

Does protected area connectivity moderate the efficacy of protection on tropical biodiversity? Evidence from a replication of Brodie et al. 2023

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1 Introduction

This study is a *computational reproduction* of:

Brodie, J.F., Mohd-Azlan, J., Chen, C. et al. Landscape-scale benefits of protected areas for tropical biodiversity. *Nature* 620, 807–812 (2023). <https://doi.org/10.1038/s41586-023-06410-z>

Using a causal framework that controls for forest structure, site accessibility, and geographic location through matching, Brodie et al. (2023) find evidence that protected areas (PA) preserve vertebrate biodiversity within their boundaries and in the adjacent unprotected landscape.

In this reproduction, we attempt to identically reproduce the primary results of the original study. The results of interest include:

1. Six measures of the effect of PA status on bird and mammal biodiversity,
2. Six measures of the effect of adjacency to a large PA on bird and mammal biodiversity at unprotected sites
3. Six measures of the effect of distance from a PA on bird and mammal biodiversity at unprotected sites.

We attempt the reproduction using data and code files published with an author correction in April 2024. A successful reproduction should recreate the numerical results published in Brodie et al. (2023), or the those published with the correction in April 2024.

All materials and procedures used in this reproduction are publicly available at GitHub (**LINK**) with the identifier **PROJECT DOI**. That repository also contains a series of scripts and functions to re-execute this reproduction attempt and a related replication attempt. We implemented the reproduction in platform x86_64-w64-mingw32 using R programming language (Version 4.3.1). Structural causal modeling was performed using the DAGITTY package (Version 0.3.1). We used the MatchIt package (Version 4.5.5) to perform propensity score matching and the NLME package (Version 3.1.164) to fit the linear mixed effects regression models.

2 Study design

We attempt to reproduce the statistical results of the original authors by implementing their workflow as identically as possible. This effort allows us to assess study design and conclusion validity of the original study. The spatial extent of this reproduction attempt is Southeast Asia, matching the area studied by the

original authors. The spatial scale of our statistical analysis is the observation site level with national scale adjustments for human development levels. Our primary data source is the data files publicly shared by Brodie et al. (2023). All data acquisition from original sources followed the procedures presented by the authors. Both the original study and our reproduction attempt were conducted in R.

2.1 Original Study Design

The original study uses a quasi-experimental design with the objective of identifying the causal effect of PAs on tropical biodiversity in Southeast Asia while deconfounding for the influence of site accessibility and habitat quality. The authors use three measures of bird and mammal biodiversity as their response variables - Species richness (SR), Functional richness (FR), and Phylogenetic diversity (PD). Bird observations were gathered from 1,079 sampling locations in the eBird database spanning the period between January 2015 and August 2021. Mammal observations were assembled by the authors from camera traps 1,365 camera stations deployed across the region.

The primary predictors of interest were:

1. A binary measure indicating whether a observation site was located inside or outside a PA
2. a binary indicator that identified if the PA closest to an unprotected site as larger than 500 sq km
3. a binary indicator that identified if the PA closest to an unprotected site was within 2km.

Primary predictors measuring PA status were derived from the World Database of Protected Areas. Additional predictors used to deconfound for site accessibility, forest structure, understory density, and human development pressure were derived from the NASA Global Ecosystem Dynamics Investigation (GEDI) mission, and the UN Development program Human Development Index. Site accessibility was measured using circuit theory-based metrics of proximity to human development¹. Forest structure and understory density were measured use three-dimensional metrics derived from GEDI mission. Code to produce these predictors was not provided by the authors.

Using propensity score matching to control for the confounds of location, site accessibility, and forest structure, Brodie et al. fit a linear mixed-effects models to estimate the PA related effects. The authors completed two sets of statistical analyses. First, the authors estimated the the effect of a site being located inside or outside a PA on bird and mammal biodiversity. In total, the authors fit six separate regression models - two taxons (birds, mammals) for three biodiversity measures (SR, FR, PD) - testing the null hypothesis that:

OR-Ho-1: The protected area status of a site has no effect on the level of mammalian or avian biodiversity observed at that site when adjusting for the confounds of site accessibility, habitat condition, and the socioeconomic development.

Brodie et al. find evidence that the legal designation of PAs provides statistically significant benefits to Southeast Asian bird biodiversity. The authors did not find the same effect for mammals. None of the three measures of mammalian biodiversity was significantly different inside v. outside or PAs.

Second, Brodie et al. tested whether the biodiversity preserving effects of PA status have positive (spillover) or negative (leakage) effects on the biodiversity of unprotected areas surrounding PAs. Within the subset of observation sites outside PA, the authors tested for these effects using the same propensity score matching procedure and statistical framework presented above, but replaced the binary PA status predictor with either the size of the nearest PA or the distance to the nearest PA in separate models. The authors also alternatively included nearest PA distance or size as a control in models testing one of these effects. In total, the authors fit 12 separate regression models - two response variable taxons (birds, mammals), by three biodiversity measures (SR, FR, PD), by two PA measures (area, distance). The null hypothesis tested were:

¹“circuit theoretical models parameterized with human travel speeds across different terrains and the locations of populations centers and transportation networks” (Brodie et al. 2023)

OR-Ho-2a: Being located within 2km of a protected area of at least 500 km^2 in size has no effect on the level of mammalian or avian biodiversity observed at an unprotected site when adjusting for the confounds of site accessibility, habitat condition, the socioeconomic development, and distance to that protected site.

OR-Ho-2b: The distance to the protected area located closest to an unprotected observation site has no effect on the level of mammalian or avian biodiversity observed at that site when adjusting for the confounds of site accessibility, habitat condition, the socioeconomic development, and adjacency to a large protected area.

Brodie et al. find evidence that large PAs are associated with higher biodiversities for mammals and birds in surrounding unprotected areas. However, size effects were only observed for two of the three response variables for birds. The authors found that distance to the nearest PA was significantly associated with only the species richness of birds.

2.2 Study-level metadata

- **Key words:** Biodiversity, Conservation, Protected Areas, Connectivity, 30x30
- **Subject:** Ecology and Evolutionary Biology, Natural Resources and Conservation,
- **Date created:** August 23, 2023
- **Date modified:** August 23, 2023
- **Spatial Coverage:** Southeast Asia
- **Spatial Resolution:** Species observations - GPS located point data, GEDI - derived forest structural covariates - 1 km raster, HDI - country-level, Protected Areas - PA Polygons
- **Spatial Reference System:** WGS84, UTM
- **Temporal Coverage:** 01-2015 to 08-2021
- **Temporal Resolution:** Varies with data set

2.3 Data-level Metadata

We use the author corrected dataset available at https://figshare.com/authors/Jedediah_Brodie/9745991 to conduct our reproduction . The authors' originally published dataset (available at <https://doi.org/10.6084/m9.figshare.22527298.v1>) is missing the country-level measure of the Human Development Index used in biodiversity modeling. For completeness, we gathered and include here metadata on the datasets used by the original authors to construct their shared analytical datasets.

2.3.1 eBird

Brodie et al. use the eBird database to construct the biodiversity measures for birds that are then used as response variables in statistical modeling. The authors did not provide scripts on how they derived the biodiversity metrics.

- **Title:** eBird.
- **Abstract:** A community science platform for reporting bird sightings.
- **Spatial Coverage:** Tropical region (overlapping countries of Brunei, Cambodia, China, Indonesia, Laos, Malaysia, Singapore, Thailand, and Vietnam).
- **Spatial Resolution:** Vector data model with point observations of species occurrence.
- **Spatial Reference System:** Not specified.
- **Temporal Coverage:** 2015/01 - 2021/08.
- **Temporal Resolution:** Not applicable.

- **Lineage:** Brodie et al. (2023) queried and subset data directly from eBird website or its R package or API.
- **Distribution:** eBird webpage and other download methods.
- **Constraints:** Non-commercial use.
- **Data Quality:** Although a direct data quality layer is not associated, Brodie et al. (2023) stated that they followed recommendations from existing studies to filter out data points.

2.3.2 Camera traps

Brodie et al. assembled camera trap data in the study region and pre-processed these data to construct the biodiversity measures for mammals that are then used as response variables in statistical modeling. The authors did not provide scripts on how they derived the biodiversity metrics.

- **Title:** Camera traps.
- **Abstract:** Data from 1,365 camera stations in 65 plots in the study region.
- **Spatial Coverage:** Southeast Asia (overlapping countries of Brunei, Cambodia, China, Indonesia, Laos, Malaysia, Singapore, Thailand, and Vietnam).
- **Spatial Resolution:** Cleaned to vector data model with point observations of species occurrence.
- **Spatial Reference System:** Not specified.
- **Temporal Coverage:** Not specified.
- **Temporal Resolution:** Not applicable.
- **Lineage:** Brodie et al. (2023) cleaned, filtered, and standardized data, and used data from the most recent year if a station contains records of more than one year.
- **Distribution:** Not applicable.
- **Constraints:** Non-commercial use.
- **Data Quality:** Unknown.

2.3.3 The World Database on Protected Areas

The original study used protected area boundaries to derive the three treatment variables (Table 2). Brodie et al. (2023) did not specify a data processing procedure or provide code from the preparation of protected area boundaries.

- **Title:** The World Database on Protected Areas (WDPA).
- **Abstract:** A global database on protected areas (PAs) and other effective conservation measures (OECM).
- **Spatial Coverage:** Tropical region (overlapping countries of Brunei, Cambodia, China, Indonesia, Laos, Malaysia, Singapore, Thailand, and Vietnam).
- **Spatial Resolution:** Vector.
- **Spatial Reference System:** WGS 84.
- **Temporal Coverage:** Accessed sometime in 2023
- **Temporal Resolution:** Updated monthly.
- **Lineage:** Brodie et al. (2023) subset from the dataset, but procedures are unknown.
- **Distribution:** WDPA webpage.
- **Constraints:** Non-commercial use.
- **Data Quality:** Unknown.

2.3.4 GEDI L2 metrics

The Global Ecosystem Dynamics Investigation (GEDI) is a spaceborne light detection and ranging (LiDAR) mission monitoring forest structure on earth. The original study derived both ground elevation and forest

structure metrics from the Level 2 dataset of GEDI. Level 2 GEDI data are at footprint level, so Brodie et al. (2023) used kriging interpolation to create wall-to-wall layers at 1-km resolution.

Level 2 GEDI data includes elevation data. Brodie et al. computed slope and topographic position index (TPI) to represent topographic traits at each site. The authors originally gathered five L2B metrics, canopy height (relative height at 95%), plant area volume density (PAVD) between 0 and 5 m (represents understory density), cumulative plant area index from ground to canopy top, foliage height diversity of plant area index, and proportional canopy cover. The authors found the five forest structure metrics to be highly correlated and retained only canopy height and understory density in statistical models.

Raster files at 1-km resolution for GEDI derived metrics and circuit-based accessibility were shared through a weblink. The authors did not provide code for the calculation of GEDI metrics.

- **Title:** The Global Ecosystem Dynamics Investigation Level 2 Elevation and Height Metrics.
- **Abstract:** Global footprint level observations from GEDI on ground elevation and forest structure.
- **Spatial Coverage:** Tropical region (overlapping countries of Brunei, Cambodia, China, Indonesia, Laos, Malaysia, Singapore, Thailand, and Vietnam).
- **Spatial Resolution:** Footprints are of 25-m resolution and extrapolated into 1-km resolution.
- **Spatial Reference System:** WGS 84.
- **Temporal Coverage:** 2019/04/17 to 2022/04/12
- **Temporal Resolution:** Not applicable.
- **Lineage:** Brodie et al. (2023) used kriging to interpolate GEDI footprints into wall-to-wall raster data of 1-km resolution.
- **Distribution:** Original GEDI L2 metrics can be derived from NASA website and Brodie et al. (2023) shared krigged results on a webpage.
- **Constraints:** Non-commercial use.
- **Data Quality:** Original GEDI L2 metrics have quality and degrade flags and Brodie et al. (2023) kept only data points of satisfying quality.

2.3.5 Human Development Index (HDI)

Data on this measure are missing from the analysis file originally shared by Brodie et al.. We gathered HDI values for each country from the Human Development Report 2020 following the citation provided by the authors. This data omission was corrected in the authors update. Our HDI addition to the original file matched the authors updated inclusion, other than cases where the authors noted that they hand corrected certain measures. Clear reasoning for those adjustments was not provided in the note on author corrections.

- **Title:** Human Development Index
- **Abstract:** An index on the level of human development by country.
- **Spatial Coverage:** Tropical region (overlapping countries of Brunei, Cambodia, China, Indonesia, Laos, Malaysia, Singapore, Thailand, and Vietnam).
- **Spatial Resolution:** Not applicable.
- **Spatial Reference System:** Not applicable.
- **Temporal Coverage:** 2020.
- **Temporal Resolution:** Not applicable.
- **Lineage:** Direct query through the official website.
- **Distribution:** Acquired directly through Human Development Report 2020.
- **Constraints:** Non-commercial use.
- **Data Quality:** Unknown.

2.4 Statistical Approach

Brodie et al. use propensity score matching to control for the potential confounding effects of site accessibility and habitat quality when estimating the efficacy of protected areas at improving bird and mammal

biodiversity. In the PA efficacy models, observations were matched based on their geographic locations (i.e., latitudes and longitudes), forest canopy height, accessibility, and HDI. In spillover models, observations were matched based on these same factors and either adjacent PA size or distance to the nearest PA. Weights produced by propensity score matching were then used in mixed-effects linear regression models that estimated the treatment effect - PA status, nearest PA size, or nearest PA distance - while adjusting for forest canopy height, site accessibility, and HDI (Table 1).

2.5 Observations Preceding the Reproduction Attempt

Before beginning our reproduction attempt, we had observed the analysis file and code published by Brodie et al.. We noticed the following issues in the script and analysis file originally published by the authors.

- 1) The HDI measure was missing from the original analysis file.
- 2) The procedure for computing biodiversity metrics, GEDI metrics, and the circuit-based accessibility metric was not provided in the scripts and not presented in detail in the methodological supplement.
- 3) The procedure for preparing PA boundaries for analysis was unclear.
- 4) The procedure for identifying and eliminating outliers was not included in the script. Only a hand coded list of outliers was provided and removed in the code.

The script and analysis file published by the authors with their correction in April 2024 addressed the first issue above. However, the other issues remain. We did not manipulate the corrected data file before beginning our reproduction attempt.

Table 1 Response, treatment, and predictor variables generated by Brodie et al (2023).

Label	Alias	Definition	Type	Accuracy	Domain	Missing Data Value(s)	Missing Data Frequency
eBird & camera traps							
SR.mean	Species richness	Number of species	Float	Unknown	Equal or greater than 0	Not applicable	Unknown
maxFRic	Functional richness	Diversity of species functional traits	Float	Unknown	Equal or greater than 0	Not applicable	Unknown
asymptPD	Phylogenetic diversity	Cumulative evolutionary time of the species assemblage	Float	Unknown	Equal or greater than 0	Not applicable	Unknown
WDPA PA							
	Within or outside PAs	Whether the point is inside a PA or not	Binary	Not applicable	1 for inside and 0 for outside	Not applicable	Unknown
PA_size_km2	PA size	The area of nearest PA in sq km	Float	Unknown	Equal or greater than 0	Not applicable	Unknown
dist_to_PA	Distance to PA	The distance to the nearest PA in km	Float	Unknown	Equal or greater than 0	Not applicable	Unknown
GEDI L2 Metrics							
elev	Elevation	Ground elevation at the site (krigged)	Integer	Unknown	Equal to or greater than 0 (terrestrial observations)	Unknown	Unknown
slope	Slope	Slope of topography	Float	Unknown	0 to 90	Unknown	Unknown
TPI	Topographic Position Index	Difference between the elevation of a focal raster cell with those of its neighbors (not mentioned in paper)	Float	Unknown	Not bounded	Unknown	Unknown
rh_95_a0.pred	Relative height at 95%	Roughly the top canopy height (krigged)	Float	Unknown	Equal to or greater than 0	Unknown	Unknown
pavd_0_5.pred	Plant area volume density from 0 to 5 m	A proxy of understory forest density (krigged)	Float	Unknown	Equal to or greater than 0	Unknown	Unknown
pai_a0.pred	Plant area index	Cumulative PAI from ground to canopy (krigged)	Float	Unknown	Equal to or greater than 0	Unknown	Unknown
fhd_pai_1m_a0.pred	Foliage height diversity	Shannon's diversity of PAI across heights (krigged)	Float	Unknown	Equal to or greater than 0	Unknown	Unknown
cover_a0.pred	Proportional coverage	Openness or closeness of canopy (krigged)	Float	Unknown	0 to 1	Unknown	Unknown
HDI							
HDI	Human Development Index	Level of human development	Float	Unknown	0 to 1	Not applicable	Not applicable

Table 2. Variables used in statistical modeling

Name	Source	Usage
Biodiversity metrics - mammals	Authors	Outcome variable
Biodiversity metrics - birds	eBird	Outcome variable
Protected area boundaries	WDPA	Treatment variables (whether inside PAs)
Ground elevation	NASA GEDI L2B	Predictor - elevation and topography
Circuit-based site accessibility (log transformed)	Authors	Predictor - site accessibility
Human Development Index	Human Development Report 2020	Predictor - Human development index
Forest structure metrics	NASA GEDI L2A	Predictor - forest structure

3 Reproduction Attempts

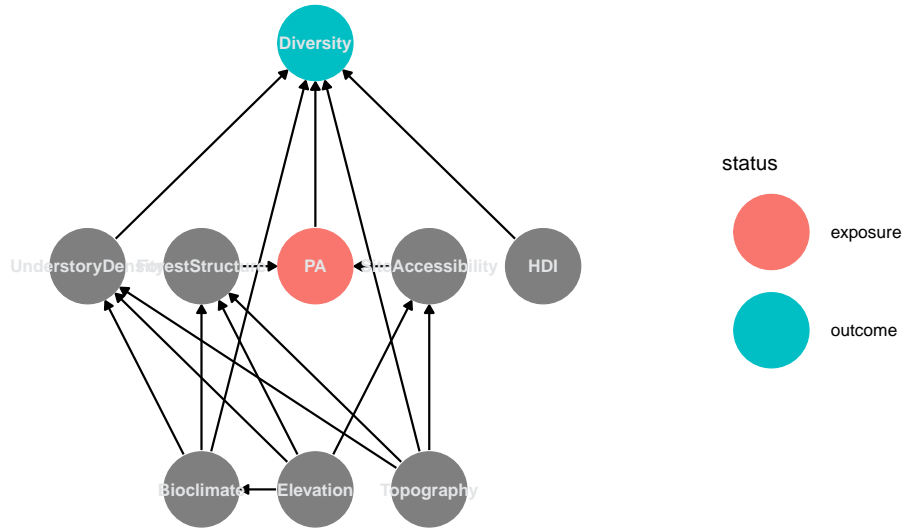
We were able to statistically reproduce the results of Brodie et al. using an unaltered version of the their corrected data and code files. In an attempt to remain consisted with the original authors, we use the most recent package versions at the time of the author corrected analysis - April 26, 2024. No additional preparation was needed for our reproduction using these materials.

For brevity and legibility, this rendered report suppresses the code used to prepare and re-execute the analysis. However, that code is recorded and accessible in the RNotebook file that forms the basis of this report. That file and all related research materials are available in this projects online repository. The computational setup for the analysis was:

```
# , results = 'hide', message = FALSE, warning = FALSE, eval = FALSE
# Load required packages and scripts
# We made minimum changes to the original script
library(groundhog)
pkgs <- c("tidyverse", "Hmisc", "MatchIt", "optmatch", "lme4", "nlme",
          "lmerTest", "cowplot",
          "here", "modelsummary", "dagitty", "ggdag", "kableExtra",
          "MuMIn", "tibble", "broom.mixed" )
# We follow the recommendation to set the time for groundhog two weeks before
# when the original script was edited
# groundhog.library(pkgs, "2024-03-03")

lapply(pkgs, library, character.only=TRUE) # use this line if groundhog returns error
here('')
```

For completeness, we first reproduced the causal diagram underlying the original analysis and used the diagram to identify the predictors necessary for estimation of the causal effect of the PA treatment.



```
## { Bioclimate, Topography, UnderstoryDensity }
## { Bioclimate, Elevation, Topography }
## { Elevation, ForestStructure, Topography }
## { ForestStructure, SiteAccessibility }
```

To assess **OR-Ho-1** we reproduced the propensity score matching procedure and linear mixed-effects modeling conducted by the Brodie et al. for each the three biodiversity response variables for each taxon. This procedure resulted in six fitted regressions. Our results (Table 3) correspond to the top third of Table 1 of the corrected supplemental materials presented by Brodie et al.. While we were not able to computationally reproduce their exact coefficient values, our results are similar in magnitude, direction, and statistical significance. Of principle interest, we were able to reproduce the statistical results for the PA treatment for both birds and mammals. Bird models produced significant positive effects for location within a PA, while no significant effects were observed for mammals.

Table 3: Reproduction results from mixed-effects linear regression for species richness (SR), functional richness (FR), and phylogenetic diversity (PD). Following Brodie et al., bolding indicates predictors with estimated coefficients with $p < 0.05$

Variable	Bird			Mammal		
	SR	FR	PD	SR	FR	PD
All sites						
R^2	0.308	0.247	0.343	0.350	0.356	0.478
Intercept	135.425 (12.745; 0.000)	212.569 (10.176; 0.000)	2.962 (0.272; 0.000)	9.450 (1.274; 0.000)	11.577 (1.675; 0.000)	2.129 (0.248; 0.000)
Forest canopy height	21.396 (2.167; 0.000)	32.957 (2.997; 0.000)	0.079 (0.032; 0.014)	0.343 (0.223; 0.124)	1.357 (0.352; 0.000)	0.055 (0.030; 0.069)
Site accessibility	7.004 (1.761; 0.000)	-1.716 (2.349; 0.465)	-0.091 (0.025; 0.000)	-0.332 (0.329; 0.313)	-0.348 (0.526; 0.508)	-0.013 (0.045; 0.781)
HDI	-5.259 (10.012; 0.616)	-19.422 (7.843; 0.042)	0.026 (0.212; 0.905)	-0.464 (0.853; 0.615)	0.273 (1.201; 0.831)	0.062 (0.161; 0.721)
PA	24.724 (4.955; 0.000)	24.629 (6.441; 0.000)	0.384 (0.075; 0.000)	-0.195 (0.518; 0.707)	-0.885 (0.823; 0.283)	-0.056 (0.070; 0.423)

To assess **OR-Ho-2a** and **OR-Ho-2b** we reproduced the propensity score matching procedure and linear mixed-effects modeling of PA size and PA distance spillovers for each the three biodiversity response variables

for each taxon. This produced 12 fitted regressions. Our results (Table 4) match the bottom two-thirds of Table 1 of corrected supplemental materials presented by Brodie et al.. We were again unable to computationally reproduce the exact coefficient values for the ‘PA size’ effects or the ‘Distance to PA’ effects, but did produce coefficients with similar directions, magnitudes, and statistical significance. The one difference between our results and the original authors was the coefficient for the distance to PA estimated for birds using SR.

Table 4: Reproduction results from mixed-effects linear regression for species richness (SR), functional richness (FR), and phylogenetic diversity (PD) for spillover effects. Following Brodie et al., bolding indicates predictors with estimated coefficients with $p < 0.05$

Variable	Bird			Mammal		
	SR	FR	PD	SR	FR	PD
Outside protected areas - ‘PA size’ effect						
R^2	0.381	0.482	0.350	0.477	0.453	0.511
Intercept	111.888 (18.836; 0.000)	208.019 (29.734; 0.000)	2.998 (0.301; 0.000)	8.219 (1.659; 0.000)	4.863 (2.168; 0.025)	1.811 (0.196; 0.000)
Forest canopy height	17.954 (2.822; 0.000)	23.233 (2.646; 0.000)	-0.051 (0.035; 0.154)	0.564 (0.372; 0.130)	1.008 (0.677; 0.137)	0.090 (0.044; 0.040)
Site accessibility	-5.425 (3.246; 0.095)	-12.086 (3.747; 0.001)	-0.291 (0.045; 0.000)	-0.583 (0.422; 0.168)	-2.195 (0.693; 0.002)	-0.098 (0.045; 0.029)
HDI	-5.263 (14.710; 0.731)	-7.251 (23.394; 0.766)	0.213 (0.236; 0.398)	0.001 (1.080; 0.999)	2.544 (1.367; 0.136)	0.163 (0.125; 0.263)
Distance to PA	-48.331 (8.535; 0.000)	-17.712 (8.054; 0.028)	-0.219 (0.103; 0.034)	-0.132 (0.419; 0.754)	-1.578 (0.723; 0.029)	-0.127 (0.050; 0.012)
PA size (binary)	6.364 (6.290; 0.312)	19.455 (6.512; 0.003)	0.409 (0.089; 0.000)	2.297 (0.623; 0.000)	10.080 (1.115; 0.000)	0.424 (0.074; 0.000)
Outside protected areas - ‘Distance to PA’ effect						
R^2	0.370	0.312	0.461	0.376	0.290	0.278
Intercept	113.260 (15.404; 0.000)	220.549 (14.540; 0.000)	2.896 (0.296; 0.000)	8.832 (1.515; 0.000)	12.395 (1.316; 0.000)	2.221 (0.097; 0.000)
Forest canopy height	24.085 (2.313; 0.000)	32.203 (2.849; 0.000)	0.178 (0.035; 0.000)	0.657 (0.323; 0.043)	2.947 (0.516; 0.000)	0.160 (0.039; 0.000)
Site accessibility	5.796 (2.799; 0.039)	-4.917 (3.520; 0.163)	-0.223 (0.045; 0.000)	-0.605 (0.487; 0.215)	-0.846 (0.776; 0.276)	-0.104 (0.057; 0.067)
HDI	-7.385 (12.379; 0.570)	-22.621 (11.486; 0.090)	0.041 (0.238; 0.868)	-0.136 (0.987; 0.897)	0.552 (1.193; 0.667)	0.115 (0.088; 0.200)
PA size	0.844 (2.796; 0.763)	2.501 (4.030; 0.535)	0.180 (0.047; 0.000)	1.041 (0.662; 0.116)	0.828 (0.962; 0.390)	0.119 (0.070; 0.089)
Distance to PA (binary)	10.328 (5.928; 0.082)	7.382 (6.908; 0.286)	0.007 (0.086; 0.934)	1.734 (0.701; 0.014)	1.557 (1.177; 0.186)	0.163 (0.090; 0.072)

4 Discussion & Conclusion

The goal of the report is to reproduce analysis and results from Brodie et al. (2023) on the effect of protected areas to preserve tropical bird and mammal biodiversity after removing confounding effects of site accessibility and forest structure. Our statistical reproduction produced results that were consistent with the main findings of Brodie et al. (2023). Our numerical results similarly supported rejection of OR-H0-1 (i.e., similar coefficient values and significance), although we were unable to reproduce exact results as Brodie et al. (2023). Our numerical results similarly supported rejection of OR-H0-2a and a failure to reject OR-H02b.

While our numerical results aligned with those of Brodie et al., the limited information about how variables were constructed restricted our ability to directly assess the outcomes and interpretations of the original paper. The scripts can be used to recreate the numerical results, but did not include data preprocessing steps such as the procedure for cleaning protected area boundaries, or computing secondary variables from raw data (e.g., GEDI metrics and circuit-based accessibility metrics). Provided datafiles also did not include raw observation data needed to recreate variables, or an extensive metadata file documenting those data

sources. Omission of the processing steps used to create the analytical datafile meant that we could only directly assess the statistical analysis of the authors, as we could not retrace the variable creation process.

4.1 Bias and threats to validity

There remain minor concerns about statistical bias and construct validity. The original models account for location and potential spatial autocorrelation in both the matching procedure and the clustering of errors in regression models. However, the authors did not present any formal testing of remaining spatial autocorrelation in the residuals. The paper does not include an extensive discussion of measurement uncertainty issues that could lead to concerns about construct validity (e.g., biodiversity measures, forest structure measures created through kriging.) Independent investigation of these issues cannot be easily undertaken given the lack of documentation of variable construction and processing.

5 Acknowledgements

This report is based upon the template for Reproducible and Replicable Research in Human-Environment and Geographical Sciences, DOI:10.17605/OSF.IO/W29MQ(<https://doi.org/10.17605/OSF.IO/W29MQ>)

6 References

Brodie, J.F., Mohd-Azlan, J., Chen, C. et al. Landscape-scale benefits of protected areas for tropical biodiversity. *Nature* 620, 807–812 (2023). <https://doi.org/10.1038/s41586-023-06410-z>