

1 **Mapping and understanding the digital biodiversity knowledge about vertebrates in the**  
2 **Atlantic Rainforest**

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15

## Abstract

16 Biodiversity data are fundamental for macroecological studies. Recent efforts on gathering  
17 global data have not been sufficient to surpass biases and gaps. This incompleteness has serious  
18 consequences on conservation and ecological understanding, therefore it is of major importance  
19 to map, quantify and describe these flaws. In this paper we aimed to assess inventory  
20 incompleteness for the Atlantic Rainforest, concerning amphibians, birds, mammals and reptiles.  
21 We also investigate if some environmental variables are correlated to biodiversity knowledge.  
22 Our results suggest that this biome is not well known, with clusters of quality information near  
23 big conservation centres. Environmental variables commonly referred to as indicators of species  
24 richness were not correlated to inventory completeness, but when only well-sampled units were  
25 analysed, mammals' rarefaction slopes could be considered correlated with potential  
26 evapotranspiration. Impacted regions which are underexplored need urgent investments in  
27 sampling efforts so we can know the real biodiversity of this biome and efficiently measure  
28 environmental impacts.

29

30 Keywords: inventory completeness, rarefaction curves, data bias, Atlantic Rainforest.

31

## 32 **Introduction**

33 Information about life diversity and distribution is a fundamental tool for understanding  
34 evolutionary and ecological processes (Graham et al. 2004; Rocchini et al. 2011; Jetz et al. 2012;  
35 Ladle and Hortal 2013; Meyer et al. 2015). Since the 19th century, naturalists, taxonomists and,  
36 more recently, citizen scientists have been collecting global biodiversity information, resulting in  
37 the current knowledge of species' distribution on the planet (Humboldt et al. 1850; Hawkins  
38 2001; Willig et al. 2003; Chase 2012). Museum data has been stored in electronic catalogues at  
39 slow pace since the 1970's and more recently has been connected through web-based initiatives,  
40 improving biodiversity data gathering (Graham et al. 2004). As a result, we now have big  
41 databases such as Global Biodiversity Information Facility (GBIF; <http://www.gbif.org/>) and  
42 Map of Life (<https://mol.org/>) providing accessible and extensive information on biodiversity,  
43 compiling museum, survey and observation data (Graham et al. 2004; Jetz et al. 2012; Beck et al.  
44 2013). However, despite these recent efforts, our knowledge on species diversity and distribution  
45 is still biased and full of gaps due to the complex nature of these information (Brown and  
46 Lomolino 1998; Whittaker et al. 2005). These shortfalls have been recently revised (Hortal et al.  
47 2015) and there are growing evidence that they can compromise ecological, evolutionary and  
48 conservation analyses (IUCN 2012; Ladle and Hortal 2013; Ficetola et al. 2014; Hortal et al.  
49 2015).

50 The wallacean shortfall (the lack of information about species real distribution) is present  
51 in every spatial and temporal scales (Whittaker et al. 2005; Hortal 2008; Hortal et al. 2015) and  
52 is a consequence of a myriad of biological, environmental and social factors. Characteristics of  
53 the species (such as crypsis, its natural history and behaviour), political borders and topography,  
54 for example, can lead to biases in biodiversity surveys and form gaps in information. On the

55 other hand, clustered information also can lead to biased surveys, since researchers may prefer to  
56 assess places knowingly species-rich or that are undergoing a process of ecological change  
57 (Boakes et al. 2010; Ahrends et al. 2011; Rocchini et al. 2011; Yang et al. 2014). Information  
58 gaps may also be a consequence of data quality decay in space (e.g., when we extrapolate the  
59 distribution of a species based on polygons or species distribution models) and time (due to  
60 taxonomic reviews, climate change, land use, habitat loss, extinction and migration) (Ladle and  
61 Hortal 2013). Therefore, the measurement of geographical variation of biodiversity on the planet  
62 (represented by distribution maps) has an error associated that must be assessed (Hortal 2008;  
63 Rocchini et al. 2011; Ladle and Hortal 2013; Yang et al. 2013).

64         The acknowledgement of error in biodiversity information is of major importance. The  
65 underestimation of species distribution can have consequences in conservation planning, since  
66 range restriction is a classification criterion of species in risk of extinction (IUCN 2012; Ladle  
67 and Hortal 2013; Ficetola et al. 2014; Hortal et al. 2015). Furthermore, bias can influence and  
68 even reverse ecogeographical patterns, leading us to associate certain factors to species richness  
69 when they are only proxies for sampling quality (Ficetola et al. 2014). It has been recommended  
70 to include maps of ignorance in the results or to map data quality and use only well sampled  
71 locations on analyses (Hortal 2008; Ladle and Hortal 2013; Ficetola et al. 2014; Yang et al.  
72 2014). Once researchers are aware of the error in their data sets, they can try to correct or  
73 diminish it and better analyse the results. This practice, in addition to guide future researches,  
74 produces more reliable results, since the exact measure of uncertainty clarifies how explicative  
75 an inference can be.

76         There is a growing interest in biodiversity data biases in literature (see Boakes et al. 2010;  
77 Yang et al. 2013; Sousa-Baena et al. 2014). Nevertheless, studies mapping South American

78 under-sampled sites are relatively few. This is worrying especially for the Atlantic Forest since it  
79 is an important biodiversity and socio-climatic hotspot (Scarano and Ceotto 2015). Human  
80 activities and the growth of urban centres have reduced its original area to only 8% (Galindo-  
81 Leal and Câmara 2003; Scarano and Ceotto 2015), resulting in substantial loss of habitat.  
82 Conservation units can decelerate this process, but their implementation need good biodiversity  
83 data. The Atlantic Rainforest is also a good model for ecological and evolutionary research  
84 because of its large latitudinal and altitudinal range, high endemism, variation in temperature  
85 and precipitation, and historical connexion with other biomes (Silva and Casteleti 2003; Ribeiro  
86 et al. 2009; Batalha-Filho et al. 2013). Furthermore, its natural resilience allows the persistence  
87 of biodiversity and it hosts 1-8% of the world's total species (Silva and Casteleti 2003).  
88 Therefore, biodiversity data biases must be studied in the Atlantic Forest in order to provide  
89 good quality inputs for all of these applications and guide new surveys.

90         Given that the Atlantic Rainforest is a biodiversity hotspot, with a high rate of  
91 deforestation, it becomes urgent to describe and map the digital accessible knowledge gaps in  
92 this ecoregion. Here we aim to map and quantify these gaps with occurrence data of terrestrial  
93 vertebrates, and to identify environmental variables that may be related to these shortfalls (mean  
94 annual temperature, altitudinal range, potential evapotranspiration and vegetation). We expect  
95 that regions with high environmental heterogeneity and productivity would attract more  
96 researchers because of their relationship with high biodiversity.

## 97 **Methods**

98         The inventory completeness of Atlantic Rainforest fauna was analyzed for amphibians,  
99 birds, mammals and reptiles. We used occurrence data from the Global Biodiversity Information  
100 Facility (on 20 June 2015), which was downloaded by classes' names, using geometric filtering

101 and excluding fossil records. We excluded records dated before 1900 and marine animals, as  
102 well as incomplete taxonomic identifications (when the taxon was not monospecific). We also  
103 merged infraspecific taxa to species level. After that, we checked scientific names for validity  
104 using the “taxize” R package (Chamberlain and Szöcs 2013; Chamberlain et al. 2014), based on  
105 Catalogue of Life (<http://www.catalogueoflife.org/>), National Center for Biotechnology  
106 Information Taxonomy Database (<http://www.ncbi.nlm.nih.gov/taxonomy>), AmphibiaWeb  
107 (<http://amphibiaweb.org/>), Avibase (<http://avibase.bsc-eoc.org/>), Handbook of the Birds of the  
108 World Alive (<http://www.hbw.com/>), Mammal Species of the World (3<sup>rd</sup> edition,  
109 <http://vertebrates.si.edu/msw/mswcfapp/msw/index.cfm>) and The Reptile Database  
110 (<http://reptile-database.reptarium.cz/>). We filtered the remaining occurrence points by the  
111 Atlantic Rainforest domain *sensu* Olson et al., 2001 (Olson et al. 2001) (Fig. 01) and then  
112 assessed species richness and number of occurrences for grid cells of 60 arc-minutes (110km at  
113 Equator) (Fig. 2), which we used for calculating inventory completeness.

114 Two approaches were used to evaluate inventory completeness on Atlantic Forest: the  
115 species accumulation curve for the whole region followed by the analysis of its final 10% slope  
116 (Yang et al. 2013), and a rarefaction method for each sampling unit (SU), also assessing the  
117 sample slope. The species accumulation curve is a sample-based method for assessing sampling  
118 effort and estimate species richness (Colwell and Coddington 1994; Gotelli and Colwell 2001).  
119 This approach was performed with the method ‘exact’ of the function ‘specaccum’ and the final  
120 10% slopes were extracted with function ‘specslope’ in the R package VEGAN (Oksanen et al.  
121 2015). The output of this function was analysed according to Yang et al. (Yang et al. 2013) and  
122 slopes  $> 0.05$  were considered as indicators of inventory incompleteness (Fig. 3). Rarefaction  
123 curve is an individual-based method that represents the sampling effort needed to reach total

124 estimated richness within an area (Gotelli and Colwell 2001). The ‘rarefy’ and ‘rareslope’  
125 functions calculate the rarefaction and slopes of each SU, both operating in the same package  
126 abovementioned.



127  
128 **Figure 1 – The Atlantic Rainforest *sensu* Olson et al. 2001 and its main conserved areas**  
129 **(Serra do Mar and Iguazu).**

130 Additionally, we investigated if four environmental variables were correlated with  
131 inventory completeness. These variables were chosen based on previous studies indicating their  
132 influence on data bias or if they are commonly mentioned as proxies for species richness (Currie  
133 1991; Sánchez-Fernández et al. 2008; Toranza and Arim 2010; Martin et al. 2012; Ficetola et al.

134 2014; Vasconcelos et al. 2014; Yang et al. 2014). We used annual mean temperature and  
135 altitudinal range downloaded from WorldClim (Hijmans et al. 2005; <http://www.worldclim.org/>;  
136 resolution 10'), potential evapotranspiration (PET) data from the Consortium for Spatial  
137 Information of the Consultative Group for International Agricultural Research (Trabucco and  
138 Zomer 2009; <http://www.cgiar-csi.org/>; resolution 30"), and Normalized Difference Vegetation  
139 Index (NDVI) from NASA's Earth Observatory Group (Stockli 2015). These last two variables  
140 and temperature represent ecosystems' energy income, while altitudinal range represents  
141 topographical and, therefore, habitat homogeneity. All variables were also rescaled to 60 arc-  
142 minutes resolution grids.

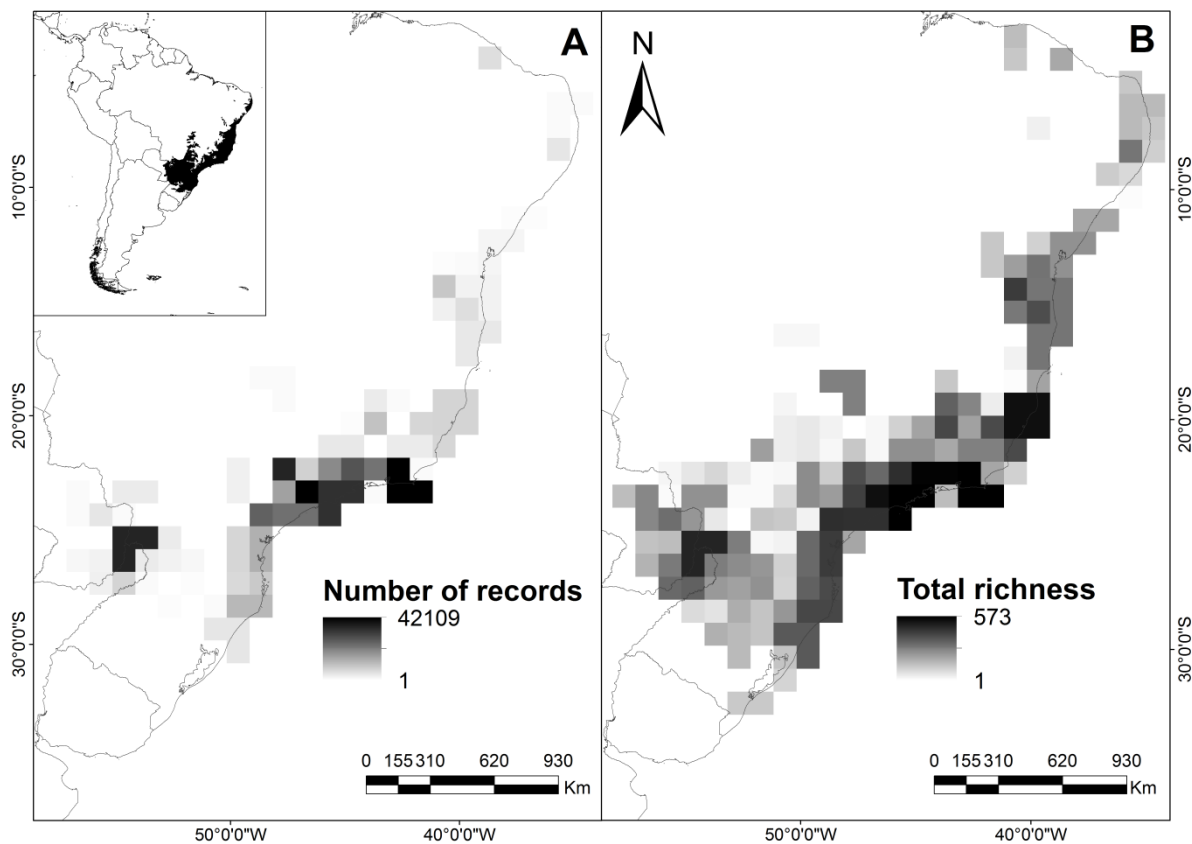
143 We performed Pearson's correlation tests between the final 10% of each class's slopes  
144 (extracted from the 'rareslope' function) and environmental variables, both for the whole study  
145 area and only for the sample units considered well sampled. This procedure was repeated for  
146 total observations and the rarefaction slope considering total species richness. Statistical  
147 analyses were performed using the computing environment R 3.4.0 (R Development Core Team  
148 2017).

## 149 **Results**

150 The terrestrial vertebrate biodiversity of the Atlantic Rainforest is not well known,  
151 according to our results. All the species accumulation curves had a final slope higher than 0.8  
152 (Table 1), indicating that the biome is still sub-sampled according to GBIF. After data processing  
153 and cleaning, the database comprised 143 sampling units and 169472 records, 85.2% of which  
154 was from bird occurrences. Mammalian, amphibian and reptile classes represented 7.71%, 6.27%  
155 and 0.81% of the records. The same pattern was identified for species richness: from 17875  
156 species, 84.7% were birds, 5.3% were mammals, 6.7% were amphibians and 3.2% were reptiles.



157 Both total occurrences (Fig. 2A) and total species richness (Fig. 2B) were clustered in  
158 southeastern Brazil (Serra do Mar) and northeastern Argentina (Iguazu).



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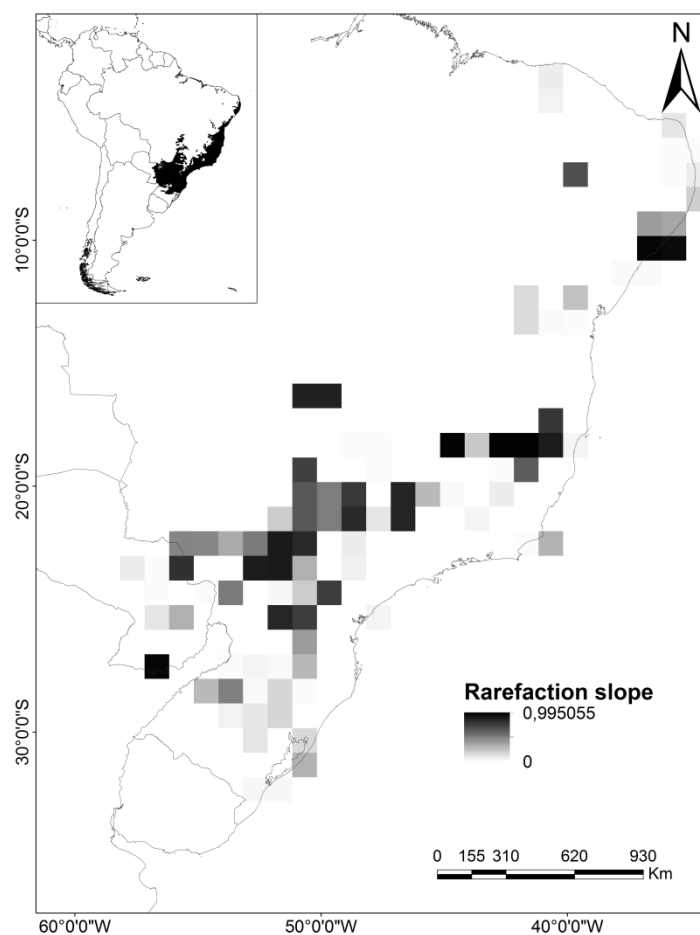
160 **Figure 2 – Distribution of sampling effort (A) and total species richness (B) for the four**  
161 **groups.**

162

163 **Table 1- Inventory completeness for all the Atlantic Rainforest. Slopes close to 1**  
164 **characterizes a growing curve, which indicates that much sampling effort is still needed to**  
165 **reach the actual richness. Slopes close to 0 indicate that the species accumulation curve**  
166 **reached its asymptote and the probability of finding new species is low (Yang et al. 2013).**

<b>Richness</b>	<b>Slopes of the last 10% of the rarefaction curves</b>
Total	0.995
Amphibians	0.992
Birds	0.998
Mammals	0.790
Reptiles	0.924

167 Rarefaction slopes for each SU corresponding to total records varied from 0 to 0.99, with  
168 a median of 0.19. Only 31.47% of the Atlantic Rainforest could be considered well sampled  
169 according to the threshold of 0.05 applied by Yang et al. (2013) (Fig. 3). When each class was  
170 assessed separately, the amount of well sampled SU varied from 6.99% for birds to 0% for every  
171 other class.



172  
173 **Figure 3 – Map of inventory completeness for the Atlantic Rainforest. Only sampling units**  
174 **with slopes between 0 and 0.05 are considered well sampled.**

175 There was no significant association between corrected variables either using all the  
176 knowledge of the whole biome or only the well known regions. However, the mammalian

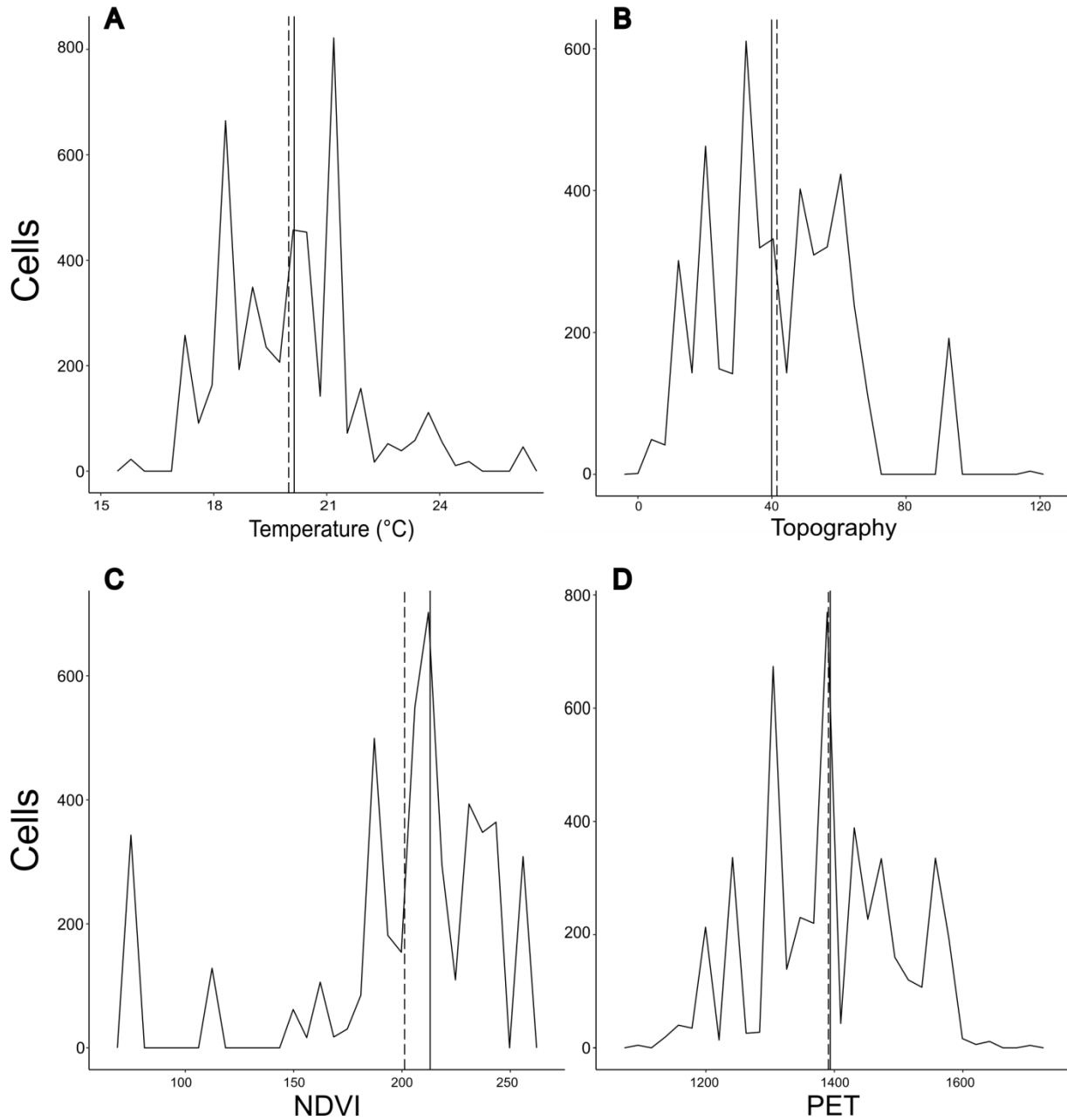
177 inventory completeness was significantly correlated to potential evapotranspiration ( $R = -0.3$ ,  $p$   
 178  $= 0.048$ ) (Table 3). There was little difference in the environmental characteristics of the SU  
 179 when only the well sampled cells were analysed (Fig. 04). Nevertheless, all variables means  
 180 were lower in these regions, except for the terrain roughness index, which was slightly higher at  
 181 well sampled units (Table 04).

182

183 **Table 3 – Pearson’s correlation coefficient (R) between environmental variables, species**  
 184 **richness and slopes of the rarefaction curve for all vertebrates and for each class, both in**  
 185 **the whole study area and only in the sample units considered well sampled (slope $\leq$ 0.05).**  
 186 **All correlations were statistically significant ( $p < 0.01$ ). There are empty cells when there are**  
 187 **no well sampled units for that class.**

All cells						
	Total observations	Slopes				
		Total richness	Amphibians	Birds	Mammals	Reptiles
PET	0.20	0.05	0.12	0.14	-0.26	0.10
NDVI	0.27	-0.03	0.25	-0.04	-0.18	0.22
Temp.	-0.22	0.19	0.24	-0.27	-0.34	-0.04
Topog.	0.09	-0.18	-0.37	-0.29	0.35	0.20

Only well-sampled cells						
PET	0.24	-0.19	-	0.12	-	-
NDVI	0.28	-0.02	-	-0.49	-	-
Temp.	-0.18	-0.14	-	0.08	-	-
Topog.	0.04	0.38	-	-0.49	-	-



189

190 **Figure 4 – Frequency distribution of temperature (A), topography (B), NDVI (C) and PET**191 **(D) values on well sampled units. Means are represented by dashed lines, while medians are**192 **solid lines.**

193

194

195 **Table 4 – Differences in variables means between all cells and only well sampled units**  
 196 **(WSU).**

Variable	All cells (mean)	WSU (mean)	T-test		
			t	df	p
Temperature	20.036	19.990	12.517	950620	<0.01
Altitude	40.999	41.484	-12.039	950270	<0.01
NDVI	201.406	201.213	2.0753	949620	0.038
PET	1393.420	1390.767	11.584	950650	<0.01

197

## 198 Discussion

199

200 There is a natural tendency for natural history studies being made at knowingly  
 201 biodiverse locations. A study with the Brazilian flora aimed to identify sites with insufficient  
 202 sampling in order to guide future survey efforts. They used a Brazilian database, speciesLink  
 203 (<http://www.splink.org.br/>) and metrics of inventory completeness as described by Colwell &  
 204 Coddington (Colwell and Coddington 1994). Well preserved sites close to important research  
 205 centres were pointed as well-sampled: three of the highest scores in inventory completeness are  
 206 located in the Atlantic Rainforest (Sousa-Baena et al. 2014). This may be the case of our data.  
 207 Well-known SU are located in areas with a few large or several small protected areas, such as the  
 208 Iguazu (Argentina-Brazil) and Serra do Mar region (Brazil) (Fig. 1; Fig. 03). Additionally, our  
 209 analyses indicated that potential evapotranspiration (PET) and the normalized difference  
 210 vegetation index (NDVI) can explain 20-27% of the variation in records frequency, but they  
 211 explain almost nothing in the variation in species richness (Tab. 3). This reinforces our

212 hypothesis that highly known and predictably biodiverse areas (based on environmental  
213 variables, such as preserved vegetation) are being frequently visited, but biodiverse sites with  
214 little vegetation may have been ignored. There are also indications that researchers are choosing  
215 places that do not represent the Atlantic Rainforest's environmental variability (Tab. 4). . Some  
216 social variables which also characterize these mentioned regions, such as the number of research  
217 centres, accessibility and infrastructure, can also help explain these biases (Ficetola et al. 2014;  
218 Yang et al. 2014).

219         Sampling bias can have serious consequences in conservation and ecological  
220 understanding. For instance, a study with the diverse Chinese flora tried to quantify inventory  
221 incompleteness and evaluate the influence of database biases in ecological analyses. They found  
222 that 91% of Chinese counties do not have complete inventories and this affected the explicative  
223 power of predictive environmental variables (Yang et al. 2013).

224         However, this “feedback” causes a practical paradox: a well studied site may highlight a  
225 certain area if it is recognized as biodiverse; subsequently, protected areas typically attract more  
226 research while undersampled sites are ignored by funding projects (Ahrends et al. 2011; Boakes  
227 et al. 2016). Some protected areas achieved that status because of other several reasons to protect  
228 a site, such as its natural beauty, its cultural value, its geological conformation or its importance  
229 to the ecosystem (Margules and Pressey 2000; Yang et al. 2014). Nevertheless, even when  
230 reserves aim to protect things other than species, they may create an opportune place for  
231 biodiversity research.

232         Local or private data sources could add important information and allow a more precise  
233 representation for the Atlantic Rainforest. There are important independent national databases in  
234 Brazil that could add substantial information to the global biodiversity knowledge, such as



235 speciesLink and “Portal da Biodiversidade” (<https://portaldabiodiversidade.icmbio.gov.br>). On  
236 the other hand, the process of transferring data from natural history collections to online  
237 databases is naturally slow and is not a solidified activity yet because it requires trained  
238 technicians and infrastructure (Sousa-Baena et al. 2014). Also, there is a growing overlap  
239 between local and global databases, which leads us to think that, in the near future, researchers  
240 will take a “shortcut” and feed global databases directly.

241         There is a major need for sampling effort in non-protected sites, with intense human  
242 activities. The inventory completeness tended to be lower in sites knowingly fragmented, such as  
243 the Brazil’s Northeast and central region (Fig. 3). These are regions highly explored by the  
244 tourism industry and farmers, with neglected environmental policy. The assessment of  
245 biodiversity in those places is important in order to accurately measure human impact on nature.  
246 As highlighted by Martin et al., a great amount of ecological knowledge is based on a narrow  
247 variety of ecosystems, since researchers tend to study only well preserved sites (Martin et al.  
248 2012; Boakes et al. 2016). These biases surely difficult our perception of patterns and real  
249 impacts (Ficetola et al. 2014).

## 250 **Conclusion**

251         The Atlantic Rainforest fauna is not well known by the scientific community. Our  
252 analyses suggest that the current digital accessible knowledge is insufficient about its  
253 biodiversity and there is a bias towards two remarkable areas: Iguazu and Serra do Mar, which  
254 are known for their protected areas.

255         We could not indicate an environmental variable that would be related to this bias. Social  
256 variables might explain better this trend, once well sampled sites are located close to populated  
257 areas and research centres, in addition to the conservation actions aforementioned.

258           Despite the flaws of GBIF data, it still is one of the best tools available for  
259 macroecological studies. A reasonable practice would be use more than one data source when  
260 feasible. The user must be aware of its incompleteness and profoundly analyse its errors,  
261 especially when dealing with species distribution modelling. On the other hand, users are also  
262 responsible for furnishing good quality, open access data. The expectation is that this  
263 incompleteness will be soon bypassed.

264

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