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A practical overview of transferability in species distribution modelling

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1 **A practical overview of transferability in species distribution**

2 **modelling**

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11 **Abstract**

12 Species distribution models (SDMs) are basic tools in ecology, biogeography and

13 biodiversity. The usefulness of SDMs has expanded beyond the realm of ecological

14 sciences, and their application in other research areas is currently frequent, e.g., spatial

15 epidemiology. In any research area, the principal interest in these models resides in their

16 capacity to predict species response in new scenarios, i.e. the models' transferability.

17 Although the transferability of SDMs has been the subject of interest for many years,

18 only in the 2000s did this topic gain particular attention. This article reviews the concept

19 of the transferability of SDMs to new spatial scenarios, temporal periods and/or spatial

20 resolutions, along with the potential constraints of the model's transferability, and more

21 specifically: (i) the type of predictors and multicollinearity, (ii) the model complexity,

22 and (iii) the species' intrinsic traits. Finally, we describe a practicable analytical

23 protocol to be assessed before transferring a model to a new scenario. This protocol is

24 based on three fundamental pillars: the environmental equilibrium of the species with

25 the environment, the environmental similarity between the new scenario and the areas

26 used to model parametrisation, and the correlation structure among predictors.

27 Key words: species distribution model, spatially explicit model, spatial transferability,

28 temporal transferability, downscaling, multicollinearity

29

30   **Introduction**

31   The study of species distributions developed significantly during the last decades of the

32   Twentieth Century. The first theoretical models and predictive approaches appeared in

33   the late 1970s and during the 1980s (Kessel 1979; Busby 1986; Nix 1986; Austin 1987;

34   see also Booth et al. 2014). The increasing use and development of geographic

35   information systems and the growing ability and capacity to handle large databases

36   provided fundamental tools with which to carry out large-scale studies on species

37   ranges (e.g. Guisan and Zimmermann 2000; see also Elith and Leathwick 2009).

38   Nowadays, species distribution models (SDMs) have become basic tools in ecology,

39   biogeography, biodiversity and conservation (e.g. Franklin 2010).

40   An SDM is basically a correlative or mechanistic model that relates the localities in

41   which one species is present – or its abundance – with the ecological and geographical

42   characteristics of the territory (Guisan and Zimmermann 2000). These kinds of spatially

43   explicit models make it possible to determine the main environmental gradients to

44   which species are able to respond, and to predict the potential of a territory for the

45   species according to the local environmental characteristics. Scientific literature has

46   denominated these models in accordance with the interpretation that is made of their

47   outcomes, and the terms 'niche models', 'predictive models of habitat' or 'suitability

48   models' have, for example, been used. Researchers are currently attempting to reach a

49   consensus as to what name to apply to these approaches, and the term 'species

50   distribution models' is now becoming generalised as a more theoretically neutral term

51   (Mateo et al. 2011).

52   The applications of SDMs in ecology are varied and numerous: from basic studies

53   whose aim is to determine the ecogeographical determinants of species ranges, to

54   multispecies interdisciplinary studies focused on relevant ecological questions, both for

55   basic and applied ecology (e.g. Guisan et al. 2006; Acevedo et al. 2010; Franklin 2013).

56   However, the principal driving force behind SDMs was their use to predict species

57   response in unsampled spatio-temporal scenarios. Models can be used to forecast the

58   distribution of a species in different scenarios, such as past climatic scenarios in order

59   to reconstruct the evolutionary history of the species (e.g. Nogues-Bravo 2009), future

60   scenarios of climate and land-use changes to assess species sensitivity to environmental

61   changes (e.g. Pearson and Dawson 2003; Acevedo et al. 2011), for an invasive species

62   in a new territory to assess potential invasion patterns (e.g. Peterson and Vieglais 2001;

63   Peterson 2003)*,* or similarly, for a species in unsampled territories (e.g. Randin et al.

64   2006; Barbosa et al. 2009). This concept of the cross applicability of the models in both

65   space and time has been defined as generality (Fielding and Haworth 1995) or

66   transferability (e.g. Thomas and Bovee 1993; Glozier et al. 1997; hereafter

67   transferability) and it is now widely used to expand the potential of SDMs. But the

68   transference of a SDM is not a straightforward task (see below) and requires to handle

69   both a conceptual background and analytical procedures in order to avoid the inclusion

70   of bias in the results. However, most of the SDMs transferences in studies not directly

71   focused in testing transferability are uncritically performed (but see e.g. Acevedo et al.

72   2014a; Ray et al. 2016). In this context, we provide a practical overview of SDMs

73   transferability aimed to i) define the concept of the transferability of SDMs to new

74   spatial scenarios, temporal periods and/or spatial resolutions, and identify the potential

75   constraints of the model's transferability, and ii) describe a practicable analytical

76   protocol to be assessed before transferring a model to a new scenario.

77

The transferability of SDMs

79   Modellers employ SDMs when seeking the environmental conditions of the species and

80   when interested in registering general responses to environmental gradients and not only

81   to local conditions. The fit among predictions and observed data – when available – is

82   an empirical validation of the ecological significance of the model; a general and

83   validated model can therefore be transferred to other scenarios so as to predict the

84   pattern of the species in a scenario in which very little sampling has taken place. The

85   validation of the model is a key step for getting success in its transference. In the last

86   years further advances were produced on validation step in SDM and nowadays there

87   are both conceptual framework and analytical protocols to consistently perform it (e.g.

88   Roberts and Hamann 2012; Muscarella et al. 2014; Radosavljevic and Anderson 2014).

89   Finally, the transference of an SDM to outside the context used for model calibration

90   helps drive return on investment for the development of the model, which often requires

91   intensive fieldwork and/or laboratory analyses. At times of low investment in science in

92   general and in the management of natural resources in particular, the use of published

93   models to predict species patterns in areas for which little information is of the species

94   available is an extremely interesting line of research (Acevedo et al. 2014b).

95   Models can be transferred to different spatial scenarios, temporal periods and/or spatial

96   resolution. *Spatial transferability* is a means to assess the degree to which a

97   parameterised model can be generalised to other territories (Randin et al. 2006; Barbosa

98   et al. 2009). It is possible to differentiate two types of spatial transferability as regards

99   whether predictions are made within (interpolation) or outside (extrapolation) the

100   geographical domain of the model (Elith and Leathwick 2009). Spatial transferability

101   has been used widely to improve sampling design (e.g. Rebelo and Jones 2010), to

102   determine the environmental potential for invasive/introduced species (e.g. Jimenez-

103   Valverde et al. 2011; Torres et al. 2016), or to assess the niche similarities between

104   related taxa (e.g. Acevedo et al. 2014a**)**, among others. For instance, SDM extrapolation

105   was recently used to evaluate niche relationships between two allopatric species, *Lepus*

106   *castroviejoi* and *Lepus corsicanus*, which inhabit the northern Iberian Peninsula and

107   mainland Italy and Sicily, respectively (Acevedo et al. 2014a), in order to reinforce the

108   molecular evidence on their status as sister species (Alves et al. 2008). In the study in

109   question, individual models were transferred to the territory of the sister species in order

110   to evidence their ecological similarities.

111   The transferability of the model to other periods of time is known as *temporal*

112   *transferability*. It permits the evaluation of the effects that environmental changes have

113   had and will have on species ranges (e.g. Dobrowski et al. 2011; Tuanmu et al. 2011) –

114   i.e. to determine the species' sensitivity to environmental changes – in order to

115   anticipate the effects of global change on species distributions (e.g. Brook et al. 2008),

116   and to design conservation plans in the context of environmental change (Araújo et al.

117   2011; Thuiller et al. 2011). The transference of SDMs to future climate change

118   scenarios was the area that stimulated further progress in both conceptual and analytical

119   strategies of SDMs. It is not, however, possible to adequately assess predictions for

120   future scenarios owing to the obvious lack of data (but see Araújo et al. 2005a).

121   Therefore, predictions should be considered with relative caution since several sources

122   of uncertainty emerge at each step (e.g. Real et al. 2010) and propagate throughout the

123   modelling procedure (e.g. Rocchini et al. 2011). A huge amount of studies are based on

124   the temporal transferability of SDM. For instance, Maiorano et al. (2011) assessed the

125   future of terrestrial mammals in the Mediterranean basin in climate change scenarios.

126   These authors concluded that a substantial number of species, and mainly endemic

127   species, will have been severely affected by the ongoing climate change by 2100.

128   The integration of macroecology and phylogeny is currently a cutting-edge research

129   area in biogeography. In this respect, SDMs are hindcasted to past environmental

130   scenarios as a means to provide ecological scenarios in which to test evolutionary

131   hypotheses (e.g. Wielstra and Arntzen 2012). However, SDMs can perform poorly

132   when projected to distant time periods and climatic dissimilar scenarios (Maguire et al.

133   2016). Thus, predictions for past scenarios should be validated by using fossil records

134   and/or phylogenies (e.g. Collevatti et al. 2013; Diniz-Filho et al. 2013; Maguire et al.

135   2015). For instance, the application of SDMs in evolutionary studies allows researchers

136   to propose and validate hypotheses regarding the existence and location of glacial

137   refugia (e.g. Carnaval and Moritz 2008; Acevedo et al. 2012), to explore ecological

138   relationships within and between phylogenetically related taxa (Peterson et al. 1999;

139   Wiens and Graham 2005), or to reconstruct the conditions that allowed, among other

140   things, historical hybridisation and genetic introgression to occur (Acevedo et al. 2015).

141   The resolution at which distribution data are available does not always coincide with the

142   interests of conservation and management. The *changes in the spatial resolution* of a

143   model's predictions – i.e. the projection of models built at one resolution to a larger

144   (upscaling) or a finer (downscaling) spatial resolution – are potentially highly beneficial

145   for ecology and conservation (Araújo et al. 2005b). The large-scale data available are

146   usually too coarse to enable spatial resolutions to be applied in local conservation

147   planning, while the collection of data at a finer resolution requires high sampling

148   efforts, which are only feasible for a few species and over small areas. For instance,

149   Barbosa et al. (2010) successfully downscaled SDMs for a restricted endemic

150   insectivore, the Iberian desman (*Galemys pyrenaicus*), and a more widespread

151   carnivore, the Eurasian otter (*Lutra lutra*), in the Iberian Peninsula. This and other

152   studies suggest the potential usefulness of downscaled projections of environmental

153   quality as a proxy for expensive and time-consuming field studies when field studies are

154   not feasible.

155   The opposite process, upscaling, is not as frequent as downscaling in studies on species

156   distribution (but see Harvey 2000). Data on species distribution at fine spatial resolution

157   is able to contain more reliable and precise information on species ecology than data

158   obtained for coarser resolutions, but the former are patchy within the species range.

159   However, factors that are associated with the occurrence of individuals on a local scale

160   may not be associated with factors explaining a large-scale species distribution range

161   (Jimenez-Valverde et al. 2008)**,** and SDMs derived from fine resolution data are,

162   therefore, sometimes not able to provide a good explanation of data represented at

163   coarser resolutions. This indicates that SDMs at both fine and coarse resolution do not

164   explain the same species distribution pattern, as was discovered by Marcer et al. (2012)

165   when studying vascular plants in Spain; the models at a fine resolution probably explain

166   the habitat selection within the area favourable for species distribution, but they fail to

167   discriminate between the areas that are favourable and unfavourable for the species.

168   Despite the relevance of this topic in order to both fit the spatial resolution of SDM

169   adequate to data and goals, and determine the limits for changing spatial resolution, the

170   studies are scarce and, therefore, further research would be valuable in this area.

171

172   **Potential constraints as regards the model's transferability**

173   Researchers have, for many years, found the transferability of statistical models to be a

174   subject of interest, but it was not until the 2000s that this topic gained particular

175   attention (Randin et al. 2006; Vanreusel et al. 2007; Barbosa et al. 2009). Many studies

176   have indicated factors that may affect and hinder the model's transferability, such as the

177   type of predictor variables and their multicollinearity, the model complexity

178   (dimensionality and algorithm), and the species' intrinsic traits (see Figure 1).

179   *Type of predictors and multicollinearity*

180   The choice of predictor variables for modelling affects the model's predictive

181   performance (e.g. Synes & Osborne 2011) and, therefore, the SDM's transferability.

182   Most of the abiotic predictors used for modelling explain animal distribution indirectly,

183   through their correlation with ecological functional resources (Austin 2002; Guisan and

184   Thuiller 2005; Austin et al. 2006). Extrapolations will be particularly error-prone if only

185   indirect predictors are used, because the correlations between them and the functional

186   resources vary in both space and time (Austin 2002). When these correlations depend

187   on area-specific conditions, models could be overfitted to the local conditions, which

188   may compromise the model's transferability (Luoto et al. 2002) – in SDMs overfitting

189   occurs when a model closely fits the calibration data and, thus, fails when predicting on

190   independent data. The use of more ecologically relevant predictors is now increasingly

191   possible as remotely sensed data are more readily available (e.g. Pettorelli et al. 2016).

192   Remote sensing therefore provides data that can play a role in improving the

193   performance of SDMs and, therefore, their transferability (e.g. He et al. 2015),

194   especially spatial transferability and changes in spatial resolution, since remote sensing

195   data are not available for different past, e.g. in an evolutionary context, or future

196   temporal scenarios. Despite these advances, many studies appear to use only data that

197   are readily available, while failing to explain the relevance of the predictors selected,

198   and probably missing important ecological drivers.

199   When an SDM is extrapolated, the proper quantification of the effect of each predictor

200   on current geographic ranges is a must for an accurate estimation of the potential for the

201   species (Braunisch et al. 2013). But the effect of a factor can only be adequately

202   estimated in the context of the other influential factors (e.g. Márquez et al. 2011). This

203   signifies that the real effect of a factor on species distributions could be masked (under

204   or overrated) by confounding correlated factors, becoming evident only when the effects

205   of the other factors are subtracted from the weights of the predictors and subsequently

206   from the predictions of the models (e.g. Lavergne et al. 2005; Real et al. 2013; Record

207   et al. 2013). One of the main challenges in this respect is to filter out (control for) the

208   variation caused by spatial structures (Griffith and Peres-Neto 2006; Dormann et al.

209   2007*;* Hawkins et al. 2007), since the spatial structure in species distribution and

210   environmental processes can increases type I errors and can potentially affect model

211   estimations (e.g. Legendre et al. 2002). Briefly, the solution is again to produce

212   combined models in which both environmental and spatial gradients should be

213   considered (for details, see Peres-Neto and Legendre 2010). For instance, Real et al.

214   (2013) estimated the pure climatic effect (i.e. not affected by covariation with non-

215   climatic factors) and the apparent climatic effect (i.e. including shared effects between

216   climate and non-climatic factors) on species distribution, and suggested that both the

217   pure and apparent fractions could be interpreted as the lower and upper bounds of a

218   range of possible scenarios for the future climatic potential for the species.

219   *Model complexity*

220   Model complexity can be characterized with the number of predictors (dimensionality),
221   the algorithm and the parameters within the same algorithm (e.g. Merow et al. 2014;
222   Duque-Lazo et al. 2016). A simpler model typically has relatively fewer parameters and
223   fewer relationships among predictors compared to a more complex model. Simple
224   models, with insufficient flexibility to describe occurrence-environment relationships,
225   can be misunderstanding the factors driving species distributions. Complex models,
226   with excessive flexibility and number of parameters, can be inadvertently ascribing
227   pattern to noise. Therefore, in the framework of the transferability, complex models
228   should be avoided.

229   The dimensionality – i.e. number of predictors – of the models determines the
230   transferability of SDMs (e.g. Peterson 2011) and must be declared and weighed
231   carefully from the beginning of the analysis (see also Warren et al. 2014).
232   Transferability decreases as the number of predictors in the model increases; models
233   developed through too many dimensions may run the risk of overfitting to local
234   conditions that restrict the predictive power of the model.

235   The complexity associated to the algorithm is, in this case, characterised as the shape of
236   the inferred occurrence–environment relationships that are closely related to the number
237   of parameters. Briefly, environmental envelopes (e.g. BIOCLIM or DOMAIN) and
238   distance-based approaches in multivariate environmental spaces (e.g. ENFA,
239   Malahanobis) are considered to be the simplest SDMs. Their response curves are simple
240   functions with a reduced number of parameters (e.g. linear, hinge or step; Hirzel et al.
241   2002; Elith et al. 2005). Generalised linear models (GLM), which are typically fitted
242   with linear or polynomial features up to second order terms (rarely third or fourth order)
243   for SDMs, are considered to be simple even when they admit more complexity.
244   However, this relative simplicity applies to the relationship between probability, which
245   is the output of the model, and the logit function, whereas the relationship between
246   probability and individual variables tends to be more complex owing to the collinearity
247   between predictors (Acevedo and Real 2012). GARP and MAXENT are considered to
248   be complex algorithms since they allow high flexibility (Stockwell and Peters 1999;
249   Phillips et al. 2006). Generalised additive models (GAM) are also complex techniques
250   because they allow non-parametric smooth functions of variable flexibility (Hastie and

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251   Tibshirani 1990). Decision trees (Breimann et al. 1984) can also become quite complex
252   because they may use a large number of step functions (each requiring a parameter) and
253   can implicitly include high order interaction terms with which to depict response curves
254   of arbitrary complexity. In addition to the analytical protocols involving the use of a
255   single modelling technique, "ensemble models" in which predictions from several
256   techniques are considered, such as BIOMOD (Thuiller et al. 2009), are also frequently
257   used. Different modelling techniques can achieve variable performance in the data-
258   training set, even when they are calibrated with the same data (e.g. Segurado and Araújo
259   2004; Benito de Pando and Peñas de Giles 2007; Mateo et al. 2011). The capability of
260   the different techniques to be transferred is consequently also widely variable (e.g.
261   Peterson et al. 2007). In addition, only models that produce commensurate outcomes,
262   such as probability or favourability (see Acevedo & Real 2012), can be adequately
263   combined in ensemble models, whereas models yielding suitability values that are
264   idiosyncratic for each modelling technique lack the commensurability required for
265   combination (Romero et al. 2016). However, the ensemble models does not necessarily
266   control or fix biases and/or improve transferability (see e.g. Rodríguez-Rey et al. 2013).

267   Several studies were performed to assess the relationship between model complexity
268   and predictive performance, both on the training and transference area. For instance,
269   Tsoar et al. (2007) compared the performance of six algorithms and concluded that
270   flexible algorithms attain a higher predictive performance in the training data set than
271   do non-flexible ones. This result resembles the insight provided by Elith et al. (2006),
272   who also concluded that those which are able to fit complex responses are preferable to
273   simple algorithms. However, complex algorithms are not preferred when the models
274   should be transferred to new scenarios, because flexible algorithms tend to overfit to
275   local conditions, thus losing generality (Jimenez-Valverde et al. 2008). A good
276   transferability has been suggested for algorithms such as GLM and GAM (e.g. Austin et
277   al. 2006; Meynard and Quinn 2007; Wenger and Olden 2012). Randin et al. (2006)
278   reported that GLM was more robust than GAM, suggesting that overfitting can reduce
279   the transferability of GAM models. With regard to GARP and MAXENT, two
280   techniques based on data of presence, Peterson et al. (2007) compared these techniques
281   and found the latter to be overfitted. However, if the sample size is small, it can
282   extrapolate better than GARP (Papes and Gaubert 2007). Other techniques have proved
283   to have worse predictive power and accuracy, such as GARP, Random Forest and

284   MARS (e.g. Prasad et al. 2006). Determining the most appropriate amount of

285   complexity to be included in SDMs is therefore crucial for biological applications

286   (Merrow et al. 2014). Researchers must constrain model complexity on the basis of data

287   attributes and study objectives, and an understanding of how they interact with the

288   underlying biological processes.

289

290   *Species intrinsic traits*

291   Lack of transferability can be also caused by species specific traits not included in the

292   model, for instance dispersal capacity, changes in the role of biotic interactions and/or

293   changes in the realized niche (e.g. Urban et al. 2013; Williams et al. 2013). Despite this,

294   the relationship between specific traits and model transferability has rarely been studied.

295   Vanreusel et al. (2007) related model spatial transferability to the range of habitat use of

296   two butterfly species. These authors observed that the model for the species with the

297   smallest range of space use (*Callophrys rubi*) was more transferable than the model for

298   a more mobile species (*Hipparchia semele*). Kharouba et al. (2009*),* also with

299   butterflies, found that transferability declined for widely distributed species over time

300   and showed inconclusive results for dispersal capability. After working with 133

301   vascular plant species, Dobrowski et al. (2011) found that models for non-endemic

302   species with a greater dispersal capacity, intermediate levels of prevalence, and a low

303   capacity to adapt to fire had a higher transferability over time than did endemic species

304   with a limited dispersal capacity that rely on fire for reproduction (disturbance

305   response). Heikkinen et al. (2012) found differences in models' spatial transferability

306   between taxonomic groups; the best transferability was specifically found for birds,

307   followed closely by butterflies, whereas plant species were found to have a weak

308   transferability capability. There is thus a need for further research that will relate

309   species' taxonomical and functional traits to model's transferability, taking into account

310   potential discrepancies in their effects as regards the type of transferability: spatial *vs.*

311   temporal.

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313   **Checking the model's transferability: analytical protocol**

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314   Before transferring an SDM beyond the data-training set, three fundamental

315   requirements should be checked (see Figure 1):

316   i) Transferability requires the target species to have environmental equilibrium

317   throughout its entire distribution area (Nogues-Bravo 2009). Species are said to be at

318   equilibrium with the environment if they occur in all climatically suitable areas whilst

319   being absent from all unsuitable ones (Araújo and Pearson 2005). However, even when

320   the results obtained from a model suggest a climatic equilibrium, the model's

321   transferability does not necessarily provide realistic results. This was the case of a study

322   on *Crocuta crocuta* in which predictions for the last interglacial period were incoherent

323   because the current geographical range does not allow estimations of all of the

324   environmental requirements of the species to be made (Varela et al. 2009).

325   Paradoxically, the opposite – e.g., a model in disequilibrium that produce good

326   predictions – can also occur when working, for instance, with an introduced invasive

327   species (Muñoz and Real 2006; but see Jimenez-Valverde et al. 2011). A proxy metric

328   of equilibrium between species distribution and the environment is the realised/potential

329   range size ratio (Svenning and Skov 2004).

330   ii) The environmental similarity of the new scenario with regard to the training area

331   should be evaluated. As a general rule, SDMs may only be transferred to scenarios

332   which are similar in environmental terms to that in which the model was calibrated.

333   Similarity can be assessed using Mahalonobis distances and/or multivariate

334   environmental similarity surfaces (e.g. Elith et al. 2010). This kind of analyses also

335   allow to identify the predictor that is driving to a given locality to be environmentally

336   dissimilar (the most dissimilar predictor can thus be recognized). To remove of the

337   modelling procedure these dissimilar predictors is a way to improve the transferability

338   of the model.

339   iii) High levels of multicollinearity between the predictors included in a model can bias

340   predictions when the model is transferred to a situation in which the correlation matrix

341   between predictors is different. Collinearity can be quantified using the variance

342   inflation factor (VIF), which should be calculated for each of the predictors in the model

343   (see Zuur et al. 2010). There are more ways in which to detect collinearity, such as by

344   examining the matrix of correlation coefficients between predictors in order to avoid

345   including those that are highly correlated (r>|0.8|) in the model. However,

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346   multicollinearity is a real phenomenon in nature, and it cannot therefore be avoided in

347   all cases, although it should be managed. When possible, the best ways in which to

348   manage multicollinearity are by increasing the sample size by including external

349   information and by removing highly correlated variables (e.g. Doran 1989). The

350   maintenance of the correlation structure among predictors between training and

351   transference areas should be assessed. As the coefficient for a predictor in a model

352   depends on the coefficients for the other predictors (Fox 1997), changes in the

353   correlation structure may include severe bias in models' predictions in the transference

354   area. A Mantel test (Mantel 1967), or another similar means to determine the

355   association between matrices (see Guillot and Rousset 2013), should therefore be

356   carried out in order to avoid biased results.

357   In summary, various methodological requirements should be taken into account before

358   transferring a model to another spatial/temporal scenario. This means that if the

359   objective is to transfer a model, special attention should be paid to the species-

360   environment equilibrium and to the selection of predictors. What is more, a calibrated

361   model cannot be transferred just anywhere, but only to those scenarios that are

362   environmentally similar to the scenario in which the model was calibrated. Despite the

363   importance of transferring distribution models, studies designed to explore this feature

364   and to assess the methodological and ecological factors which determine it are still

365   scarce (e.g. Dobrowski et al. 2011). This is a line of interesting and timely research,

366   given the high number of models that have been published in recent years (Lobo et al.

367   2010).

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738   Figure 1. Overview of the model building process when the dataset is split into two

739   parts, one with which to fit and another with which to evaluate the model. The

740   transferability of the model to a new scenario is also schematised. In each step, the main

741   factors that can compromise the model's transferability are highlighted in red, along

742   with the three (1-3) fundamental requirements that should be checked before the

743   transference of the model to the new scenario (see text for details).
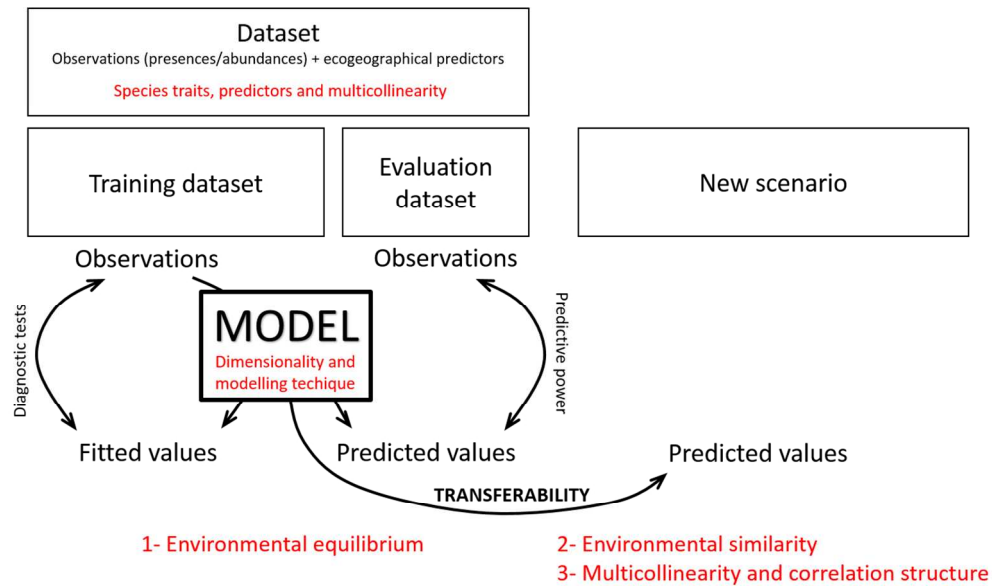
Overview of the model building process when the dataset is split into two parts, one with which to fit and another with which to evaluate the model. The transferability of the model to a new scenario is also schematised. In each step, the main factors that can compromise the model's transferability are highlighted in red, along with the three (1-3) fundamental requirements that should be checked before the transference of the model to the new scenario (see text for details).
Figure 1
368x219mm (96 x 96 DPI)