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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Abstract

This study is a 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

We replicate the analysis of Brodie et al. (2023) and introduce protected area (PA) connectivity as a statistical moderator of the effect PA status has on biodiversity. We find KEY FINDINGS. 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) do preserve vertebrate biodiversity within their boundaries and in the adjacent unprotected landscape. Brodie et al. provides evidence of the efficacy of protected area status, they do not assess whether the effect they observe is altered by network connectivity.

1 Study metadata

This replication uses the data file provided by Brodie et al. (2023) at https://doi.org/10.6084/m9.figshare.22527298.v1. We independently accessed the World Database on Protected Areas https://www.protectedplanet.net/en/thematic-areas/wdpa?tab=WDPA to construct our site and PA connectivity measures.

- Key words: Biodiversity, Conservation, Protected Areas, Connectivity, 30x30
- Subject: Ecology and Evolutionary Biology, Natural Resources and Conservation,
- Date created: November 8, 2023
- Date modified: date of most recent revision
- 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: Specify the geographic or projected coordinate system for the study, e.g. EPSG:4326
- Temporal Coverage: $01\text{-}2015 \ \mathrm{to} \ 08\text{-}2021$
- Temporal Resolution: Specify the temporal resolution of your study—i.e. the duration of time for which each observation represents or the revisit period for repeated observations

2 Study design

This study consists of a reproduction of the original work by Brodie et al. (2023) and a replication to analyze how connectivity influences protected area efficacy in preserving tropical biodiversity. We first implement the workflow as described and shared in Brodie et al. (2023) as identically as possible to reproduce the original study. We then compute and add connectivity measures at the sample points to the original dataset to further examine the effect of connectivity.

Brodie et al. (2023) formulated hypotheses to assess protected area effectiveness and tested them with structural causal modeling. Hypotheses concerned overall protected area effectiveness (H1) and PAs' size (H2) and closeness (H3) effects on biodiversity in unprotected lands to infer implications for spillover and leakage effects.

2.1 Protected area effectiveness on overall biodiversity

OR-H1: Biodiversity is higher within protected areas than outside (after removing effects of site accessbility and habitat condition).

Debates exist on whether protected areas are effective because of their remote location and good habitat conditions or conservation status itself. Motivated by such, Brodie et al. (2023) estimated protected areas efficacy for conserving tropical mammal and bird diversity after de-confounding the effects of site accessibility and habitat condition (H1). Their outcome variables are various aspects of biodiversity. The treatment variable is whether the observation point is within or outside a reserve. If the treatment variable is significant in a causal model, it supports H1 and adds evidence for the effectiveness of protecting lands.

To do so, they removed confounding effects and built causal models for birds vs mammals, and different biodiversity outcome metrics. Two major confounders identified were site accessibility and habitat quality. Site accessibility was proxied using Human Development Index (HDI), circuit theory-based measures of proximity to human development¹, and an interaction term of the two variables. Habitat quality was proxied using three-dimensional habitat structure metrics derived from the Global Ecosystem Dynamics Investigation (GEDI) mission. Confounding effects were removed using statistical matching based on propensity scores. Biodiversity metrics used as outcome variables include species richness (SR), functional richness (FR), and phylogenetic diversity (PD). PA effects were estimated using separate mixed effects linear regression for different biodiversity metrics and for birds vs mammals.

Brodie et al. (2023) found protection status increased all facets of bird biodiversity but the effects were not significant for mammals.

2.2 Spillover and leakage effects on unprotected lands

Spillover and leakage effects are two ways protected areas could have regional impacts on biodiversity beyond their boundaries. Spillover effect refers to enhanced biodiversity in unprotected lands near PAs whereas leakage effect refers to increased conservation pressure (e.g., unregulated hunting and displaced disturbances) in nearby unprotected lands because of PA establishment. Brodie et al. (2023) tested the effects of PA sizes (H2) and closeness (i.e., distance, H3) to neighboring unprotected lands.

OR-H2: Biodiversity outside protected areas is higher when they are near large ones (size effect).

They built separate models for birds and mammals on three different diversity metrics and tested H2 using observations outside protected areas. They went through the same matching steps as above.

Brodie et al. (2023) found that PA size is a significant predictor of all facets of birds and mammals diversity outside PAs in the study region. Effects for mammals were smaller than those for birds.

^{1&}quot;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-H3: Biodiversity outside protected areas is higher when they are closer (distance effect).

They tested the effect of proximity to PAs on biodiversity outside PAs. Distance was computed as the Euclidean distance to the nearest reserve.

In the original paper, the authors reported that no significant effects of distance were observed. However, regression summary for H3 was incomplete in Extended Data Table 1 so that a direct comparison could not be made.

2.3 Adding connectivity

We ask the research question of whether protected areas moderate the efficacy of protection on tropical biodiversity. We formulate the hypothesis is as follows:

RPL-H1: Connectivity mdoerates the efficacy of protection on biodiversity.

We build upon the existing structural causal models by Brodie et al. (2023) to test the hypothesis. The original study archetype is quasi-experimental as it uses a matching strategy to perform causal analysis.

3 Materials and procedure

3.1 Computational environment

The reproduction of the original study is conducted in MacBook Pros. Brodie et al. (2023) cleaned up the variables and performed propensity score matching and causal analysis in R. They did not provide scripts on how they derived the biodiversity metrics, circuit theory-based metrics, HDI, and the GEDI metrics. We built upon and annotated R scripts shared by the original study, and added missing information on HDI and GEDI metrics to the scripts. // Is this accurate?

Required packages are as follows:

3.2 Data and variables

In the original study, outcome variables for the causal models are biodiversity metrics (i.e., species richness, functional richness, and phylogenetic diversity) derived from species observations. Mammal observations were assembled by the authors from camera traps in 65 study areas in the study region. Bird observations were gathered from eBird from 2015/01 to 2021/08 following a set of filtering procedures.

Treatment variables for ORIG-H1, H2, H3 were derived from the World Database on Protected Areas (WDPA) by UNEP-WCMC. Specifically, they are 1) a binary variable on whether the sampling point is within protected areas or not (H1), 2) relative size of the closest protected area (i.e., large or small, H2), and 3) euclidean distance to the closest protected area (H3). For H2, PAs equal to or larger than 500 km2 are considered large and otherwise small. The size threshold was determined by testing a series of values with the best model fits for birds and mammals (Extended Data Table 4 in Brodie et al. 2023).

Observations were matched based on propoensity scores of their geographic locations (i.e., latitudes and longitudes), forest canopy height, accessibility, and HDI. Predictors in the mixed-effects linear regression models were forest canopy height, site accessibility, HDI, and treatment variables.

We gathered data shared by Brodie et al. (2023). Tabular data of most model inputs were provided in a figshare. Raster files at 1-km resolution for GEDI derived metrics and circuit-based accessibility were shared through a weblink.

Table 1. Variables used in Brodie et al. (2023)

Name	Source	Usage
Biodiversity metrics - mammals	Authors	Outcome variable (ORIG-H1, H2, H3)
Biodiversity metrics - birds	eBird	Outcome variable (ORIG-H1, H2, H3)
Protected area boundaries	WDPA	Treatment variables (whether inside PAs: ORIG-H1, distance to PAs: ORIG-H2, and size of PAs: ORIG-H3)
Elevation	NASA SRTM	Predictor - elevation and topography
Circuit-based site accessibility (log transformed)	Authors	Predictor - site accessibility
Human Development Index	Human Development Report 2020	Predictor - HDI
GEDI metrics	NASA GEDI L2	Predictor - forest structure

3.2.1 Bird observations

- Title: eBird.
- Abstract: A community science platform for reporting bird sightings.
- Spatial Coverage: Tropical region (overlapping countries of Brunei, Cambodie, China, Indonesia, Laos, Malaysia, Singapore, Thailand, and Vietnam).
- Spatial Resolution: Vector.
- 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) followed recommendations from existing studies to filter out data points.

Variables constructed were as follows:

Table 2 Variables created from bird observations via eBird.

Label	Alias	Definition	Type	Accuracy	Domain	$egin{aligned} ext{Missing} \ ext{Data} \ ext{Value(s)} \end{aligned}$	Missing Data Frequency
SR.mean	Species richness	Number of species	Float	Unknown	Equal or greater than 0	Not applicable	Unknown

Label	Alias	Definition	Type	Accuracy	Domain	Missing Data Value(s)	Missing Data Frequency
maxFRic	Functional richness	Diversity of species functional traits	Float	Unknown	Equal or greater than 0	Not applicable	Unknown
asymptPD	Phylogenetic diversity	Cumulative evolution- ary time of the species assemblage	Float	Unknown	Equal or greater than 0	Not applicable	Unknown

3.2.2 Protected area boundary

- Title: The World Database on Protected Areas (WDPA).
- Abstract: A global database on protected areas (PAs) and other effective conservation measurers (OECM).
- Spatial Coverage: Tropical region (overlapping countries of Brunei, Cambodie, China, Indonesia, Laos, Malaysia, Singapore, Thailand, and Vietnam).
- Spatial Resolution: Vector.
- Spatial Reference System: WGS 84.
- Temporal Coverage: Latest.
- Temporal Resolution: Updated monthly.
- Lineage: Brodie et al. (2023) queried and subset data directly from eBird website or its R package or API.
- Distribution: WDPA webpage.
- Constraints: Non-commercial use.
- Data Quality: Unknown.

Brodie et al. (2023) did not specify how they cleaned up protected area boundary. We dissolved PAs and then converted them from multi-parts to single-parts. For mammals, we excluded marine protected areas.

// needed to confirm with Lei.

Table 3 Variables created from protected area boundaries.

Label	Alias	Definition	Type	Accuracy	Domain	Missing Data Value(s)	Missing Data Frequency
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_k	m2Functional richness	Diversity of species functional traits	Float	Unknown	Equal or greater than 0	Not applicable	Unknown
dist_to_PA	A Phylogenetic diversity	Cumulative evolution- ary time of the species assemblage	Float	Unknown	Equal or greater than 0	Not applicable	Unknown

- Variables: SR.mean, FR, and PD
 - Label: variable name as used in the data or code
 - Alias: intuitive natural language name
 - Definition: Short description or definition of the variable. Include measurement units in description.
 - Type: data type, e.g. character string, integer, real
 - Accuracy: e.g. uncertainty of measurements
 - Domain: Range (Maximum and Minimum) of numerical data, or codes or categories of nominal data, or reference to a standard codebook
 - Missing Data Value(s): Values used to represent missing data and frequency of missing data observations
 - Missing Data Frequency: Frequency of missing data observations

3.2.3 Elevation

- Variables: SR.mean, FR, and PD
 - Label: variable name as used in the data or code
 - Alias: intuitive natural language name
 - Definition: Short description or definition of the variable. Include measurement units in description.
 - Type: data type, e.g. character string, integer, real
 - Accuracy: e.g. uncertainty of measurements
 - Domain: Range (Maximum and Minimum) of numerical data, or codes or categories of nominal data, or reference to a standard codebook
 - Missing Data Value(s): Values used to represent missing data and frequency of missing data observations
 - Missing Data Frequency: Frequency of missing data observations

3.2.4 Circuit-based accessibility

3.2.5 Human Development Index (HDI)

3.2.6 GEDI-based metrics

Label	Alias	Definition	Type	Accuracy	Domain	Missing Data Value(s)	Missing Data Frequency
variable1 variable2	• • •		• • •				• • •

^{...} same form as above...

3.3 Prior observations

At the beginning of this analysis, we had observed the dataset provided by Brodie et al with their publication. We did not manipulate the data before beginning our replication attempt.

3.4 Bias and threats to validity

Given the research design and primary data to be collected and/or secondary data to be used, discuss common threats to validity and the approach to mitigating those threats, with an emphasis on geographic threats to validity.

These include: - uneven primary data collection due to geographic inaccessibility or other constraints - multiple hypothesis testing - edge or boundary effects - the modifiable areal unit problem - nonstationarity - spatial dependence or autocorrelation - temporal dependence or autocorrelation - spatial scale dependency - spatial anisotropies - confusion of spatial and a-spatial causation - ecological fallacy - uncertainty e.g. from spatial disaggregation, anonymization, differential privacy

3.5 Data transformations

Describe all data transformations planned to prepare data sources for analysis. This section should explain with the fullest detail possible how to transform data from the **raw** state at the time of acquisition or observation, to the pre-processed **derived** state ready for the main analysis. Including steps to check and mitigate sources of **bias** and **threats to validity**. The method may anticipate **contingencies**, e.g. tests for normality and alternative decisions to make based on the results of the test. More specifically, all the **geographic** and **variable** transformations required to prepare input data as described in the data and variables section above to match the study's spatio-temporal characteristics as described in the study metadata and study design sections. Visual workflow diagrams may help communicate the methodology in this section.

Examples of **geographic** transformations include coordinate system transformations, aggregation, disaggregation, spatial interpolation, distance calculations, zonal statistics, etc.

Examples of **variable** transformations include standardization, normalization, constructed variables, imputation, classification, etc.

Be sure to include any steps planned to **exclude** observations with *missing* or *outlier* data, to **group** observations by *attribute* or *geographic* criteria, or to **impute** missing data or apply spatial or temporal **interpolation**.

3.6 Analysis

Describe the methods of analysis that will directly test the hypotheses or provide results to answer the research questions. This section should explicitly define any spatial / statistical models and their parameters, including grouping criteria, weighting criteria, and significance thresholds. Also explain any follow-up analyses or validations.

4 Results

Describe how results are to be presented.

5 Discussion

Describe how the results are to be interpreted vis a vis each hypothesis or research question.

6 Integrity Statement

Include an integrity statement - The authors of this preregistration state that they completed this preregistration to the best of their knowledge and that no other preregistration exists pertaining to the same hypotheses and research. If a prior registration *does* exist, explain the rationale for revising the registration here.

7 Acknowledgements

• Funding Name: name of funding for the project

• Funding Title: title of project grant

• Award info URI: web address for award information

• Award number: award number

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8 References