

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (<i>n</i>) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☒	☐ The statistical test(s) used AND whether they are one- or two-sided <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☐	☒ A description of all covariates tested
☐	☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☒	☐ For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☐	☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐ Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection	Existing datasets were used with detailed description of data collection at Asner et al. (2017, Science, doi: 10.1126/science.aaj1987), BirdLife DataZone (https://datazone.birdlife.org), EltonTraits 1.0 (Wilman et al. 2014, Ecology, doi: 10.1890/13-1917.1), and AVONET database (Tobias et al. 2022; Ecology Letters, doi:10.1111/ele.13898).
Data analysis	We used the following published packages of R-statistics (version 4.3.2) for data analysis and visualisation: factoextra, # v1.0.7 - PCA visualization glmmTMB, # v1.1.7 - GLMMs tidyverse, # v2.0.0 - Data manipulation car, # v3.1.2 - Regression tools parallel, # Base R - Parallel processing forcats, # v1.0.0 - Factor manipulation FactoMineR, # v2.8 - PCA analysis MuMIn, # v1.47.5 - Model selection (dredge) ggpubr, # v0.6.0 - Plot arrangement patchwork, # Panel stacking for split FFG plot flextable, # v0.9.2 - Table formatting officer, # v0.6.2 - Word document export The code used in this study is available at FigShare: https://doi.org/10.6084/m9.figshare.12894230

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

All derived analytical data generated during this study (including principal component loadings, comprehensive model selection tables, model summaries, and variance partitioning results) are provided in the Supplementary Data 1–14. FFC and FFG maps are available in GeoTIFF format at <https://zenodo.org/records/4602641>. Bird range polygons and trait database used in this study are available at Figshare: <https://doi.org/10.6084/m9.figshare.12894230>. The sources of raw datasets analysed (detailed in Methods and Supplementary Table 1) are available from public repositories, including BirdLife DataZone (<https://datazone.birdlife.org>), AVONET (<https://figshare.com/s/b990722d72a26b5bfead>), Tobias & Pigot (2019; <https://doi.org/10.1098/rstb.2019.0012>), and EltonTraits 1.0 (<https://doi.org/10.6084/m9.figshare.c.3306933>).

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.

Reporting on race, ethnicity, or other socially relevant groupings

Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status). Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.) Please provide details about how you controlled for confounding variables in your analyses.

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."

Recruitment

Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.

Ethics oversight

Identify the organization(s) that approved the study protocol.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description

We assessed how the mapped canopy functional diversity of Peruvian forests relates to its birds. We assessed how mapped canopy functional diversity (i.e. how forests function, including productivity, nutrient cycling, and resilience) of forests throughout Peru relates to 1,492 forest-dwelling bird species. We modelled the distribution, natural history traits, and conservation status of birds, and compared these to the mapped forest functional diversity using an information-theoretic model selection framework.

Research sample

The study involved the analysis of the following existing datasets (detailed data sources are listed in Supplementary Table 1 of our manuscript):

- Remotely sensed environmental data and forest functional data (Asner et al., 2017, Science, doi: 10.1126/science.aaj1987)
- Data maps are available at: <https://zenodo.org/records/4602641>

- BirdLife DataZone (<https://datazone.birdlife.org>)
 - Tobias & Pigot (2019; <https://doi.org/10.1098/rstb.2019.0012>)
 - EltonTraits 1.0: Species-level foraging attributes of the world's birds and mammals (Wilman et al., 2014 Ecology, doi: 10.1890/13-1917.1, <https://doi.org/10.6084/m9.figshare.c.3306933>).
 - AVONET database: Tobias et al. 2022; Ecology Letters, doi:10.1111/ele.13898 (<https://figshare.com/s/b990722d72a26b5bfead>)

Sampling strategy No sample-size calculations were performed. We assembled a database of all extant bird species of Peru using biological attributes for 1,492 bird species in total.

Data collection We used existing datasets with detailed description of data collection at Asner et al. (2017, Science, doi: 10.1126/science.aaj1987), BirdLife International (<https://datazone.birdlife.org>), Tobias & Pigot (2019; <https://doi.org/10.1098/rstb.2019.0012>), Wilman et al. (2014, Ecology, doi: 10.1890/13-1917.1), and AVONET database (Tobias et al. 2022; Ecology Letters, doi:10.1111/ele.13898).

Timing and spatial scale We used existing datasets with detailed description on timing and spatial scale of the data collected at Asner et al. (2017, Science, doi: 10.1126/science.aaj1987), BirdLife International (DataZone), Tobias & Pigot (2019; <https://doi.org/10.1098/rstb.2019.0012>), Wilman et al. (2014, Ecology, doi: 10.1890/13-1917.1), and AVONET database (Tobias et al. 2022; Ecology Letters, doi:10.1111/ele.13898). Spatial scale included the forested area of Peru.

Data exclusions We evaluated the listed bird species by consulting with the Committee of Peruvian Bird Records (Comité de Registros de Aves Peruanas) about the official bird list, after which we excluded species with no real Peruvian distribution and included birds recently reported for Peru, resulting in 1,893 bird species. Of these, we used data on 1,492 species that are forest-dependent to some degree. In a final filtering, we used the geographic distribution available for 1,470 forest-dependent bird species to calculate spatial statistics. We excluded species with missing values in any of the selected functional, threat, or taxonomic variables to ensure consistent input across analyses. This left 1,303 forest-dependent bird species with complete trait records.

Reproducibility We made the maps, trait data, and code available for reproducibility.

Randomization Grouping species was not relevant in this study as traits of all forest-dependent bird species living in Peru were analysed together.

Blinding Blinding was not relevant in this study as we analysed all available forest functional data and bird species traits living in Peru.

Did the study involve field work? ☐ Yes ☒ No

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Plants

Seed stocks Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.

Novel plant genotypes Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.

Authentication Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.