**Supplementary material S1**

Supplementary information for ‘atolls are globally significant hubs for tropical seabirds’

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1. ***Reference list for seabird nesting censuses on atolls***

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1. ***Seabird foraging ranges***

**Table S1: Foraging ranges of atoll seabirds during breeding and chick-rearing season.** Average ± standard deviation foraging ranges in km around nesting colony calculated based on available literature data of seabird tracking studies, see reference list below. For five species, species-level information was not available and foraging ranges were approximated based on available data of closely-related species (see upper case letters): a range data from *Hydrobates* spp. b range data from *Onychoprion fuscatus*. c range data calculated as average of *Pterodroma* spp. ranges, d range data from *Sternula albifrons*.

|  |  |  |
| --- | --- | --- |
| **Species** | **range [km]** | **reference** |
| *Anous ceruleus* | 5.5 ± 4.9 | [1] [2] |
| *Anous minutus* | 80.0 ± 54.0 | [3] |
| *Anous stolidus* | 71.8 ± 24.4 | [1] [4] [5] [6] |
| *Anous tenuirostris* | 108.1 ± 101.6 | [7] [8] |
| *Ardenna pacifica* | 212.8 ± 204.8 | [9] [10] [11] [12] [13] |
| *Bulweria bulwerii* | 153.0 ± 46.6 | [6] [11] |
| *Fregata ariel* | 141.6 ± 26.0 | [14] [15] |
| *Fregata minor* | 303.3 ± 274.2 | [14] [16] [17] [18] [19] |
| *Gygis alba* | 42.5 ± 53.0 | [8] [20] |
| *Hydrobates tristrami* | 282.3 ± 233.5 | [21] [22] [23] a |
| *Hydroprogne caspia* | 28.0 ± 18.6 | [6] |
| *Nesofregetta fuliginosa* | 282.3 ± 233.5 | [21] [22] [23] a |
| *Onychoprion anaethetus* | 40.0 ± 20.0 | [24] |
| *Onychoprion fuscatus* | 374.2 ± 404.2 | [1] [6] [25] [26] [27] |
| *Onychoprion lunatus* | 248.9 ± 351.3 | b |
| *Phaethon lepturus* | 79.2 ± 41.9 | [1] [6] [28] [29] [30] |
| *Phaethon rubricauda* | 213.2 ± 161.0 | [31] [32] |
| *Phoebastria albatrus* | 1500.0 ± 755.0 | [11] |
| *Phoebastria immutabilis* | 1226.7 ± 986.1 | [11] [33] |
| *Phoebastria nigripes* | 885.1 ± 694.8 | [11] [33] [34] [35] |
| *Pterodroma alba* | 210.0 ± 1273.4 | [11] |
| *Pterodroma heraldica* | 195.0 ± 1273.4 | [11] |
| *Pterodroma hypoleuca* | 898.5 ± 1273.4 | c |
| *Pterodroma neglecta* | 318.0 ± 182.3 | [11] [36] |
| *Pterodroma ultima* | 1943.0 ± 1736.7 | [11] [37] |
| *Puffinus bailloni* | 795.8 ± 357.3 | [13] |
| *Puffinus nativitatis* | 179.5 ± 45.9 | [38] |
| *Sterna dougallii* | 11.6 ± 7.5 | [23] [39] [40] |
| *Sterna sumatrana* | 3.0 ± 7.5 | [40] |
| *Sternula nereis* | 2.0 ± 3.0 | [41] |
| *Sternula saundersi* | 6.3 ± 3.0 | [23] d |
| *Sula dactylatra* | 57.7 ± 36.4 | [6] [25] [42] [43] [44] |
| *Sula granti* | 177.5 ± 112.4 | [45] |
| *Sula leucogaster* | 42.8 ± 10.5 | [6] [25] [43] [46] [47] [48] |
| *Sula sula* | 62.4 ± 30.7 | [42] [43] [49] |
| *Thalasseus bengalensis* | 3.0 ± 18.6 | [50] |
| *Thalasseus bergii* | 25.4 ± 19.0 | [40] [51] |

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***3. Principal component analysis of environmental parameters***

A screenshot of a computer screen

Description automatically generated**Figure S1: Principal component scores of environmental parameter.** To handle issues of potential multicollinearity between environmental parameters and extract relevant features to describe the atoll environmental conditions for the Bayesian modelling, we computed a principal component analysis (PCA). The first six principal components explain a relevant proportion of the total variance in the data and were used for subsequent Bayesian predictive modelling. Colour code indicate the loadings of each principal component (PC1-6) for the respective environmental parameter.

1. ***Presence model, prior predictive check***

*A graph of a line

Description automatically generated with medium confidence***Figure S2: Prior predictive check for the default prior used in the presence model.**

1. *A screenshot of a graph

   Description automatically generated****Presence model, posterior predictive check***

**Figure S3: Posterior predictive checks of the presence model.** Blue bars indicate observed (blue) absence (0) or presence (1), distributions are the cumulative predicted probability distributions (orange) of the logistic regression for seabird presence or absence. Dashed vertical line indicates the threshold of 80% probability that was set as a cut-off for predicted presence. Sensitivity to this cut-off was also assessed against less (65%, 70%, 75%) and more (85%, 90%) restrictive cut-offs and found to be robust.

1. ***Count model, prior predictive check***

*A graph of a log-count

Description automatically generated***Figure S4: Prior predictive check using the default prior set for the count model.**

1. ***Count model, posterior predictive check***

*A screenshot of a graph

Description automatically generated***Figure S5: Posterior predictive checks for the abundance model.** Predictive checks between observed (orange) and predicted (blue) abundance estimates for each seabird species.

1. ***Sensitivity of global count predictions to different prior settings***

*A graph with different colored lines

Description automatically generated***Figure S6: Prior sensitivity analysis.** Sensitivity of the model to prior settings was evaluated using default, narrow (1/3x), wide (3x), global, and mean prior sets (see colour code). Global population predictions are robust to prior specifications.

1. ***MCMC diagnostics***

In the presence model, no R\_hat score was larger than 1.0011. Minimum effective sample size (ESSbulk) was 3685 and tail effective sample size (ESStail) was 3349. No divergent transitions occurred (0 out of 40,000).

In the abundance model, no R\_hat was larger than in 1.0006. Minimum effective sample size (ESSbulk) was 23,659 and tail effective sample size (ESStail) was 13945. 0.19% of chains ended in divergent transitions (76 out of 40,000).

1. ***Out-of-sample validation***