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12 Abstract: Estimating the number of dolphins in a group is a challenging task. To assess the 13 accuracy and precision of dolphin group size estimates, observer estimates were compared to 14 counts from large-format vertical aerial photographs. During 11 research cruises, a total of 2,435 15 size estimates of 434 groups were made by 59 observers. Observer estimates were modeled as a 16 function of the photo count in a hierarchical Bayesian framework. Accuracy varied widely 17 among observers, and somewhat less widely among dolphin species. Most observers tended to 18 underestimate, and the tendency increased with group size. Groups of 25, 50, 100, and 500 were 19 underestimated by <1%, 16%, 27%, and 47%, respectively, on average. Precision of group size 20 estimates was low, and estimates were highly variable among observers for the same group. 21 Predicted true group size, given an observer estimate, was larger than the observer estimate for 22 groups of more than about 25 dolphins. Predicted group size had low precision, with coefficients 23 of variation ranging from 0.7 to 1.9. Studies which depend on group size estimates will be 24 improved if the tendency to underestimate group size and the high uncertainty of group size 25 estimates are included in the analysis.

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Keywords: group size estimation, abundance estimation, aerial photography, Bayesian
hierarchical model, random-effects model, reverse jump MCMC

Introduction

32	Estimation of group size is an important component of ecological and behavioral studies
33	of animals which occur in groups. However, estimation of group size in wildlife studies can be
34	difficult. Replicate counts of birds showed high variation (Ryan and Cooper 1989), the number
35	of birds was undercounted in aerial surveys (Bayliss and Yeomans 1990), and known group sizes
36	of elk were underestimated from a helicopter (Cogan and Diefenbach 1998). Even counting the
37	number of birds in photographs had a negative bias (Erwin 1982). Experiments in visual
38	perception have shown a tendency to underestimate the size of large groups of objects (Krueger
39	1972), apparently related to distortions produced by saccadic ("jerky") eye movements (Binda et
40	al. 2011). Determining the size of a group of cetaceans is particularly challenging because of
41	several characteristics that make group size estimation difficult: (1) the animals are moving; (2)
42	an unknown fraction of the group is underwater at any moment; (3) the fraction underwater
43	changes with behavior; (4) groups can be large; and (5) the distribution of group sizes is usually
44	skewed, with a few groups much larger than the mean.

45 Accurate estimation of group size is necessary for unbiased estimation of abundance. In 46 standard distance sampling (e.g., line transects), the density of groups is estimated and then 47 multiplied by an estimate of expected group size (Buckland et al. 2001). Alternatively, group 48 size may be a covariate of the detection process and expected group size is not estimated 49 explicitly (Borchers and Burnham 2004). In either case it is assumed that group sizes are 50 measured accurately. Using earlier subsets of the photographic calibration data presented here, 51 some line-transect analyses have used group size estimates corrected by observer-specific 52 calibration factors (Gerrodette and Forcada 2005, Barlow and Forney 2007). In most studies, 53 however, correction factors for group size estimation are not available.

Assessing precision of group size estimates is equally important. Even if group sizes were to be estimated accurately on average, there is measurement error associated with each group size estimate. Including the variability associated with group size estimates is necessary for proper assessment of uncertainty. If measurement error is not included, variance of estimates of abundance and other quantities that depend on group size estimates will be too small. In other words, an important source of uncertainty will not be included in the analysis, and conclusions may appear to be more precise than they should be.

61 In this large field study, we measured the accuracy and precision of dolphin group size 62 estimates. True group size was assessed with counts from high-quality vertical aerial 63 photographs, and ship-based observer estimates were calibrated against these counts. The 64 tendencies of different individual observers to under- or over-estimate group size were estimated 65 in a hierarchical Bayesian framework, for different group sizes, species, and sea-state conditions. 66 The performance of a new (out-of-sample) observer was predicted by integrating over observer 67 and/or species effects. Given an observer estimate, we inferred true group size by sampling 68 posterior distributions.

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Methods

71 Field methods

Photographs of dolphin groups were collected during 11 research cruises between 1987
and 2006 in the eastern tropical Pacific Ocean. During all cruises except the last, the NOAA
vessel *David Starr Jordan* carried a Hughes 500D helicopter equipped with two large-format
military reconnaissance cameras mounted below the fuselage. During the 2006 cruise, images

76 were collected with the same camera systems mounted in a NOAA Twin Otter fixed wing 77 aircraft. Under conditions of sun angle (generally mid-morning and mid-afternoon) and sea state 78 (generally Beaufort 0-4) that allowed dolphins to be clearly visible from above, vertical 79 photographs of dolphin groups were taken from an altitude of 200-300m (Gilpatrick 1993). The 80 camera recorded images on 114mm negatives, and had a motion-compensation system that 81 moved the film at the same speed that the image was moving within the camera, thus eliminating 82 blurring due to the forward motion of the aircraft. The cycle rate of the camera was adjusted to 83 achieve 80% overlap between adjacent frames during a photographic pass over a dolphin group. 84 The number of photographic passes of each dolphin group varied with group size, configuration and behavior. 85

86 After a group of dolphins had been photographed, the group was approached by the ship 87 in a way to give the marine mammal observers on the ship the best possible view of the whole 88 group, considering wind, swell, and sun angle. All observers who had adequate views of the 89 group, usually all six observers on the ship, made their best estimates of group size. We refer to these estimates as the "observer estimates." Observers usually first detected dolphins with 25X 90 91 binoculars, but switched to 7X binoculars and then to naked eye as the ship approached the 92 group. The minimum approach distance varied with group size and behavior, but typically was 93 10-50m. Observers made group size estimates independently and did not discuss their estimates 94 with each other, either during the sighting or afterward. Independence in this context refers to 95 the behavioral independence of the observers, not to the statistical independence of their 96 estimates. All observers had previous experience in cetacean field work. Before each cruise, 97 observers were given training on group size estimation, including tests with known numbers of

static objects, computer simulations of moving, intermittently visible objects, and instruction on
counting by subgroups (*e.g.*, by tens or fifties) for more consistent estimation.

100 *Laboratory methods*

101 The aerial photographs of dolphin groups were reviewed on light tables equipped with 102 dissection microscopes (Gilpatrick 1993). Photographs were compared with notes recorded 103 during the photographic passes to ensure that the entire group was captured within the series of 104 images that made up a photograph pass. For groups that were successfully photographed, the 105 best pass was selected, and three readers independently counted the number of dolphins in the 106 group from the series of images. If the CV among counts was > 0.1, or if notes by aerial and 107 shipboard observers indicated that there was confusion over the identity of the group, the group 108 was not included in the data analyzed here (Gilpatrick 1993).

109 To qualify as a "calibration school" for this analysis, the whole group had to be 110 photographed from the air with a series of overlapping photographs, the photo counts of the three 111 independent readers had to agree closely, and the shipboard observers had to view the whole 112 group for a sufficient time to make good estimates. Calibration schools were thus not a random 113 sample of all dolphin groups, but rather a selected set for which we were confident that true 114 group size could be accurately determined. We omitted as outliers eight cases for which there 115 was a large (greater than a factor of four) discrepancy between mean photo count and mean 116 observer estimate, probably a result of undetected splitting or coalescence of groups after 117 photography but before observer estimates. A total of 434 groups met these criteria as 118 calibration schools, with 2,435 estimates of group size by 59 observers.

119 Statistical model

120 To evaluate observer estimates of group size, we used the mean of the counts by the three 121 photograph readers for each calibration school, and refer to this as the "photo count." This 122 measure of true group size had some error (variation among the three readers), but this variation 123 (mean photo count CV over all groups = 0.047) was much smaller than the variation among 124 observer estimates of the same groups (mean CV = 0.42). Preliminary exploration of the data 125 suggested that, on a log-log scale, observer estimates could be linearly related to photo counts 126 and that variance was approximately constant over a large range of group sizes (Fig. 1A). In 127 addition, observers varied widely in the accuracy of their group size estimates (Fig. 1B). We 128 evaluated a variety of linear and nonlinear models in a frequentist setting, with both fixed and 129 random effects, with R function *lmer*, and used likelihood ratio tests, information criteria such as 130 AIC and DIC, and visual examinations of residual and q-q plots to identify a reasonable set of 131 candidate models. We found that dolphin species and Beaufort sea state could possibly affect the 132 accuracy of group size estimates, and that a linear model of the logarithm of photo counts 133 provided a more parsimonious fit to the data than a quadratic model.

134 Let y_{ij} be the observer estimate of the size of group *i* by observer *j*, and let x_i be the photo 135 count of group *i*. We modeled differences among observers as random effects, and dolphin 136 species and wind conditions as fixed additional effects that might affect group size estimates. 137 The full hierarchical model may be written as

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$$\log(y_{ij}) = \alpha_{0j} + (\alpha_{1j} + \beta_1)\log(x_i) + \sum_{k=2}^{7} \beta_k S_{ik} + \beta_8 B_i + \varepsilon_{ij}$$

$$\begin{pmatrix} \alpha_{0j} \\ \alpha_{1j} \end{pmatrix} \sim N \begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_{\alpha 0}^2 & \rho \sigma_{\alpha 0} \sigma_{\alpha 1} \\ \rho \sigma_{\alpha 0} \sigma_{\alpha 1} & \sigma_{\alpha 1}^2 \end{pmatrix} \end{pmatrix}$$

$$\varepsilon_{ij} \sim N(0, \sigma_{\varepsilon}^2), \qquad (1)$$

where β_1 was the coefficient associated with the log of the photo counts, β_k were coefficients 139 140 associated with six species S_{ik} , k=2,...7, and β_8 was the coefficient associated with Beaufort sea state B_i . Two random effects, α_{0i} and α_{1i} , allowed the relationship between $\log(y_{ij})$ and $\log(x_i)$ 141 to vary among observers, α_{0j} in terms of the intercept and α_{1j} in terms of the slope coefficient 142 β_1 . The two sets of random-effects coefficients had means of zero, variances $\sigma_{\alpha 0}^2$ and $\sigma_{\alpha 1}^2$, and 143 144 correlation ρ . The assumption was that the 59 observers were a random selection from a larger 145 pool of possible observers whose group size estimation tendencies were normally distributed. 146 Species S_{ik} entered the model as an indicator variable, with a value of 1 if group *i* was 147 species k and 0 otherwise. Species were recorded in the field at the lowest possible taxonomic 148 level, including subspecies. We combined the field identifications into six species categories: 149 pantropical spotted dolphins (Stenella attenuata, 51 groups), spinner dolphins (S. longirostris, 40 150 groups), mixed spotted-spinner dolphin groups (78 groups), striped dolphins (S. coeruleoalba, 151 114 groups), common dolphins (Delphinus delphis and D. capensis, 87 groups) and other (64 groups). "Other" was a heterogeneous category including Risso's dolphins (Grampus griseus), 152 153 common bottlenose dolphins (*Tursiops truncatus*), rough-toothed dolphins (*Steno bredanensis*), 154 short-finned pilot whales (Globicephalus macrorhynchus), and other groups which did not fit 155 into the previous categories, such as mixed common-striped dolphin groups. In the eastern 156 tropical Pacific Ocean, mixed spotted-spinner dolphin groups are common, so we included these 157 as a distinct category. Sea state B was recorded on the Beaufort scale as an integer from 0 to 5; 158 however, only one of the 434 calibration schools occurred in Beaufort 5 conditions, so the 159 effective range of the model was Beaufort 0-4. Because the Beaufort scale is ordered, we 160 modeled sea state as a continuous variable with a single linear coefficient. Models with sea state

161 as a categorical variable are addressed in the Discussion. S_i and B_i were the same for all 162 observers for a given group *i*, so we omitted subscript *j* for these covariates in Eq. 1.

We considered four variants of Eq. 1 as candidate models: model 1, without species or sea-state effects ($\beta_k=0$ and $\beta_8=0$); model 2, with species but without sea-state effects ($\beta_8=0$); model 3, with sea-state but without species effects ($\beta_k=0$); and model 4, the full model with both species and sea-state effects. All four models included observers as a random effect.

167 Bayesian inference

168 To include model selection in a Bayesian framework, we fitted the models in R using 169 reversible jump Markov Chain Monte Carlo (RJMCMC) methods (King et al. 2009, Oedekoven 170 et al. 2014). In this approach, the model itself was treated as an additional parameter to be 171 estimated, and the joint posterior distribution included both parameters and models (Appendix 172 1). A uniform discrete prior was specified for the four models, and uniform continuous priors 173 were specified for all coefficients β and standard deviations σ in Eq. 1. Model probabilities 174 were calculated as the fraction of iterations of the RJMCMC chain in each model after burn-in 175 (Appendix 1).

The four models were also fitted in the BUGS language (Lunn *et al.* 2000) and compared
with the Watanabe-Akaike (or Widely Applicable) Information Criterion (WAIC) (Watanabe
2010). WAIC can be viewed as an improvement to the Deviance Information Criterion (DIC)
(Spiegelhalter *et al.* 2002), which has some shortcomings for hierarchical models (Plummer
2008, Millar 2009, Lunn *et al.* 2013). WAIC was calculated using pointwise predictive density
at the observer level from the MCMC posterior samples for each model (Gelman *et al.* 2014,
Vehtari *et al.* 2016). We used standard procedures to assess burn-in, autocorrelation, and

convergence of the MCMC samples (Appendix 2). BUGS code is given in Appendix 3 and Rcode for the RJMCMC analysis in Appendix 4.

185 For prediction, we sampled from the BUGS posterior samples of model 2, which had the 186 most support (see Results). We made two kinds of predictions: an observer estimate given true 187 group size and true group size given an observer estimate. For each, we predicted conditionally 188 and unconditionally on both observer and species. A conditional prediction for an observer or 189 species meant a prediction given that it was made by a particular observer or given that it was 190 made of a group of a particular species. An unconditional prediction was calculated to infer 191 estimation tendencies for a new (out-of-sample) observer and/or species – that is, estimation 192 tendencies integrated over observers or species effects. Unconditional predictions were 193 approximated by sampling observers and/or species randomly. We sampled the MCMC chain 194 50,000 times with replacement, each time also randomly sampling an observer and a species for unconditional inference. For the model error term σ_{ϵ}^2 , we made random draws from normal 195 196 distributions with the MCMC sample variances. To preserve the covariance structure, we used 197 the whole set of parameter values for each selected MCMC iteration, and computed observer 198 estimate y given group size, or group size x given observer estimate, based on Eq. 1. We 199 checked the accuracy of our predictions by comparing them to the photo counts (Appendix 5). 200 For each of the 2,435 observer estimates, we determined if the central 95% credibility interval of 201 predicted size included the photo count.

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Results

204 Calibration schools

205 Group sizes of calibration schools ranged from 5 to 6.012 (Fig. 1). The set of 434 206 calibration schools represented about 8% of dolphin groups of the same species detected during 207 the 11 surveys. On average, calibration schools were larger in size (because we did not 208 photograph groups containing only a few dolphins) and were photographed in lower Beaufort sea 209 states (because it was harder to obtain clear images in windy conditions) than for all dolphin 210 groups. Importantly, the variation among independent observer estimates for a dolphin group 211 was similar for calibration schools (mean CV 0.42, interquartile range 0.29-0.50) and all detected 212 groups (mean CV 0.39, interquartile range 0.24-0.51). The number of calibration schools per 213 observer ranged from 6 to 159, with a median of 33 and a mean of 41.3.

214 Observer estimates of dolphin group size

215 The raw data indicated that observers generally tended to underestimate dolphin group 216 size; 69% of observer estimates were less than the photo count (Fig. 1). Both model selection 217 methods indicated that the accuracy of observer estimates was affected by the species of the 218 group but less so by Beaufort sea state. Posterior model probabilities indicated by the RJMCMC 219 chain were 0.0, 0.984, 0.0, and 0.016 for models 1-4, respectively (Fig. 2). With proper selection 220 of proposal distributions, models 2 and 4 had stationary distributions throughout the history of 221 the chain (Fig. A1 in Appendix 1). WAIC scores showed a similar pattern favoring model 2 but 222 with some support for model 4, with values of 3766.0, 3596.0, 3769.3, and 3598.5 for models 1-223 4, respectively.

224 Marginal posterior distributions of parameters for models 2 and 4 were similar (Table 1). 225 For model 4, the sea-state coefficient β_8 was small in absolute value and the 95% credibility 226 interval included 0, further indications that wind conditions in the range Beaufort 0-4 had little

effect on the accuracy of group size estimation. The coefficient for log(photo count), β_1 , was effect on the accuracy of group size estimation. The coefficient for log(photo count), β_1 , was
example 1.0 (mean 0.80, 95% credibility interval 0.76 to 0.83 for model 2), which meant that the
tendency to underestimate increased with group size. Species coefficients decreased in the order
mixed spotted-spinner, common, spotted, spinner, striped, and other (Fig. 3A). However, the
posterior distributions of species coefficients overlapped (Table 1), indicating that the differences
among species were modest. The random-effects coefficients were negatively correlated (mean $\rho = -0.79$, 95% credibility interval -0.59 to -0.91).

234 Observers differed in accuracy of group size estimation (Fig. 3B). Among the 59 235 observers, some tended to underestimate and others tended to overestimate. For spotted dolphin 236 groups of 25, 50, 100, and 500 animals, the observers with the lowest estimation tendency had 237 mean posterior estimates of 18, 29, 45 and 132, respectively, while the observers with the highest 238 estimation tendency had mean posteriors of 42, 72, 125, and 585 (Table 2). The "average 239 observer" (actually four different observers, one for each of the four group sizes in Table 2) had 240 estimates of 25, 44, 78, and 290 for spotted dolphin groups of 25, 50, 100, and 500, respectively. 241 Thus, over all observers, groups of 25 spotted dolphins were estimated accurately on average, 242 but the range among observers was from underestimation by 29% to overestimation by 66% 243 (Table 2). There were similarly large ranges in accuracy among observers for larger groups: for 244 groups of 50, -43% to +45%; for groups of 100, -55% to +25%; and for groups of 500, -74% to 245 +17%. The "average observer" underestimated spotted dolphin groups of 50, 100, and 500 246 animals by 11%, 22%, and 42%, respectively. We chose spotted dolphins for these numerical 247 comparisons because spotted dolphins were near the middle of the species effect (Table 1). 248 There would be less underestimation of group size for common dolphins and mixed groups of 249 spotted-spinner dolphins, and more underestimation of group size for spinner, striped, and other

dolphins. Averaged over all species, the mean figures of underestimation were <1%, 16%, 27%,
and 47% for groups of 25, 50, 100, and 500 animals.

The random-effects model allowed intercept and slope parameters to be estimated for each observer (Fig. 4), constrained by the hierarchical assumptions of normal distributions and correlation between slope and intercept. Visually, the greater importance of the observer effect relative to the species effect can be judged by comparing Fig. 3B with Fig. 3A. Numerically, the range of plausible values for observer intercepts $(1.5 \approx \pm 2 \sigma_{\alpha 0})$ was greater than the range of species effects (≈ 0.4), based on the mean posterior values in Table 1.

Accuracy decreased with group size (Fig. 5). Groups of 25 spotted dolphins were slightly underestimated, but groups of 500 were severely underestimated. For groups of 25, 50, 100, and 500 dolphins, posterior means for an out-of-sample observer (gray lines in Fig. 5) were 24.2, 42.2, 73.1, and 264.4, respectively. To show conditional estimates, we used observer #53 as an example. The black lines in Fig. 5 for observer #53 were slightly to the left of the gray lines unconditioned on observer, indicating that this observer tended to underestimate more than the average over all observers.

The posterior distributions of observer estimates were approximately normal on a natural logarithmic scale (Fig. 5). The distributions were quite wide, illustrating the high uncertainty (or low precision) in observer estimates of group size. Conditional estimates had higher precision than unconditional estimates. Estimates made by a particular observer (observer #53) for a particular species (spotted dolphins) had slightly higher precision (less uncertainty) than estimates by the same observer for an unknown species (compare thin dashed with thick solid black lines in Fig. 5). Unconditional estimates for any observer or species had the least precision

(thick gray lines in Fig. 5). The differences between conditional and unconditional estimates
were small, however, in the context of the overall high variability of group size estimates.

274 Predictions of dolphin group size from observer estimates

275 Conversely, given an observer estimate, predicted true group size was usually larger than 276 the estimate, especially for larger groups (Fig. 6). For observer estimates of 25, 50, 100, and 500 277 dolphins, posterior means were 26.0, 63.5, 154.0, and 1,194.5, respectively, for an out-of-sample 278 observer (gray lines in Fig. 6). As with posterior distributions of observer estimates given group 279 size, predicted group sizes conditional on observer and species had higher precision than 280 unconditional estimates (compare black and gray lines in Fig. 6). Because observer #53 tended 281 to underestimate more than average, predicted group size was larger for this observer than for the 282 average over all observers.

283 Dolphin group size predicted from an observer estimate had high uncertainty. 284 Coefficients of variation for predicted group size conditional on species ranged from 285 approximately 0.7 to 0.9 (Table 3). Coefficients of variation for unconditional predictions were 286 even larger, ranging from 0.9 to 1.9, due to the additional uncertainty of predicting group size for 287 an unknown species. Given an observer estimate of 100 dolphins, the 95% credibility interval 288 for the true size of the group ranged from 43 to 621 for a group of spotted dolphins, and from 37 289 to 776 for a group unconditional on species. Posterior distributions accurately captured the 290 uncertainty in predicting dolphin group size from an observer estimate (Appendix 5, Fig. A4).

The degree to which an observer estimate was increased to estimate true group size depended on species. For an observer estimate of 25 dolphins, for example, the median predicted group size was smaller than 25 for mixed spotted-spinner and common groups, and

294	larger than 25 for spotted, spinner, striped, and other groups (Table 3). Because the
295	exponentiated posterior distributions were lognormal, means were larger than medians.
296	Therefore, we used the median (50% quantile) as the best measure of central tendency for these
297	distributions, because there was equal probability of a value being higher or lower than the
298	median. Integrated over species and observer effects, estimates of 25, 50, 100, and 500 were
299	increased by 4%, 24%, 47%, and 122%, respectively, to obtain the medians of the posterior
300	distributions of predicted group size (Table 3). In other words, given an observer estimate of 500
301	dolphins, the most probable true size of the group would be more than twice that number.
302	
303	Discussion
304	Accuracy and precision
305	The discrepancy between an observer estimate of dolphin group size and the true number
306	can be discussed in terms of two components: accuracy and precision. Accuracy is measured by

307 the difference between the true number and the mean of repeated observations. Inaccurate 308 measurement of group size leads to biased results. Precision is assessed by the random error 309 among repeated observations. Random error will be positive for some observations and negative 310 for others, but with a mean of zero. Low precision means high variance and greater uncertainty 311 in results.

We found that accuracy of dolphin group size estimates depended on group size, observer, and species. Within the Beaufort 0-4 range of the calibration schools, Beaufort sea state had less effect on accuracy, once group size and observer effects had been accounted for.

315 There was a general tendency to underestimate dolphin group size, and this tendency 316 increased with group size. The coefficient of the log of photo count (β_1 , Table 1) was < 1.0, 317 which meant that large groups were underestimated more than small groups. Observer estimates 318 were accurate (on average) for dolphin groups of 25 animals, but were too low by 16% for 319 groups of 50, too low by 27% for groups of 100, and too low by 47% for groups of 500 (Fig. 5). 320 These estimates of accuracy averaged over all observers do not measure the accuracy of a 321 particular observer, nor the discrepancy between an observer estimate and true group size for a 322 particular group. Accuracy of dolphin group size estimation in this study applies within the 323 range of calibration school sizes with a reasonable number of samples, roughly between 10 and 324 1000 animals (Fig. 3).

These results were broadly consistent with previous studies which showed that humans tend to underestimate group sizes in wildlife studies (Caughley 1974, Bayliss and Yeomans 1990, Cogan and Diefenbach 1998). The rate of decline in accuracy with group size ($\beta_1 = 0.80$, Table 1) falls in the range of perceptual experiments measuring underestimation of the number of dots on paper (Krueger 1972). Underestimation of large groups may have a physiological basis related to eye movement; estimation of small groups (about 10 or fewer objects) does not have this negative bias and seems to involve a different perceptual mechanism (Binda *et al.* 2011).

The degree of underestimation also varied by species. For the six species categories in this study, dolphin group size estimates were lower in the order: mixed spotted-spinner,

common, spotted, spinner, striped, and other (Table 1, Fig. 3A). This order of species

335 coefficients corresponded roughly to mean group size among the six species groups, with mixed

336 spotted-spinner and common dolphin groups being largest, and striped and other dolphin groups

337 smallest. This correspondence suggests that the effects of group size and species were somewhat338 confounded.

339 Accuracy varied among the 59 observers. While there was an overall tendency to 340 underestimate dolphin group size, some observers had a stronger tendency to underestimate, 341 while others had a tendency to overestimate (Table 2). The random-effects model allowed the 342 estimation of separate effects for each observer (Fig. 3B), but connected the observers as a group 343 and allowed the tendency of all observers together to support estimation for each single observer 344 (Fig. 4). A random-effects model is often understood in terms of "partial pooling." It represents 345 an intermediate approach between complete pooling (treating all observers as a single group, Fig. 346 1A) and no pooling (treating each observer independently, Fig. 1B). The random-effects 347 approach spans a range of models between these extremes, and includes complete pooling and 348 complete separation as special cases at the limits (Gelman and Hill 2007). The degree of pooling 349 is related to the amount of shrinkage of individual effects toward the mean (Gelman and Pardoe 350 2006).

Precision of observer estimates of dolphin group size was strikingly low (Fig. 5). For a group of 100 dolphins, for example, estimates could range from about 30 to 200 with 95% probability. Regardless of an observer's accuracy, it was common for the observer to estimate 50% high for one group and 50% low for the next. As a consequence, there was high variability among the independent observer estimates of group size, both for calibration schools as well as for non-calibration dolphin groups. The mean CV among observer estimates was 0.4 across a wide range of group sizes. Clearly, estimating the size of a dolphin group is a challenging task.

358 Statistical issues

As a measure of true group size, we used the mean of photo counts by three independent readers. A binomial moment estimator has been proposed for repeated counts with imperfect detection, *i.e.*, false negatives (DasGupta and Rubin 2005, Walsh *et al.* 2009), but in our study variation among counts of the three readers was also due to false positives. Large tuna, which frequently accompany dolphin groups in the eastern tropical Pacific, can be mistaken for a submerged dolphin in the photographs. Splashes and reflections might also be counted as a partially hidden dolphin.

366 RJMCMC and WAIC are two fully Bayesian approaches to model selection (Hooten and 367 Hobbs 2015). RJMCMC treats the model itself as an additional unknown parameter to be 368 estimated, while WAIC is a score function based on the predictive ability of the model. Both 369 indicated that the accuracy of dolphin group size estimates varied by observer and species 370 (model 2). There was little posterior support for model 4, which included Beaufort sea state 371 (Fig. 2). The posterior odds of models 2 and 4 (the Bayes factor, Kass and Raftery 1995) was 372 60.6, indicating strong support for model 2 over model 4. The WAIC difference of 2.5 also 373 indicated support of model 2 over model 4. If sea state was modeled as a categorical variable, 374 model 4 had a posterior probability of zero (it was never selected in the RJMCMC algorithm), 375 but if sea state was modeled as a continuous variable, model 4 was selected 2% of the time (Fig. 376 2, Fig. A1 in Appendix 1). Thus, it appeared that modeling sea state as a continuous variable 377 rather than as separate factor variables was a more parsimonious approach. As there was little 378 support for model 4, and because parameter estimates were similar for models 2 and 4 (Table 1), 379 we focused on model 2 for inference and did not use model-averaged estimates.

Because Bayesian inference is based on conditional probabilities, it was possible to make
 inference regardless of observer and/or species, by integrating over observer and species effects.

The estimation tendency of a new, out-of-sample observer included the uncertainty of not knowing which observer, out of the "universe" of possible observers with different estimation tendencies, might be chosen. Such estimates unconditional for observer and species are shown as gray lines in Figs. 5 and 6. The greater uncertainty of the unconditional estimates is indicated by the wider probability distributions in those figures, relative to the conditional estimates shown with black lines.

388 Application of results

389 To obtain the best estimates of group size, we can use the estimation tendencies revealed 390 in this study to adjust observer estimates of dolphin group size. We wish to predict true group 391 size, given an observer estimate. The Bayesian approach allowed us to solve this inverse 392 problem with proper accounting of uncertainty. Since, for groups larger than about 25 dolphins, 393 there was a tendency to underestimate group size, predictions of true group size tended to be 394 larger than the estimate (Fig. 6). Because the degree of underestimation depended on group size, 395 species, and observer, the amount that a group size estimate had to be increased to predict true 396 group size also depended on group size, species, and observer (Table 3). The amount that an 397 estimate had to be increased could be substantial. For example, a group size estimate of 100 398 dolphins had to be increased by 47% to obtain the unconditional best (median) estimate of true 399 group size.

Because an estimate of group size had low precision, predicted group size based on an estimate also had low precision. Posterior distributions had CVs of approximately 0.7 to 0.9 for groups of known species, and 0.9 to 1.9 for groups of any species (Table 3). For an out-ofsample observer estimate of 25 dolphins, for example, median predicted true group size was 25.9

animals (accuracy was good), but the 50% credibility interval extended from 16 to 42 dolphins,
and the 95% credibility interval from 6 to 111 dolphins (Table 3). This source of uncertainty is
usually ignored in distance sampling analyses, although Gerrodette and Forcada (2005) included
uncertainty in group size through a bootstrap procedure. Most line-transect analyses compute the
variance in expected group size from the sizes of the observed groups.

409 On cetacean line-transect surveys conducted by the Southwest Fisheries Science Center, 410 three independent estimates of group size are recorded for each sighting. For the best estimate of 411 group size, Gerrodette and Forcada (2005) used an average of the three calibration-adjusted 412 observer estimates, weighted by the inverse of the group size estimation variance of each 413 observer. The value of making several independent estimates of group size will be examined in 414 a future paper.

415 Given our findings of inaccuracy for groups larger than 25 dolphins and low precision for 416 groups of all sizes, it is worth noting that the estimates of group size in this study were a selected 417 set of estimates made in optimal circumstances. Each group was approached with the specific 418 objective of obtaining group size estimates, the observers had good views of the entire group, 419 and the ship remained with the group until the observers had made their best possible estimates. 420 Almost certainly the behavior of dolphin groups affects the accuracy and precision of group size 421 estimates, but our set of calibration schools consisted of well-behaved groups that could be 422 observed and photographed in their entirety.

Accuracy and precision may be lower for groups estimated in less optimal conditions.
Schwarz *et al.* (2010) found that estimates of delphinid group sizes were 58% lower when the
ship did not approach groups (passing mode) than when it did (closing mode). Barlow *et al.*

426 (1997) also found that group size estimates were smaller in passing mode. Barlow and Taylor 427 (2005) found that an extended 90-min period of observation improved group size estimates of 428 asynchronously diving sperm whales (*Physeter microcephalus*). The position of the observer 429 may also matter. The estimates of group size in this study were made from a platform 430 approximately 10 m above the water. The estimation tendencies reported here may not apply to 431 other situations, such as estimates made from higher or lower platforms on a ship, or estimates 432 made from land at various elevations and distances to sightings. Caughley *et al.* (1976) found 433 that the accuracy of aerial counts varied with aircraft speed, height, and observer.

434 We conclude with two recommendations for studies that depend on estimates of cetacean 435 group size. First, we recommend training to improve group size estimation. Although we were 436 not able to measure how our pre-cruise training affected observers' estimates, we believe that the 437 training had a positive effect. Training may include displays of groups of objects of known size, 438 and instructions on estimating group size by counting subgroups of multiple animals. Second, 439 we recommend assessment of accuracy and precision of group size estimation under the 440 particular conditions of a study. The large budget of this study is unlikely to be replicated, but 441 digital photography by drones is a more economical and much safer option today. Laake *et al.* 442 (2012) used two observer teams to assess the accuracy of pod size estimates for migrating gray 443 whales (*Eschrichtius robustus*). Although pod size was usually only one or two animals, 444 correcting pod size estimates had an important effect on abundance estimates and inferred 445 population trajectory.

If a study is unable to assess accuracy of group size estimates, the results of this study can be applied with appropriate caution. We have noted that biases might be different for group size estimates made under other conditions, such as greater distances. One of our central results was

449 that people varied widely in their group size estimation tendencies; therefore, the ideal is to 450 calibrate particular individual observers. However, the random-effects model for the observer 451 effect allowed inference for observers outside this study. Table 3 and Figures 5 and 6 show 452 posterior distributions for a new, out-of-sample observer – that is, accuracy and precision of 453 group size estimates which include the uncertainty of not knowing which observer, out of the 454 large number of possible observers with different estimation tendencies, might have been chosen. 455 Unless more specific information can be obtained, it would be reasonable to assume that the 456 estimation tendencies of the 59 observers in this study are representative of all observers.

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546	information criterion in singular learning theory. Journal of Machine Learning Research
547	11: 3571-3594.

- 550 Table 1. Marginal posterior distributions of parameters for the two models with posterior
- 551 support. Distributions are summarized by means, standard deviations (SD) and three quantiles.
- All parameters had uniform prior distributions. RE = random effects for observers. See Eq. 1
- 553 for definitions of parameters.

		Model 2					Model 4					
Parameter	Mean	SD	2.5%	50%	97.5%	Mean	SD	2.5%	50%	97.5%		
Log(photo count), β_1	0.796	0.018	0.761	0.796	0.832	0.797	0.018	0.760	0.798	0.831		
Sp: spotted-spinner, β_2	0.805	0.087	0.635	0.803	0.974	0.818	0.087	0.653	0.816	0.995		
Sp: common, β_3	0.757	0.084	0.592	0.755	0.926	0.776	0.087	0.613	0.774	0.951		
Sp: spotted, β_4	0.656	0.082	0.497	0.654	0.816	0.674	0.083	0.521	0.672	0.843		
Sp: spinner, β_5	0.603	0.088	0.433	0.604	0.778	0.620	0.091	0.448	0.618	0.806		
Sp: striped, β_6	0.513	0.075	0.370	0.511	0.660	0.531	0.078	0.386	0.530	0.687		
Sp: other, β_7	0.423	0.076	0.273	0.424	0.576	0.442	0.079	0.291	0.440	0.601		
Beaufort sea state, β_8	na	na	na	na	na	-0.010	0.010	-0.030	-0.010	0.010		
SD intercept RE, $\sigma_{\alpha 0}$	0.382	0.073	0.245	0.377	0.534	0.385	0.073	0.252	0.381	0.540		
SD slope RE, $\sigma_{\alpha 1}$	0.104	0.017	0.073	0.102	0.138	0.104	0.017	0.073	0.103	0.139		
Correlation RE, ρ	-0.792	0.085	-0.912	-0.808	-0.586	-0.792	0.088	-0.912	-0.809	-0.578		
SD model, σ_{ε}	0.497	0.008	0.482	0.497	0.512	0.497	0.007	0.482	0.497	0.511		

Table 2. Summary of estimation tendencies among observers. For each group size, the entries in the table show the distribution of the means of the posteriors of the 59 observers for estimates of a group of spotted dolphins. "Mean diff.", "Min diff." and "Max diff." are the differences between the mean (or minimum or maximum) of the mean observer estimates and true group size, expressed as percentages of group size.

ſ	Group	D	istribution	Mean	Min	Max				
	size	Mean Min 25% 50% 75% Max						diff.	diff.	diff.
Ī	25	25.4	17.7	21.2	25.9	28.7	41.5	2%	-29%	66%
	50	44.4	28.5	35.5	45.0	51.1	72.4	-11%	-43%	45%
ſ	100	77.7	44.9	60.3	78.3	89.1	124.6	-22%	-55%	25%
ſ	500	289.7	131.7	201.8	293.0	355	585.3	-42%	-74%	17%

Table 3. Predicted dolphin group sizes given observer estimates of 25, 50, 100, and 500 animals by a new (out-of-sample) observer, for six dolphin species and integrated over species ("any species"). Posterior distributions have been exponentiated to show values on the scale of the number of dolphins. Distributions of predicted group size are approximately lognormal, and are summarized by means, standard deviations (SD), coefficients of variation (CV) and five quantiles. "Difference" is the difference between the median (the 50% quantile) of predicted group size and observer estimate, expressed as a percentage of the observer estimate.

Observer	Dolphin	Predicted group size								
estimate	species	Mean	SD	CV	2.5%	25%	50%	75%	97.5%	chee
	spotted-spinner	26.4	19.6	0.74	5.3	13.3	21.2	33.3	78.2	-15%
	common	28.2	21.1	0.75	5.5	14.3	22.6	35.8	83.4	-10%
	spotted	32.3	24.4	0.76	6.6	16.3	25.9	40.8	95.7	4%
25	spinner	34.6	26.3	0.76	6.9	17.4	27.7	43.6	103.6	11%
	striped	39.0	29.1	0.75	7.9	19.9	31.4	49.3	113.9	26%
	other	43.8	33.3	0.76	8.8	22.1	35.2	55.3	130.3	41%
	any species	34.1	30.0	0.88	6.2	16.1	25.9	42.0	110.6	4%
	spotted-spinner	66.6	50.4	0.76	13.9	33.8	53.5	83.6	196.6	7%
	common	70.7	53.2	0.75	14.7	36.1	56.7	88.7	209.9	13%
	spotted	81.1	61.6	0.76	17.0	41.2	65.1	101.4	239.7	30%
50	spinner	87.3	66.7	0.76	18.1	44.3	70.3	110.1	256.5	41%
	striped	98.6	75.2	0.76	20.2	49.9	78.6	123.9	294.5	57%
	other	110.6	84.1	0.76	23.1	56.1	88.8	138.8	325.8	78%
	any species	84.5	79.6	0.94	15.7	38.8	62.1	102.6	286.9	24%
	spotted-spinner	167.2	128.0	0.77	34.7	84.6	133.2	208.8	502.4	33%
	common	179.5	137.4	0.77	37.7	90.9	143.3	224.6	538.7	43%
	spotted	206.2	160.0	0.78	43.4	103.9	163.4	257.5	620.8	63%
100	spinner	222.2	175.1	0.79	46.7	111.4	175.4	276.6	680.3	75%
	striped	247.3	191.0	0.77	52.7	124.6	195.8	308.9	748.2	96%
	other	281.7	219.6	0.78	59.4	142.1	223.3	349.7	847.5	123%
	any species	211.2	241.4	1.14	37.4	90.2	147.4	248.5	776.3	47%
	spotted-spinner	1466.7	1215.5	0.83	305.0	723.5	1137.9	1810.4	4557.1	128%
	common	1581.4	1335.3	0.84	326.1	766.7	1218.6	1956.9	4981.8	144%
	spotted	1801.7	1518.8	0.84	367.9	876.1	1386.9	2227.2	5629.0	177%
500	spinner	1941.8	1651.7	0.85	400.7	938.3	1490.8	2399.8	6192.8	198%
	striped	2181.9	1972.4	0.90	447.1	1057.2	1674.9	2689.5	6898.4	235%
	other	2483.6	2145.0	0.86	498.4	1190.7	1892.8	3053.4	7876.5	279%
	any species	1944.2	3600.3	1.85	250.6	626.9	1108.2	2103.6	8468.8	122%

Figure captions

575 Fig. 1: Dolphin group size calibration data plotted on logarithmic scales. (A) Photo counts and 576 observer estimates of group size for 434 calibration schools. The size of each group was 577 estimated independently by multiple (usually 6) shipboard observers. The dashed line is a 578 regression of log(observer estimate) on log(photo count), while the solid gray line is a 1:1 579 relationship. (B) Regressions of log(observer estimate) on log(photo count) for each of the 59 580 observers. 581 Fig. 2. Prior and posterior probabilities of four models of dolphin group size estimation based on 582 RJMCMC. Differences among observers were modeled as random effects (RE) in all four 583 models; species and sea state were fixed effects. 584 Fig. 3. Estimates of (A) species and (B) observer effects on dolphin group size estimation. 585 Regression lines are based on means of posterior distributions. Fig. 4. Posterior distributions of random effects for each observer for (A) intercept α_0 and (B) 586 587 slope α_1 (see Eq. 1). Points are means and lines are central 95% credibility intervals. 588 Fig. 5. Posterior distributions of observer estimates for dolphin groups of 25, 50, 100, and 500 589 animals. Thin dashed lines are the distributions of estimates for a given observer (#53) whose 590 tendencies were estimated in this study, for a given species (spotted dolphins). Thick black lines 591 are the distributions for the same observer for any species (integrated over species). Thick gray 592 lines are the distributions for a new, out-of-sample observer with unknown tendencies, for any 593 species (integrated over observers and species). The probability densities (vertical scale) of all 594 distributions are scaled relative to the maximum value.

Fig. 6. Predicted dolphin group sizes given observer estimates of 25, 50, 100, and 500 animals. Thin dashed lines are the distributions of group size for a given observer (#53) whose tendencies were estimated in this study, for a given species (spotted dolphins). Thick black lines are the distributions for the same observer for any species (integrated over species). Thick gray lines are the distributions for a new, out-of-sample observer with unknown tendencies, for any species (integrated over observers and species). The probability densities (vertical scale) of all distributions are scaled relative to the maximum density value.





608 Fig. 2





615 Fig. 4



627 Appendix 1. Reverse Jump Markov Chain Monte Carlo (RJMCMC)

628 Random-effects models such as Eq. (1) can be implemented in a Bayesian framework 629 using hierarchical models where each parameter, including the random-effects standard 630 deviations, are assumed to have a distribution. Markov Chain Monte Carlo (MCMC) simulation 631 can be used to obtain summary statistics of the posterior distributions of the parameters given the 632 data. To include model selection in our analysis, we treated the model itself as a parameter and 633 formed the joint posterior distribution of both parameters and models. An RJMCMC algorithm 634 (Green 1995) explored this posterior distribution. The RJMCMC algorithm represented a 635 random walk, where each iteration consisted of two steps: (1) the reversible jump (RJ) step 636 where we proposed to move to a different model (the between-model move), and (2) the 637 Metropolis-Hastings (MH) step where we updated the parameters from the current model (the 638 within-model move). We placed uniform priors on all parameters with an upper bound of 1, and 639 a lower bound of -1 for coefficients and a lower bound of 0 for standard deviations.

640 All models included in the analysis contained the intercept and the log of the photo 641 counts as well as their corresponding random-effects coefficients (Eq. 1). Hence, the RJ step at 642 each iteration consisted of proposing to add or delete each of the two remaining covariates (sea-643 state and species) in turn, depending on whether the covariate was in the current model or not. 644 Four different models were possible that differed only in the inclusion or exclusion of species $(\beta_k, \text{ with } k = 2,...,7)$ and sea state (β_8) coefficients in Eq.(1): for model 1, $\beta_k=0$ and $\beta_8=0$; for 645 646 model 2, $\beta_8=0$; for model 3, $\beta_k=0$; and for model 4, both species and sea-state coefficients were 647 non-zero (full model). A proposal to add a covariate to the model involved drawing random 648 samples from the respective proposal distributions for the parameters and accepting this proposal 649 based on the calculated acceptance probability (see, e.g., King et al. 2009 on how to obtain the

acceptance probability). A proposal to delete a covariate from a model involved setting its
coefficients to zero and accepting this proposal based on the calculated acceptance probability.
The four models were considered equally likely a priori.

653 The MH step at each iteration consisted of updating the parameters that were currently in 654 the model using an MH update (Metropolis et al. 1953, Hastings 1970). This included the 655 coefficient associated with the log of the photo counts, the standard deviations associated with 656 the random effects and model errors as well as the coefficients for *species* and *sea-state* if these 657 covariates were in the current model. Furthermore, all random-effects coefficients were updated 658 during each iteration. In particular, this update involved a random walk single-update with 659 normal proposal distributions, where the mean was equal to the current value of the parameter 660 (or random-effects coefficient) and the standard deviations were fine-tuned during pilot tuning to 661 achieve appropriate acceptance rates (Gelman et al. 1996).

The chain was started with the full model and completed 210,000 iterations. We discarded the first 10,000 as burn-in and thinned the chain by retaining every 50th value, thus obtaining a posterior sample of 4000 values. Posterior model probabilities were the fraction of iterations that the chain spent in the respective model. Models 1 and 3 were never selected; model 4 was selected 1.6% of the time consistently through the history of the chain (Fig. A1). Similar results were obtained regardless of which model was used to initiate the chain.

668



670 Fig. A1. Sequence of RJMCMC jumps among models after burn-in. Results were similar

671 regardless of which model was chosen to initiate the chain. To show separate points, random

672 values have been added to each point (jittering).

674 Appendix 2. BUGS models and diagnostics for MCMC sampling

675	Each of the four variants of Eq. 1 was implemented in the BUGS language. Uniform
676	priors were specified for all parameters except the random-effects coefficients, which were
677	latent. Due to the large amount of data, specification of other priors, such as normal distributions
678	(lognormal distributions for variance parameters) with means far from values supported by the
679	data, had no effect on posterior distributions. For each model, we ran three chains of 120,000
680	iterations each, discarding the first 20,000 as burn-in from different random initial starting
681	values. For the remaining 100,000 iterations, we retained every 100 th value (thinning) to reduce
682	autocorrelation. Thus the final sample consisted of 1000 values for each of three chains. The
683	effective sample size for each parameter, calculated with R package coda, was near 1000,
684	indicating that autocorrelation was low. The chains were well-mixed for all parameters (Fig.
685	A2), and converged to similar values (Fig. A3).



Fig. A2. Traces of posterior samples. Green, red and blue lines show three independent MCMC
chains of 1000 iterations each, with different initial values. See Eq. 1 and Table 1 for definitions
of parameters.



Fig. A3. Marginal posterior probability density distributions for parameters. Green, red and blue
lines show three independent MCMC chains with different initial values. The histogram is the
total sample of all three chains. See Eq. 1 and Table 1 for definitions of parameters.

```
699
       Appendix 3. BUGS code
700
       BUGS.model <- function() {
701
        for (i in 1:n) {
702
         y[i] ~ dnorm(y.hat[i],tau.model)
703
          y.hat[i] <- a0[obs[i]] + a1[obs[i]]*x[i] + b.sp[sp[i]]
                                                                    # model 2
704
       # y.hat[i] <- a0[obs[i]] + a1[obs[i]]*x[i] + b.sp[sp[i]] + b.bf*bf[i] # model 4
705
        }
706
        tau.model <- pow(sigma.model,-2)</pre>
707
        sigma.model ~ dunif(sigma.min,sigma.max) # prior
708
       for (i in 1:6) {b.sp[i] ~ dunif(b.min,b.max)} # 6 species factor levels
709
       # b.bf ~ dunif(b.min,b.max)
                                                # sea state
710
       for (j in 1:n.obs) {
711
         a0[j] <- A[j,1]
712
         a1[j] <- A[j,2]
713
         A[j,1:2] \sim dmnorm(A.hat[j,],Tau.A[,])
714
         A.hat[j,1] <- 0
                           # mean of intercept random effects
715
         A.hat[j,2] <- b1
                            # mean of slope random effects
716
       }
717
       b1 \sim dunif(b.min,b.max)
                                     # prior
718
       Tau.A[1:2,1:2] <- inverse(Sigma.A[,])</pre>
719
       Sigma.A[1,1] <- pow(sigma.a0,2)
720
       Sigma.A[2,2] <- pow(sigma.a1,2)
721
       Sigma.A[1,2] <- rho*sigma.a0*sigma.a1
722
       Sigma.A[2,1] <- Sigma.A[1,2]
723
       sigma.a0 ~ dunif(sigma.min,sigma.max) # prior
724
       sigma.a1 ~ dunif(sigma.min,sigma.max) # prior
725
       rho \sim dunif(-1,1)
                                                 # prior
726
       }
727
```

- 728 Appendix 4. R code for RJMCMC analysis
- 729 # RJMCMC calibration analysis for ETP dolphin school size estimation
- 730 #
- 731 library(tcltk2) # for progress bar
- 732 ## Proposal distributions for parameters for RJ step
- 733 rjprop.mean.sp <- rep(0,5)
- 734 rjprop.mean.bft <- 0
- 735 rjprop.sd.bft <- 0.1
- 736 rjprop.sd.sp <- rep(0.3,5)
- 737 ## Proposal distributions for parameters for MH step
- 738 mhprop.sd.int <- 0.035
- 739 mhprop.sd.ph <- 0.007
- 740 mhprop.sd.sp <- rep(0.04,5)
- 741 mhprop.sd.bft <- 0.005
- 742 mhprop.sd.sd.model <- 0.01 l
- 743 mhprop.sd.sd.obs.int = 0.01
- 744 mhprop.sd.sd.obs.ph = 0.01
- 745 mhprop.sd.params <- c(mhprop.sd.int, mhprop.sd.ph, mhprop.sd.sp, mhprop.sd.bft,
- 746 mhprop.sd.sd.model, mhprop.sd.sd.obs.int, mhprop.sd.sd.obs.ph)
- 747 names(mhprop.sd.params) <- c('sd.int','sd.ph',rep('sd.sp',5),'sd.bft',
- 748 'sd.sd.model', 'sd.sd.obs.int', 'sd.sd.obs.ph')
- 749

- 751 ## Starting values for the parameters
- 752 # fixed effects
- 753 int.0 <- 0.7 # intercept
- 754 ph.0 <- 0.8 # slope for photo
- sp.0 <- rjprop.mean.sp # factor covariate with 6 levels (first level absorbed in the intercept)
- 756 bft.0 <-rjprop.mean.bft # beaufort coefficient
- sd.model.0 <- 0.5 # standard deviation of model errors
- 758 # random effects for observers
- 759 sd.obs.int.0 <- 0.2 # intercept for regression
- 760 re.obs.int <- rnorm(n.obs,0,sd.obs.int.0)
- 761 names(re.obs.int) <- sort(unique(observers))
- 762 sd.obs.ph.0 <- 0.05
- 763 re.obs.ph <- rnorm(n.obs,0,sd.obs.ph.0)
- 764 names(re.obs.ph) <- sort(unique(observers))
- 765 params <- c(int.0,ph.0,sp.0,bft.0,sd.model.0,sd.obs.int.0,sd.obs.ph.0)
- 766 names(params) <-
- 767 c('int','ph',paste("sp",levels(species)[2:6],sep="."),'bft','sd.model','sd.obs.int','sd.obs.ph')
- 768 param.list <- matrix(0,4,8)
- 769 param.list[1,c(1,2)] <- 1
- 770 param.list[2,c(1:7)] <- 1

```
771
       param.list[3,c(1,2,8)] <- 1
772
       param.list[4,1:8] <- 1
773
774
       # choose the model
775
       cur.mod <- 1
776
       # which parameters are switched on
777
       cur.p <- param.list[cur.mod,]</pre>
778
       params[1:8] <- params[1:8]*cur.p
779
780
       ## Prior limits for parameters
781
       prior.params.lo <- -1
782
       prior.params.hi <- 1
783
       prior.sd.lo <-0
784
       prior.sd.hi <- 1
785
786
       # number of iterations, about 3000 per hour
787
       n.iter <- 3000*70
                                 # total number of iterations
788
       n.thin <- 10
                         # thinning; number of posterior samples will be floor(n.iter/n.thin) + 1
789
790
       # setting up matrices that will store the posterior samples
                                       # number of rows is thinned no. of updates + starting value
791
       nr <- round(n.iter/n.thin,0)+1</pre>
792
       params.mat <- matrix(NA,nr,length(params))</pre>
793
       colnames(params.mat) <- names(params)
794
       params.mat[1,] <- params
795
       re.obs.int.mat <- matrix(NA,nr,n.obs)
796
       colnames(re.obs.int.mat) <- paste("obs",levels(observers),".int",sep="")
797
       re.obs.int.mat[1,] <- re.obs.int
798
       re.obs.ph.mat <- matrix(NA,nr,n.obs)
799
       colnames(re.obs.ph.mat) <- paste("obs",levels(observers),".ph",sep="")
800
       re.obs.ph.mat[1,] <- re.obs.ph
801
802
       # vector for storing model choices
803
       model <- array(NA,nr)</pre>
804
       # the predictor
805
       x <- l.photo
806
       # the response
807
       y <- l.best
808
809
       ###### the likelihood equations
810
       \log_k < - function(y = y, x = x, params = params, re.obs.int = re.obs.int, re.obs.ph = re.obs.ph)
811
                                    # these will be zero if beaufort is not included in the model
        sp.params<-params[3:7]
812
                                    # these will be zero if species is not included in the model
        bft.params<-params[8]
813
        mu <- params['int'] + re.obs.int[observers] + (params['ph'] + re.obs.ph[observers]) * x +
```

814 c(0,sp.params)[match(species,levels(species))] + bft.params[1]*beaufort

```
815
        log.lik <- sum(log(dnorm(y,mu,params['sd.model']))) +</pre>
816
       sum(log(dnorm(re.obs.ph,0,params['sd.obs.ph']))) +
817
       sum(log(dnorm(re.obs.int,0,params['sd.obs.int'])),na.rm=T)
818
       log.lik
819
       }
820
821
       # test
822
       \log_{10}(y = 1.best, x = 1.photo, params = params, re.obs.int = re.obs.int, re.obs.ph = re.obs.ph)
823
824
       825
       # progress bar
826
       pb <- tkProgressBar(title = "progress bar", min = 0,max = n.iter, width = 200)
827
828
       # the RJMCMC algorithm
829
       isave <- 1
                       # set the counter; first value is starting value
830
       for (b in 2:n.iter){
831
       newparams <- params
832
833
       ##### the RJ step
834
       if(cur.p[3]==0){ # if species is currently not in the model, propose to add it
835
        newparams[3:7] <- rnorm(5,rjprop.mean.sp,rjprop.sd.sp) ##################### changed from
836
       1 to 5
837
        new.lik <- log.lik(y = y, x = x, params = newparams, re.obs.int = re.obs.int, re.obs.ph =
838
       re.obs.ph)
839
        cur.lik <- log.lik(y = y, x = x, params = params, re.obs.int = re.obs.int, re.obs.ph = re.obs.ph)
840
         num <- new.lik + sum(log(dunif(newparams[3:7],prior.params.lo,prior.params.hi))) # add
841
       priors for new parameters
842
         den <- cur.lik + sum(log(dnorm(newparams[3:7],rjprop.mean.sp,rjprop.sd.sp))) # add
843
       proposal densities for new parameters
844
        A<-min(1,exp(num-den))
845
        V < -runif(1)
846
        ifelse(V<=A,{params[3:7]<-newparams[3:7];cur.p[3:7]<-1},{newparams[3:7]<-params[3:7]})
847
       }
848
        else{ # if species is currently in the model, propose to delete it
849
        newparams[3:7] <- 0
850
        new.lik <- log.lik(y = y, x = x, params = newparams, re.obs.int = re.obs.int, re.obs.ph =
851
       re.obs.ph)
852
        cur.lik <- log.lik(y = y, x = x, params = params, re.obs.int = re.obs.int, re.obs.ph = re.obs.ph)
853
         num <- new.lik + sum(log(dnorm(params[3:7],rjprop.mean.sp,rjprop.sd.sp))) # add proposal</pre>
854
       densities for current parameters
855
          den <- cur.lik + sum(log(dunif(params[3:7], prior.params.lo, prior.params.hi))) # add priors for
856
       current parameters
857
        A<-min(1,exp(num-den))
858
        V<-runif(1)
```

859	ifelse(V<=A,{params[3:7]<-newparams[3:7];cur.p[3:7]<-0},{newparams[3:7]<-params[3:7]})
860	}
861	if(cur.p[8]==0){ # if beaufort is currrently not in the model, propose to add it
862	newparams[8] <- rnorm(1,rjprop.mean.bft,rjprop.sd.bft)
863	new.lik <- log.lik(y = y, x = x, params = newparams, re.obs.int = re.obs.int, re.obs.ph =
864	re.obs.ph)
865	cur.lik <- log.lik(y = y, x = x, params = params, re.obs.int = re.obs.int, re.obs.ph = re.obs.ph)
866	num <- new.lik + sum(log(dunif(newparams[8],prior.params.lo,prior.params.hi))) # add priors
867	for new parameters
868	den <- cur.lik + sum(log(dnorm(newparams[8],rjprop.mean.sp,rjprop.sd.sp))) # add
869	proposal densities for new parameters
870	A<-min(1,exp(num-den))
871	V<-runif(1)
872	ifelse(V<=A,{params[8]<-newparams[8];cur.p[8]<-1},{newparams[8]<-params[8]})
873	}
874	else{ # if beaufort is currently in the model, propose to delete it
875	newparams[8] <- 0
876	new.lik <- log.lik(y = y, x = x, params = newparams, re.obs.int = re.obs.int, re.obs.ph =
877	re.obs.ph)
878	cur.lik <- log.lik(y = y, x = x, params = params, re.obs.int = re.obs.int, re.obs.ph = re.obs.ph)
879	num <- new.lik + sum(log(dnorm(params[8],rjprop.mean.bft,rjprop.sd.bft))) # add proposal
880	densities for current parameters
881	den <- cur.lik + sum(log(dunif(params[8],prior.params.lo,prior.params.hi))) # add priors for
882	current parameters
883	A<-min(1,exp(num-den))
884	V<-runif(1)
885	ifelse(V<=A,{params[8]<-newparams[8];cur.p[8]<-0},{newparams[8]<-params[8]})
886	}
887	# which model did we end up with?
888	cur.mod<-match(sum(cur.p),apply(param.list,1,sum))
889	
890	##### the MH step
891	newparams <- params
892	new.re.obs.int <- re.obs.int
893	new.re.obs.ph <- re.obs.ph
894	# updating the parameters
895	# the first level of species coefficients or beaufort coefficients are always zero, don't need
896	updating
897	for (p in which(cur.p==1)) {
898	u <- rnorm(1,params[p],mhprop.sd.params[p])
899	newparams[p] <- u
900	new.lik <- log.lik(y = y, x = x, params = newparams, re.obs.int = re.obs.int, re.obs.ph =
901	re.obs.ph)
902	cur.lik <- log.lik(y = y, x = x, params = params, re.obs.int = re.obs.int, re.obs.ph = re.obs.ph)

```
903
         num <- new.lik + log(dunif(newparams[p],prior.params.lo,prior.params.hi))</pre>
904
         den <- cur.lik + log(dunif( params[p],prior.params.lo,prior.params.hi))</pre>
905
        A<-min(1,exp(num-den))
906
        V<-runif(1)
907
        ifelse(V<=A,params[p]<-newparams[p],newparams[p]<-params[p])
908
        }
909
        for (p in 9:11) {
                                       # st dev cannot be negative
910
        u <- rnorm(1,params[p],mhprop.sd.params[p])</pre>
911
        newparams[p] <- u
912
        new.lik <- log.lik(y = y, x = x, params = newparams, re.obs.int = re.obs.int, re.obs.ph =
913
       re.obs.ph)
914
        cur.lik <- \log_{10}(y = y, x = x, params = params, re.obs.int = re.obs.int, re.obs.ph = re.obs.ph)
915
         num <- new.lik + log(dunif(newparams[p],prior.sd.lo,prior.sd.hi))</pre>
916
         den <- cur.lik + log(dunif( params[p],prior.sd.lo,prior.sd.hi))</pre>
917
        A<-min(1,exp(num-den))
918
        V<-runif(1)
919
        ifelse(V<=A,params[p]<-newparams[p],newparams[p]<-params[p])
920
        }
921
922
       # random effects coefficients - no priors on the coefficients
923
        for (r in 1:n.obs){
924
        new.re.obs.int[r] <- rnorm(1,re.obs.int[r],mhprop.sd.sd.obs.int)</pre>
925
        num <- \log_{10}(y = y, x = x, params = params, re.obs.int = new.re.obs.int, re.obs.ph = re.obs.ph)
926
        den <- log.lik(y = y, x = x, params = params, re.obs.int = re.obs.int, re.obs.ph = re.obs.ph)
927
        A<-min(1,exp(num-den))
928
        V<-runif(1)
929
        ifelse(V<=A,re.obs.int[r]<-new.re.obs.int[r],new.re.obs.int[r]<-re.obs.int[r])
930
        }
931
        for (r in 1:n.obs){
932
        new.re.obs.ph[r] <- rnorm(1,re.obs.ph[r],mhprop.sd.sd.obs.ph)</pre>
933
        num <- \log_{10}(y = y, x = x, params = params, re.obs.int = re.obs.int, re.obs.ph = new.re.obs.ph)
934
        den <- \log_{k}(y = y, x = x, params = params, re.obs.int = re.obs.int, re.obs.ph = re.obs.ph)
935
        A<-min(1,exp(num-den))
936
        V<-runif(1)
937
        ifelse(V<=A,re.obs.ph[r]<-new.re.obs.ph[r],new.re.obs.ph[r]<-re.obs.ph[r])
938
        }
939
940
        # each "n.thin-th" iteration, store the parameter values in matrices
941
       if (b %% n.thin < 1) {
942
        isave <- isave + 1
943
        params.mat[isave,] <- params
        re.obs.int.mat[isave,] <- re.obs.int
944
945
        re.obs.ph.mat[isave,] <- re.obs.ph
946
        model[isave] <- cur.mod
```

947	}
948	# display progress
949	Sys.sleep(1)
950	setTkProgressBar(pb, b, label=paste(round(b/n.iter*100),"% completed",sep=""))
951	} ### end of iteration loop
952	close(pb); date()
953	
954	######################################
955	*********
956	

958 Appendix 5. Coverage of predicted group sizes

959 For each group size estimate for each observer, we predicted group size using Eq. 1 and 960 sampling the MCMC chains from model 2 as described in Methods. For each of the 2,435 961 observer estimates, we determined if the 95% credibility interval of predicted size included the 962 photo count (our measure of true group size). Coverage of the 95% interval, measured as the 963 fraction of intervals which included the photo count, was 0.955. We note that this procedure was 964 an inverse prediction – that is, although the model fitted y to x, we predicted x given y. We also 965 note that this procedure was not cross-validation, since the model was not refit for each of the 966 2,435 observer estimates. Therefore, since the value being predicted (photo count) was included 967 in the model fitting, coverage was expected to be positively biased. Given the large sample size, 968 however, we believe the positive bias due to the inclusion of a single datum would be small, as 969 indeed it seemed to be. Fig A4 shows observer estimates and posterior distributions of predicted 970 group size plotted against photo count for a selection of the 59 observers.



Fig. A4. Observer estimates (x), and group sizes predicted from those estimates, plotted relative
to photo count (gray line) for selected observers. Circles are the means and vertical line
segments the 95% credibility intervals of predicted group sizes. Cases for which the 95%
credibility interval did not include the photo count are shown in red.