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Reporting Summary

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For	all st	atistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.
n/a	Cor	nfirmed
	×	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
X		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 Only common tests should be described solely by name; describe more complex techniques in the Methods section.
	×	A description of all covariates tested
x		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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted Give P values as exact values whenever suitable.
x		For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
x		For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
x		Estimates of effect sizes (e.g. Cohen's d, Pearson's r), 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

No software was used for data collection.

Data analysis

We used R (version 3.6.0) for all analyses. All code newly developed to run these analyses (coded by the lead author) is available from: http://doi.org/10.5281/zenodo.3952401. In addition, we used the auk R package (version 0.3.2) and the mgcv R package (version 1.8-28).

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/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a <u>data availability statement</u>. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The data that support the findings of this study are all freely available for research purposes, and can either be directly downloaded from the respective website or are available on demand.

- Bird species checklists (eBird v. 12/2018), http://ebird.org;
- Bird species distribution maps (version V7.0), http://datazone.birdlife.org (available on demand);
- Bird species IUCN Red List status (IUCN Red List of Threatened Species, version 2017.1), http://iucnredlist.org;
- Protected area polygons (World Database on Protected Areas, v. 10/2018), https://www.protectedplanet.net/;
- Elevation data (GLOBE Digital Elevation Model, v.1, 1999), https://www.ngdc.noaa.gov/mgg/topo/gltiles.html;
- Biodiversity hotspots, https://www.cepf.net/our-work/biodiversity-hotspots/hotspots-defined;
- Biome boundaries, https://www.worldwildlife.org/publications/terrestrial-ecoregions-of-the-world;

• Forest cover (Climate Change Initiative Land cover data project map from 2015 v.2.0.7) http://maps.elie.ucl.ac.be/CCI/viewer/index.php,
Agricultural suitability 1981-2010 (version 1.0), https://www.ufz.de/glues/;

· Remoteness (Accessibility to Cities, version 1.0), https://malariaatlas.org/research-project/accessibility to cities/;

- · Canopy height (version 1.0), https://landscape.jpl.nasa.gov/;
- Human footprint (version 1.0), https://doi.org/10.5061/dryad.052q5;
- Forest loss (2000 to 2019, version 2019-v1.7), http://earthenginepartners.appspot.com/science-2013-global-forest.

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Life sciences	Behavioural & social sciences	x 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 compare bird occurrence records in protected versus unprotected sites in eight biodiversity hotspots across the tropics in order to measure protected areas effectiveness at conserving bird diversity. We then measure whether an effect of protected areas at mitigating forest loss and forest degradation can explain those results.

Research sample

The study is based on existing data on bird occurrence: checklists compiled through the eBird citizen science platform (version released in December 2018). Here, we analysed a total of 66,777 checklists that met the following conditions: collected between 2005 and 2018; within the study area (eight biodiversity hotspots analysed, restricted to their moist forest parts: Atlantic Forest, Tropical Andes, Tumbes-Chocó-Magdalena, Mesoamerica, Eastern Afromontane, Western Ghats and Sri Lanka, Indo-Burma, Sundaland); complete checklists only (i.e., in which observers explicitly declare having reported all bird species detected and identified); following either the 'stationary points' or the 'travelling counts' protocol; with durations of continuous observation of 0.5-10 hrs; with observers travelling distances during the checklist < 5 km; only from relatively experienced observers (≥ 10 checklists; ≥ 30 species per checklist on average; ≥ 100 different species in total). We removed potential duplicates (checklists made on the same day at the same place).

Sampling strategy

All data that meet the above mentioned conditions were included in the analyses.

Data collection

This study builds from previously existing data on bird occurrences. These data were collected in the form of checklists by volunteer observers (who also reported information on sampling effort) and then compiled and managed by the eBird team at the Cornell Lab of Ornithology.

Timing and spatial scale

Data were collected locally (points or transects < 5km), with observers providing GPS coordinates and timing of sampling sites. We considered only data from eight tropical biodiversity hotspots, between 2005 and 2018.

Data exclusions

We focused on records from 2005 to 2018, as data collected prior to 2005 were too scarce for analysis. We filtered the dataset based on the above-mentioned criteria (Research Sample) in order to obtain high-quality checklists comparable in protocol and effort. We removed potential duplicates (checklists made on the same day at the same place) to avoid pseudo-replication. We excluded hotspots for which we did not have sufficient data (<= 1000 checklists, after the above-mentioned data selection).

Reproducibility

All the data filtering and processing method is detailed, which should allow the reproductibility of this study's results. There was no experimental replication of this work as it is based on citizen science data analyses, not experiments.

Randomization

We did not apply any randomisation as we addressed sampling biases using statistical controls for sampling effort (following guidelines by eBird project managers)

Blinding

Blinding is not relevant for this study because it is an observational study (citizen science monitoring), and no experiments were

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.

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iviateriais & experimental systems			Methods		
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x	Antibodies	x	ChIP-seq		
x	Eukaryotic cell lines	x	Flow cytometry		
x	Palaeontology	×	MRI-based neuroimaging		
x	Animals and other organisms				
x	Human research participants				
x	Clinical data				