

Is my sdm good enough? insights from a citizen science dataset in a point process modeling framework

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Is my SDM good enough? Insights from a citizen science dataset in a Point 1 **Process Modeling framework** 2 3 Authors: Camila LEANDRO, Pierre JAY-ROBERT, Bruno MERIGUET, Xavier HOUARD, Ian 4 RENNER 5 Corresponding author: Camila LEANDRO camila.leandro@cefe.cnrs.fr; Bat. J. Dpt. BEE, 6 Université Paul-Valéry Montpellier 3, 34199 Montpellier, FRANCE 7 Affiliations: Camila LEANDRO [orcid.org/0000-0003-1153-326X] and Pierre JAY-ROBERT: CEFE, Univ. Paul 8 9 Valéry Montpellier 3, Univ. Montpellier, EPHE, CNRS, IRD; Montpellier, France Bruno MERIGUET and Xavier HOUARD: Office pour les Insectes et leur Environnement 10 11 (Opie), BP 30, 78041 Guyancourt cedex, France 12 Ian RENNER: School of Mathematical and Physical Sciences, The University of Newcastle, Australia 13 Abstract and keywords 14 15 Citizen science programs, and particularly atlas schemes based on opportunistic biological records, are very important sources of data for species distribution models and 16 17 conservation. Nevertheless, these data are prone to bias, particularly when they come from 18 less popular or hard to detect/identify species, such as insects. With such biased data, it is 19 important to evaluate the stability of the model predictions. In recent years, point process 20 models (PPMs) have shown their strength as a unifying framework to fit presence-only 21 species distribution models with many advantages in model implementation and 22 interpretation; PPMs are closely connected to methods already in widespread use in ecology

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such as MaxEnt and to logistic regression and benefit from being more transparent about

resource selection and absence handling. Moreover, there is a well-developed set of tools to

fit these models and assess various features of the underlying model, including model

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26 stability. However, such tools are currently unavailable when point process models are fitted 27 with a lasso penalty, which has been shown to improve predictive performance. Based on 28 the French citizen science program "Stag beetle Quest", we propose new methods to assess 29 model stability in this context. The ultimate goal was to develop a set of functions to analyze 30 PPM models with lasso penalties fitted with presence-only data. To assess model stability, 31 we randomly sampled different subsets of locations with varying size from the whole dataset 32 and used the proposed tools to compare fitted intensities and model coefficients. All the 33 developed measures are complementary and can be used to identify at what number of 34 point locations the model stabilizes, which will be dependent on the dataset. Our work 35 presents a new toolbox to explore questions around model stability based on the number of 36 locations in the context of point process models with a lasso penalty and confirms once 37 more the use of the point process modelling framework as a flexible and unifying framework to fit presence-only species distribution models. 38

Key-words: Species distribution models; Point process models; LASSO; diagnostic tools; R
functions; Lucanus cervus

41 *I. Main text*

42 **1. Introduction**

To be able to estimate accurately the decline of biodiversity, we need to be equipped with reliable tools and methods allowing a good characterization of population trends. Methods should provide a picture of the distribution of species through space and time from data which represent a subsample of the true species populations. This is especially necessary for

47 organisms that are hard to detect in their environment, such as insects (Donaldson et al.
48 2017; Leandro et al. 2017).

Species distribution models (SDMs) have become important methods to inform policy makers and conservation practitioners about biodiversity trends. Mapping the patterns of biodiversity, SDMs can be used in land use planning, leading to prioritization of conservation strategies (Devictor et al., 2010; Guisan et al. 2013). They have also been put forward as pivotal tools for the appropriate evaluation of conservation status of insects (Diniz-Filho et al., 2010; Cardoso et al., 2011; Leandro et al., 2017).

55 In order to fit a SDM, a substantial number of recorded locations is typically necessary. One 56 source of data that can be used to fit an SDM is a list of locations found in biodiversity atlas 57 schemes and citizen science programs, but such data involve the attendance of particular 58 questions related to the observation process (Alabri, 2010; Isaac & Pockok, 2015; Powney & 59 Isaac, 2015). Indeed, data can come in a number of formats, the two most common being: 60 (1) presence-absence data, which implies a clear sampling protocol and a greater effort from 61 the observer when cryptic species are considered and (2) presence-only data. Presence-only 62 data are cheaper and consequently more widely available than presence-absence data. 63 However, they are more prone to bias due to the way they are collected: presence-only data 64 can be opportunistic observations whose distribution is highly correlated with the 65 observation process (Warton et al. 2013; Guillera-Arroita, 2017).

Let us put ourselves in the place of a practitioner wanting to model the distribution of a species whose observations come from citizen science with presence-only data. Let us say that the ecology of the species is relatively well known. First we have to address the question "Which is the best statistical framework to model my data?" This question has

70 been largely explored (Aguirre-Gutiérrez et al. 2013; Guillera-Arroita et al. 2015; Duque-Lazo 71 et al. 2016) and in recent years, point process models (PPMs) have shown their strength as a 72 unifying framework to fit presence-only species distribution models (SDMs) with many 73 advantages in model implementation and interpretation, which can be obscured in popular 74 software platforms such as MaxEnt (Renner et al. 2015; Stirling et al. 2016). Indeed, easy to 75 use "click-button" platforms such as MaxEnt (Philips et al. 2017) and the Biomod R package (Thuiller et al. 2009) have been described as "black box techniques" because users can 76 77 ignore the details and nuances of their models and default parameters (Renner & Warton 78 2013; Ahmed et al. 2015; Philips et al, 2017). Point process models, on the contrary, let the 79 user have complete control over what its being modelled (Renner et al. 2015). In particular, 80 PPMs provide clearer interpretations of the model output as an intensity of reported 81 observations per unit area and as well as clarity regarding necessary choices to implement 82 presence-only models such as the choice of quadrature points (also referred to as "pseudo-83 absences" or "background points").

84 Then comes the crucial question "do I have enough data to model the distribution of the 85 species?" (Virgili et al. 2018), a question that is not new and which can be translated into the 86 important matter of "trust in models" or model accuracy and particularly in their specific 87 contexts (Stockwell & Peterson 2002; Guillera-Arroita et al. 2015; Ross et al. 2015). When fitting a point process model, we estimate the intensity of species records as a function of 88 89 the chosen environmental covariates. The stability of this intensity surface depends not only 90 on the number of records, but also on the choice of covariates used to characterize it. 91 Indeed, reducing the number of candidate variables helps to explain which biological factors 92 are important in determining a species' distribution. For example, MAXENT software by default uses a Lasso penalty, which shrinks parameter estimates $\hat{\beta}$ toward zero. While the 93

Lasso penalty is known to improve predictive performance and give numerical stability, the default penalty chosen by MAXENT software is *ad hoc*; the choice of the penalty criterion can have consequences in model interpretation, as reducing the number of candidate variables helps to explain which biological factors are important in determining a species' distribution, but some criteria impose larger penalties than others (i.e. BIC, MSI) (Renner, 2013).

100 In the point process framework, the 'spatstat' package (Baddeley & Turner, 2005; Baddeley 101 et al., 2015) offers a number of tools to test model reliability, including significance levels for 102 implemented variables and standard deviations of the predicted intensity. However, in 103 spatstat, regularization tools aimed at boosting predictive performance through reducing 104 model complexity, such as Lasso penalties, are not available. In the PPM-lasso framework of 105 the 'ppmlasso' package, a number of Lasso-type penalties are included in order to shrink 106 coefficients of point process models in a data-driven way, which tends to provide superior 107 predictive performance to MAXENT (Renner & Warton, 2013). Nevertheless, there are no 108 tools to explore model stability within the PPM-lasso framework.

109 Our goal was to develop a toolbox analogous to that of the 'spatstat' package, therefore 110 writing new functions to explore model stability for models fitted with the ppmlasso package 111 that would expand the toolkit for practitioners and researchers who want to have more 112 control over their models. Based on the French citizen science program "En quête d'insectes 113 ! Lucane cerf-volant" or "Stag beetle Quest", we explored different methods to assess model 114 stability (or the capacity to predict correctly all presence data) within the PPM perspective 115 fitted with a lasso penalty and observer bias corrections. Thanks to the extensive dataset 116 offered by this dynamic program, we used random subsets of increasing size to test the

stability of models fitted with varying numbers of points in order to determine whether the model fitted with all points could be considered to have stabilized. Such methods will contribute to an increase in the usage of SDM for a wider audience of practitioners as we provide a toolbox of different R functions which may be used to explore stability of models fitted with the ppmlasso package. We present a detailed tutorial as supplementary material demonstrating usage of these functions and interpretation of their output. By doing so, we also conducted an ecological analysis of the distribution of *Lucanus cervus* in France.

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2. Materials & Methods

125 2.1 Data

Species records were obtained from the Stag beetle Quest citizen science program launched in 2011 and managed by the Office for the Insects and their Environments (Opie) (Meriguet *et al.*, 2012). The program is focused on the French distribution of *Lucanus cervus* (Linnaeus, 1758) (Insecta, Coleoptera) and contains more than 16,000 records from 1905 onward. Data from before 2011 come from contributors who entered old records through the Stag beetle Quest online form. The database is composed of ~90 % presence-only data of which ~ 82 % of the records have a precise location.

The data retained for the study correspond to a recent and highly active period of observation (from 2007 to 2017) (Fig. 1a), thereby reducing the temporal heterogeneity of the dataset. Only verified observations (photography-based validation made by experts) were used, leaving a total of 2576 point locations.



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Figure 1. Point locations of the data used for the analysis. Map made by © OpenStreetMapcontributors

140 Saproxilic beetles are species which are involved in or dependent on wood decay; in some 141 European forests, the Lucanidae family presents the highest percentage of indicator species 142 for dead-wood amount and temperature (Lachat et al. 2012). Indeed, like other exothermic 143 insects, their life traits and abundance is related to climatic variables; additionally, as adult 144 activity has been considered as weather-dependent (Fremlin & Fremlin 2010), we 145 hypothesized that their sightings (observations) would be as well. Therefore, to model the 146 distribution of Lucanus cervus, we used six environmental variables : 2 climate variables 147 from WorldClim (Hijmans et al. 2005; Fick & Hijmans 2017) and four land use variables from 148 the Corine Land Cover (2012) and Hilda databases (Fuch et al. 2013-2014-2015) (Table 1); 149 Climatic variables were modelled with linear, interaction and quadratic terms, while land 150 use (defined as proportion of the landscape cover within grid cells) and observer bias 151 variables were entered as linear terms leading to a total of 10 covariates.

152 Variables were chosen based on the literature (Thomaes et al. 2008; Hawes 2008; Irmler et 153 al. 2010; Frank et al. 2017) and our expertise, and verified if in the suite of variables no two 154 variables have a Pearson correlation $R \ge 0.7$. Because presence-only data are prone to 155 observer bias, in which the observed pattern of points reflects not only the distribution of 156 the species but also the distribution of the observers, we added an "observer bias" variable. 157 It is common to use distances to roads or to natural areas for this purpose (Renner et al. 158 2015; Fisher-Phelps et al. 2017), nevertheless in our particular case, points seemed to be 159 clustered around cities, which led us to include the natural logarithm of human population 160 density as an observer bias variable, assuming that the species was reported more when 161 human population density was higher. Therefore we included the human population variable 162 from the SEDAC dataset (2016). All variables were available at 1 km x 1 km resolution (Table 163 1).

Table 1. Complete information of the environmental and bias variables included in the model. The climatic and human population variables' resolutions are 30 arc-seconds (approximately 1 km at the equator).

	Туре	Model form	Covariate	Source
Environmental covariates		Linear,	Mean annual Temperature (Bio 1)	
	Climatic	Quadratic	Unit: Celsius degrees (°C)	Bioclimatic variables from
		Linear,	Mean annual Precipitation rate (Bio12)	- Worldclim (2017)
		Quadratic	Unit: millimeter (mm) Resolution ~1 km ²	
		Interaction term	Mean annual temperature * Mean annual precipitation rate	-
		Linear	Percentage of broad-leaved forest cover in a 1km radius	Corine Land Cover (2012)
		Linear	Percentage of coniferous forest cover in a 1km radius	- Resolution 1 km ²
	Land Use	Linear	Percentage of arable land cover in a 1km radius	-
		Linear	Percentage of forest cover in the past (1910 and 1960) at	Hilda database (2013)
			1km radius	Resolution 1 km ²

Unovon		
Ulleveli		population of the worl
sampling	Natural logarithm of the Human Population data	SEDAC dataset (2016)
effort		Resolution ~1 km ²
	sampling effort	sampling Natural logarithm of the Human Population data effort

169 2.2 SDM Framework

170 The m = 2576 stag beetle locations, denoted by s, were modelled with a Poisson point process model. Under this model, we assume that the expected number of stag beetle 171 presence reportings per unit area, called the intensity $\mu(s)$, varies spatially (therefore 172 173 indexed by location s), according to environmental conditions x(s) and a term related to the observation process z(s). Ecologically speaking, this intensity is not a probability of 174 175 occurrence but a measure proportional to the abundance per unit area for the considered 176 species (Renner *et al.* 2015) throughout an area \mathcal{A} . In our case, the intensity of points was 177 fitted as a log-linear model of the predictors (Warton et al. 2013; Renner et al. 2015). Such 178 predictors were split into two categories: environmental variables $\mathbf{x}(s)$ parameterized by $\boldsymbol{\beta}$ 179 and the observer bias variable z(s) parameterized by gamma (γ) (eq. 1).

180 Equation 1:
$$\ln \mu(s) = \mathbf{x}(s)'\mathbf{\beta} + z(s)'\gamma$$

181 The parameters of the model are typically fitted via maximizing the log-likelihood expression 182 below (eq. 2) (Cressie, 1993) which includes an intractable integral μ_{a} .

183 Equation 2:
$$l(\boldsymbol{\beta}, \gamma; \boldsymbol{s}) = \sum_{i=i}^{m} ln \ \mu(s_i) - \mu_{\mathcal{A}}$$
, where $\mu_{\mathcal{A}} = \int_{s \in \mathcal{A}} \mu(s) ds$

Because the integral μ_A is intractable, it must be approximated via numerical quadrature (eq. 3).

186 Equation 3:
$$\mu_A \approx \sum_{i=m+1}^{m+n} w_i \mu(s_i)$$

187 This is done by introducing a set of *n* quadrature points $s_0 = \{s_{m+1}, ..., s_{m+n}\}$ throughout \mathcal{A} 188 along a regular grid and associating with the species locations *s* and the quadrature points 189 s_0 a set of quadrature weights $w = \{w_1, ..., w_{m+n}\}$, leading to the approximate likelihood 190 below (eq. 4; Berman & Turner 1992).

191 Equation 4:
$$l(\boldsymbol{\beta}, \gamma; \boldsymbol{s}) \approx \sum_{i=i}^{m+n} w_i(y_i \ln(\mu(s_i)) - \mu(s_i))$$

192 In equation 4, $y_i = \frac{I(i \in \{i,...,m\})}{w_i}$; in other words, y_i is equal to 1 over the quadrature

193 weight if s_i is one of the presence points and 0 if s_i is one of the quadrature points.

Quadrature points were initially placed on a regular 1 km x 1 km grid. However, initial analysis of the data with the findres function of ppmlasso suggested that we did not need to fit models at such a fine resolution, as the maximized log-likelihood appeared to stabilize at a spatial resolution of 4 km x 4 km (see Appendix S1 in Supporting Information, Fig. S1.1), which we hereby used in all of our models in order to reduce the time and computer power needed to run the analysis, improving the efficiency of the analysis (Renner & Warton, 200 2013).

201 In our case, we used 10 covariates to model the observed pattern of stag beetle locations. 202 With so many covariates, we run the risk of overfitting the model as some may not be 203 informative of the distribution of the observed records. Therefore, we incorporated a lasso 204 penalty (Tibshirani 1996), which shrinks coefficients toward zero and in some cases may set 205 some coefficients to be exactly zero, effectively removing the associated covariates from the 206 model (Renner et al., in press). We fitted regularization paths of 200 Poisson PPMs with 207 increasing lasso penalties, and chose the model with the smallest model selection criterion, 208 here BIC.

Analyses were performed in R 4.0.2 (R Development Core Team 2020) using the 'ppmlasso'
package (Renner & Warton, 2013) and different R functions which were written to establish

intensity and coefficient measures. These functions are the stability assessment toolbox,
hereafter referred to as "diagnostic tools". Code, simulated data and a tutorial illustrating
use of this code are provided in the supplementary material.

214 2.3 Diagnostic tools

215 We evaluated the alignment of the fitted model using all available points with models fitted 216 to random subsets of the available points with varying size using the aforementioned 217 diagnostic tools. In this way, we can assess the number of points required to ensure 218 reasonable trust in the fitted models. Our main idea was to assess model stability and 219 congruence in the ecological information inferred from the models. Therefore, 1000 220 randomizations were run in R for each experiment for each number of subsampled points (N 221 = 50, 100, 200, 500, 1000) (Fig. 2). By simulating a number of subsamples from the whole 222 dataset available, we reproduced a general framework of ecological studies, where the 223 observed dataset is a subset of the whole species pattern. The diagnostic tools we propose 224 may be broadly divided into two categories: tools that measure stability of the fitted intensity surface $\hat{\mu}(s)$ and tools that measure alignment of the fitted coefficients $\hat{\beta}$ and $\hat{\gamma}$. 225

Table 2: A short description of the supplied R functions to explore model stability, which are contained in the DiagnosticFunctions.R file supplied in the supplementary material. Full details of these functions and a demonstration of their usage appears in the RMarkdown tutorial in the supplementary material.

Function	Characteristic	Description
avg_mu_plot	Intensity surface	Produces a map of the average intensity for a
		given subset size
compute_intensity	Intensity surface	Computes the raw and rescaled intensities for a
		matrix of fitted model coefficients
Corr_plot	Intensity surface	Produces a trace plot of correlation coefficients
		between the intensity surfaces of the subset

		models compared to the model fitted with all
		available points
IMSE_plot	Intensity surface	Produces a trace plot of the integrated mean
		square error of the intensity surfaces of the
		subset models compared to the model fitted with
		all available points
makeraster	Intensity surface	Creates a raster object of a mapped measure
		from one of the other functions, with an option
		to export as a .tif file
quantilematch	Intensity surface	Produces a map of misalignment proportions of
		quantile-categorised intensity surfaces between
		the subset models of a given subset size and the
		model fitted with all available points
sd_plot	Intensity surface	Produces a map of standard deviations of the
		intensity surface for a given subset size
coef_plot	Fitted	Produces a trace plot of coefficient estimates
	coefficients	across models of various subset sizes
coef_se_plot	Fitted	Produces a trace plot of the standard deviation of
	coefficients	the coefficient estimates across models of various
		subset sizes
signcoefs	Fitted	Computes the number of positive, zero, and
	coefficients	negative coefficient estimates for each covariate
		across all subset sizes
signplot	Fitted	Produces a barplot of the estimated coefficient
	coefficients	signs for a given covariate across all subset sizes
ZeroEnvEffect	Fitted	Computes the number of fitted models of each
	coefficients	subset size where all coefficients are shrunk to 0





Figure 2. The Lucanus PPM workflow for model simulation and diagnostic tools comparison.
Diagnostic tools are functions included in the ppmlasso package for R. Vectors from
freepik.com.

235 2.3.1 Intensity measures

236 The first set of diagnostic tools assess stability of the fitted intensity surface $\hat{\mu}(s)$. As this intensity surface is typically the primary output of a species distribution model, knowing 237 238 whether the model which produced it can be assumed to have stabilized is an important 239 consideration. We do this by exploring trends in the intensity surface as subset size changes. 240 Let $\hat{\mu}_{i,N}(s)$ be the fitted intensity of the *i*th subset of size N at location s. As we will consider 241 multiple subset sizes (N = {50, 100, 200, 500, 1000}), we would expect the range of these raw fitted intensities $\hat{\mu}_{i,N}(s)$ to expand as subset size N increases. Consequently, we rescale 242 243 these fitted intensities to achieve a common scale. Because these tools are used to assess 244 stability of a model fitted with the full set of *m* species points, we will define the rescaled 245 fitted intensity $\hat{\mu}_{i,N,m}(s)$ to have the same scaling as the model which uses all m points as follows: 246

247 Equation 5 :
$$\hat{\mu}_{i,N,m}(s) = \frac{m}{N}\hat{\mu}_{i,N}(s)$$

Here, we present five diagnostic measures of intensity surface stability which are in theDiagnosticFunctions.R file in the supplementary material:

• **Standard deviation of the Intensity.** The fitted model produces an estimate of intensity at each species location in *s* and each quadrature point in s_0 . As each subset is randomly sampled, we can examine trends in the variation of intensity as subset size changes. We can thus calculate the standard deviation of the rescaled intensities $\hat{\mu}_{i,N,m}(s)$ across all random subsets, and visualize them in a map produced by the function sd_plot. These standard deviations can be used to quantify the likely variation in intensity at each location *s* for a given subsample size.

• Average rescaled intensity. We can calculate the average rescaled intensity $\hat{\mu}_{avg,N,m}(s)$ across all random subsets of size N. Mapping these can indicate when the fitted intensity has stabilized. We provide a function avg_mu_plot in order tomap the rescaled intensity across subsets.

IMSE. The integrated mean square error (IMSE) may be used to measure alignment
 between the fitted intensity surface using the full set of *m* points with the rescaled
 intensity of a subset. Because we expect the intensity surface to be right-skewed, we
 implement the IMSE as a sum of squared differences between the natural logarithm
 of the fitted rescaled intensities at the quadrature points, as follows:

266

267 Equation 6:
$$IMSE(\hat{\mu}_{i,N,m}) = \sum_{j=m+1}^{m+n} (\ln \hat{\mu}(s_j) - \ln \hat{\mu}_{i,N,m}(s_j))^2$$

The higher the IMSE, the greater the dissimilarity between the fitted intensity surfaces. Across subsets, this tool can also be used to inform about model stability. We would expect IMSE to decrease as subset size increases. We provide a function IMSE_plot to visualize the IMSE for each simulated subset and a trace plot of the mean across subsets.

Correlation. We can also measure alignment between the fitted intensity surface 273 274 using the full set of *m* points with the rescaled intensity of a subset with a correlation 275 measure, using either Pearson's correlation coefficient or non-parametric alternatives such as Spearman's rho or Kendall's tau. Unlike IMSE, correlation 276 277 measures are bound between -1 and 1, and this scale-free property allows judgment 278 to be made about the raw correlation value in addition to relative comparisons across subset sizes. We provide a function Corr plot to visualize the chosen 279 280 correlation measure for each simulated subset and a trace plot of the mean across 281 subsets.

282 Quantile misalignment maps. While the previous tools are useful summaries of the 283 overall alignment between the fitted intensities of the model using all the points $(\hat{\mu}(s))$ with the rescaled intensities of the models fitted to the subsets $(\hat{\mu}_{i,N,m}(s))$, 284 285 they do not indicate where the intensity surfaces differ (Pontius and Millones 2011). We provide a function quantilematch that produces a map of quantile misalignment 286 287 between the models that use random subsets and the model that uses the full data. 288 With this function, the user can supply the desired quantile cutoffs to determine the ordered categories. For example, if the quantiles argument is left at the default of 289 290 (0.2, 0.4, 0.6, 0.8), locations are placed into one of five categories (corresponding to 291 quantile ranges 0-0.2, 0.2-0.4, 0.4-0.6, 0.6-0.8, and 0.8-1) based on both the fitted 292 intensities $\hat{\mu}(s)$ of the model using all available points as well as the fitted intensities 293 $\hat{\mu}_{i,N,m}(s)$ of the models using random subsets. By quantifying the proportion of 294 differences in categories for each location, the quantilematch function therefore 295 highlights regions where the relative fitted intensities tend to differ between the 296 models fitted to random subsets and the model fitted with all of the data points.

297

2.3.2 Fitted coefficient measures

Ecologists interested in exploring the effects of the environmental covariates \mathbf{x} and the observer bias covariates \mathbf{z} on the fitted model can explore all covariate effects included in the model. Consequently, we present two tools to measure the stability of the coefficient estimates $\hat{\boldsymbol{\beta}}$ and $\hat{\boldsymbol{\gamma}}$ for the environmental parameters $\boldsymbol{\beta}$ and the observer parameters $\boldsymbol{\gamma}$. Let $\hat{\beta}_{j,i,N}$ and $\hat{\gamma}_{k,i,N}$ be the *j*th environmental and *k*th observer bias coefficient estimates of the model fitted to the *i*th subset of size *N*. Tools that may be used to explore stability in the coefficient estimates are as follows: 305 **Coefficient estimate variability**. As each subset is randomly sampled, we can examine trends in the variation of coefficient estimates as subset size changes. We 306 can thus calculate the standard deviation of the coefficient estimates $\hat{\beta}_{j,i,N}$ and $\hat{\gamma}_{k,i,N}$ 307 308 across all random subsets. We have provided a function coef_plot which constructs a scatterplot of the fitted estimates of a given coefficient across all simulated 309 subsamples, along with a trace plot of the mean. In addition to the plot, it outputs 310 311 the mean and standard deviation of the coefficient estimates for each subset size. 312 This diagnostic tool can not only inform about model stability through its dispersion, 313 but also highlight the effect of the different variables on the intensity. This second 314 point can be of major importance for the ecological interpretation of results. Thus, we added the function coef_se_plot which displays empirical standard errors of 315 coefficient estimates along with a trace plot of the standard deviation of the fitted 316 parameter estimates $\hat{\beta}_{i,i,N}$ and $\hat{\gamma}_{k,i,N}$ for each subset size across all environmental 317 318 and observer bias parameters.

319 Signs of coefficient estimates. The sign of a coefficient estimate indicates whether it has a positive, neutral, or negative effect on the predicted species distribution, 320 321 providing insight for ecologists. Consequently, exploring trends in the signs of the fitted coefficients can provide insight into the level of agreement in terms of 322 323 ecological information. Across subsets, we can compute the proportion of fitted 324 coefficients that have the same sign as the model which uses all *m* points and thus 325 inform about model stability. We have provided a function signcoefs which outputs 326 an array which counts the number of negative, zero, and positive signs for each 327 subset size and coefficient and a function signplot to visualize bar plots of the sign of

328 the fitted parameter estimates $\hat{\beta}_{j,i,N}$ and $\hat{\gamma}_{k,i,N}$ for each subset size across all 329 environmental and observer bias parameters.

330 3. Results

Full results of the Lucanus analysis are presented below and the supplementary material; we also provide a simulated dataset and stability screening results for this dataset in a separate tutorial.

334 3.1 Predicted intensity, IMSE and misalignment

335 As we modelled the intensity of the stag beetle across 1000 random subsets of points for 336 different subset sizes, we compared the average intensity of each subset and the fitted 337 intensity for the PPM which uses all 2576 points. As some fitted intensities are very low, we 338 truncate intensities below 10⁻⁵ (1.5% of predicted intensities). By mapping the average 339 rescaled intensity for each subset size (avg_mu_plot function), we note that a pattern 340 appears to stabilize from N = 500 points (Fig. 3a). These maps provide point estimates of the 341 intensity, but we can also assess variability by examining maps of standard deviations of the 342 rescaled fitted intensities (sd_plot function; see Appendix S1 in Supporting information, Fig. 343 S1.2). Moreover, taken one by one, visualization of intensities for models above 500 points were more consistent that those under 500. Indeed, for instance models based on subsets of 344 50 points appeared more variable between them than those using subsets of 500 points 345 346 (Supporting information, Fig. S1.3).

Such differences were also visible by plotting the average Pearson correlation (Corr_plot function) between each subset's log intensity and the whole model with all available points was moderately good at 200 points ($R \ge 0.7$) and nearly perfect ($R \ge 0.97$) for models beyond 500 points (Fig. 3b). Furthermore, correlation between subsampled models and the whole

model was greater when the subset contained more than 100 points and consistently above
0.9 with 500 points or more (99.4% of correlations greater than 0.9 when N=500).

These results were confirmed by the log IMSE of each model across subsets (IMSE_plot function; Fig. 3c). Indeed, we can see how the average log IMSE by subset significantly decreases, from around 10.7 at 50 and 100 points to 6.1 at 1000 points. Indeed, pairwise comparisons of IMSE are all significantly different at the 0.1% level (t-test). However, we noticed that the lasso penalty shrank most of the coefficients to zero in models with 200 points or less, leading to greater differences which lead to high IMSE.



Figure 3. (a) Average rescaled intensity for each subset size (avg_mu_plot function; N = 50, 100, 200, 500 or 1000 points) and the intensity of the whole model with the 2576 stag beetle observations. Maps can be used for graphical comparison. (b) Pearson correlation between

the natural logarithm of the fitted intensity surface from the model using all 2576 points and the rescaled intensity surface from the models using random subsets; the dotted line shows the below which the correlation is considered as low (R >= 0.7) (Corr_plot function). (c) A logarithmic transformation of the integrated mean squared error (IMSE) for each simulation depending on the subset of given points (yellow) (IMSE plot function).

Furthermore, regarding the quantile matching (quantilematch function), we observed that the level of misalignment is initially very high, because most of the models for subset sizes N = 50 and N = 100 set all coefficients to 0 (Fig. 4). Once we reach a subset size of N = 500, the level of misalignment is much lower. Even at N = 1000, however, there are certain regions where there is relatively high misalignment. Therefore, the interpretation of the intensity surfaces should be more prudent in such areas.



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Figure 4. Maps of the proportion of subsets which place the locations into different categories defined by the quantiles 0.2, 0.4, 0.6, and 0.8 than the model using all available points (quantilematch function), for each subset size (50, 100, 200, 500 and 1000 points). The intensity surface (2) of the model using the all N = 2576 available points is graphically illustrated next to the 1000 points misalignment map in order to show the areas were the interpretation must be nuanced, particularly the southwest of France and in the east, near the Swiss border. 382

383 3.2 Covariate effects (β dispersion and ecological agreement)

384 The plots of the fitted coefficients (coef_plot function) likewise suggest that the model stabilizes when the subset size reaches 500, as the mean values of $\hat{eta}_{j,i,N}$ appeared to 385 converge to the values \hat{eta}_j obtained from fitting a model to the full set of 2576 points and the 386 variation in $\hat{eta}_{j,i,N}$ likewise appeared to decrease with increasing subset size (Supporting 387 information, Figure S1.4). Indeed, the standard deviation of coefficient estimates $\hat{\beta}$ 388 389 consistently decreased when the number of points increased beyond 200 (coef_sd_plot 390 function; Fig. 5a). This result can be seen as congruent with the measures of intensity from 391 Section 3.1, which suggested the stability of models with a number of points of 500 or more.



Figure 5: (a) Trace plot of the standard deviation of the fitted parameter estimates $\hat{\beta}_{j,i,N}$ and $\hat{\gamma}_{k,i,N}$ for each subset size across all environmental and observer bias parameters (coef_sd_plot function. (b) Bar plots of the sign of the fitted parameter estimates $\hat{\beta}_{j,i,N}$ for each subset size across all environmental and observer bias parameters (signplot function).

397 It may seem counterintuitive that the average standard deviation, in some cases, increases 398 from N=50 to N=200 and then decreases (Fig. 5a). As many of the coefficient estimates are 399 set to 0 for models of subset size N= 50, this has the effect of decreasing the standard 400 deviation across all simulations. Those coefficients which are non-zero tend to have a large spread, as shown in the graph with a large range of values for $\hat{\beta}_{i,i,50}$ (Supporting information, 401 402 Figure S1.3). In other words, there is a strong pull toward 0 for N= 50 (as shown in the 403 analysis of coefficient signs in the next subsection), but those coefficients which are not set 404 to 0 tend to be more variable. As subset size increases, the range of the fitted coefficients 405 tends to decrease, but as fewer coefficients are set to 0, the overall standard deviation may 406 be higher across all 1000 simulated subsets for N= 100 and N= 200. Once the subset size 407 reaches 500, however, the range becomes small enough that the overall standard deviation 408 starts to decrease, despite very few coefficients being set to 0.

The sign of the fitted coefficients $\hat{\beta}$ (signplot function) informed us about the contribution of 409 410 each environmental variable to the potential distribution of the Stag beetle in France (Fig. 411 5b; Supporting information, Figure S1.4). Mean annual temperature and mean annual 412 precipitation rate, the percentage of forest cover in the past and the current presence of 413 broad-leaved forest and the natural logarithm of the human population were positively 414 associated with the presence of the species. On the other hand, the percentage of arable 415 land and coniferous forest as the quadratic term of the temperature and the interaction 416 term of climatic variables, were negatively associated with Lucanus presence. The sign of the 417 fitted coefficient estimate $\hat{\gamma}$ (log of the human population variable) were always 100 % 418 positive, whatever the subset size (Supporting information, Figure S1.5).

Hence, we looked at the agreement between the signs of $\hat{\beta}$ and $\hat{\gamma}$ across subset models, as shown in Figure 5b, with the signs of the coefficients from the model using all the available data. For the temperature or ancient forest variables, for instance, even if the coefficients were shrunk to zero in many cases (particularly models with less than 200 points) the sign 423 was always positive when it was non-zero. Coefficients of the other variables fluctuate from 424 positive to negative signs, particularly for models with 200 points or less. For example, the 425 estimated coefficients for precipitation or the interaction term were equally negative and 426 positive until models with 500 points or more. Therefore, getting sign congruency is a sign of 427 model stability. Nevertheless, we got a clear sign tendency with 200 points and more.

428 The tools are therefore congruent in their conclusions: to model the stag beetle distribution 429 at the French mainland scale and with the given choice of variables and lasso penalty 430 criterion, 500 points are needed to get stabilized models, and consequently in our point of view, also trustworthy conclusions. With a different choice of variables, the number of 431 432 points necessary for reliable conclusions may differ – in general, the more variables included 433 in the model, the more variation is expected in the fitted intensity surfaces, requiring larger 434 numbers of points to stabilize. Regardless, the tools presented here can be tailored to 435 different spatial scales and choices of variables to investigate model stability.

436 **4. Discussion**

437 **4.1 Assessing PPM stabilization**

438 By departing from our particular data and environmental context, we were able to explore 439 the question of "at what point do my models stabilize?". Our suite of diagnostic tools 440 provides a way to assess the stability of the model in its particular context. Hence, this 441 methodology could be used in order to verify how stable a Poisson point process model 442 fitted with a lasso-type penalty is. Moreover, if the models stabilize at a relatively low 443 number of points, it might mean that the dataset could be divided into shorter periods and 444 used for species distribution analysis across time. For instance, in our case, 500 points seem enough to have a reasonably trustworthy model of the stag beetle. We could have 445

446 potentially split the dataset in two and see the differences in the distribution between 2007-447 2012 and 2012-2017, but in our case temporal heterogeneity of the records did not permit 448 this. Participation in the Stag beetle Quest significantly increased in 2015, and since the 449 average number of records per year is 1000, this implies that a future comparison of models 450 for different time periods could be possible.

451 As these diagnostic tools rely on exploring stability across different subset sizes, it is 452 important to consider which subset sizes to specify in the simulations. In our context, we 453 fitted models using 10 covariates with over 2500 point locations. We considered subset sizes 454 ranging from N = 50 to N = 1000, thus representing between about 2% and 40% of the total 455 number of points. Indeed, allowing the maximum subset size to be too large could give a 456 false impression of stability due to the fact that there are fewer possible subsets and an 457 increasing number of shared records across subsets. For instance, if we allow the subset size 458 to be 80% of the number of available records, different subsets are guaranteed to share at 459 least 60% of the records in common. As a general recommendation, we advise practitioners 460 to consider subsets ranging in size from a minimum greater than the number of covariates 461 and a maximum less than half of the total number of available records, though this may be 462 quite limiting for data sets with few available records relative to the number of covariates.

While there are certainly other ways to create subsamples aside from sampling at uniform from the available points (i.e half split or block-crossed validation (Roberts et al. 2017), which are certainly preferable for validating models to independent data), such schemes do not seem appropriate for our work. In our model, we also include a term related to sampling bias, and incorporating different subsampling schemes could make it difficult to disentangle effects of the environment from effects of this sampling bias. In this work we want to call

469 attention to the fact that any given set of observed points represents some (likely biased) 470 subsample of the true point pattern, and by sampling randomly, we thereby preserve any 471 underlying bias patterns of the observed data set. Without direct information regarding 472 sampling effort, creating random subsamples from the observed data set thus mimics the 473 setting in which the observed point pattern is some random subsample of the true point 474 pattern.

475 We also want to highlight that the criterion we used to select the optimal lasso penalty was 476 the BIC. As we have seen that stability is greatly influenced by the proportion of models for which the coefficients are set to 0, the choice of the criterion for the lasso penalty will also 477 478 impact the model complexity and hence the number of points necessary for the models to 479 adequately stabilize. If we had instead chosen the AIC, which tends to choose lower 480 penalties than the BIC, model stabilization might have been achieved with smaller subset 481 sizes. Consequently, the effect of criterion choice for the lasso penalty on model stability is a 482 potential area of future research.

If after using these tools, the model does not appear to have adequately stabilized, we recommend results be interpreted with corresponding caution, particularly when the model may be used to inform management or conservation actions. Greater model stability could be achieved by considering a smaller set of covariates, acknowledging that this would lead to less sophisticated ecological understanding of the species distribution and the environmental factors that drive it.

It is important to note that the tools presented in this paper require an adequate number of points in the original pattern to create reasonably-sized subsets. When presence records are rare (around the same number as the number of modelled covariates), it is impractical to

492 produce subsets to assess model stability as there is an increased risk of model convergence 493 problems when fitting models with small numbers of points. However, the spirit of this 494 paper is to explore questions related to the amount of trust that can be placed in a fitted 495 model, and a model fitted using a small number of records is unlikely to be very informative 496 or reliable.

497 Our approach exploits already existent tools in the ppmlasso package and can therefore be 498 already used. In principle, these tools could also be adapted for use with models fitted using 499 other software platforms, such as spatstat. However, these functions were specifically built 500 to extract information from objects with a ppmlasso class, so adaptation of the functions to 501 objects with other classes may be challenging. Moreover, spatstat provides its own functions 502 to assess model stability. Our functions explore model stability through subsetting largely 503 due to the fact that classical statistical estimators such as standard errors are not available 504 when fitting models with a lasso penalty, and the ppmlasso package is specifically designed 505 for the setting of our paper in fitting species distribution models with lasso penalties.

This data-driven scrutiny of sample size and model stability is more tailored to analysis of different data sets than ad hoc rules for choosing the number of points to model a certain species. Moreover, it helps us explore trust in the conclusions from the fitted model, particularly for those who use SDMs to inform decisions for conservation.

510 4.2 Ecological insight

Lucanus cervus is a saproxylophagous beetle of conservation interest at the European scale (cited in the 3rd appendix of the Berne convention of 1979 and the 2nd appendix of the Habitat Directive of 1992), that is, subservient to dead or decaying wood; it is observable near old trees, in forest but also in wooded and urban areas. It is a relatively common

515 species in France, and more largely in Europe (Paulian & Baraud, 1982; Bensettiti & 516 Gaudillat, 2004).

517 Using the SDM framework to have ecological insight about the distribution pattern of stag 518 beetles, we observed that climate variables dominated the spatial characterization of the 519 species, particularly the annual temperature (with $\hat{\beta}$ coefficients furthest from 0). This was 520 not a surprise as adults' activity is considered weather-dependent, particularly to conditions 521 of temperature and humidity (Fremlin & Fremlin 2010; Lachat et al. 2012). Indeed, the whole 522 model (Supporting information, Figure S1.2) shows that the species drastically rarifies in 523 mountainous regions where temperatures are lower and humidity higher (massif of the 524 Cevennes, the Pyrenees and the Alps). As the overall alignment between the fitted 525 intensities of the models above 500 points is high (less than 20 % misalignment; fig. 4) in the 526 mountainous areas, we can validate that Lucanus cervus sightings are weather related.

Land use plays a significant but secondary role. The extent of agriculture, an environmental variable previously thought to be unfavorable for the species was useful. The influence of broad-leaved vs coniferous forests became unambiguous (respectively positive and negative) above 50 points, which may be due to the mixture of trees in forests and the way in which Corine Land cover classifies landscape features (through a visual interpretation of satellite images) at small scale.

The abundance of ancient forest was positively associated and plays a significant role in the Lucanus distribution among the land use variables. Perhaps it is due to the selection of local broad-leaved oaks and beeches (Bazire & Gadant, 1991) and availability of dead wood in such plots of old forest. The influence of this variable confirms the influence of the landscape matrix and its history in the current distribution of the stag beetle, as old-growth deciduous

forests favor the presence of this saproxylophagous species; it also underlines the inertia of
forest systems and should warn us about the potential consequences of the large
domination of coniferous plantations occurring for the last 70 years in France (Bazire &
Gadant, 1991; Boutefeu 2005).

542 In France, broad-leaved forests are mainly in the plains or at medium altitude. Coniferous 543 stands are mainly in mountainous areas, in the Landes highlands and in recent plantations in 544 western France (Garnier et al., 2018). It is known that coniferous forests are not favorable 545 for this species, even if some Lucanus can breed on Pinus spp and Thuja spp (Paulian & Baraud, 1982; Bensettiti & Gaudillat, 2004). The bar plots of the sign of the fitted parameter 546 547 estimates showed us that above 500 points the sign is mainly negative. Ecologically, we 548 expected a negative sign, and we only consistently see it from N = 200 onward, so models 549 fitted with fewer than 100 points could have led to conclusions contradictory to ecological 550 knowledge. In interaction with other variables, such as the climatic ones, this can also 551 explain the absence of Lucanus cervus in mountainous areas and could be therefore 552 explored in future models.

553 Complementary variables, such as biotic interactions with fungi in decaying wood or other 554 invertebrate species, wood species selection for breeding or micro-climatic variables, which 555 are important for invertebrate development and suggested as important for saproxilic 556 beetles (Diniz-Filho *et al.*, 2010; Quinto *et al.*, 2015; Ulyshen *et al.*, 2017; Garrick *et al.*, 557 2019), were not included as they were not available.

558 The importance of the bias covariate (human population) was significant, showing once 559 again the importance of variables that can correct for sampling bias to accurately model 560 species distributions.

561 The conclusions inferred from a fitted SDM may be incomplete from an ecological point of 562 view or even inaccurate at small scales. Here we want to underline the important role of 563 experts of the target species and the fact that models approximate a complex reality and 564 should be used with parsimony and caution, especially in conservation contexts. 565 Furthermore, we encourage practitioners to always keep in mind the areas where categories 566 of intensity are most likely to differ between the models fitted to random subsets and the 567 model fitted with all available points (misalignment map). In our case, precautions must be 568 taken before interpreting the whole model in the south-west of France (west part of the 569 Landes highlands) and in particular in the east near the border with Switzerland (Massif du 570 Jura), even though in this second area we had some observations (fig. 1).

571 **5. Conclusion**

572 PPMs not only offer a unifying framework to fit presence-only species distribution models 573 with many advantages in model implementation and interpretation, but also possess a 574 number of ready-to-use diagnostic tools that can inform about model consistency and 575 stability. Without any rule of thumb or an obscure single metric, the number of needed 576 points in a particular environmental and spatial context to achieve model stability can be 577 explored from perspectives relating to both the fitted intensity surface and the fitted model 578 coefficients. All of the diagnostic tools are congruent and can be used for any kind of point 579 process model. Above all, we recommend collaboration between species experts and 580 researchers in ecology and statistics to build realistic, field-informed, trustworthy models 581 and test them before applying them. Thanks to the diagnostic tools offered by PPMs, a 582 constructive step-by-step process may allow us to rapidly increase our knowledge of species 583 distributions, even for the less studied ones.

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