Data sharing among protected areas shows advantages in Habitat Suitability Modelling performance

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Abstract

Context. Most of the effort dedicated to the conservation of biodiversity in the European Union is applied through the establishment and maintenance of the Natura 2000 network, the world's most extensive network of conservation areas. European Member State must actively manage these sites and report the state of the species listed in the Annexes of the Habitat and Birds Directives. Fulfilling these duties is a challenging task, especially when money available for conservation is limited. Consequently, how to optimise the use of the available economic resources is a primary goal for reserve managers.

Aims. In this study, we focused on data sharing, and we analysed whether data sharing among institutions may boost the performance of Habitat Suitability Models (HSMs).

Methods. We collected presence data about three species of reptiles in three different protected areas of Northern Italy. Then, we built HSMs under two different data-sharing policies: data sharing of species' occurrence among the different managers of the protected areas, and not sharing the occurrence data among the different managers. To evaluate how sharing the occurrence data influence the reliability of HSMs in various situations, we compared models' performance under several sampling-effort levels.

Key results. Results show that data sharing is usually the best strategy. In most cases, models built under the Data-Sharing (DS) strategy showed better performance compared to Data-Un-sharing (DU) models. The data-sharing strategy showed advantages in model performance, notably at low levels of sampling effort.

Conclusions. Overcoming administrative barriers and share data among different managers of protected areas allows obtaining more biologically meaningful results.

Implications. Data-sharing among protected areas could allow improving the reliability of future management actions within the Natura 2000 network.

Additional keywords: common wall lizard, green whip snake, Habitat Suitability Models, Habitats Directive, Natura 2000 network, resource optimisation, western green lizard.

Introduction

The Natura 2000 network is the cornerstone of the biodiversity conservation in the European Union (EU) (Strange *et al.* 2007). It is the world's most extensive network of conservation areas, which encompasses 27,758 protected areas distributed across the 28 EU countries, and covers 18% of the European lands and seas (Natura 2000 Barometer, 2017). The network nodes (i.e. Sites of Community Importance and Special Protection Areas) are landscape patches, often surrounded by urban and agricultural areas (Fig. 1). The management of this network is regulated by the Habitats Directive (92/43/EEC) and the Birds Directive (2009/147/EC), which require monitoring and periodical reporting about the status of conservation of species and habitats listed in the Annexes of the Directives. Achieving these goals imposes the allocation of economic resources because the starting point for most management actions is the systematic collection of species occurrence data, which implies the recruitment of experienced workers, instruments, and time; in other words, money. Considering that money available for conservation are usually limited (Mikkonen and Moilanen 2013), adequately addressing the resources to manage Natura 2000 sites is a primary goal. In this context, the choice of appropriate sampling design is crucial to make the best use of the available economic resources (Marta *et al.* 2019). Additionally, collaboration among managers of neighbour protected areas may result in a better quality of the collected information. Although some data-sharing platforms already exist at a national (e.g. UK National Biodiversity Network; https://nbn.org.uk/) and global scale (e.g. Global Biodiversity Information Facility; www.gbif.org), these databases are spatially biased and targeted surveys are essential for small-scale assessments (Beck *et al.* 2014).

Habitat Suitability Models (HSMs) are tools to estimate the relationships between species records at sites and the environmental characteristics of those sites (Elith *et al.* 2011). HSMs can be a powerful tool for conservation purposes. For instance, HSMs can be employed in assessing the impact of climate and land-use change on population trends (Rondinini *et al.* 2011; Falaschi *et al.* 2019), to assess the effectiveness of protected areas in preserving proper habitats (Maiorano *et al.*

2007; Hanson *et al.* 2020), or to make predictions about possible range shifts of either native or alien species (Fouquet *et al.* 2010; Falaschi *et al.* 2018; Ramellini *et al.* 2019; Mori *et al.* 2020). Within the Natura 2000 network, Member States are required to take measures to assure the favourable conservation status of habitats and species listed in the Directives (Epstein *et al.* 2016). In this context, HSMs can provide useful insights on how to plan future management of protected areas. For example, Araújo *et al.* (2011) found that most species occurring in Natura 2000 areas are likely to be threatened by climate change. Another study by Johovic *et al.* (2020) found that, within the Natura 2000 network, suitable habitat for invasive American bullfrogs is likely to triplicate by 2050, potentially threatening protected amphibians.

This work aims to evaluate if and how data sharing/un-sharing policies affect the reliability of HSM predictions, given different levels of sampling effort. Indeed, the usefulness of HSMs crucially depends on the ecological information they can capture (Sillero 2011; Araújo and Peterson 2012). The amount of captured information is strongly related to the quality of the collected data and to the sampling design adopted (Guillera-Arroita *et al.* 2015; Marta *et al.* 2019). When dealing with neighbouring, environmentally homogeneous sites, a key question could be if multiple, independent site-specific samplings (i.e. a data un-sharing policy) supply better predictions than a single among-site census (i.e. a data sharing policy), given the same sampling effort (i.e. the total money allocated for monitoring). In terms of HSM this means that under a data-sharing policy (DS) data collected in all the neighbouring sites can be pooled to build up a single HSM (that makes a single prediction all over the sites), whereas, under a data un-sharing policy (DU), each site uses its own data to obtain a site-specific HSM (that make independent predictions, one for each site).

In this study, we compared the performance of HSMs under DS and DU policies, at different levels of sampling effort. We adopted a case study approach, using presence data of three reptile species from six-years monitoring in three neighbouring, environmentally homogeneous, protected areas located in Northern Italy.

Materials and methods

Study area

The study area is located in Northern Italy and includes three protected areas, managed by three different stakeholders (Fig. 1): the *Pineta di Appiano Gentile e Tradate* Regional Park (PP), managed by a consortium of 15 municipalities and two provinces, with an extension of 4800 ha, and including the Natura 2000 area *Pineta Pedemontana di Appiano Gentile* (IT2020007); the *Groane* Regional Park (PG), managed by a consortium of 17 municipalities and two provinces, with an extension of 3800 ha, and including two Natura 2000 areas, *Pineta di Cesate* (IT2050001), and *Boschi delle Groane* (IT2050002); the *Brughiera Briantea* Park (BB), managed by a consortium of 10 municipalities, with an extension of 2600 ha, and including the Natura 2000 area *Fontana del Guercio* (IT2020008).

The study area was chosen in order to have different protected areas, managed by different stakeholders, but close to each other and sharing similar environmental characteristics (Supplementary Fig. 1). To test whether the environmental features used in the analyses were comparable among the three parks, we assessed the similarity of the environmental characteristics by performing a Multivariate Environmental Similarity Surfaces analysis (Elith *et al.* 2011). In this analysis, we considered all the variables used in the subsequent modelling (Supplementary Table 1) and results highlighted no particular dissimilarities between the three parks (few cells with negative values; Supplementary Fig. 2).

Study species and occurrence data

Targeted surveys were carried out in the three protected areas from 2009 to 2015. Notably, we collected presence data about three reptile species: two lizards, the common wall lizard (*Podarcis muralis*, annex II Habitat Directive), and the western green lizard (*Lacerta bilineata*, annex II Habitat Directive), and one snake, the green whip snake (*Hierophis viridiflavus*, annex II Habitat

Directive). Presence data were collected through visual encounter surveys (Blomberg and Shine 2006) and georeferenced with a GPS.

Reptiles are good biological models when dealing with small areas, and many examples of the application of HSMs to this taxon are available (e.g. Ficetola *et al.* 2012; McPherson 2014; Ihlow *et al.* 2015). Though other reptiles were monitored during the study, our subsequent modelling framework needs a good amount of presence data, so we chose these three species because they are the most abundant and widespread reptiles in the area.

Environmental predictors

We used seven variables as informative layers in HSM building: cover of agricultural area, forest cover, scrubland cover, cover of permanent meadows, presence/absence of streams, presence/absence of carriageable roads, and slope. The four land cover variables were derived from a land use map of Lombardy region (ground resolution: 3 m) updated to 2012; slope was derived from a digital elevation model (ground resolution: 20 m); the presence/absence of streams and carriageable roads were derived from vectorial maps of streams and roads. The original cartography from which we derived environmental predictors is available at the geoportal of Lombardy region (http://www.cartografia.regione.lombardia.it). All the environmental predictors were rasterized at a 20 m resolution (using the digital elevation model as a mask for rasterization). Then, to consider processes acting at the landscape scale, the value of each cell was calculated over a 9 × 9 matrix centred on the cell (i.e. the focal cell and the 80 surrounding cells). For the four land cover variables, we calculated the percentage of cells occupied by each land cover category in the matrix; for the slope, we calculated the average slope of the cells included in the matrix; for streams and roads, we calculated the presence/absence within the 9 × 9 matrix. The correlation among variables was weak (all Pearson's correlation coefficients $r_p < 0.39$), so we decided to keep all the variables for model fitting.

Maxent models

HSMs were built using Maxent (Phillips *et al.* 2004), version 3.4.1 (http://biodiversityinformatics.amnh.org/open_source/maxent/). All models were obtained using 'linear', 'quadratic' and 'product' features, excluding 'threshold', 'hinge' and 'autofeature' features, to avoid the risk of overfitting (Warren and Seifert 2011). Maxent require the selection of pseudo-absences or background points, so we randomly selected ten thousand cells from each park as background. All the other settings were left as default.

Reference models

The evaluation of the relative performance of HSMs according to DS/DU and sampling-effort constraints requires an absolute reference. This reference model should represent the 'truth', i.e. the realized ecological niche of the species (Sillero 2011; Araújo and Peterson 2012), which is typically unknown for real data. Thus, we adopted two different proxies for the realized niche, each representing a different perspective on the question. In the first approach, we generated a single reference model using all the points available in the whole dataset: this model incorporates the maximum achieving information, given the data, and it describes the general habitat preferences of the species, independently of park's peculiarities. We defined this reference as the Broad Reference Model (hereafter BRM). In the second approach, we generated three different reference models, one for each park. Each model was fitted using all the points available for a given park (Fig. 2). These reference models were named Local Reference Model (LRM).

The ability of BRM and LRMs to capture non-random ecological relations was tested comparing their AUC (Area Under the receiver-operating Curve; Fielding and Bell 1997) values to those obtained by null models having the same structure but built on randomly chosen occurrence cells (999 replicates; Raes and ter Steege 2007). The AUC for a random, i.e. not informative, model should be near 0.5, while for an ideal model should be one. For presence-background models (like MaxEnt) the maximum achieving value is less than one but cannot be estimated (Phillips *et al.*

2006; Jiménez-Valverde 2012). Thus, a null-hypothesis comparison allows testing if the model is better than random (Raes and ter Steege 2007; Hijmans 2012).

For each species, BRM and LRM models were projected in geographical space to obtain reference maps of habitat suitability. BRM was projected three times, once for each park; while each of the three LRM was projected once. We obtained a total of 18 maps to use as reference: three species × three parks × two reference models (BRM and LRM).

Performance comparison at different levels of sampling effort

To evaluate the performance of HSMs under DS and DU policies at different levels of sampling effort, we assumed that the number of presence points was a proxy for the sampling effort (or money available for field sampling). We simulated the effect of reduction of sampling effort by gradually reducing the number of presence points available for modelling from 95% to 10%, by 5% decrease (Fig. 2a). We then simulated the data-policy by defining two ways of subsampling the available occurrence data (Fig. 2b): (i) following the DS strategy (i.e. institutions collaborate and share occurrence data), the data reduction was performed on the whole dataset and a single multi-park HSM fitted; (ii) according to DU strategy (institutions do not collaborate and each one uses occurrence data only from within their boundaries), the data reduction was performed on the within-park data and three separate HSMs fitted, one for each park. Thus, for each combination of sampling-effort reduction and data-sharing strategy, we built four models, one for the DS and three for the DU strategy.

HSMs were then projected in geographical space to obtain maps of habitat suitability (Fig. 2a): DS models were projected three times, once for each park; while DU models were projected once. Hence, we obtained a habitat suitability map for each combination of park and data-policy (DS and DU). Further, to account for the bias due to the random subsampling procedure, we ran ten replicates for each level of sampling effort, leading to a total of 3,240 projections (3 parks × 2 data policies × 18 levels of sampling effort × 10 replicates × 3 species).

For each level of sampling effort, the performance of the HSMs was assessed by comparing the obtained projections to the corresponding reference projections of both BRM and LRM references (leading to a total of 6,480 comparisons; Supplementary Table 2). The similarity of the maps was obtained by calculating the ‘relative rank score’ (RR; Warren and Seifert 2011): RR ranges from zero (completely different models) to one (completely overlapping models) and it quantifies the ability of two HSMs to equally rank randomly chosen cells (Warren and Seifert 2011). To calculate the relative rank score, two cells of a suitability map (A and B) are randomly sampled and the relationship between them (A > B or A < B) is compared to the one of the corresponding cells of the reference suitability map. If the relationship is maintained a value of 1 will be assigned, if not, the assigned value will be 0. The process can be repeated until all the possible combinations of cell pair are sampled, and the RR score will be the sum of the assigned values divided by the number of comparisons.

To visually compare the performance of DS and DU strategies at different levels of sampling effort, we built Generalized Additive Models (GAMs; Hastie and Tibshirani 1986), using RR as the response, the sampling-effort as the predictor, and fitting separate GAMs for each combination of species, park, strategy, and reference model. We performed two separate analyses: one using RR values obtained comparing projections to BRM reference, and one using RR values obtained comparing projections to LRM reference. In DS models, similarly to BRM, occurrences are sampled from all the three parks; while in DU models, similarly to LRM, occurrences are sampled from a single park at a time. So, if the performance of different strategies depends only on the similarity of structure to the reference model, we expect that: when BRM is used as a reference, DS models perform better; while when LRM is used as a reference, DU models perform better.

Furthermore, we performed a linear mixed model using the RR values as the response variable and strategy (DS or DU), sampling-effort (fraction of used occurrences), and their interaction as fixed effects, while species and parks entered the model as random terms. Before running the linear mixed model, RR values where logit transformed.

All analyses where performed in R environment (R Core Team 2018), using ‘raster’ package for map processing (Hijmans 2019), ‘dismo’ package for running MaxEnt from R (Hijmans *et al.* 2015), ‘lmerTest’ package to fit and test mixed models (Kuznetsova *et al.* 2017), and ‘mgcv’ package for GAM modelling (Wood 2011). The function to compute RR was implemented *ad hoc*, following Warren and Seifert (2011).

Results

Testing assumptions

A total of 1,407 occurrence cells constituted the raw dataset used to build the reference models (Table 1). Observations were not equally distributed among species (*P. muralis*: 1234; *L. bilineata* 101; *H. viridiflavus* 72) nor among sites (PP 484; PG 569; BB 354), reflecting the natural abundance of the species, the surfaces and the characteristics of the sites.

All reference models obtained good AUC values, (range: 0.733 - 0.951; Table 1) and they all performed significantly better than null-models ($P < 0.001$).

Strategy comparison

When BRM was set as the absolute reference, all DS models outperformed DU models at almost all the sampling effort levels (Fig. 3). For *P. muralis* and *L. bilineata* models, the performance advantage was constant along the entire cost axis. The *H. viridiflavus* models maintained the advantage until around 0.2 sampling effort, then all the models underwent a rapid decrease up to 0.05 sampling effort, where both DS and DU models had very low similarity values compared to the reference models, failing to estimate habitat suitability well (Fig. 3).

By changing the reference to LRM, the situation became more complex (Fig. 4). All DU models started with a huge advantage over DS models. Despite this initial advantage, DU models underwent a faster decline compared to DS models, which seemed to have a more stable behaviour. This pattern can be seen in all nine comparisons, and in most of them, there was a threshold at which DS models were more similar to reference models than DU models (Table 2). This sampling effort threshold ranged from 0.09 to 0.62 (mean: 0.32) and it varied according to both species and sites. An exception was *H. viridiflavus*-BB comparison, where DS strategy outperformed DU between 0.4 and 0.1, then, below 0.1, the similarity value of DS was smaller than DU.

The previous outcomes were coherent with those from the linear mixed model. As expected, decreasing the budget constraint, i.e. increasing sampling effort, positively affected RR ($F_{1,6372.1}$ = 2494.62; $P < 0.001$; $\beta_{\mathrm{effort}} \pm SD = 1.965 \pm 0.051$); DS strategy significantly increased HSM performance ($F_{1,6372.2}$ = 131.86; $P < 0.001$; $\beta_{\mathrm{DS\ strategy}} = 0.477 \pm 0.042$); also, the interaction between the two variable is significant ($F_{1,6372.1}$ = 85.35; $P < 0.001$), meaning that DU and DS had different slopes for the relation linking performance and sampling-effort (Fig. 5). Notably, the DS slope is less steep than the DU one ($\beta_{\mathrm{effort} \times \mathrm{DS\ strategy}} = -0.415 \pm 0.070$).

Discussion

In this study, we analysed the combined effects of collaboration level (i.e. data sharing policy) and resources allocated for species monitoring (i.e. sampling effort) on the quality of predictions by HSMs fitted on neighbouring Natura 2000 protected areas. When the aim is to model the species habitat suitability at a broad scale (BRM as a reference), results point the collaboration framework as the best choice, regardless of budget availability. In fact, using BRM as a reference, DS outperforms DU consistently. This result was expected, because the structure of DS models is similar to the one of BRM, with occurrences sampled from all three parks (Fig. 2b).

Conversely, the structure of DU models is similar to the one LRM, with occurrences sampled from a single park at a time (Fig. 2b). However, DU models did not always perform better than DS models when LRM was used as a reference. With a high sampling effort, DU provides better predictions, while with low sampling effort DS strategy outperforms DU strategy. Indeed, the cost-performance relation follows two different trends according to the adopted data-sharing policy (Fig. 5). Notably, DS is more stable against the reduction of the sampling effort than DU, and then there is a point where DS strategy starts outperforming DU (Fig. 3, 4). While it is true that DS models are built on a higher number of occurrences (i.e. fraction of points from the focal park + from the other two parks), more points do not necessarily correspond to better information. When using LRM as a reference, we assumed that each park is interested in knowing the habitat preferences of a species just within the park's boundaries. Hence, if habitat preferences change across space, adding more occurrences would not result in gaining information for HSMs. In our analyses, we demonstrate that occurrences from neighbouring protected areas, with similar environmental characteristics, can be informative for HSMs. Therefore, data-sharing among managers of protected areas appears to be preferable even to project suitability at a local scale.

The sharing of information has already proven its effectiveness in various fields and at different scales, overall providing several advantages (Lejano and Ingram 2009; Susskind *et al.* 2012; Wyborn and Bixler 2013; Hill *et al.* 2015). In the field of biodiversity monitoring, for example, knowledge-sharing helped in the identification of significant areas for the monitoring of the northern Rocky Mountain wolf (Wyborn and Bixler 2013). Moreover, data collected from different sources (meta-analyses) allowed to assess the status of conservation of different species at large scale (Bonardi *et al.* 2011). Aside from the evaluation of broad-scale conservation status, we showed that smaller scale data-sharing can improve local biodiversity assessment. The intrinsic nature of Natura 2000, which has been thought and planned as a network of conservation areas in a human-dominated landscape, has facilitated the origin of many nearby protected areas rather than few very large entities (Evans 2006). Those areas are usually managed by different stakeholders, but this policy-based partitioning usually doesn't reflect natural processes. The incorporation of natural processes in biodiversity conservation is at the same time challenging and essential if we want to preserve biodiversity in the long-term (Maiorano *et al.* 2007). Results obtained in this work could lead one step closer, making us imagine a scenery where multiple groups Natura 2000 areas, grouped by environmental and species similarity, cooperate to the conservation of nature, creating a real network of European protected areas. Following this framework, the use of economic resources could be optimised to better accomplish Habitat Directive duties, improving the quality of the work without increasing the outlay for the single reserve manager or, vice versa, achieving better results when economic resources are limited from the beginning.

The Habitat Directive requires the standardised monitoring of biodiversity in the Natura 2000 areas, and in this context HSMs can provide a standardised and objective tool for biodiversity assessments (Ficetola *et al.* 2012; Funk *et al.* 2013; Mangiacotti *et al.* 2013). First of all, HSMs can improve the knowledge about the habitat preferences of a species, helping to identify which are the habitat features crucial for specie's occurrence (e.g. Peterman *et al.* 2013; Ficetola *et al.* 2020). HSMs have been widely used for exploring possible locations for new Natura 2000 areas and also to evaluate the efficiency of Natura 2000 network in protecting the potential distribution of endangered species to the real area protected by Natura 2000 network (Buse *et al.* 2007; Embling *et al.* 2010; Bosso *et al.* 2013; Rubio-Salcedo *et al.* 2013; Amici *et al.* 2014). Furthermore, HSMs can help evaluate relationships between the temporal trend of populations and changes in environmental characteristics (Rondinini *et al.* 2011; Falaschi *et al.* 2019). Moreover, projections of HSMs on future conditions can suggest how biodiversity will respond to expected environmental changes, suggesting if the future conservation status is likely to improve or get worse (Araújo *et al.* 2011; Thuiller *et al.* 2011). These examples show that HSMs can be a powerful tool when employed in biodiversity conservation, helping to identify critical areas and also present and future threats to species conservation.

Choosing the best spatial distribution of sampling effort is crucial should we want to optimize available resources. For instance, Marta *et al.* (2019) found that when the aim is to gather information about species' ecology for conservation purposes, uniform sampling of the study area is preferable compared to stratified (habitat-specific) sampling. Similarly, in our study, we demonstrate that when the aim is to collect information about general patterns of species distributions, data-sharing is always preferable (Fig. 3). Additionally, when the within-park sampling effort is limited, data sharing is the best choice even if the aim is to obtain information about park-specific habitat preferences of species (Fig. 4). In this study we showed that overcoming administrative barriers and share data among different managers of protected areas enhances the performance of Habitat Suitability Model. As a consequence, data-sharing has the potential to improve the reliability of future management actions.

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Conflicts of Interest

The authors declare no conflicts of interest.

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Species	**Reference model**			
	BRM	**LRM**		
		PP	PG	BB
Podarcis muralis	0.811 *(1234)*	0.733 *(403)*	0.880 *(516)*	0.846 *(315)*
Lacerta bilineata	0.876 *(101)*	0.762 *(51)*	0.951 *(27)*	0.923 *(23)*
Hierophis viridiflavus	0.837 (*72*)	0.846 *(30)*	0.887 *(26)*	0.893 *(16)*

Table 1. Area under the receiver-operating curve (AUC) for the reference models. Final sample size, i.e. the total number of raster cells used to build HSMs, is reported between brackets.

Park **Species**	**PP**	**PG**	**BB**	**Species mean**
Podarcis muralis	0.23	0.18	0.11	0.17
Lacerta bilineata	0.55	0.09	0.15	0.26
Hierophis viridiflavus	0.62	0.43	0.51	0.52
Park mean	0.47	0.23	0.26	0.32

Table 2. Sampling effort at which DS strategy overcomes DU strategy when LRM is used as a reference. The threshold was estimated as the value of relative sampling effort at which the confidence area of the DS curve intersects that of DU curve (Fig. 5).

Captions to figures:

Fig. 1. The Italian Natura 2000 network and study area. The network is showed in green and consists of neighbouring landscape patches surrounded by urban and agricultural areas. The study area is shown in the bottom left and consists of three protected areas located in Northern Italy (Lombardy region is highlighted in grey). BB: *Brughiera Briantea* park; PG: *Groane* regional park; PP: *Pineta di Appiano Gentile e Tradate* regional park.

Fig. 2. Flow-diagram of the analytic approach. The process shown here was repeated for each species and for 18 different levels of sampling effort. a) First, we randomly selected a subsample of points from the complete dataset (1). Sampled points were used to run a single Data-Sharing Habitat Suitability Model (HSM) for all three park, and one Data-Un-sharing HSM for each park (2). For each level of sampling effort, the points selection process was repeated ten times (3). HSMs were projected in geographic space to obtain values of estimated suitability: the Data-Sharing HSM was projected three times, once for each park; while each of the three Data Un-Sharing HSMs was projected once (4). The six projections obtained were compared to the corresponding Local Reference and Broad Reference projections, through the calculation of the relative rank score (5). Relative rank score values were stored for statistical analyses (6). b) Schematic representation of the points selection process: the point sample was used altogether for Data-Sharing HSM, while it was separated according to the park for the Data-Un-sharing HSMs. Also background used is shown. HSM: Habitat Suitability Model; LRM: Local Reference Model; BRM: Broad Reference Model; GAM: Generalized Additive Model; LMM: Linear Mixed Model.

Fig. 3. Models performance comparison using BRM as a reference. Lines represent the performance of the models under the two data-sharing policies, with the 95% credible interval. DU: data-un-sharing; DS: data-sharing; BB: *Brughiera Briantea* park; PG: *Groane* regional park; PP: *Pineta di*

Appiano Gentile e Tradate regional park; Pmur: *Podarcis muralis*; Lbil: *Lacerta bilineata*; Hvir: *Hierophis viridiflavus*.

Fig. 4. Models performance comparison using LRM as a reference. Lines represent the performance of the models under the two data-sharing policies, with the 95% credible interval. Vertical dashed lines represent one-sixth of the maximum sampling effort (i.e. one year of monitoring instead of six years). DU: data-un-sharing; DS: data-sharing; BB: *Brughiera Briantea* park; PG: *Groane* regional park; PP: *Pineta di Appiano Gentile e Tradate* regional park; Pmur: *Podarcis muralis*; Lbil: *Lacerta bilineata*; Hvir: *Hierophis viridiflavus*.