Appendix S1. Characteristics of mechanistic and phenomenological models in ecology. A distinction is made in the literature between mechanistic and phenomenological models (Hilborn & Mangel 1997; Clark & Gelfand 2006; Stouffer 2010), which can be seen as the two ends of a continuum of ecological understanding (Clark & Gelfand 2006; Dormann *et al.* 2012). Mechanistic models are based on clearly identified biological mechanisms linked into a process based framework while phenomenological models are built on empirically derived statistical relationships between the variables of interest. In practice though this distinction is not that obvious, as what can be seen as a mechanism at one scale may be perceived as a correlative response at a lower level of organization (Anderson 1972). For instance, the classical Lotka-Volterra model is considered phenomenological by community ecologists: there is no explicit mechanism of competition (it is only approximated through the use of competition coefficients and density dependent growth function). However this same model, when included into biogeographic model of species distribution, is considered as mechanistic (Godsoe & Harmon 2012), as species interactions were initially not included into these phenomenological models of species distribution. The distinction between mechanistic and phenomenological is however useful as it helps to differentiate between the need to understand and the need to predict (i.e. explanatory vs. anticipatory predictions), which are not always associated in research agendas. Mechanistic models are usually considered more robust to extrapolation outside the range of current conditions than are phenomenological models, because the functional forms of some processes (but not all) are likely to be conserved (e.g., Levin 1992; Dormann *et al.* 2012). Here we compare the principles, assumptions, and limitations associated to both extremes of the continuum, using species distribution models as an example.

	Mechanistic models	**Phenomenological models**
Principle		
	Prediction and input are of a different nature. Known biological mechanisms link the two.	Input data and predictions constitute both the input and output of the model. Observed patterns of species distribution are related to spatial patterns in environmental variables; the relationship is used to predict abundance or occurrences.
Assumptions		

	Assumptions are guided by the conceptual framework and associated simplification choices. They vary among models and are usually well-defined (e.g., concerning inter- or intraspecific interactions, or the biological mechanisms underlying growth, fecundity or survival).	Assumptions are guided by the conceptual framework (e.g., ecological niche estimation) and available information. The models assume that (i) observed spatial patterns of abundance or occurrence result from (hidden) mechanisms that vary with the environmental variables taken into account; (ii) environmental variables are relevant to define the species' fundamental niche. (iii) the realized niche is representative of the fundamental niche; (iiv) the species is in quasi-equilibrium with the environment.
Choices left to the modeler		
Processes	Which processes govern life history traits.	None
Environmental drivers	Which environmental variables affect these processes? What is the optimal resolution of the environmental variables? What resolution is available? Which processes must be accounted for and which process might be ignored?	Which environmental variables might indirectly affect the species' occurrence? What is the optimal spatial resolution? Note that climatic data are not necessarily available at spatial scales matching that relevant to the niche.
Transferability		
Within and among taxa	Each model is usually defined for a small number of taxa [e.g., lizards (Buckley 2008) or temperate trees (Chuine & Beaubien 2001)]. Parameters derived at the species (e.g., Chuine & Beaubien 2001) or population level (Gritti *et al.* 2013), or for different ages (with implications for demography Smith, Prentice & Sykes 2001).	The same approach can be used for any taxon. Only the set of environmental variables would vary. Model parameters may vary among species (e.g., Thuiller *et al.* 2011), subspecies (Pearman *et al.* 2010) or even SNP-variants (Banta *et al.* 2012).
Among environmental spaces	First principles should hold outside the environmental range used for calibration. Extrapolation outside the environmental range used for calibration may be safer than for phenomenological models, because the functional responses of some – but not all – processes are likely to hold under a wider range of environmental conditions (Dormann *et al.* 2012). Yet, the variation of particular mechanisms may not be foreseen under new combinations of environmental variables.	Phenomenological models often show low transferability outside the environmental range used for model calibration (e.g., Heikkinen, Marmion & Luoto 2012).
Validation		
	Purely mechanistic models do not use observed distributions as inputs: these can be used as an external validation tool. Some validation attempts have used long term past data (Saltré *et al.* 2013).	Usually performed using cross-validation procedure, which may over-estimate the predictive accuracy of the approach (Araujo *et al.* 2005). Some validation attempts have used recent past data (Araujo *et al.* 2005) and long term past data (Pearman *et al.* 2008).
Ease of use		
Data availability	Gathering data for calibrating the reaction norms of biological processes to environmental variables may require much time and/or money.	Data on environmental variables and species occurrences or abundances are often publicly available.
Mathematical skills	Mathematical skills may be implied to formulate the model. New developments in statistical parameterization ask for complementary knowledge in inverse modeling and inferential statistic.	Stand-alone softwares allow non-specialists to easily fit any model on their own, although a good knowledge of what lies behind the algorithm is strongly recommended.
Implementation	Model implementation may take time as they are often built from the	User-friendly modeling tools have been setup (Phillips, Anderson & Schapire

	ground up.	2006; Qiao *et al.* 2012), most of which have been ported to R (Thuiller *et al.* 2009; Hijmans *et al.* 2012).
Computer time	May be computationally intensive depending on the model and area considered.	Results can be obtained within minutes or hours for a given species.
Communication		
Replicability	Because model implementation takes time, model code is often not open source (and may be patented, e.g., Porter & Mitchell 2006), thus often hampering result replication.	Model outputs can be replicated due to data availability, open source code, and relatively low computation needs.
Complexity	Models may be complex and imply numerous mechanisms. Their complexity may be an obstacle to communication with stakeholders.	Even though some algorithms are complex, the rationale *i*s simple. Communication to stakeholders is easier.
Models explicitly account for		
Biotic interactions	Some intrinsically do (e.g., Smith, Prentice & Sykes 2001; Buckley 2008).	Absent from most models but can be implemented (e.g., Boulangeat, Gravel & Thuiller 2012).
Dispersal	Can be implemented (e.g., Saltré *et al.* 2013).	Absent from most models but can be implemented (e.g., Boulangeat, Gravel & Thuiller 2012; Meier *et al.* 2012).
Local adaptation	Can be implemented (e.g., Chuine & Beaubien 2001; Gritti *et al.* 2013).	Absent from most models but can be implemented (e.g., Pearman *et al.* 2010; Banta *et al.* 2012).
Age structure	Can be implemented (e.g., Smith, Prentice & Sykes 2001).	Can be implemented (e.g., McLaughlin & Zavaleta 2012).
Phenotypic plasticity	Some intrinsically do (e.g., Chuine & Beaubien 2001; Smith, Prentice & Sykes 2001).	Not explicitly accounted for, and not possible if plasticity enables persistence outside the environmental range used for model calibration.
Microevolution	Can be implemented (e.g., Kearney *et al.* 2009).	Not possible

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