Delphi survey to assess the spatial distribution of sea turtles in the Pacific Ocean

Report to the Pacific Community (SPC)

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1. INTRODUCTION

Fisheries worldwide interact with a range of non-target species, resulting in the incidental capture of marine mammals, seabirds, and marine turtles (e.g., Lascelles et al. 2014, Lewison et al. 2014). For a number of megafaunal species, this fisheries bycatch is a significant source of mortality, leading to population declines and threatening the viability of populations. For sea turtles, incidental captures in fisheries have been identified as a primary threat to their populations in different regions, including the Atlantic and Pacific oceans (Wallace et al. 2011, Clarke et al. 2014).

In the Pacific Ocean, four sea turtles species are considered vulnerable to fisheries interactions, including green (*Chelonia mydas*), leatherback (*Dermochelys coriacea*), loggerhead (*Caretta caretta*), and olive ridley (*Lepidochelys olivacea*). Each of these species is ranked as either endangered or vulnerable by the International Union for Conservation of Nature, and the reduction of bycatch mortalities has been highlighted as a priority for their conservation.

The incidental capture of sea turtles in tuna longline fisheries has led to concerted efforts to reduce and mitigate their bycatch. These efforts include a set of workshops under the Areas Beyond National Jurisdiction (ABNJ, or Common Oceans) Tuna Project (see Western and Central Pacific Fisheries Commission 2016). The first workshop was held in February 2016, and focused on characterising the current interactions and mortality rates of sea turtles in pelagic longline fisheries in the Pacific Ocean. The investigation into the effectiveness of sea turtle mitigation measures included the use of simulation models to determine the overlap between sea turtles and longline fisheries. These models require information of the spatial distribution of sea turtles, and although some of this spatial information is currently available, these data are considered to be incomplete.

The simulation models developed in the first workshop used basic relative abundance surfaces of the four sea turtle species, based on maps of regional management units used by the State of the World's Sea Turtles (SWOT) project. It was acknowledged at the workshop that the maps represent the best information available, but contain a number of uncertainties, and also need revision in some key areas. For this reason, it was recommended that the spatial information be updated and review by experts in the future. The current project followed this recommendation by conducting an Internet-based Delphi survey of expert knowledge of the spatial distribution of green, leatherback, loggerhead and olive ridley sea turtles in the Pacific Ocean, based on SWOT data. The survey was aimed at augmenting existing information by soliciting expert knowledge.

The Delphi technique is a research method for data-poor situations, as it provides a structured approach for obtaining expert opinion in a systematic and transparent way (Linstone & Turoff 2002, MacMillan & Marshall 2006, Cole et al. 2013). The Delphi process allows experts to contribute their information independently, and experts are able to participate in the survey remotely. This technique involves an iterative process based on existing information, facilitating contributions by participating experts, and includes a feedback approach to build consensus, including a measure of uncertainty. Through this technique, it is possible to capture information that is otherwise not available.

This report presents the findings from the Delphi survey that was conducted to support subsequent workshops on sea turtle bycatch mitigation in pelagic longline fisheries in the Pacific Ocean.

2. METHODS

2.1 Practical implementation: the Delphi web application

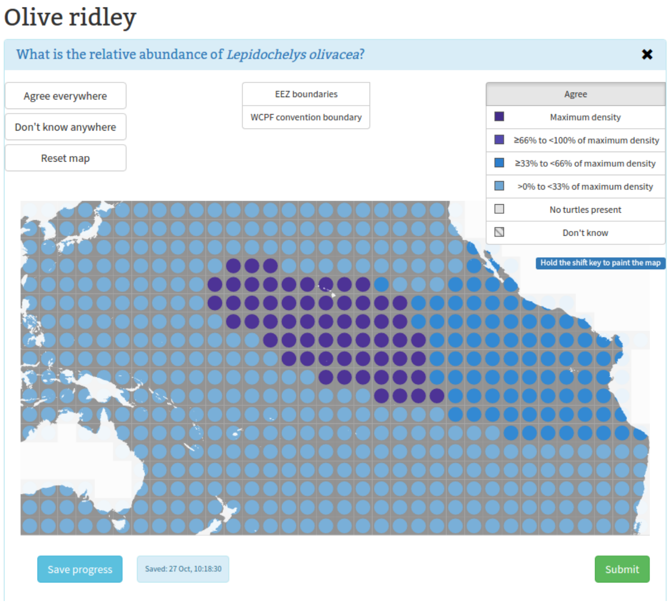
The Delphi survey sought expert knowledge to obtain estimates of the relative abundance of the four sea turtle species included in the assessment, green (*Chelonia mydas*), leatherback (*Dermochelys coriacea*), loggerhead (*Caretta caretta*), and olive ridley (*Lepidochelys olivacea*). The survey was implemented as a web application, which allowed participants to use an e-mail link to log in and complete the survey. All contributions remained anonymous, participants were not expected to share confidential data.

The survey consisted of two rounds. In the first round, participants were asked to independently estimate the relative abundance of each sea turtle species. In the second round, a summary of the previous results was provided to the participants, who were invited to confirm or update their responses in view of the other participants' answers.

The web application consisted of a map for each sea turtle species, showing a prior distribution of the species across the Pacific Ocean (Figure 1), based on expert-drawn maps from SWOT data during the "Workshop on joint analysis of sea turtles mitigation effectiveness". The relative abundance of each species was standardised across the four sea turtle species, so that abundances were on the same relative scale. To provide spatial guidance, respondents had the option to add Exclusive Economic Zone (EEZ) and Western Central and Pacific Fisheries (WCPF) convention area boundaries to the sea turtle base maps.

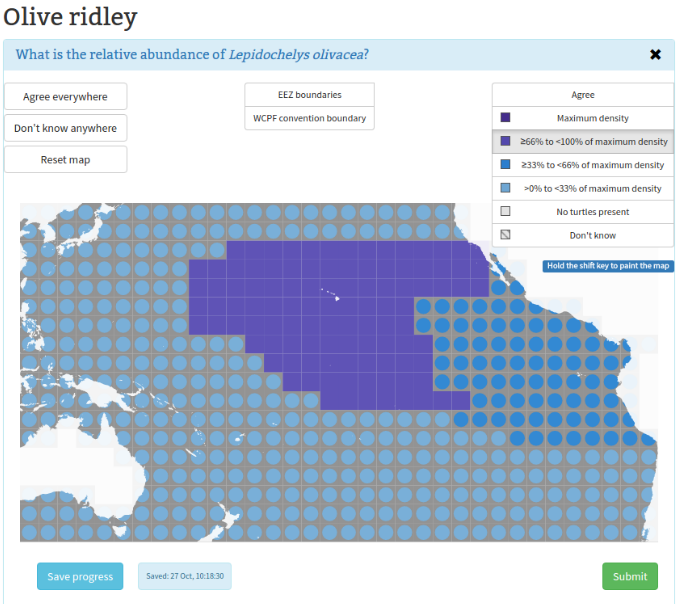
Each map contained a raster grid representing 5° by 5° cells, resulting in 545 squares (cells) across the Pacific Ocean. Respondents were asked to categorise each cell into one of five categories:

- Absence (<1% of maximum density),
- Low density (1–33% of maximum density),
- Medium density (34–66% of maximum density),
- High density (67–99% of maximum density),
- Maximum density.


Olive ridley

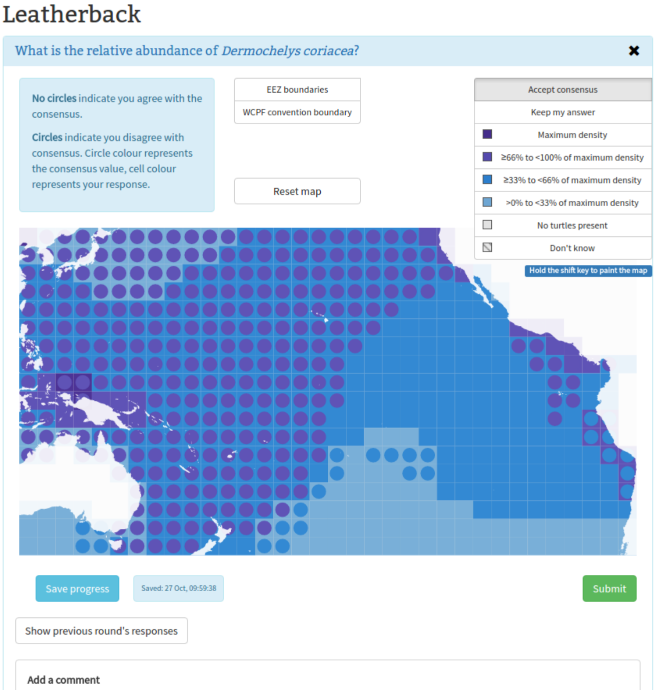
What is the relative abundance of *Lepidochelys olivacea*?

Figure 1: Partial screenshot of the initial web-app display for the first round of the Delphi survey of the relative abundance of sea turtles in the Pacific Ocean. Circles indicate the category from the prior distribution. Buttons in the top right corner allowed participants to choose the category to use with the colouring tool, including the option to agree with the prior map.


Olive ridley

What is the relative abundance of *Lepidochelys olivacea*?

Figure 2: Partial screenshot of a participant using the web-app during the first round of the Delphi survey of the relative abundance of sea turtles in the Pacific Ocean. Colouring is arbitrary for illustrative purposes, with the participant providing information. Circles indicate the category from the prior distribution, while filled squares indicate the respondent's categorisation. Buttons in the top right corner allowed participants to choose the category to use with the colouring tool, including the option agree with the prior map.



Leatherback

What is the relative abundance of *Dermochelys coriacea*?

No circles indicate you agree with the consensus.

Circles indicate you disagree with consensus. Circle colour represents the consensus value, cell colour represents your response.

Saved: 27 Oct, 09:59:38

Figure 3: Partial screenshot of the web-app display for the second round of Delphi survey of the relative abundance of sea turtles in the Pacific Ocean. The image shows the display for a randomly chosen participant. Buttons in the top right corner allowed participants to choose the category to use with the colouring tool, including the option to keep previous answers.

A colouring tool was implemented to allow respondents to colour parts of the map according to the categories listed above (Figure 2). Additional options allowed respondents to agree with the prior distribution, to leave parts of the map blank or to reset the map to the prior distribution. All submitted responses were saved in a database for analysis, and imported to R for modelling.

The display on the website was round-specific. The first round was the initial stage in which respondents answered independently of each other, with only the prior map for guidance. For the second round, the display of the prior distribution was replaced by the consensus map (see 2.2 below), and each participant's answers were overlaid to highlight where their answers differed from the consensus map (Figure 3). Participants also had the option to access the responses from the other participants, which were displayed anonymously as individual maps below their own response. Participants were then able to alter their answers or to retain them.

2.2 Consensus maps: Modelling respondents' data

The following model description uses the generic term "turtle" as the model was identical for all species. A consensus map for each species was derived from respondents' answers within a Bayesian modelling framework. This framework allowed accounting for incomplete answers, and the possibility that respondents who submitted partial maps may have had different perceptions about the maximum density for any species. Furthermore, the approach allowed us to explicitly model the un-evenness of the categories in terms of actual underlying relative abundance. Lastly, the model-based approach allowed for a model-based smoothing of the consensus map, which avoids a patchy consensus distribution map.

The consensus model for each turtle species had two layers: the first layer modelled the categorical answer $y_{i,s}$ by respondent i for cell s as a draw from a categorical distribution (i.e., a multinomial with a single draw). Thus

$$y_{i,s} \sim \text{Cat}(\mathbf{p_{i,s}}). \tag{1}$$

The categorical response depends on probabilities $\mathbf{p_{i,s}} = p_{i,s,1}, ..., p_{i,s,5}$, with $p_{i,s,k}$ the probability that participant i answers category k for cell s. These probabilities were determined by the latent, continuous density of turtles (i.e., the second layer of the model). Thus, $p_{i,s,k} = P(Y_{i,s} = k)$, which we modelled using a beta density evaluated at the mid-point of category k, given beta parameters α_s and β_s. The latter are determined by the underlying turtle density in cell s. Thus

$$P(Y_{i,s} = k \mid \alpha_s, \beta_s) = \text{Beta}(\lambda_i x_k \mid \alpha_s, \beta_s), \tag{2}$$

where x_k is the mid-point of the category and λ_i is a "shift" parameter for respondents that did not provide an answer for all cells on the map. This parameter scales the categories of incomplete response relative to those of all other responses. The beta distribution was modelled using the mode α_s and concentration parameter β_s. This approach is more convenient for the beta distribution than a formulation for the mean and variance, which have to follow reciprocal constraints. The mode of the beta distribution represents the continuous underlying turtle density, which varies between zero (turtles absent, category 1) to 1 (maximum density, category 5). The concentration parameter models the level of agreement about the location of the mode (i.e., about the true density, and the density category; see Figure 4 for an illustration). Both parameters were modelled using a conditional auto-regressive spatial model on the lattice covering the map.

For the latent spatial model, the beta mode α_s at location s was logit-transformed (giving α'_s), whereas the concentration parameter was log-transformed (giving β'_s). We then applied the auto-regressive model as:

$$\alpha'_s \mid \alpha'_q, q \neq s \sim \text{Normal}(\rho \sum_{q=1}^{545} A_{ij}\alpha'_q, \tau_\alpha^{-1}), \tag{3}$$

$$\beta'_s \mid \beta'_q, q \neq s \sim \text{Normal}(\rho \sum_{q=1}^{545} A_{ij}\beta'_q, \tau_\beta^{-1}), \tag{4}$$

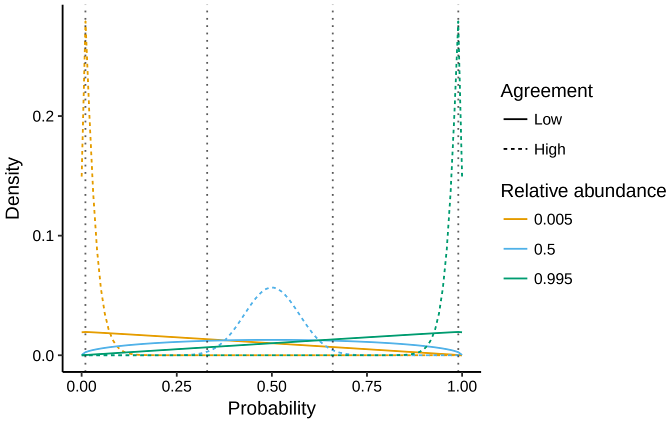


Figure 4: Example of the beta-distribution model used to derive the probabilities for each relative abundance category. Three relative abundance categories are illustrated here, with the mode centred at the mid-point of the category and two levels of agreement. At high agreement (large β), the probabilities are concentrated at the category mid-point, whereas with low agreement, probability densities are spread more evenly over the `[0,1]` interval.

where ρ is a common auto-regressive parameter, A is an adjacency matrix, and τ is a precision parameter. All priors were vaguely informative relative to the true scale of the parameters. The prior for λ_i was beta distributed with shape parameters $a_\lambda = 2$ and $b_\lambda = 1$, introducing a prior that is slightly in favour of equally aligned categories. Similarly, the prior for the spatial auto-correlation was chosen to give more weight to a map with auto-correlated cells by setting $a_\rho = 4$ and $b_\rho = 1$. Both τ_α and τ_β were given half-Cauchy priors with scale parameter $c_\tau = 5$.

The model was implemented in Stan (Carpenter et al. 2015), a Bayesian modelling language that implements efficient No-U-Turn Markov Chain Monte Carlo (MCMC) sampling based on automatic differentiation. The MCMC was run with two chains per species for 2500 iterations. 500 iterations per chain were discarded as burn-in, and as nearly no auto-correlation was evident, every fourth sample of the MCMC was kept for further analysis, leaving 1000 samples per species in total between the two chains. Convergence was assessed visually and using Gelman-Rubin diagnostics as calculated by rStan, the R interface to the Stan library (see Appendix A for the full model code, and Appendix B for a simulated example).

3. RESULTS

3.1 Delphi survey participation

Participation in the survey varied between rounds and also across the four sea turtle species (Table 1). In the first round, there were 9 to 13 participants, depending on the species. Fewer participants responded in the second round, ranging from 7 participants for *Caretta caretta* and 8 participants for *Chelonia mydas* (see Appendices C and D for individual responses in the first and second rounds).

Table 1: Number of participants in the Delphi survey of the spatial distribution of sea turtles in the Pacific Ocean. Total indicates the number of unique participants for each species.

Round	*Caretta caretta*	*Chelonia mydas*	*Dermochelys coriacea*	*Lepidochelys olivacea*
1	11	13	12	9
2	7	8	7	7
Total	12	14	12	11

3.2 Delphi survey responses—Round 1

Information from the participants in the first round of the survey was used to generate the modal map of sea turtle abundances (Figure 5). The consensus model converged quickly and provided qualitatively sensible answers, both on the continuous scale of the underlying estimated turtle densities (Figure 6) and density categories. Due to a lack of complete agreement, the categories on the consensus maps were condensed towards categories for low to high densities. This effect can be reversed by re-scaling the estimated density field to a maximum of one, thus assuring that the estimated distribution falls within the maximum category in at least some cells (Figure 7). The level of agreement was quantified spatially using the estimates of β_s (Figure 8).

3.3 Delphi survey responses—Round 2

Although fewer people updated their answers in round two, these updates led to a smoother modal map, suggesting increased agreement (Figure 9). The posterior distribution for the agreement measure, β_s was higher overall on the maps (Figure 10). Although the continuous response was generally similar between rounds (Figures 6, 11), the categorical map for round two was more nuanced, with smaller areas of maximum abundance (Figure 12).

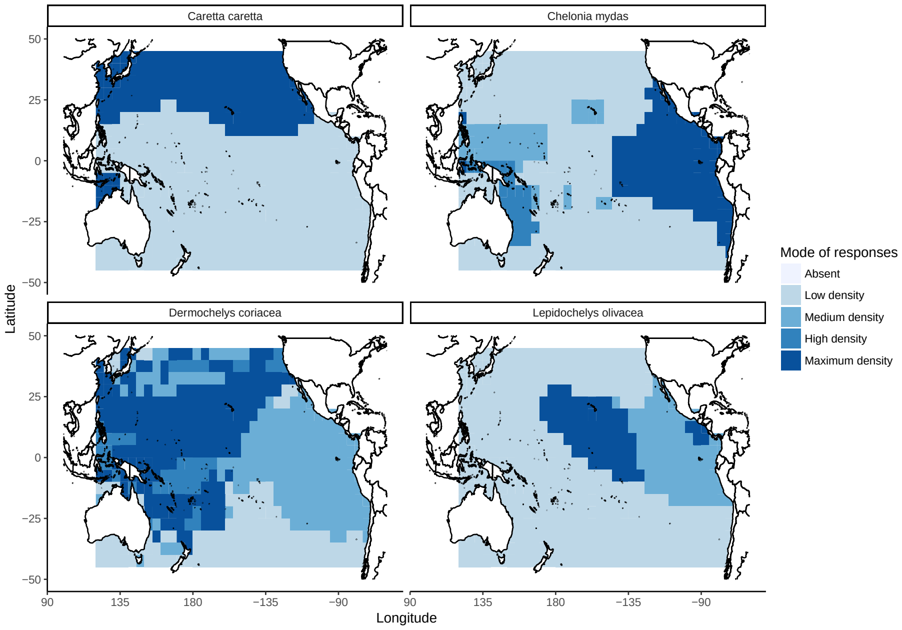


Figure 5: Modal response (i.e., the most frequent response) across all respondents in the first round of the Delphi survey. Colour shading indicates the relative abundance of each of the four sea turtle species in the Pacific Ocean, based on categories used in the survey.

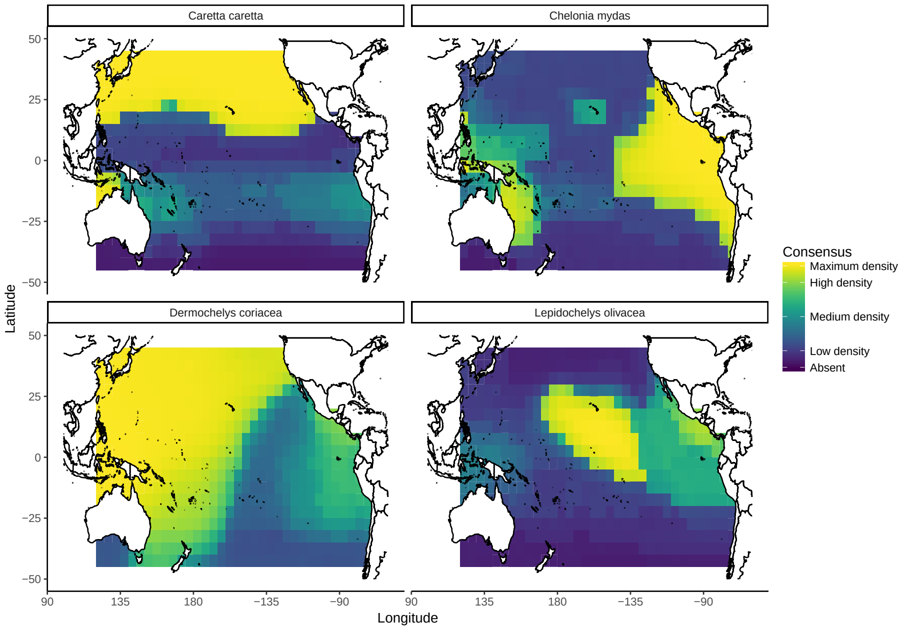


Figure 6: Estimate of the latent continuous density of sea turtles in the consensus model run for responses in the first round of the Delphi survey. Colour shading indicates the relative abundance of each of the four sea turtle species in the Pacific Ocean, based on categories used in the survey.

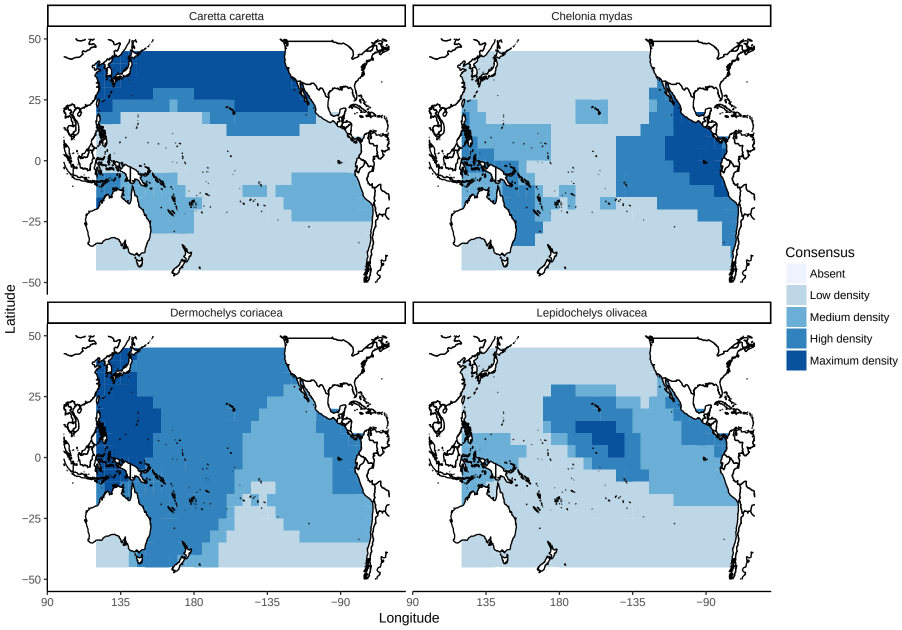


Figure 7: Consensus map from the first round of the Delphi survey. The map was produced by scaling the latent continuous density to a maximum of one and converting the estimated density of sea turtles in the consensus model to a categorical distribution, based on categories used in the survey.

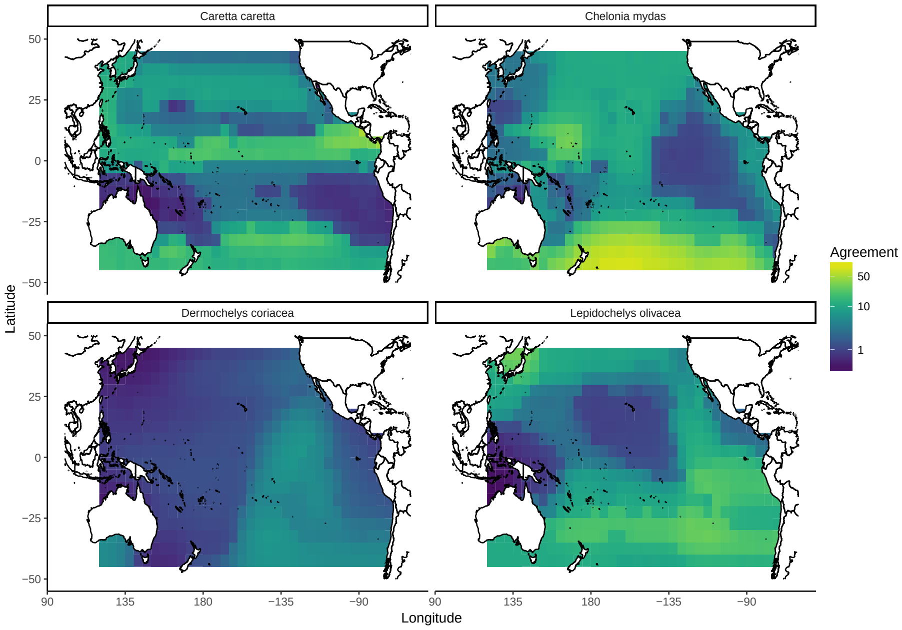


Figure 8: Beta weight parameter (on $\log_{10}$ scale), quantifying the level of consensus on the map for answers from the first round of the Delphi survey.

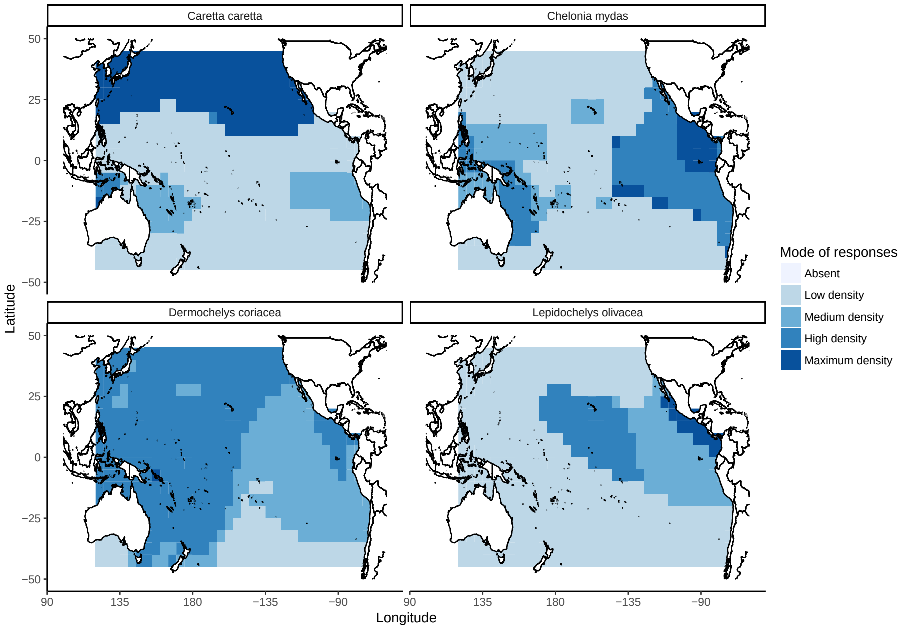


Figure 9: Modal response (i.e., the most frequent response) across all respondents in the second round of the Delphi survey. Colour shading indicates the relative abundance of each of the four sea turtle species in the Pacific Ocean, based on categories used in the survey.

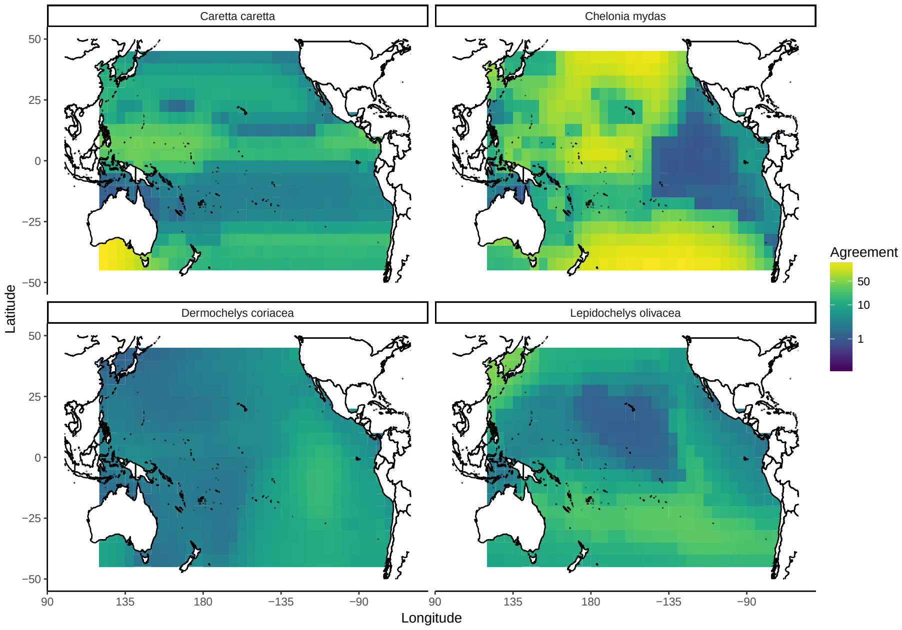


Figure 10: Beta weight parameter (on $\log_{10}$ scale), quantifying the level of consensus on the map for answers from the second round of the Delphi survey.

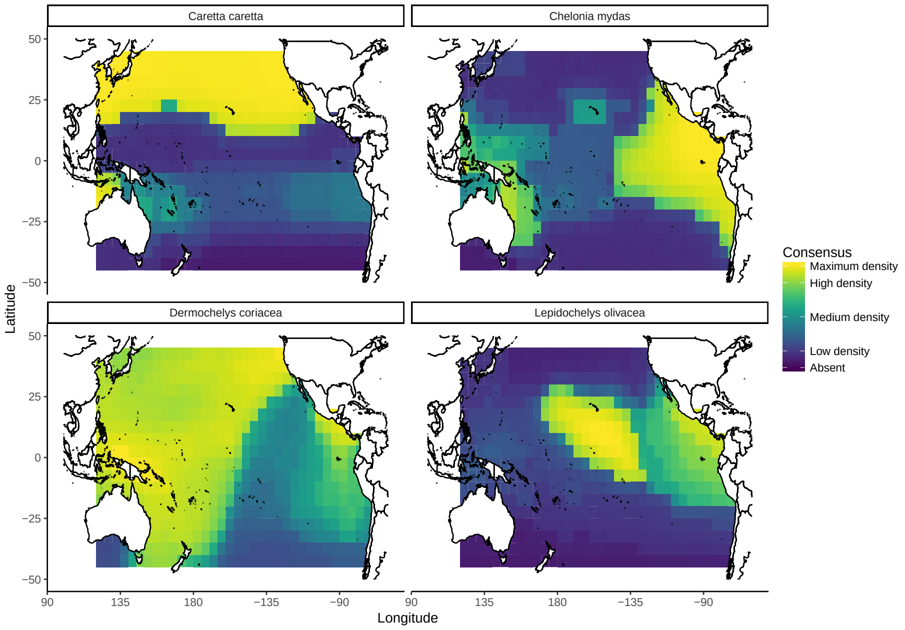


Figure 11: Estimate of the latent continuous density of sea turtles in the consensus model run for responses in the second round of the Delphi survey.

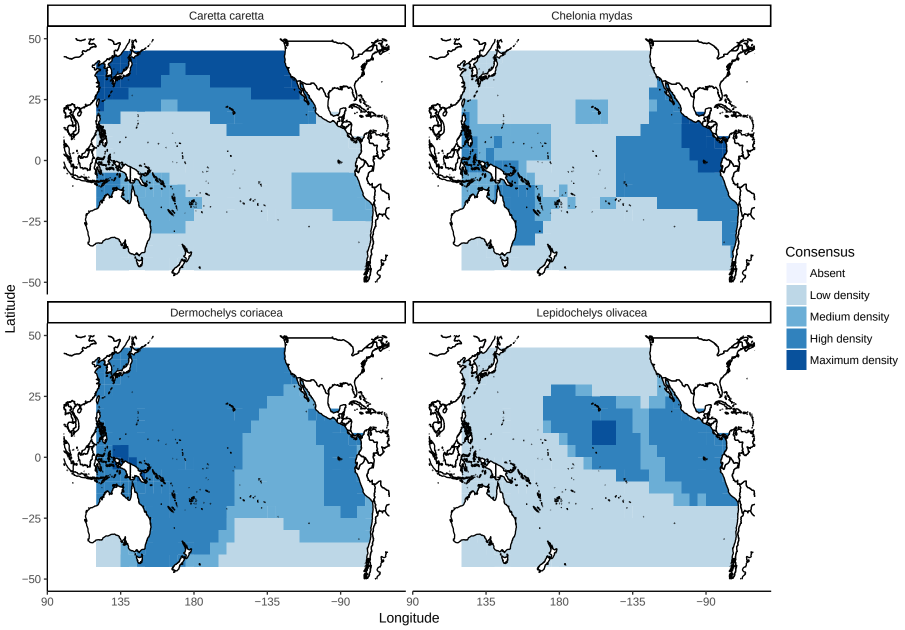


Figure 12: Consensus map from the second round of the Delphi survey. The map was produced by scaling the latent continuous density to a maximum of one and converting the estimated density of sea turtles in the consensus model to a categorical distribution, based on categories used in the survey.

4. DISCUSSION

This project implemented a Delphi process in the form of an online application. The goal of the Delphi survey was to elucidate a consensus distribution of relative abundances for each of four species of sea turtles from expert knowledge. Although uptake was slow initially, ultimately, a minimum of 11 experts filled out distribution maps for each of the four turtle species. The round-based system allowed for feedback between rounds, and led to greater consensus during the second round of the survey.

The Bayesian consensus model allowed us to explicitly model the underlying relative abundance distribution with a smooth latent model, which in turn accomodated incomplete answers. The estimated relative abundance was associated with a spatially varying measure of agreement, which would allow for uncertainty to be carried forward into a risk assessment for sea turtles.

5. ACKNOWLEDGMENTS

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APPENDIX A Consensus model code

Stan model code used to derive the consensus maps of the relative abundance of each of the four sea turtle species included in the Delphi survey. The survey sought expert knowledge to obtain estimates of the relative abundance of green (*Chelonia mydas*), leatherback (*Dermochelys coriacea*), loggerhead (*Caretta caretta*), and olive ridley (*Lepidochelys olivacea*) sea turtles in the Pacific Ocean.

```
data {
  int<lower = 1> nsamp;
  int<lower = 1> ngrid;
  int<lower = 1> nresp;
  int<lower = 1> ncat;
  int ts[nresp];
  real x[ncat+1];
  real y[ncat];
  int dist_samp[nsamp];
  int idx[nsamp];
  int resp_ix[nsamp];
  int W_n;                // number of adjacent region pairs
  int W1[W_n];            // first half of adjacency pairs
  int W2[W_n];            // second half of adjacency pairs
 vector[ngrid] D_sparse;    // diagonal of D (number of neigbors for each site)
 vector[ngrid] lambda;     // eigenvalues of invsqrtD * W * invsqrtD
}
parameters {

  vector[ngrid] phi;
  real<lower = 0> tau;
  #real<lower = 0> mu_phi;
  #real<lower = 0> mu_tau;
  vector[ngrid] tau_beta;
  real<lower = 0> tau2;
  real<lower = 0, upper = 1> alpha;
  real<lower = 0, upper = 1> est_y[nresp];
}
transformed parameters{
  vector[ngrid] itau;
  vector[ngrid] a;
  vector[ngrid] b;
  vector[ngrid] iphi;
  vector[ncat] p[ngrid,nresp];
  vector[ncat] ys[nresp];


  for(i in 1:ngrid){

     itau[i] = exp(tau_beta[i]);
```

```
     iphi[i] = inv_logit(phi[i]);

     a[i] = iphi[i]*itau[i]+1;
     b[i]=  (1-iphi[i])*itau[i]+1;

     for (s in 1:nresp){

      for(k in 1:ncat) {
           ys[s,k] = ts[s]==1 ? y[k] : y[k]*est_y[s];

           p[i,s,k] = exp(beta_lpdf(ys[s,k]|a[i],b[i]));
          }
          p[i,s,] = p[i,s,]/sum(p[i,s,]);
     }
  }
}
model {
  row_vector[ngrid] phit_D; // phi' * D
  row_vector[ngrid] phit_W; // phi' * W
  vector[ngrid] ldet_terms;
  row_vector[ngrid] taut_D; // phi' * D
  row_vector[ngrid] taut_W; // phi' * W
  vector[ngrid] ldet_terms_tau;

#  tau_beta ~ cauchy(0,50);

 for (s in 1:nsamp) dist_samp[s] ~ categorical(p[idx[s],resp_ix[s],]);

  phit_D = (phi .* D_sparse)';
  phit_W = rep_row_vector(0, ngrid);
  for (i in 1:W_n) {
    phit_W[W1[i]] = phit_W[W1[i]] + phi[W2[i]];
    phit_W[W2[i]] = phit_W[W2[i]] + phi[W1[i]];
  }

  // prior for phi
  for (i in 1:ngrid) ldet_terms[i] = log1m(alpha * lambda[i]);
  target += 0.5 * ngrid * log(tau)
  + 0.5 * sum(ldet_terms)
  - 0.5 * tau * (phit_D * phi - alpha * (phit_W * phi)) ;
  tau ~ cauchy(0,5);

  ### tau
  taut_D = (tau_beta .* D_sparse)';
  taut_W = rep_row_vector(0, ngrid);
  for (i in 1:W_n) {
    taut_W[W1[i]] = taut_W[W1[i]] + tau_beta[W2[i]];
    taut_W[W2[i]] = taut_W[W2[i]] + tau_beta[W1[i]];
  }
```

```
  // prior for phi
  for (i in 1:ngrid) ldet_terms_tau[i] = log1m(alpha * lambda[i]);
  target += 0.5 * ngrid * log(tau2)
  + 0.5 * sum(ldet_terms_tau)
 - 0.5 * tau2 * (taut_D * tau_beta  - alpha * (taut_W * tau_beta)) ;
  tau2 ~ cauchy(0,5);


  #mu_tau ~ normal(0,10);
  #mu_phi ~ normal(0,10);
  alpha ~ beta(4,1);
  est_y ~ beta(2,1);
}
```

APPENDIX B Simulated example

The current analysis included an assessment of the robustness of the model to incomplete answers and "shifted" baselines for different experts participating in the Delphi survey (i.e., different perceptions of maximum sea turtle densities). This testing of the model used a set of simulations on a small grid. The simulations used the model as a generating model, starting with a continuous, auto-correlated density map (Figure B-1). This map can then be transformed into a categorical map using the abundance categories used in the Delphi survey.

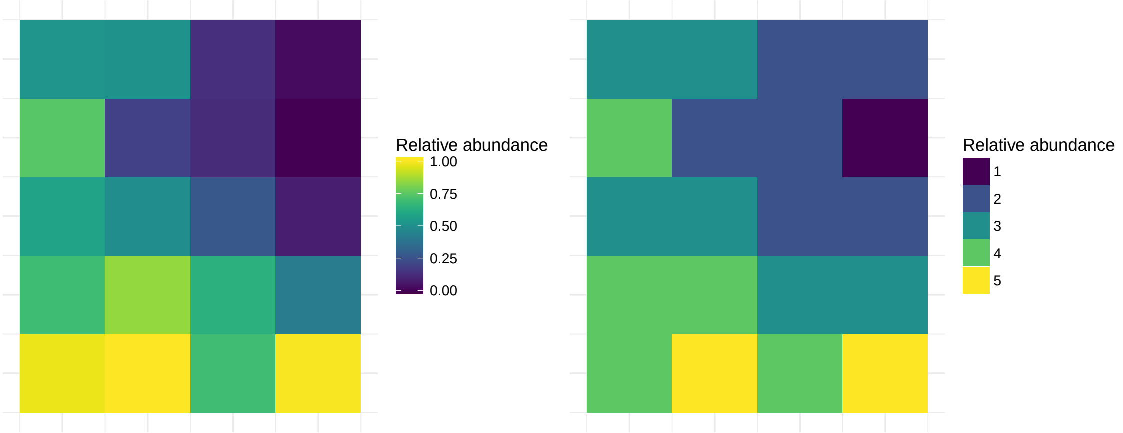

Figure B-1: Simulated continuous (left) and resulting categorical (right) relative abundance maps on a 5×4 lattice. Simulations were used to assess the model used for deriving consensus maps in the Delphi survey of sea turtle abundance in the Pacific Ocean.

Participants' answers were simulated with a value of $\beta = 10$ as the level of agreement. For a subset of four participants, parts of the answers were restricted to parts of the map only (Figure B-2), with relative abundance rescaled to the maximum abundance found on the incomplete maps (Figure B-3).

Simulations illustrate how the model estimated scaling factors for incomplete responses (Figure B-4), and used these scaling factors to determine the underlying relative density (Figure B-5).

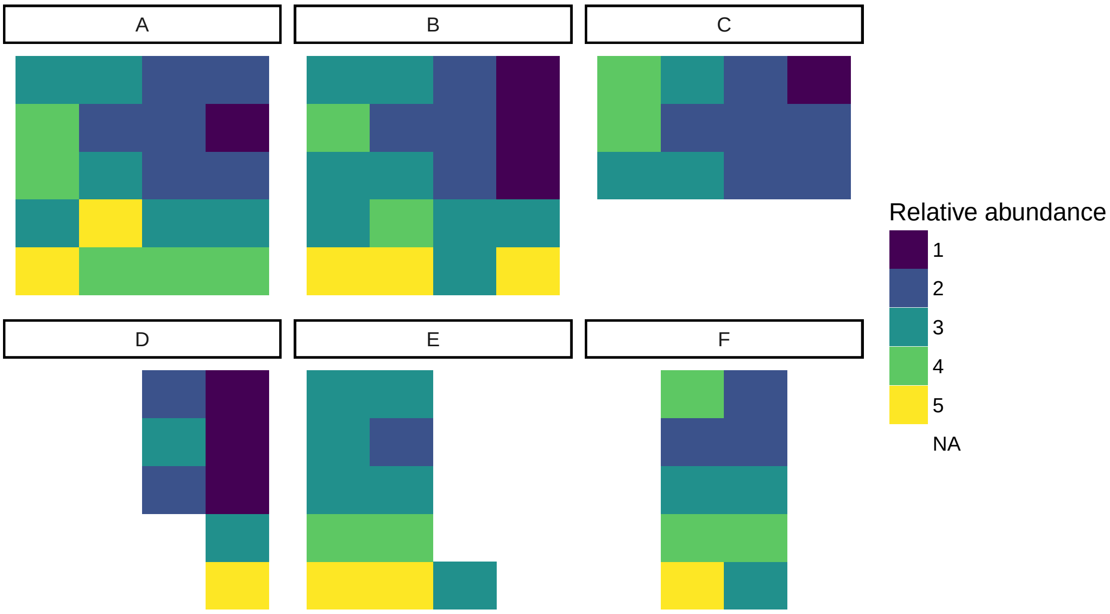

Figure B-2: Simulated answers for six of ten simulated participants, showing four incomplete answers. Simulations were used to assess the model used for deriving consensus maps in the Delphi survey of sea turtle abundance in the Pacific Ocean.

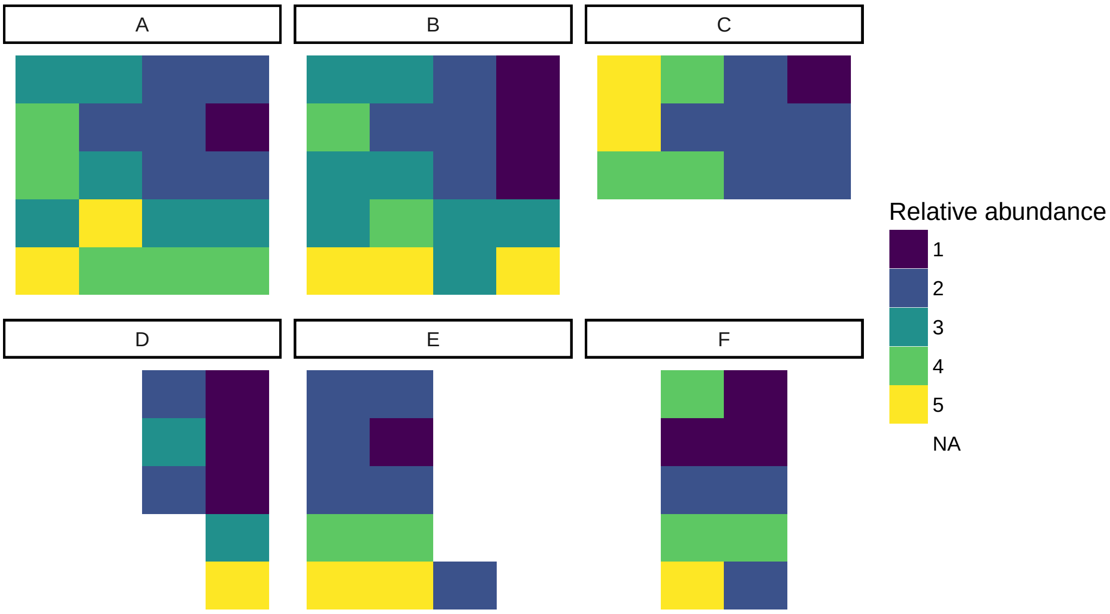

Figure B-3: Simulated answers for six of ten simulated participants, showing four incomplete answers, re-scaled to the maximum of the lattice for each participant. Simulations were used to assess the model used for deriving consensus maps in the Delphi survey of sea turtle abundance in the Pacific Ocean.

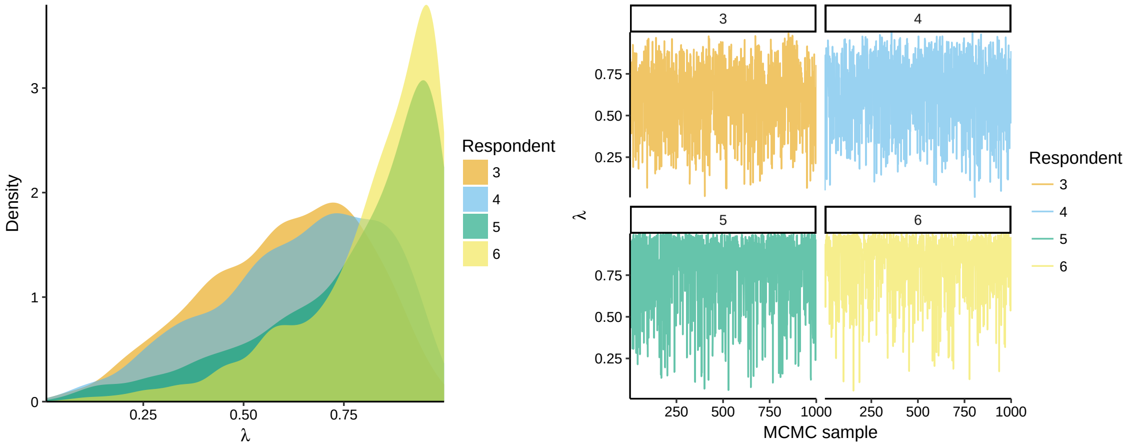

Figure B-4: Estimated scaling factors (λ) for incomplete answers in the Delphi survey, including Markov Chain Monte Carlo (MCMC) sampling. Scaling factors were estimated by the model for deriving consensus maps in the Delphi survey of sea turtle abundance in the Pacific Ocean.

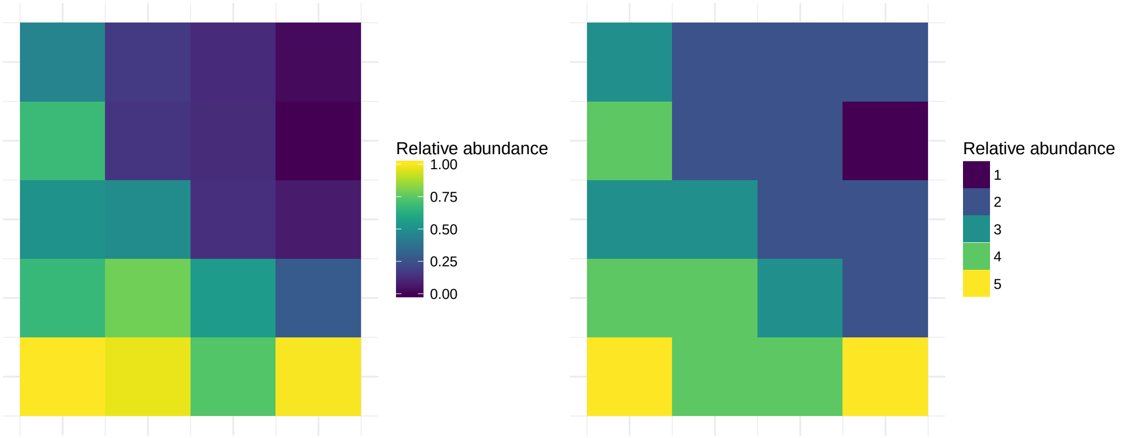

Figure B-5: Estimated continuous (left) and resulting categorical (right) relative abundance maps on a 5×4 lattice. Relative abundances were estimated using the model applied to derive consensus maps in the Delphi survey of sea turtle abundance in the Pacific Ocean.

APPENDIX C Respondent maps—Round 1

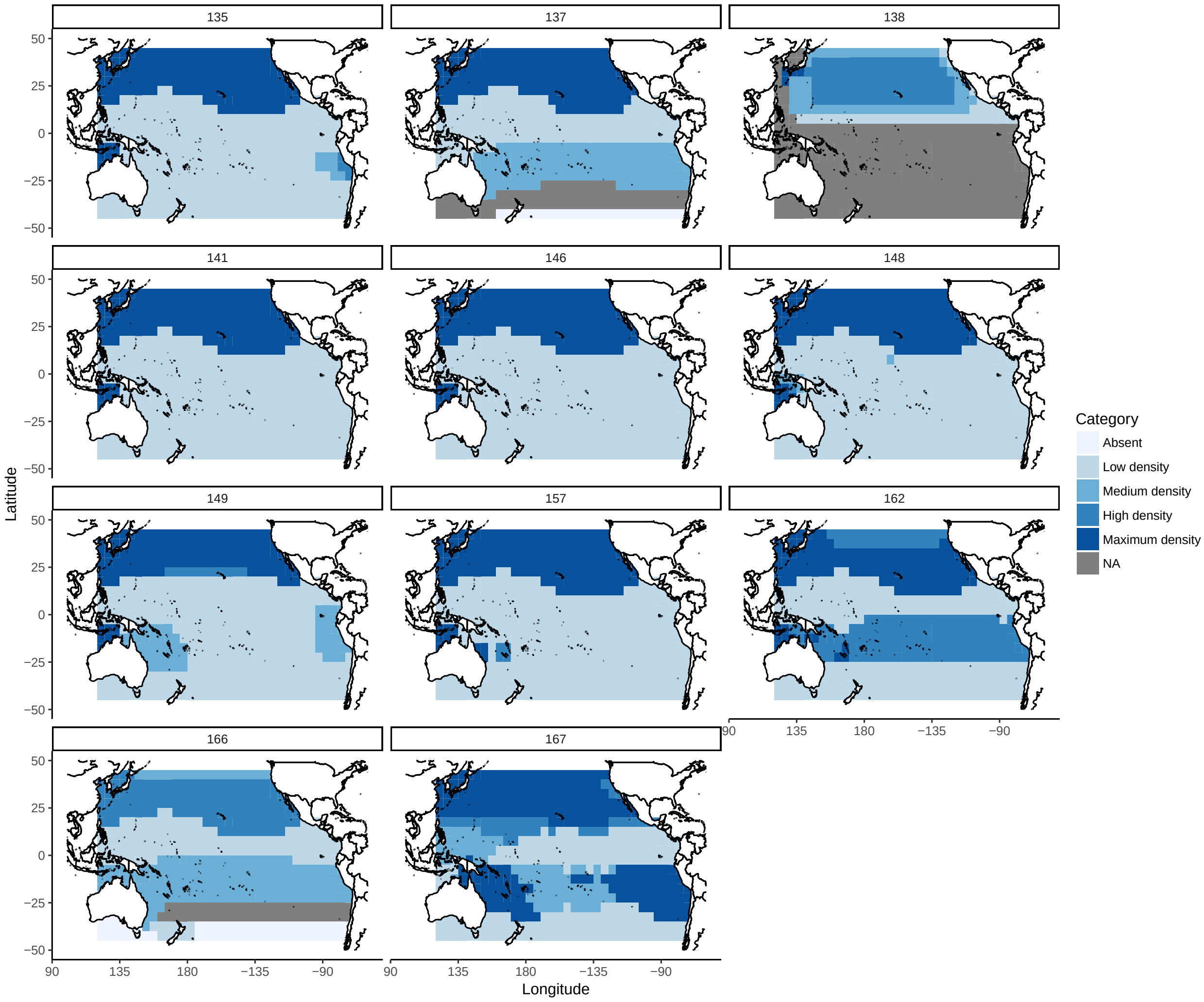

Figure C-6: Relative abundance maps for *Caretta caretta* from the individual participants in the first round of the Delphi survey. Colour shading indicates the abundance categories used in the survey.

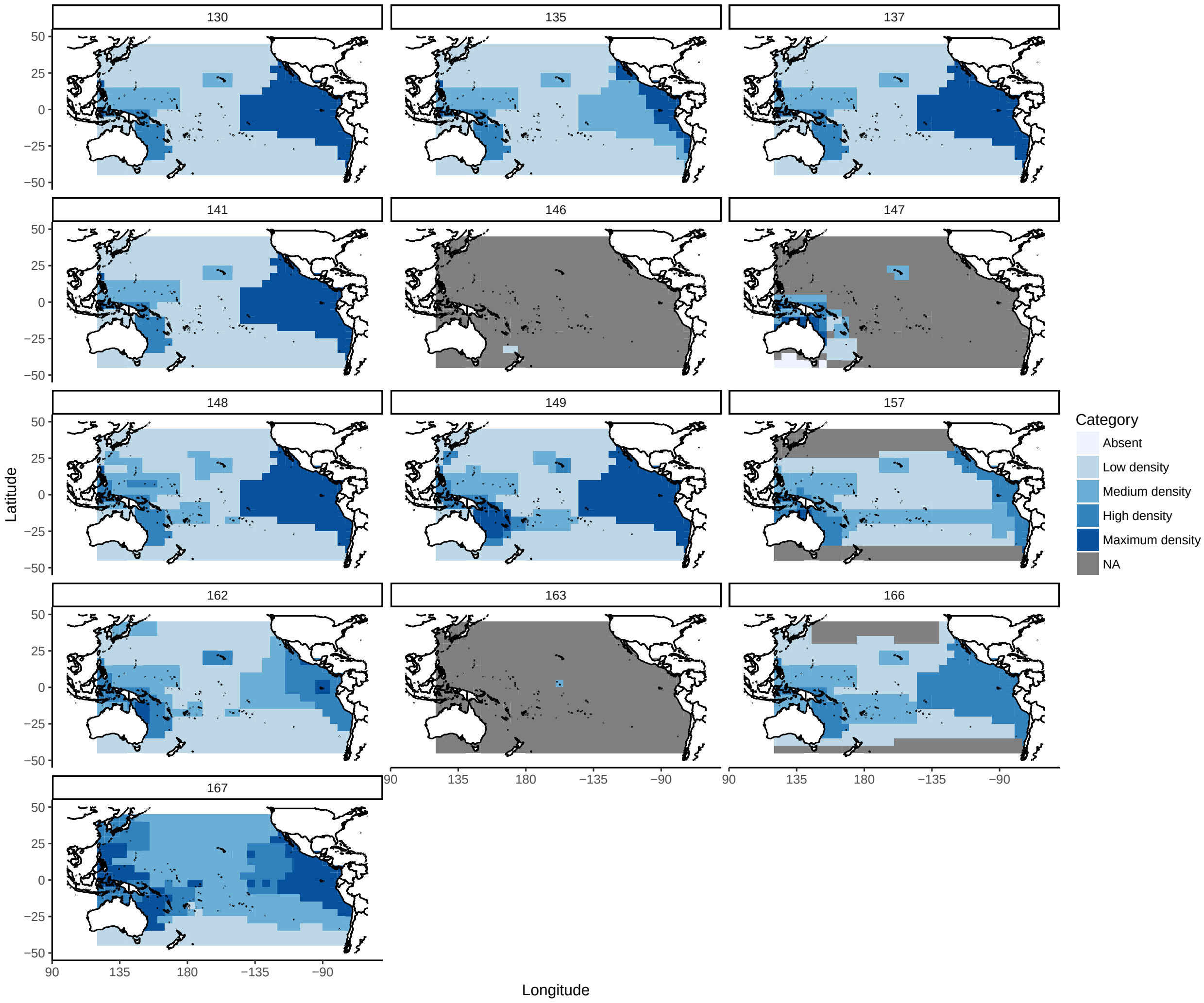

Figure C-7: Relative abundance maps for *Chelonia mydas* from the individual participants in the first round of the Delphi survey. Colour shading indicates the abundance categories used in the survey.

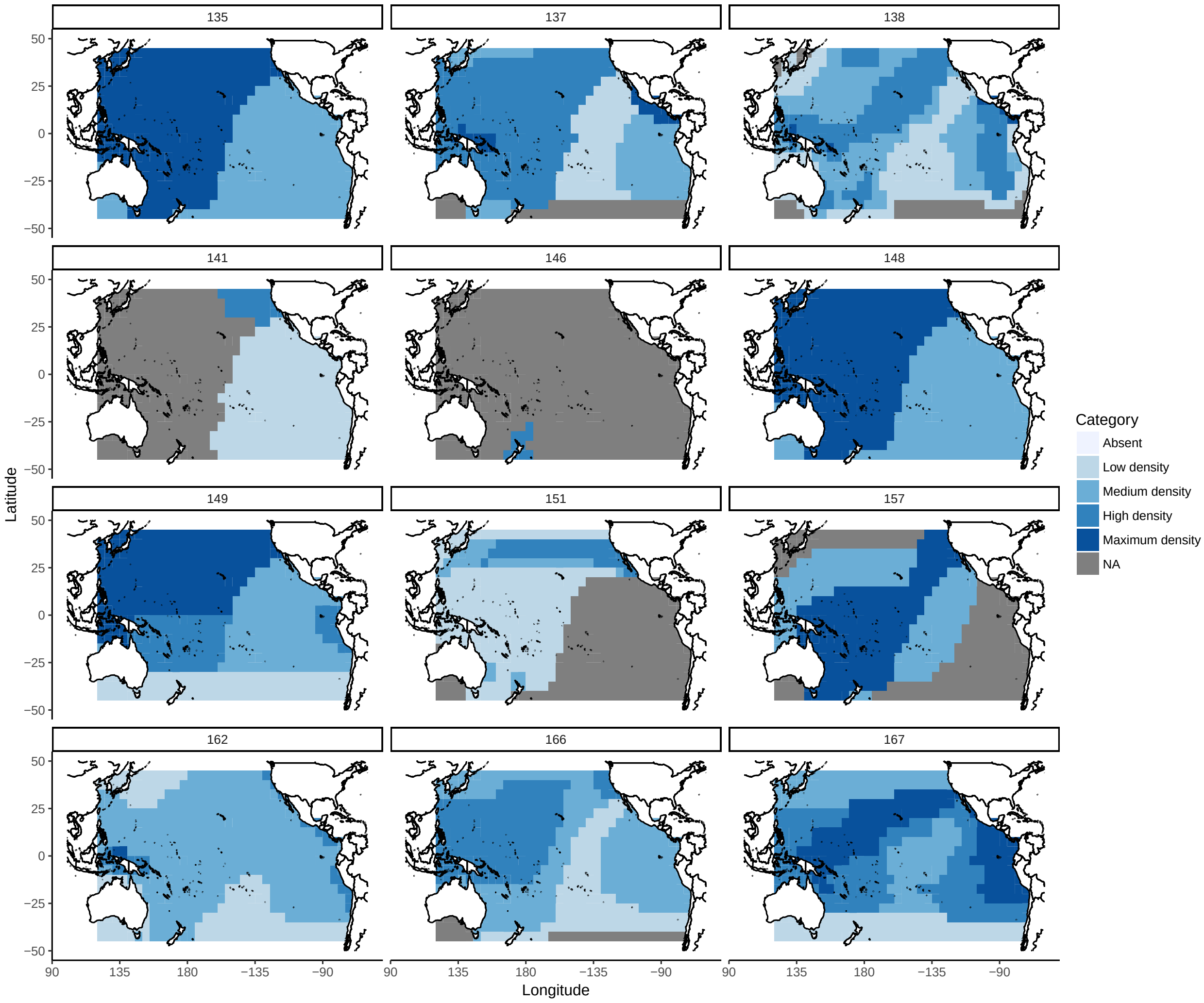

Figure C-8: Relative abundance maps for *Dermochelys coriacea* from the individual participants in the first round of the Delphi survey. Colour shading indicates the abundance categories used in the survey.

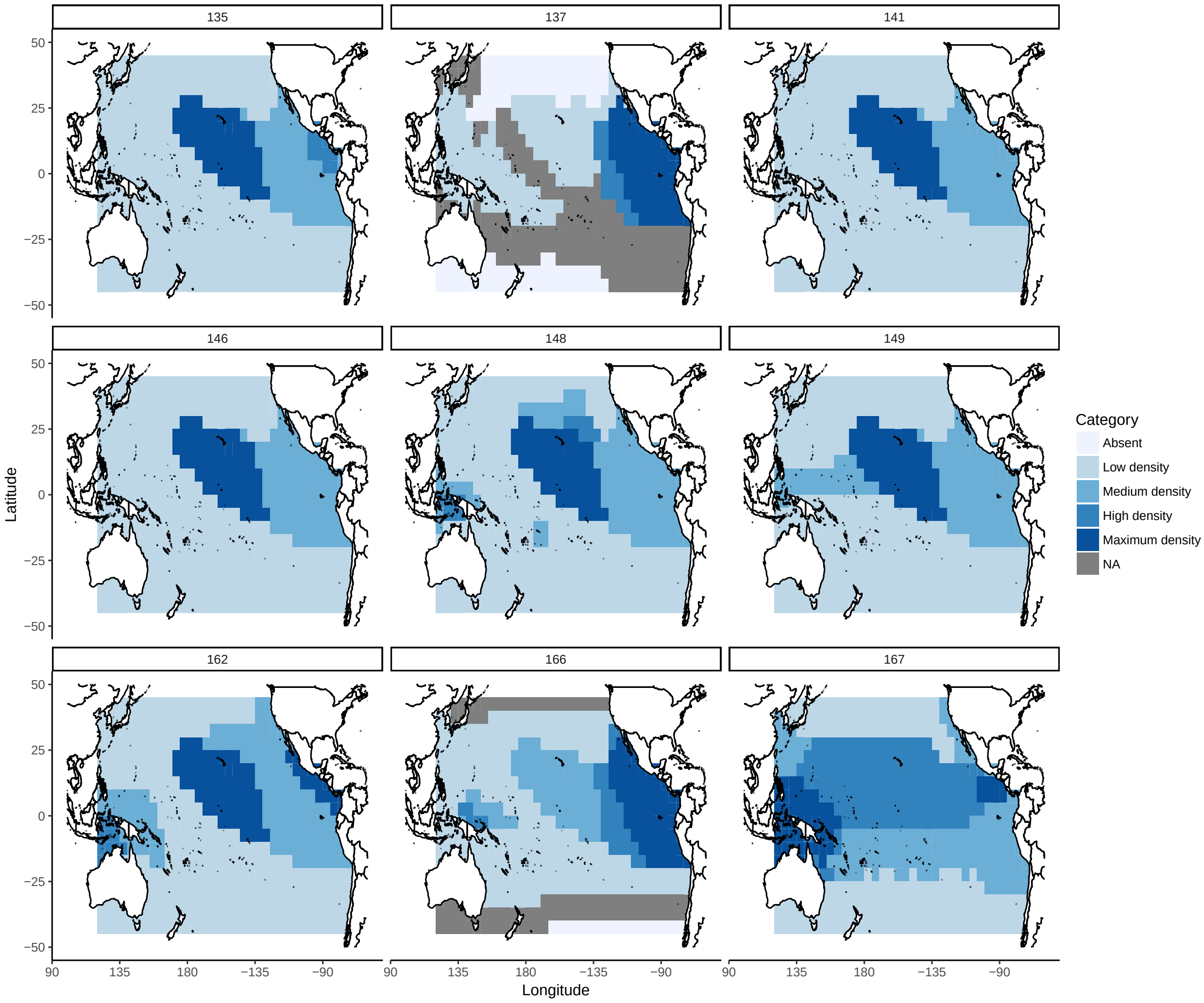

Figure C-9: Relative abundance maps for *Lepidochelys olivacea* from the individual participants in the first round of the Delphi survey. Colour shading indicates the abundance categories used in the survey.

APPENDIX D Respondent maps—Round 2

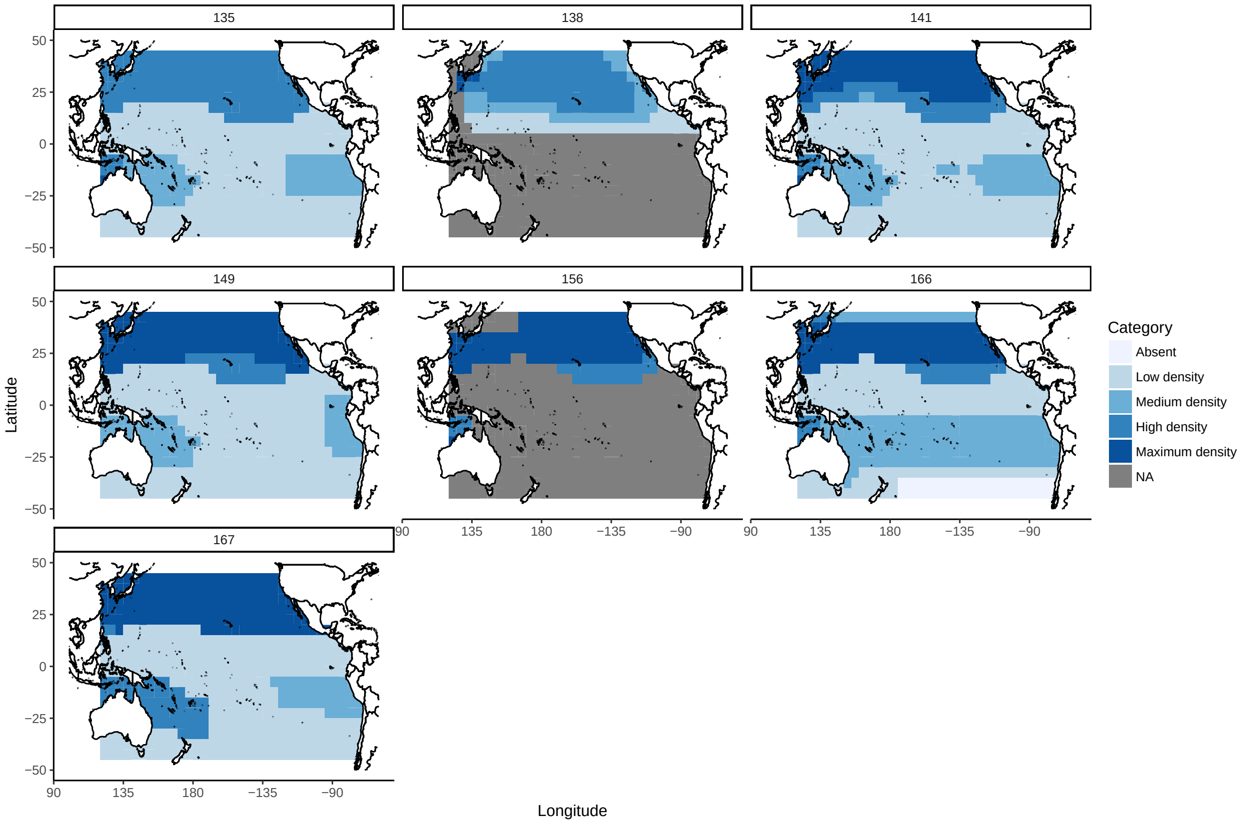

Figure D-10: Relative abundance maps for *Caretta caretta* from the individual participants in the second round of the Delphi survey. Colour shading indicates the abundance categories used in the survey.

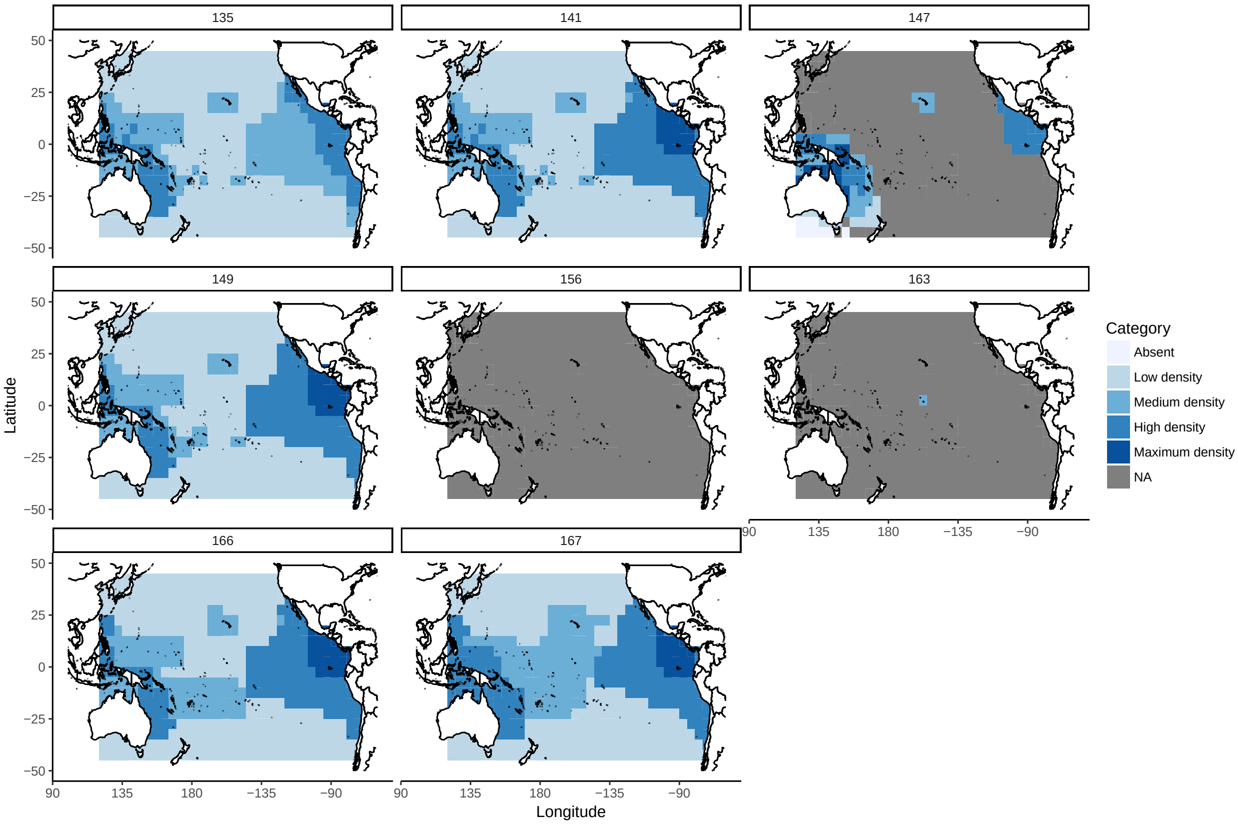

Figure D-11: Relative abundance maps for *Chelonia mydas* from the individual participants in the second round of the Delphi survey. Colour shading indicates the abundance categories used in the survey.

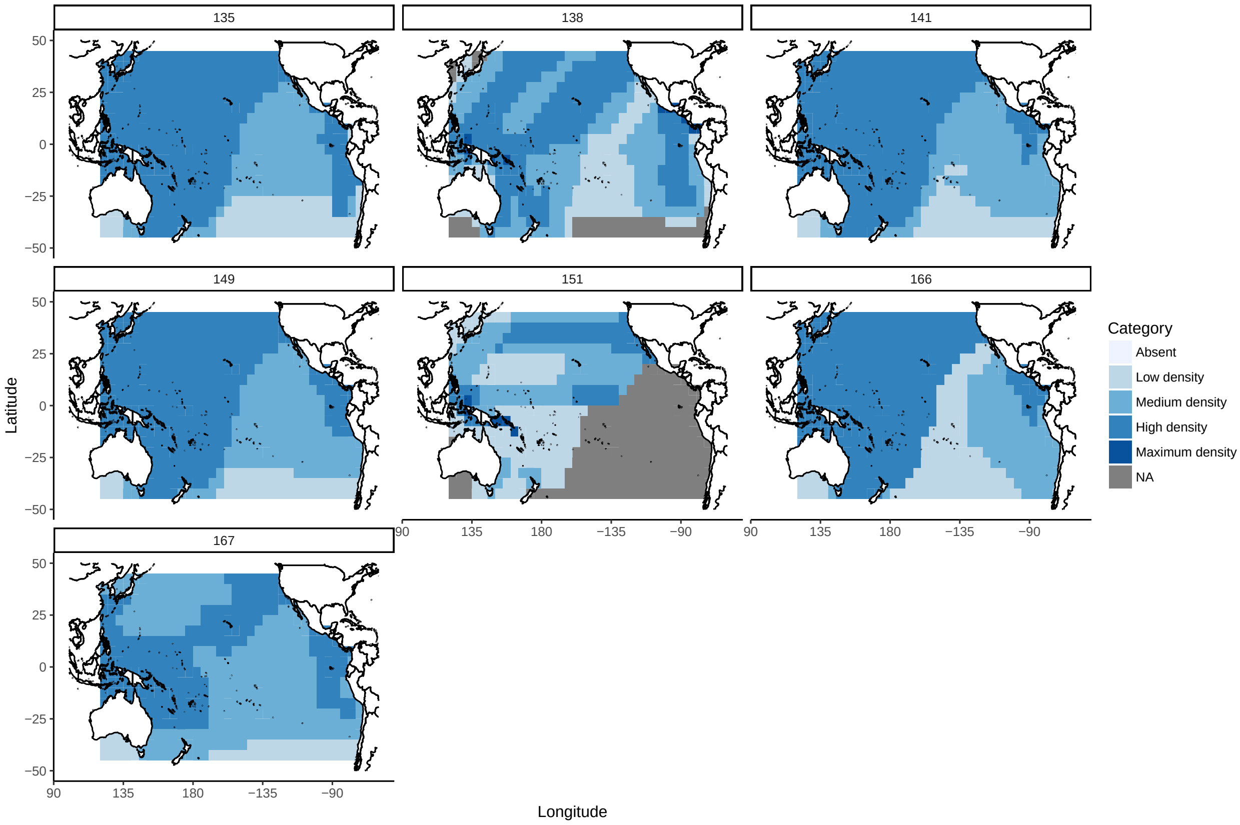

Figure D-12: Relative abundance maps for *Dermochelys coriacea* from the individual participants in the second round of the Delphi survey. Colour shading indicates the abundance categories used in the survey.

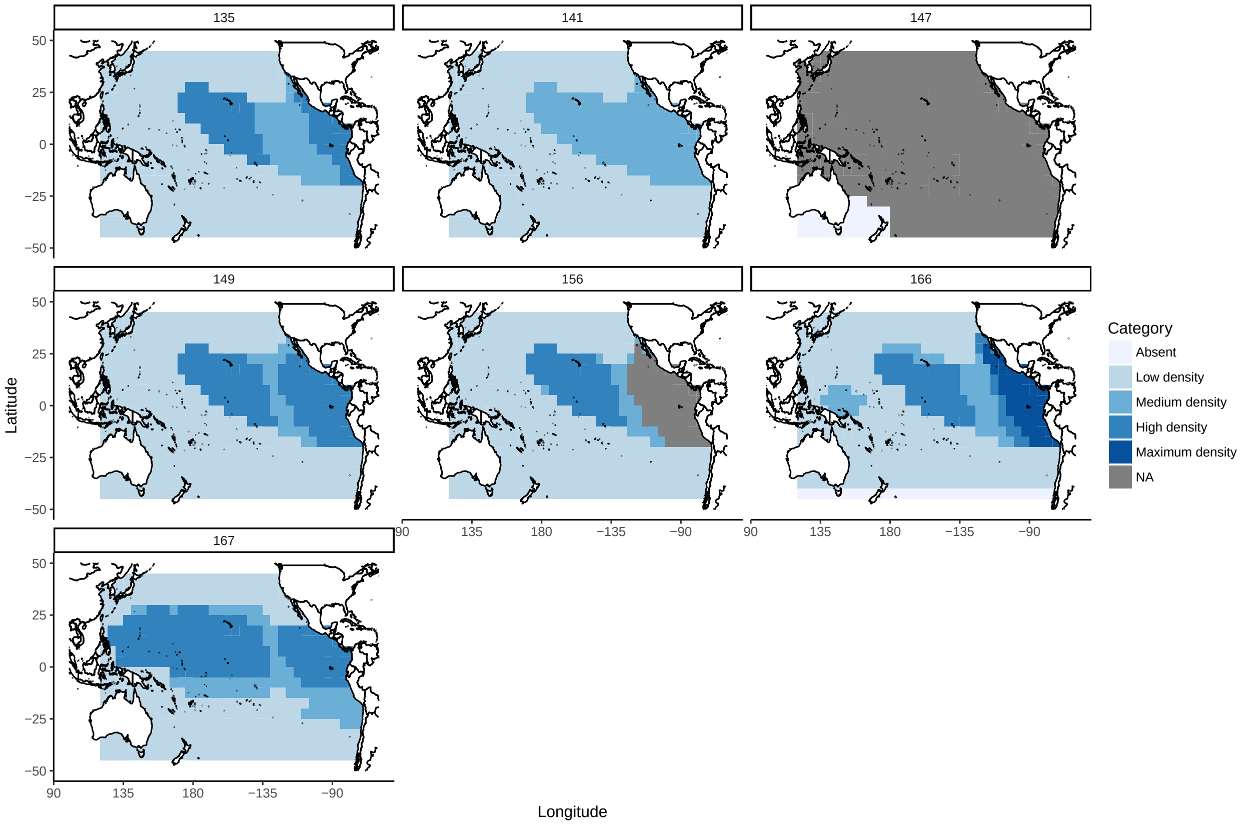

Figure D-13: Relative abundance maps for *Lepidochelys olivacea* from the individual participants in the second round of the Delphi survey. Colour shading indicates the abundance categories used in the survey.