

COMPUTATIONAL METHODS IN ECOLOGY AND EVOLUTION:
MINIPROJECT

**Using different measures of biodiversity to
investigate global drivers of local Avian
biodiversity**

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1 **Abstract**

2 Our planet's biodiversity is declining at an alarming rate. To stop it, we must
3 know exactly where and why it is happening. Being able to predict biodiversity's
4 responses to climate change and land-use change allows us to pinpoint the most
5 impacted areas and predict biodiversity change into the future. If we can deter-
6 mine the state of a community by simply counting species rather than doing more
7 time-intensive sampling, we can assess and protect sites faster. In this study, I
8 investigate a) whether using measures of evenness reveal different predictors than
9 using species richness as a biodiversity measure and b) what factors predict lo-
10 cal Avian community biodiversity on a global scale. I show that species richness
11 comes to the same conclusions as both Shannon's and Simpson's measures - that
12 land-use intensity is the single most important predictive variable - without losing
13 any significant information. This suggests that species richness is able to produce
14 meaningful models with less sampling effort. It also shows that land-use intensity
15 is a hugely impactful factor for global Avian biodiversity declines, highlighting
16 the importance of conserving primary and secondary vegetation where possible.

17 1 Introduction

18 We are currently losing species at a rate comparable to previous mass extinctions
19 (Ceballos et al. 2015). The 2002 Convention on Biological Diversity contained
20 the target to “to achieve by 2010 a significant reduction of the current rate of
21 biodiversity loss at the global, regional and national level...to the benefit of all life
22 on earth.” (Balmford et al. 2005). In order to achieve this reduction in the rate
23 of biodiversity loss the current rate needs to be known, and methods of tracking
24 it going forward must be produced. Choosing a measure of biodiversity that
25 contains the maximum amount of information about a system while also being
26 easy to measure is vital to facilitate this tracking.

27 Measures of biodiversity tend to look at one of two aspects of a community:
28 richness (i.e. the number of different species) and evenness of the number of
29 individuals of those species. Richness is obviously much easier to measure. As
30 long as a species is known to be present in an area, it can be recorded. This means
31 that camera trapping, signs of activity and even environmental DNA analysis can
32 be used to work out the species richness of a site (Li et al. 2016; Rovero et al. 2014).
33 Calculating evenness requires knowledge of the abundance of each species. This
34 often requires repeated sampling of a site (multiple quadrats, transects, traps etc.)
35 to get an estimate of abundance for each species. However measures of evenness
36 can identify situations where a community is dominated by one or two species.

37 Other ways to measure biodiversity include measuring genetic, taxonomic or
38 functional diversity instead of species diversity, or relative biodiversity (for ex-
39 ample the biodiversity intactness index (Scholes and Biggs 2005) which measures
40 relative biodiversity between a human-impacted habitat and a pristine habitat
41 that are otherwise the same). These all require more data, either of the species

42 or the area in which they reside. This study aims to look at more basic measures
43 of biodiversity as they are more widely used and easier to measure.

44 In this study I will be investigating 3 measures of biodiversity:

45 **Species Richness:**

46 This is simply calculated by counting the number of different species in an
47 area (N). As such, this measure is easy to calculate and requires only pres-
48 ence/absence data for a site. It values each species the same amount, meaning
49 rare and common species have the same weight. As such, species richness val-
50 ues rare species more highly than their relative contribution to the ecosystem.
51 This may overestimate diversity where there is largely mono dominance with
52 a few rare species, but also accounts for the fact that rare species often have
53 important functional roles (Bunker et al. 2013; Leitão et al. 2016).

54 **Simpson's Index of Biodiversity:**

55
$$D = \sum \left(\frac{n_i}{N} \right)^2$$

56 n_i = no. of individuals of one species N = total no. of individuals

57 Simpson's Index (Simpson 1949) is a measure of similarity and evenness.
58 It is a value between 0 and 1 where values close to 0 indicate less similar
59 (more diverse) communities. This index is highly impacted by dominant
60 species, with rare species making little impact on the final measure (Dejong
61 1975). It is also possible to convert Simpson's Index to a continuous measure
62 of diversity with higher numbers indicating a more diverse community by
63 taking the reciprocal of the index ($\frac{1}{D}$), known as the reciprocal Simpson's
64 Index. This also fixes the issue of the model converging close to it's final
65 value with only the first two or three most dominant species.

66 **Shannon's Measure of Diversity:**

67
$$H' = \sum \left(\frac{n_i}{N} \times \ln \frac{n_i}{N} \right)$$

68 n_i = no. of individuals of one species N = total no. of individuals

69 Shannon's measure (Shannon and Weaver 1949) is also a measure of evenness,
70 but due to the inclusion of a \ln , it is less affected by highly dominant species
71 than Simpson's Index. The least diverse communities have a Shannon's mea-
72 sure of close to 0, while increasingly diverse communities have increasingly
73 higher H' values. This is because Shannon measures the uncertainty that one
74 individual from a community will be of a specific species.

75 Birds are a good model species for several reasons. Firstly they are widely
76 studied, being popular and easy to ID. We have lots of bird data, both contem-
77 porary and historical, for areas where we may be lacking data for other taxa. For
78 example, birds were the first taxa to be included on the Red List Index due to hav-
79 ing sufficient data (Butchart et al. 2004). Secondly, birds can be used as umbrella
80 species due to being wide ranging species (Suter, Graf, and Hess 2002), are varied
81 in their level of specialisations and are impacted by changes further down the food
82 chain in flora in insect communities (Burghardt, Tallamy, and Gregory, Shriver
83 2009). This means that they can potentially act as indicators for the health of the
84 community as a whole. Birds are undergoing large worldwide declines following
85 the same pattern as global declines (Pimm et al. 2006).

86 Several studies have been carried out trying to discern traits that can predict
87 either individual species threat/loss (Ameca y Juárez et al. 2014; Cardillo et al.
88 2004; Purvis et al. 2000) or community biodiversity loss (De Palma et al. 2016).
89 Using habitat level traits to predict biodiversity change is particularly powerful
90 as these habitat level traits (change in climate, land-use etc.) can be predicted

91 into the future. This means that where patterns are present those traits can be
92 used to predict biodiversity/species change into the future, which can in turn be
93 used to test future scenarios and inform policy (Newbold et al. 2015).

94 This study looks at three aspects of global, abiotic factors that may influence
95 biodiversity. Latitude represents geographical scale effects, accounting for habitat
96 variation and climatic variables, and has been shown to correlate with biodiversity
97 (Gaston 2000). Diversity is larger in the tropics than outside of them, and so it
98 is important to test for geographic variation. GDP is used as several human level
99 factors have been shown to influence biodiversity including inequality of wealth
100 and political instability (Hanson et al. 2009; Mikkelsen, Gonzalez, and Peterson
101 2007). Finally land-use intensity is included because habitat loss and fragmen-
102 tation are considered the leading causes of global biodiversity decline (Dirzo and
103 Raven 2004).

104 The aim of this study is firstly to determine whether biodiversity measures
105 that include a measure of evenness show different patterns in explanatory vari-
106 able, and so see if the extra data needed to calculate these measures is worth
107 collecting. Secondly this study aims to determine what, if any, factors correlate
108 with biodiversity in birds across the globe.

109 2 Methods

110 All species abundance data were collected from the 2016 public release version
111 of the PREDICTS database (Hudson et al. 2016). It consists of 3250404 species
112 records from 17650 sites over 370 studies, and contains data on the geography of
113 the records (mainly related to geographic position but also on the habitat of the
114 area) as well as land-use intensity of each site.

115 Using Python (Rossum 2016) and the package pandas (McKinney 2010) the
116 data were subsetting to only include avian abundance data (i.e. presence/absence
117 data were discarded). I also discarded any sites with fewer than 5 species for the
118 evenness calculations. This resulted in 49742 records from 2456 sites. The species
119 richness, reciprocal Simpson’s index and Shannon’s measure of diversity were
120 calculated for each site (hereafter referred to as Richness, Simpson and Shannon).
121 The reciprocal Simpson’s index was used to enable linear models to be used with
122 all three measures, as Simpson’s index is bounded and is thus non-normal. Each
123 site was given a weighting based on geographic realm to enable weighting in the
124 linear models, and each land-use class was given a value. These were:

- 125 1. Primary vegetation
- 126 2. Secondary vegetation
- 127 3. Plantation forest
- 128 4. Agricultural land (both pasture and cropland)
- 129 5. Urban.

130 I also calculated the Gross Domestic Product (GDP) of the country in which the
131 site was located, from the year of sampling (where sampling occurred over several
132 years this was the midpoint). The GDP values were obtained from The World
133 Bank Group (2018).

134 2.1 Modelling

135 All modelling was carried out in R v3.4.4 (Core Team 2019). The factors that
136 I included within the maximal model were Land-use class, Latitude (absolute
137 values, i.e. measures of distance from the equator) and GDP at year of study.
138 I did not include habitat patch area or years since fragmentation/conversion of
139 the patch although these data were available for 482 and 358 sites respectively,
140 because area data were largely only collected for primary vegetation sites (76%)
141 and only 87 sites have data for both factors. This would sacrifice statistical power
142 if the data were to be reduced to less than 4% of its size. I also included the
143 original study as a random effect, so that variation due to different sampling
144 techniques, recorders, time of year, study focus etc. would not mask other trends.

145 Both the Simpson and Richness measures were heavily right skewed (Simpson:
146 range = 1.2 to 130.9, median = 9.8 and mean = 12.7; Richness: range = 5 to 474,
147 median = 16, mean = 20.3) so these were log transformed for all further analyses.
148 I checked for normality of the three diversity measures using quantile-quantile
149 plots (via the ggqqplot() function from ggpubr (Kassambara 2018)), and as the
150 main portion of the points lay across the reference line normality was inferred. I
151 did not carry out shapiro-wilkes tests or other normality tests as with very large
152 sample sizes normality isn't required for parametric tests so a visual test was all
153 I deemed necessary.

154 Linear mixed models were fitted using the R package lme4 (Bates et al. 2015).
155 First a maximal model was used to test whether inclusion of study as a random
156 effect had a significant impact on the results, then it was used to test if weighting
157 by geographic realm had a significant impact on the results. This was done by
158 fitting linear (mixed) models to both hypotheses and using an anova and the AIC

159 values of the models to decide if there was a significant difference and which model
160 provided a better fit.

161 Linear mixed models were then fitted to every combination of explanatory
162 variables for each diversity metric. Akaike information criterion (AIC) values
163 (Akaike 1974) - a measure of goodness of fit - were calculated for every model,
164 and then converted to relative AIC values based on the smallest AIC. The R
165 package xtable (Dahl et al. 2018) was used to format the AIC tables for L^AT_EX.

166 2.2 Computing Languages

167 This project used 3 main coding languages to carry out the data manipulation,
168 analyses and to construct a reproducible workflow.

169 Python: Used for initial data manipulation, calculation of diversity metrics
170 and creating the final subsetted dataframe. Python was used as it
171 can handle large files more efficiently than R (the initial database was
172 2.7GB) and can apply functions to these large dataframes efficiently
173 by use of the pandas package.

174 R: Used for fitting the linear mixed models, calculating AIC values and
175 plotting the data. R was chosen as the lme4 package is useful for
176 fitting mixed models, and subsequently the inbuilt AIC() function can
177 be used directly on the mixed model. The package GGPlot2 also
178 makes creating attractive plots very simple.

179 Bash: Used to glue the workflow together so that the project becomes fully
180 reproducible. Using bash means that the L^AT_EX file could be compiled
181 with references directly as opposed to using subprocess modules in
182 Python.

3 Results

The final database contained data for 2456 sites from 49 studies, a total of 49742 bird species records.

Including species richness as a random effect accounted for a significant amount of variation (ANOVA, $p < 0.005$) and produces a better fitting model (AIC = 3918 with study and 5831 without using the maximal species richness model). When weighting by geographic realm, the AIC values produced were different enough that the uneven geographical distribution of sites must be producing biases in the results (AIC=3000 for non-weighted model and AIC=3918 for weighted model, again using the maximal species richness model). Geographic weighting was therefore included in all models despite not being significantly different to the unweighted model (ANOVA, $p=1$).

AIC values were calculated for each possible combination of variables (GDP at year of sampling, Latitude of site and Land-use intensity) for all three measures of diversity (Table 1).

Table 1: Relative AIC values for all variations of the linear mixed models for each diversity metric. All values are relative to the smallest AIC value (Richness, Latitude + Land-use intensity) for which AIC=3956. Values in brackets are the AIC relative to the smallest for that diversity metric. Values with a * are the best fitting models for that diversity metric.

	Δ AIC	Richness	Simpson	Shannon
Null Model	121		687(141)	350(142)
GDP	125		692(146)	355(147)
Land-use	0*		546(0)*	208(0)*
Latitude	129		694(148)	358(150)
GDP + Land-use	5		551(5)	213(5)
GDP + Latitude	135		701(155)	364(156)
Latitude + Land-use	8		553(7)	216(8)
Maximal Model	14		560(14)	222(14)

198 From these AIC values it can be seen that land-use intensity is the main
 199 explanatory variable for biodiversity. Models containing land-use intensity as a
 200 variable are the best fitting for all three measures, and for all metrics the best
 201 fitting model contains only land-use intensity - although the fit is very similar to
 202 both GDP + land-use and latitude + land-use models. We can also see that, in
 203 general, species richness fits the data the best followed by Shannon then Simpson.
 204 The general trend is of decreasing biodiversity as land-use intensity increases
 205 (Figure 1). Models not containing land-use intensity as a variable tend to fit less
 206 well for the evenness measures than for species richness (Table 1).

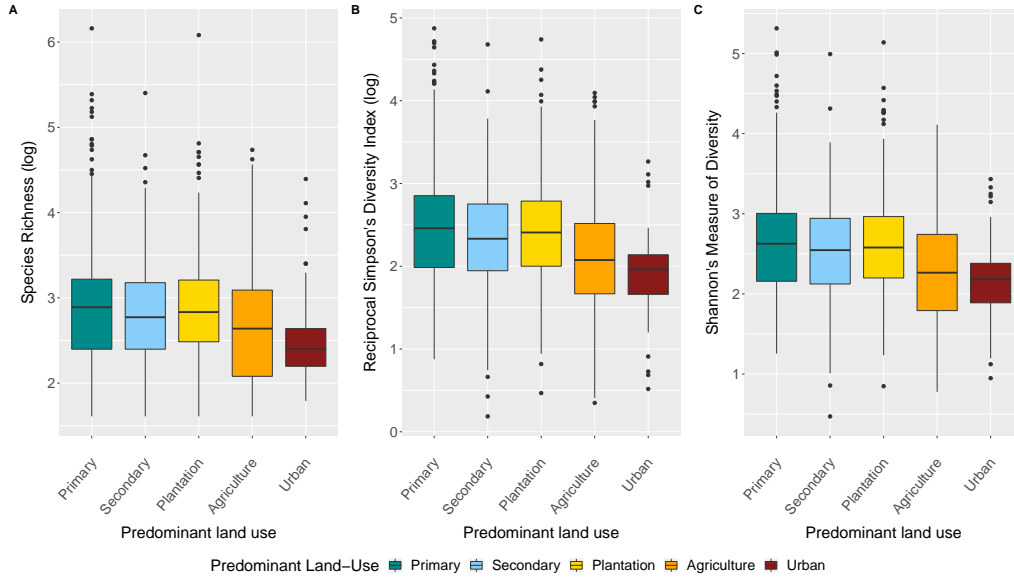


Figure 1: Site biodiversity across different land-use classes measured by A) species richness, B) reciprocal Simpson's Index and C) Shannon's measure of diversity.

207 4 Discussion

208 This study aimed to look at whether diversity measures that incorporated a mea-
209 sure of evenness can give us different outcomes from predictive models than species
210 richness alone. It also aimed to discern what variables can predict biodiversity on
211 a global scale.

212 4.1 Geographic Bias

213 Geographic bias has been shown to exist in many studies and papers, as most data
214 on biodiversity is collected where scientists live and work - primarily temperate
215 regions such as North America and Western Europe (Trimble and Aarde 2012) -
216 although threatend species have recieved more attention in recnet years (Roberts
217 et al. 2016). It has also been shown that these biases can influence attempts to
218 correlate biodiversity change with other factors as there can be interactive effects
219 (De Palma et al. 2016) such as Europe with has been largely without primary
220 forest for the last few hundred years in comparison to Central and South America
221 for which any habitat destruction is largely more recent.

222 I decided to follow a similar strategy to that of the weighted Living Planet
223 Index (Hudson et al. 2016) and weight each site so that the contribution of each
224 realm to the model was equal. This reduced the goodness of the fit of the model,
225 but mean that predictions made from the model are able to be applied globally.

226 Future studies could look at modelling each realm individually, which would
227 enable any differences between them to be more easily identified. It would also
228 mean that the predictions for each realm would be more precise. For this do be
229 achieved, more data needs to be acquired on the under-represented realms. For

230 example in these data 1166 sites were located in the Afrotropics, compared to
231 only 95 in Australasia.

232 4.2 Measures of Diversity

233 Species richness produced the best fitting models of all three measures. However
234 all three measures showed the same pattern of fit given the same combinations
235 of variables (i.e. models containing land-use intensity produced the best fit).
236 This suggests that there is little benefit to using measures of evenness instead of
237 species richness. Species richness contains less information about the community,
238 but from these models it appears that the predictive variables correlate mainly
239 to species richness rather than species composition. This is interesting, as several
240 studies have shown that dominance of some species increases and specialist species
241 decline with increasing habitat degradation (Devictor, Julliard, and Jiguet 2008).
242 What this study may be capturing, therefore, is the influx of generalist species and
243 invasive species to impacted areas (With 2004). In this case, looking more closely
244 at the species identities of a community to produce a measure of biodiversity could
245 produce different or varying strengths of predictive effects. It would also mean that
246 invasive species presence could be identified, a leading cause of Avian biodiversity
247 loss (Clavero et al. 2009) For example the Biodiversity Intactness Index (BII)
248 looks at species composition in pristine and impacted sites, and doesn't include
249 any species that are only present in the impacted site. Future studies could
250 look into this, and compare species richness to measures that take community
251 composition into account, as well as repeating this study for other taxa to see if
252 the same trends exist.

253 4.3 Predictive Variables

254 Land-use change in the form of habitat loss and fragmentation has been identified
255 as the leading cause of biodiversity and species loss both globally and in birds
256 (Gaston, Blackburn, and Klein Goldewijk 2003; Dirzo and Raven 2004). This
257 study confirms that finding, models that included land-use intensity more accu-
258 rately fit the data than those that didn't. The best model fit land-use alone, but
259 the fit was only minorly worse when including GDP, latitude, or both. This shows
260 that including GDP and latitude does not explain much meaningful variation, and
261 so they are not significant predictive variables of local biodiversity.

262 Three factors that are closely related to land-use intensity are the amount of
263 time since any land-use change, the size of the area and distance to the nearest
264 disturbed or undisturbed habitat. Edge effects, extinction debt and spillover
265 effects are all factors that can be hugely impactful on a community that has been
266 impacted by land-use change (Banks-Leite, Ewers, and Metzger 2010; Ford et al.
267 2009; Robinson et al. 1995). These factors were measured for some data in this
268 database, but unfortunately not enough to include in the model. Future studies
269 could focus on obtaining these data, as including them in models could show that
270 land-use is not in fact the most important determining factor. Also expanding
271 this to non-Avian species may also produce different results, birds are a highly
272 mobile taxa and so issues such as fragmentation tend to impact them less than
273 others such as reptiles (Keinath et al. 2017; Villard and Taylor 1994).

274 Conclusion

275 This study has shown that both species richness and measures of evenness are
276 useful measures of biodiversity. Species richness provides an easy way to assess a

community, and can produce predictions that are more precise than other measures. It may miss some patterns that measures of evenness are able to capture, but the difference does not seem significant enough to warrant the extra effort needed to measure evenness. Additionally using only species richness data allows the use of presence/absence data, and so increases the pool of data available for meta-analyses.

Land-use intensity was shown to be the single most important factor in predicting differences in biodiversity. This is consistent with other studies and the view that habitat loss and fragmentation are the largest threats to this planet's biodiversity at this time. Future studies should focus on determining if there are geographic differences in effect sizes of predictive variables and the predictive variables themselves. It would also be useful to investigate other measures of biodiversity, such as looking more closely at species composition.

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