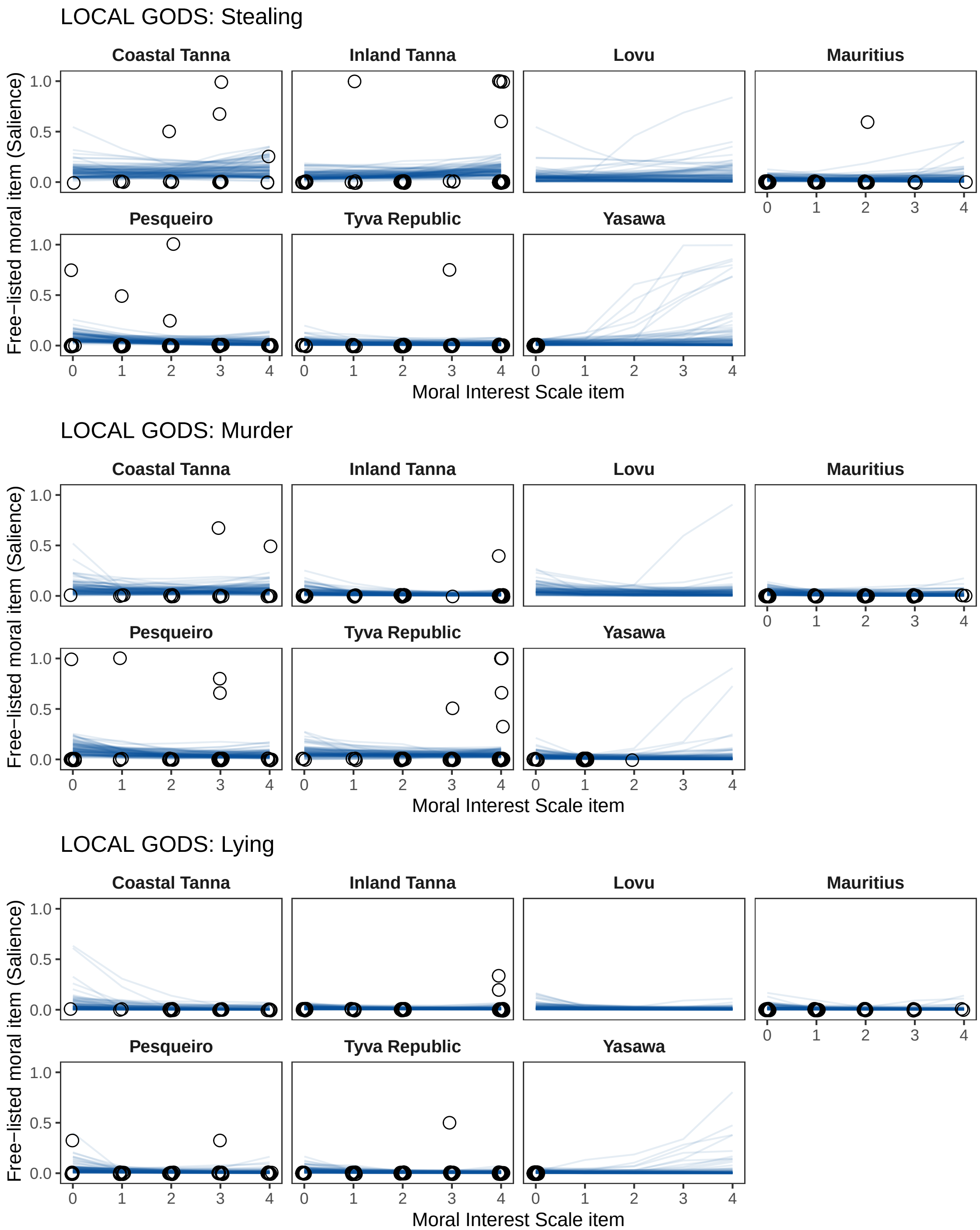
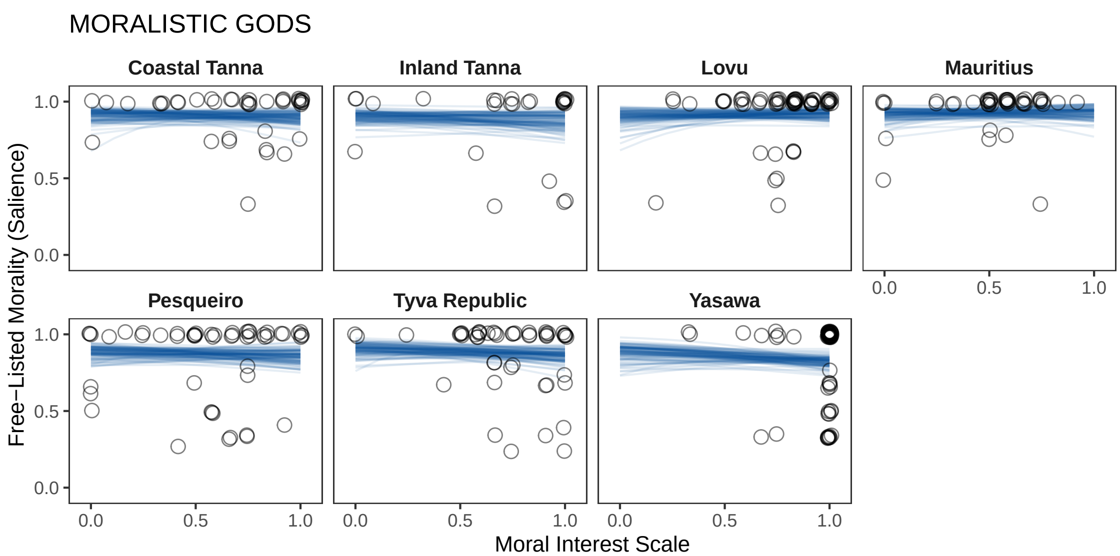


Figure 11. Posterior predictions for each field site from Model 6 through 8 on the relationship between the moral interest scale items (x-axis) and salience of the corresponding free-listed code (y-axis). Lines are draws of expected values from the posterior predictive distributions. Raw data points are slightly jittered.



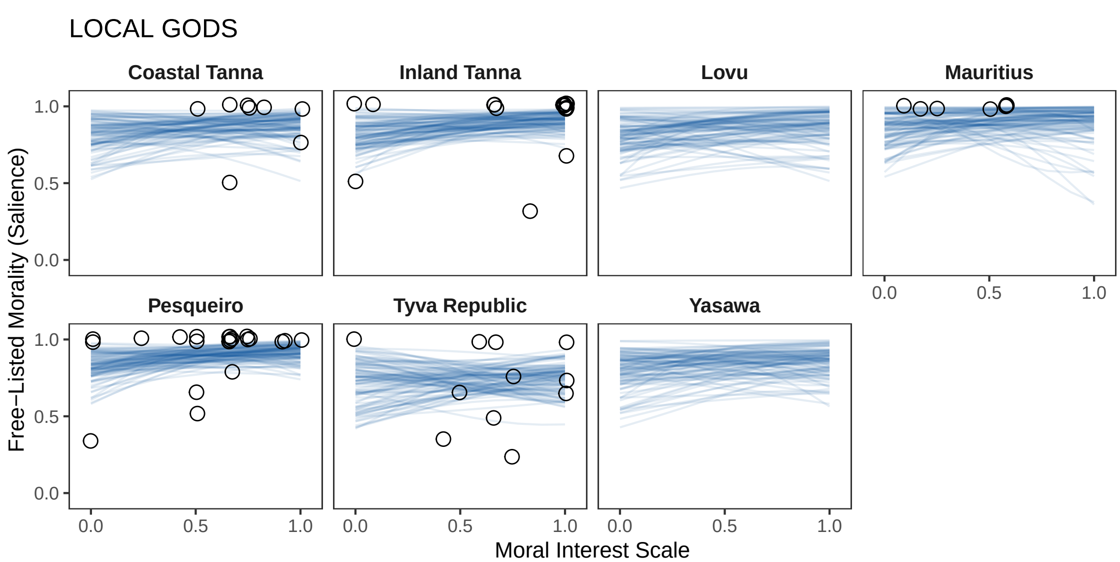


Figure 12. **Reduced models**. Posterior predictions for each field site from Model 1 and 2 on the relationship between the moral interest scale (x-axis) and salience of free-listed Morality (y-axis) with only non-zero free-list responses. Lines are draws of expected values from the posterior predictive distributions. Raw data points are slightly jittered.

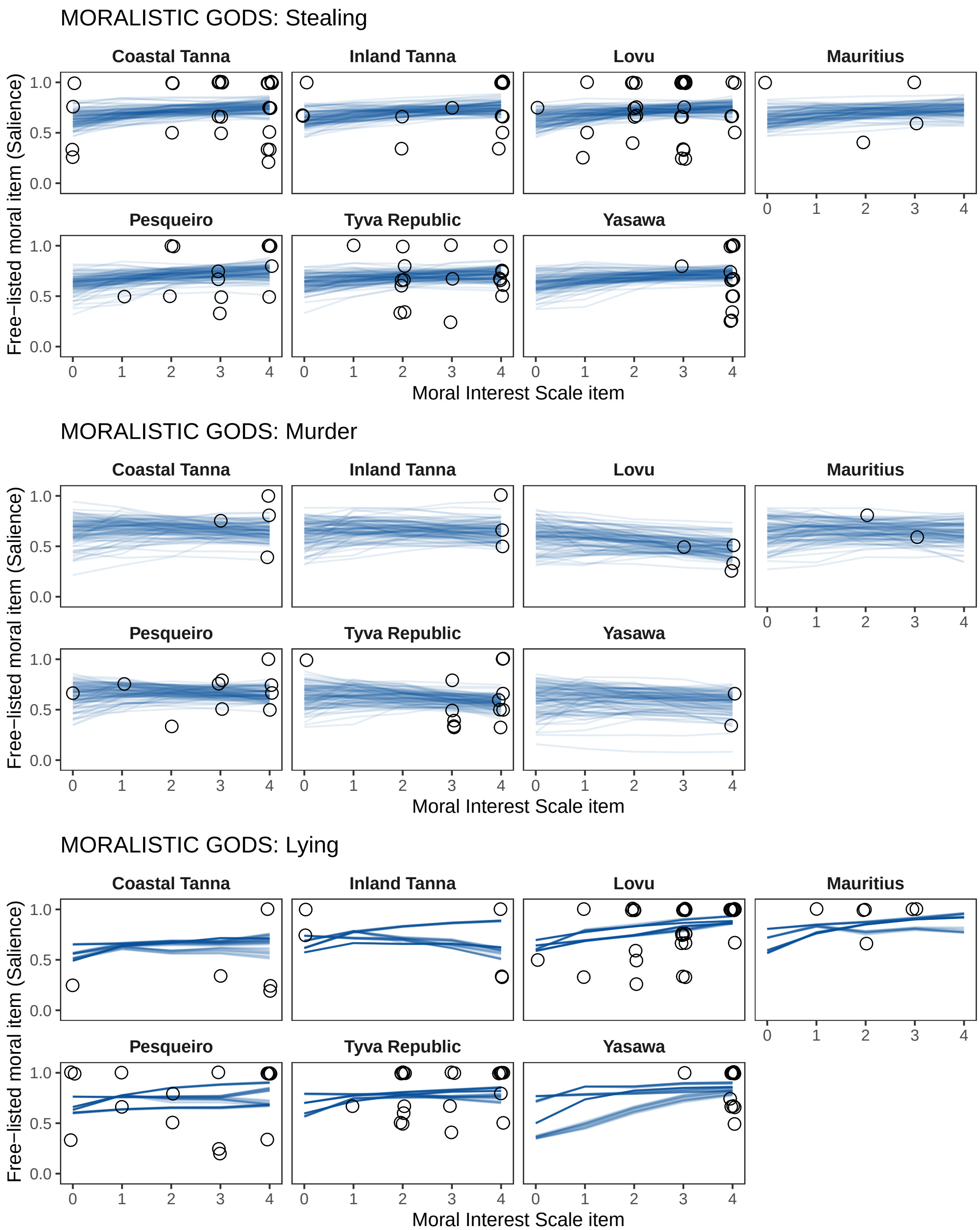


Figure 13. **Reduced models**. Posterior predictions for each field site from Model 3 through 5 on the relationship between the moral interest scale (x-axis) and salience of the corresponding free-listed code (y-axis) with only non-zero free-list responses. Lines are draws of expected values from the posterior predictive distributions. Raw data points are slightly jittered.

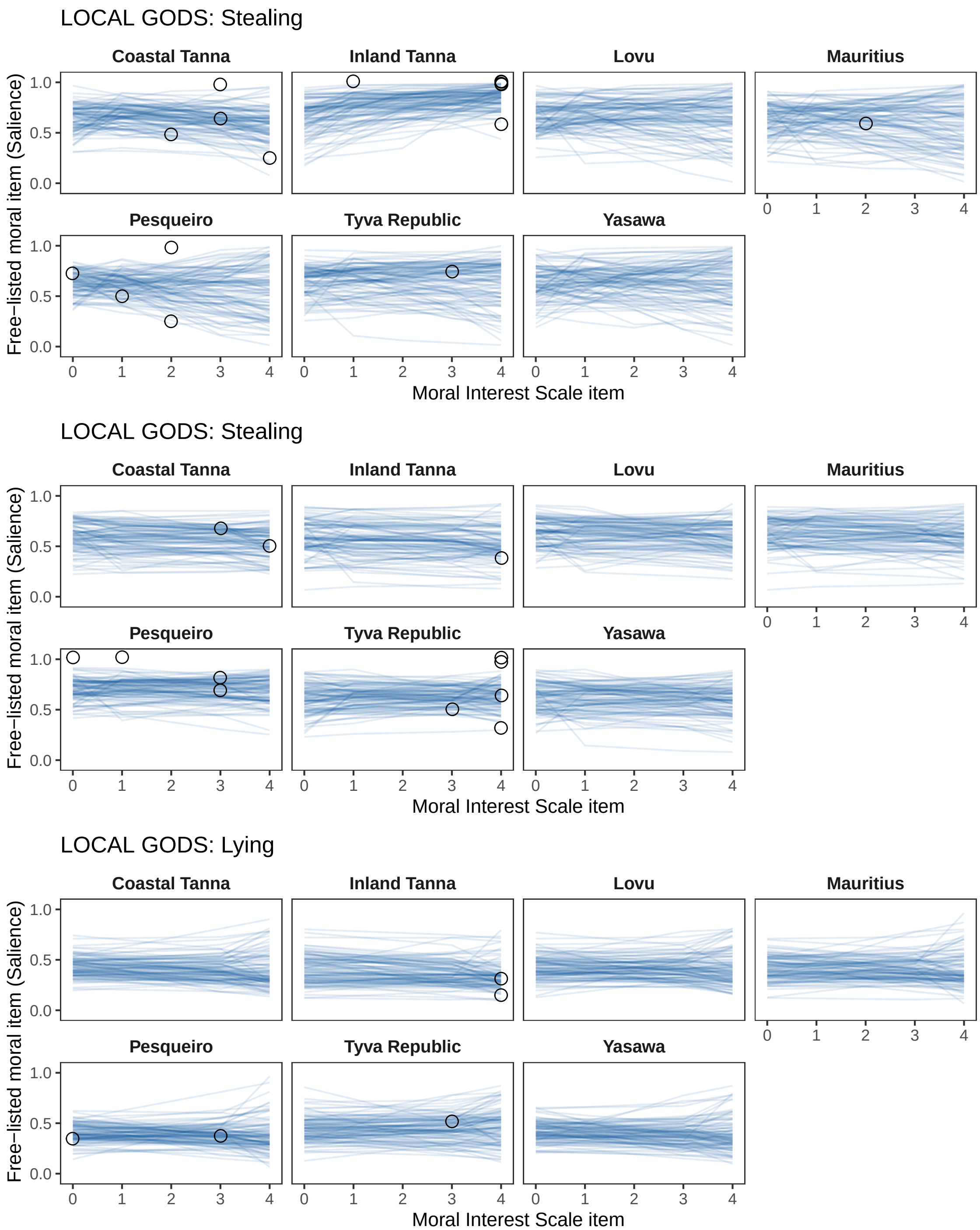


Figure 14. **Reduced models**. Posterior predictions for each field site from Model 6 through 8 on the relationship between the moral interest scale (x-axis) and salience of the corresponding free-listed code (y-axis) with only non-zero free-list responses. Lines are draws of expected values from the posterior predictive distributions. Raw data points are slightly jittered.

Table 2

Results from leave-one-group-out cross-validation (LOGO-CV).

	Akaike weights	ELPD [SE]
`m1`	0.30	-0.96 [2.13]
`m1_null`	0.70	*
`m2`	1.00	*
`m2_null`	0.00	-8.8 [3.84]
`m3`	0.00	-2.56 [1.25]
`m3_null`	1.00	*
`m4`	0.00	-1.64 [1.58]
`m4_null`	1.00	*
`m5`	0.36	*
`m5_null`	0.64	-6.55 [10.86]
`m6`	0.00	-5.32 [1.01]
`m6_null`	1.00	*
`m7`	0.50	*
`m7_null`	0.50	-2.54 [5.17]
`m8`	0.00	-15.23 [12.37]
`m8_null`	1.00	*

Note. ELPD = differences in expected log posterior density between model pairs; SE = standard error of ELPD differences. Asterisks denote the best performing model in each model pair.

Appendix D

We used R version 4.1.2 (R Core Team, 2021) and the following R packages: abind v. 1.4.5 (Plate & Heiberger, 2016), AnthroTools v. 0.8 (Lane & Purzycki., 2016), arrayhelpers v. 1.1.0 (Beleites, 2020), askpass v. 1.1 (Ooms, 2019), assertthat v. 0.2.1 (H. Wickham, 2019a), backports v. 1.4.1 (Lang & R Core Team, 2021), base64enc v. 0.1.3 (Urbanek, 2015), bayesplot v. 1.8.1 (Gabry & Mahr, 2021; Gabry, Simpson, Vehtari, Betancourt, & Gelman, 2019), bdsmatrix v. 1.3.4 (Therneau, 2020), BH v. 1.75.0.0 (Eddelbuettel, Emerson, & Kane, 2021), bit v. 4.0.4 (Oehlschlägel & Ripley, 2020), bit64 v. 4.0.5 (Oehlschlägel & Silvestri, 2020), blob v. 1.2.2 (H. Wickham, 2021a), bridgesampling v. 1.1.2 (Gronau, Singmann, & Wagenmakers, 2020), brio v. 1.1.3 (Hester & Csárdi, 2021), brms v. 2.16.3 (Bürkner, 2017, 2018, 2021), Brobdingnag v. 1.2.6 (Hankin, 2007), bslib v. 0.3.1 (Sievert & Cheng, 2021a), cachem v. 1.0.6 (Chang, 2021a), callr v. 3.7.0 (Csárdi & Chang, 2021a), cellranger v. 1.1.0 (Bryan, 2016), checkmate v. 2.0.0 (Lang, 2017), clipr v. 0.7.1 (Lincoln, 2020), coda v. 0.19.4 (Plummer, Best, Cowles, & Vines, 2006), colorspace v. 2.0.2 (Stauffer, Mayr, Dabernig, & Zeileis, 2009; Zeileis et al., 2020; Zeileis, Hornik, & Murrell, 2009), colourpicker v. 1.1.1 (Attali, 2021a), commonmark v. 1.7 (Ooms, 2018), cpp11 v. 0.4.2 (Hester & François, 2021), crosstalk v. 1.2.0 (Cheng & Sievert, 2021), curl v. 4.3.2 (Ooms, 2021a), data.table v. 1.14.2 (Dowle & Srinivasan, 2021), DBI v. 1.1.2

(R Special Interest Group on Databases (R-SIG-DB), Wickham, & Müller, 2021), desc v. 1.4.0 (Csárdi, Müller, & Hester, 2021), diffobj v. 0.3.5 (Gaslam, 2021), digest v. 0.6.29 (Antoine Lucas et al., 2021), distributional v. 0.3.0 (O'Hara-Wild, Kay, & Hayes, 2022), DT v. 0.20 (Xie, Cheng, & Tan, 2021), dygraphs v. 1.1.1.6 (Vanderkam, Allaire, Owen, Gromer, & Thieurmel, 2018), ellipsis v. 0.3.2 (H. Wickham, 2021b), evaluate v. 0.14 (H. Wickham & Xie, 2019), extraDistr v. 1.9.1 (Wolodzko, 2020), fansi v. 1.0.2 (Gaslam, 2022), farver v. 2.1.0 (Pedersen, Nicolae, & François, 2021), fastmap v. 1.1.0 (Chang, 2021b), finalfit v. 1.0.4 (Harrison, Drake, & Ots, 2021), fontawesome v. 0.2.2 (Iannone, 2021), fs v. 1.5.2 (Hester, Wickham, & Csárdi, 2021), future v. 1.23.0 (Bengtsson, 2021a), gargle v. 1.2.0 (Bryan, Citro, & Wickham, 2021), generics v. 0.1.2 (H. Wickham, Kuhn, & Vaughan, 2022), GGally v. 2.1.2 (Schloerke et al., 2021), ggdist v. 3.0.1 (Kay, 2021), ggExtra v. 0.9 (Attali & Baker, 2019), ggridges v. 0.5.3 (Wilke, 2021), globals v. 0.14.0 (Bengtsson, 2020), glue v. 1.6.1 (Hester & Bryan, 2022), grateful v. 0.1.10 (Rodríguez-Sánchez, Jackson, & Hutchins, 2022), gridExtra v. 2.3 (Auguie, 2017), gtable v. 0.3.0 (H. Wickham & Pedersen, 2019), gtools v. 3.9.2 (Warnes, Bolker, & Lumley, 2021), HDInterval v. 0.2.2 (Meredith & Kruschke, 2020), highr v. 0.9 (Xie & Qiu, 2021), htmltools v. 0.5.2 (Cheng et al., 2021), htmlwidgets v. 1.5.4 (Vaidyanathan et al., 2021), httpuv v. 1.6.5 (Cheng & Chang, 2022), ids v. 1.0.1 (FitzJohn, 2017), igraph v. 1.2.11 (Csardi & Nepusz, 2006), inline v. 0.3.19 (Sklyar et al., 2021), isoband v. 0.2.5 (Wilke & Pedersen, 2021), jquerylib v. 0.1.4 (Sievert & Cheng, 2021b), knitr v. 1.37 (Xie, 2014, 2015, 2021a), labeling v. 0.4.2 (Justin Talbot, 2020), later v. 1.3.0 (Chang & Cheng, 2021), lazyeval v. 0.2.2 (H. 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Data Availability

Data and code to reproduce this manuscript is available at: https://github.com/tbendixen/freelist-tutorial.

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