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Ordinal response regression models in ecology

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Abstract. Although ordinal data are not rare in ecology, ecological studies have, until now, seriously neglected the use of specific ordinal regression models. Here, we present three models – the *Proportional Odds*, the *Continuation Ratio* and the *Stereotype* models – that can be successfully applied to ordinal data. Their differences and respective fields of application are discussed. Finally, as an example of application, PO models are used to predict spatial abundance of plant species in a Geographical Information System. It shows that ordinal models give as good a result as binary logistic models for predicting presence-absence, but are additionally able to predict abundance satisfactorily.

Keywords: GLM; Ordinal outcome; Statistics; Predictive distribution modeling.

Abbreviations: CR = Continuation Ratio; GIS = Geographical Information System; GLM = Generalized Linear Model; LP = Linear Predictor; LS = Least Square regression model; PH = Proportional Hazard; PO = Proportional Odds.

Introduction

Over the last century, a huge amount of ecological data became available to the scientific community, which are recorded in the taxonomic and ecological literature, herbariums, inventories from natural surveys or, in very recent years, in computer-based taxonomic and ecological data banks. Being originally of a qualitative, descriptive nature, observations of the natural world tended progressively to become more quantitative. Such change is due to progress in sampling techniques and to the recent tendency to design sampling strategies more efficiently. The later is imposed by the advance in statistical techniques and is aimed at better testing biological and ecological theory. However, one cannot always reach a high level of precision during the sampling (e.g. in vegetation science, percent cover in the ground can be difficult to measure accurately). At an intermediary level, ordinal – or semi-quantitative – data can be sampled instead (e.g. ordinal abundance classes), which save part of the quantitative information that would be lost if one had to limit the sampling to qualitative observations (e.g. presence only).

An ordinal scale is defined as an ordering of measurements, with only relative – instead of quantitative – differences between values. For instance, measurements of biological entities in classes which are e.g. ‘ shorter’, ‘darker’ or ‘more abundant’ than others are clearly ordinal. Ordinal data can also originate from ratio or interval data, by ranking or slicing a continuous or discrete scale (e.g. Poisson counts), although such a procedure would inevitably result in a loss of (possibly important) information. On the other hand, some ‘so-called’ quantitative data – such as abundance-dominance scales in phytosociology – should be best considered as ordinal in statistical analyses (see van der Maarel 1979).

The use of statistical methods for ordered data can be traced back to the late 1950s (e.g. Ashford 1959) and the first attempts to model an ordinal response by multiple regression were first published in the late 1960s (e.g. Walker & Duncan 1967). However, the first reviews on this matter did not appear until the early eighties (McCullagh 1980; Anderson 1984). Since then, ordinal regression models have been included in the broader category of Generalized Linear Models (GLMs; see McCullagh & Nelder 1989) and have been more intensively used for biometrical applications (e.g. Greenland 1985; Läärä & Matthews 1985), and even more specifically for biomedical purposes (e.g. epidemics; Armstrong & Sloan 1989).

Ordinal regression models were particularly developed in epidemic studies, toxicity assessments (bio-assays) and social sciences, as these disciplines often have to deal with semi-quantitative variables (e.g. in bio-assays, different levels of ‘tolerance’ to a pollutant). In natural sciences, although several ecological data may be modelled in an appropriate manner as ordinal data, few examples of the ordinal regression model yet exist (Schabenberger 1995; Guisan et al. 1998).

The aim of this paper is hence to present the use of ordinal regression models for ecological applications, through an example taken from the more specific context of plant distribution modeling.

Why using ordinal models ?

In phytosociological studies, for instance, a huge amount of data is still provided by attributing to each plant in a relevé a pre-definite class of percentage cover from the modified Braun-Blanquet (1964) abundance/dominance scale (Barkman et al. 1964). This scale is clearly more semi-quantitative (i.e. ordinal) than truly quantitative. It takes values 0, *r*, +, 1, 2m, 2a, 2b, 3, 4 or 5 to characterize vegetation abundance/dominance, which correspond respectively to no cover, rare species, some individuals present, less than 5% cover, less than 5% cover but very abundant, 6-12%, 13-25%, 26-50%, 51-75% and 76-100% cover. In most quantitative studies, it is transformed into an ordinal scale of linear integer values ranging from 0 to 9 (van der Maarel 1979) and is then considered a quantitative variable if calculations are to be made (see Jongman et al. 1987), using e.g. a least square (LS) regression model. Although the predictions from such a model might be acceptable, we argue that such a procedure may be statistically incorrect for four main reasons.

1. On a quantitative ratio scale, as required by an LS model, the difference in category 6 and category 5 is assumed to have the same meaning as the difference between categories 2 and 1. However, on the scale mentioned above, the values correspond to different species characteristics. Although quantitative comparisons can mathematically be made on such a linearized scale, they will use ratios to calculate coefficient estimates, and thus could mislead further interpretations because the scale actually represents intervals on an arbitrary non-linear scale.

2. The linearized abundance/dominance scale resembles the log-linear transformation used earlier (i.e. before the appearance of GLM) for achieving a Normal error distribution, but then a log-Normal distribution should also be considered in the model rather than the Normal distribution considered in LS models;

3. An ordered categorical variable is discrete with few values, including ‘floor’ and ‘ceiling’, for which a continuous probability model may cause problems (Snell 1964);

4. Unless an appropriate link function is used (i.e. other than unity or logarithm, like logit), predictions from such a model may possibly take a value much higher than the maximum theoretical abundance value, which, from both the ecological and methodological viewpoint, is not acceptable.

In this case, it is thus better to consider that each class is simply relatively higher or lower than the adjacent class, depending on its relative position along the ordinal scale. In this respect, statistical methods exist – and are now implemented in most modern statistical packages – that are applicable to ordinal data.

Amongst other ordinal outcomes that may be met in plant ecology, one can mention the successive phenological stages of a plant flowering process (e.g. Schlüssel & Theurillat 1998), categories of tree’s height or diameter in forestry (Schabenberger 1995). Tolerance levels in ecotoxicology (e.g. of an organism to a pollutant), as e.g. bio-assays conducted in ecotoxicology to assess the contamination of natural waters (see, streams, estuaries, etc.), is another example of ordinal measures in ecology.

Methodological aspects

The link with Generalized Linear Models

Most ordinal regression models have recourse, at one step or another of their calculation, to a logistic regression model, which is a particular case of Generalized Linear Model (GLM). One ordinal model can be simply fitted by rearranging the data prior to fitting a logistic model (see e.g. Armstrong & Sloan 1989) for example by writing a program based on standard binary logistic regression (see the S-Plus lrm function, Harrell 2000). The basic statistical theory for ordinal models can hence be taken from the general theory of GLM for binary and binomial responses (see McCullagh & Nelder 1989; Nicholls 1989 for their application in ecology). GLMs are an extension of classical linear models. In GLMs, the combination of predictor variables x_i ($i = 1, \ldots, p$) produces a *linear predictor* LP which is related to the expectation $E(Y)$ of the response variable Y through a *link function* g(), such as

$$g(E(Y)) = \mathrm{LP} = a + Xb \qquad (1)$$

where X is a matrix of p column vectors $\{x_1, x_2, \ldots, x_p\}$, a is the constant term to estimate and $b = \{b_1, b_2, \ldots, b_p\}$ is the row vector of p coefficients to estimate for the predictor variables. Xb denotes the matrix product, so that the ith element of $g(E(Y))$ is $a + b_1x_{i1} + b_2x_{i2} + \ldots + b_px_{ip}$.

Unlike classical linear models, which presuppose a Normal distribution and an identity link, the distribution of Y may be any of the exponential family distributions and the link function may be any monotonic differentiable function. In the case of a GLM for binary response, the distribution is Bernouilli and the link is generally logit (although probit are commonly used for bio-assays).

Different regression models for different types of ordinal data

Several types of regression models were proposed to deal with an ordinal response, their choice depending generally upon the more specific type of ordinal data.

Although McCullagh (1980) distinguishes between *Proportional Odds* (PO; see also Snell 1964; Walker & Duncan 1967; Williams & Grizzle 1972) and *Proportional Hazards* (PH) models, both arise when considering continuous outcomes that have been categorized (i.e. adjacent intervals along a continuous scale, defined by successive points of division). These responses are thus assumed to have a continuous distribution in the population.

The PO model is the most commonly used ordinal logistic model. It is based on cumulative probabilities and is often also called the *Cumulative Odds* model (e.g. Greenland 1994), although odds are never accumulated. Unlike the PO model, the *Continuation Ratio* (CR; see Armstrong & Sloan 1989) model can be considered as a discrete version of Cox PH model. It is based on conditional probabilities and is particularly suitable when subjects (i.e. observations) have to 'pass through' one category to reach the next (see Fig. 1). As an alternative to the previous models, the category of *Polytomous logistic* models – of which the *Stereotype model* (Anderson 1984; Greenland 1985) is an example – seems more suited for ordinal response variables that are not considered as discrete versions of a continuum (Fig. 1). This is for instance the case when dealing with sums of qualitative indicators, such as the discrete stages of a pathologic process (Greenland 1994).

Mathematical rational

Besides GLM theory, the mathematical rational of three important ordinal models – the Proportional Odds (PO), the Continuation Ratio (CR) and the Stereotype (S) models - are given in Greenland (1994), although he calls the PO model the *Cumulative-Odds* model.

The *Proportional Odds* model is not based on the individual probability of each class (as would be the case with qualitative variables), but on the *cumulative* probabilities g_i of the class considered j and the $(j-1)$ precedent classes (McCullagh 1980)

$$g_j = P(Y \leq \mathrm{j} \mid X) = 1 / (1 + \exp[-(a_j + Xb)]) \qquad (2)$$

In order to make the model consistent with the binary model in the case where $j = 1$, this model can also be written, by redefining g_j, in term of $P(Y \geq j \mid X)$,

$$g_j = P(\mathrm{Y} \geq j \mid X) = 1 / (1 + \exp[-(a_j + Xb)]). \qquad (3)$$

The model calculation hence involves parallel GLM regressions on the ordinal scale, such as (McCullagh & Nelder 1989)

$$\ln[g_j / (1 - g_i)] = a_j - Xb \text{ with } j = 1, ..., J-1 \qquad (4)$$

where J is the total number of ordinal classes. The logit link function on cumulative probabilities is here called *log-odds*. Other links can sometimes alternatively be used such as the *log-log* – $\ln(-\ln g_j)$ – or *complementary log-log* – $\ln[-\ln(1 - g_j)]$ – link (see McCullagh & Nelder 1989). Peterson & Harrell (1990) developed an extended version of the PO model – which they called the *partial PO* model – that allows for unequal slopes for some or all Xs in some or all classes of Y to be adjusted. In application, the PO model translates into a series of J GLM equations of the type:

$$\begin{aligned} g(\gamma_1) &= \alpha_1 + Xb \\ g(\gamma_2) &= \alpha_2 + Xb \\ &[...] \\ g(\gamma_J) &= \alpha_J + Xb \end{aligned} \qquad (5)$$

where g is here the appropriate link function (e.g. log-odds, logit). For example, the PO model states that

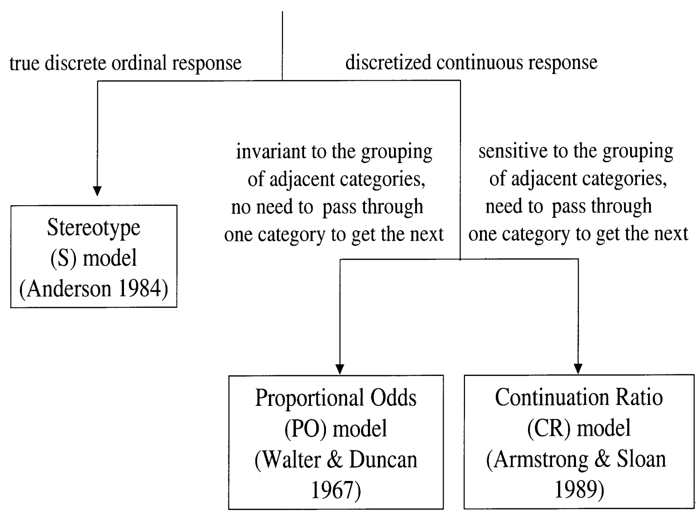

Fig. 1. Distinct models that might be used when dealing with an ordinal response in ecology. This figure should not obliterate the primary need to rely on goodness-of-fit testing and empirical evaluations when choosing an adequate model. See text for details.

$g\,(P(Y \geq 2 \mid X)$ is $\alpha_2 + Xb$, where $g\,(\gamma_2) = \log(\,\gamma_2/(1-\gamma_2))$. Like the PO model, the *Continuation Ratio* model is not based on the individual probability of each ordinal class, but on the *conditional* distribution probability P_j of the *j*-st class of response. The model calculates the probability of falling in category *j*, given the fact that one is in category *j* or higher, as

$$P_j = P(Y = j \mid Y \geq j, X) = 1 / (1 + \exp[-(\alpha_j + Xb)]) \quad (6)$$

which involves (as for the PO model) parallel GLM regressions on the ordinal scale.

As shown by their respective mathematical formulation, the PO and CR models are very close to each other. Läärä & Matthews (1985) demonstrated their equivalence when the complementary log-log link is used with grouped continuous data with known cutpoints, although the PO model is called the grouped continuous model by these authors.

The CR model translates in the same type of equations (5), with e.g. $P\,(Y = 1 \mid Y \geq 1)$ in place of $P(Y \geq 1)$. As in the case of PO models, an extended version of the CR model exists that allows for different slopes for some *X*s in some class of *Y* to be adjusted. In this later model, lines of *X* are duplicated and cohorts (or 'risk sets', if one wants to be consistent with continuous Cox regression) of the *Y* variable are defined as $Y \geq 0$, $Y \geq 1$, ..., $Y \geq J-1$. As *Y* is always greater than zero by definition, this first risk set is actually not needed in model formulation. These successive conditions are converted into binary responses (value 1 = TRUE) and the cohort variable is added to the explanatory part of a classical binary GLM equation, as e.g. specified in *S*-Plus:

$$\mathrm{Y} \sim \mathrm{cohort} + X \quad (7)$$

Non-constant slopes can in this way be easily taken into account in the model, for instance, for x_1 and x_2, in the following way

$$Y \sim \mathrm{cohort} * (x_1 + x_2) + ... + x_p. \quad (8)$$

More details on this procedure can be obtained in Harrell et al. (1998. From a practical point of view, both the PO and CR models are implemented in the *S*-Plus' Design library (Harrell 2000; lrm function).

The stereotype model as proposed by Anderson (1984) originates from the ordinary polytomous model (described in Greenland 1994). It was adapted for analysing outcomes with order constraints and can be defined in the following way:

$$P(Y = j \mid X) = \exp\ (\mathrm{aj} + X\beta s_j) / S_m \exp(\alpha_m + X\beta s_m) \quad (9)$$

where s_j is the score – used to model the coefficients vector β – attached to outcome y_j and $\alpha_0 \equiv s_0 \equiv 0$. The term $\mathrm{b}_k s_m$ represents the log odds ratio for $Y = y_j$ versus $Y = y_0$ per unit increase in x_k (Greenland 1994). The scores s_j may be assigned on external grounds (fixed scores) or may be estimated from the data (estimated scores; Anderson 1984). In the later case, however, Anderson shows that the model is not better than the unordered polytomous model, so that this model is particularly valuable for fixed scores. We present the stereotype model as it may prove useful in some ecological situations, but will not present any example of its application. Besides, to our knowledge, no general software is presently available for fitting the stereotype model.

Choosing the appropriate ordinal model

The choice of an adequate ordinal model should be based primarily on goodness-of-fit testing and empirical evaluations. The assumptions that one or the other model hold for the different explanatory variables can additionally be checked graphically – see e.g. Landwehr et al. (1984) or Harrell et al. (1998) for an applied example), as shown in Fig. 2.

Alternatively, the choice might be influenced by the nature of the response variable involved (Greenland 1994), as illustrated in Fig. 1. For instance, one may wonder if the response in the true population is a true discrete ordinal response or a continuum, which might influence the use of stereotype over PO/CR models. If the true population response is considered continuous, one may then wonder if an observation needs to 'pass through' one category to reach the next, in which case the CR model may be preferred to the PO model (Harrell et al. 1998). Another possible distinction is to consider if the model is invariant to the grouping of adjacent response categories or if it is invariant to reversals of the categories (except for the sign of the regression coefficients and intercepts), in which case the PO model would be preferred to the CR model (McCullagh & Nelder 1989).

When dealing with ordinal abundance of an organism, the true population variable is obviously continuous, but had to be discretized for practical reasons. Hence, both PO or CR models might be appropriate in this case. However, when all but the lowest outcome level are rare, the PO model can also be approximated by a special case of the stereotype model (Greenland 1994). Such a situation is common in the case of natural surveys based on a systematic sampling strategy (e.g. by sampling each intersection point of a regular grid). In turn, as phenological stages might be considered well differentiated from each other, and hence constitute a

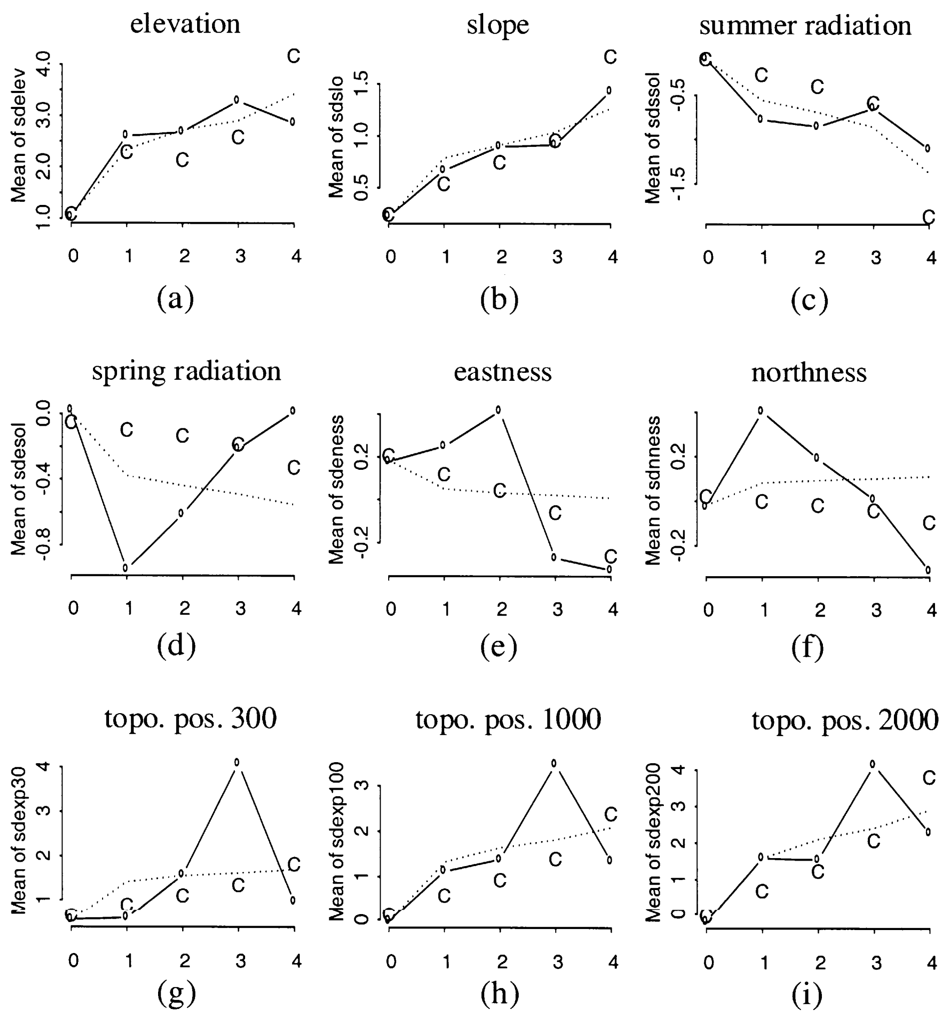

Fig. 2. Graphical checking of PO versus CR assumptions for the *Pinus longaeva* model. Means of all potential predictors are calculated for each ordinal class of the response and plotted (dotted line) against it. In the ideal case, the plain line (PO model) or the series of 'C' (CR model) should be superposed on the dotted line if the PO or CR assumptions hold. Ordinality is satisfactorily verified for PO and CR models in the cases **a**, **b**, **c**. The CR model might be more suitable in the cases **d** and **e**. Ordinality seems not be verified in case **f**. Aggregation of ordinal classes 2 to 4 is suggested by cases **g** to **i** if a PO model was to be used, whereas a CR model seems appropriate as such. Some predictors, although in ordinal relation with the response, were not kept in the final model, because they explained a similar part of the variance than another predictor previously selected (collinearity).

true discrete ordinal outcome, they might be best modelled directly by a stereotype model. These criteria may help choosing one model rather than another, although all models should be ideally tested, and the one providing the more satisfying results retained for further analyses.

Model predictions

Once the model is fitted, its primary use is generally to predict new values based on a separate set of observations. Statistical packages include usually methods for this purpose (e.g. predict() in *S*-Plus), and a new data set has simply to be specified to get estimated predicted values for each new observation. However, there are cases where the predictions might only be done in another environment, outside the statistical package that served at fitting the model. A good example is provided by static modeling (Guisan et al. 1998, 1999; see Franklin 1995 for a review) where one will generally aim at applying the fitted model to a large data set stored in several grid structures within a Geographical Information System (GIS). As we experienced, when the data set is huge (e.g. several million of geographical locations with several environmental attributes for each), it becomes difficult to transfer the data into the statistical software, and hence, the fitted model (i.e. not the fitting algorithm) has to be implemented directly into the GIS. The simplicity of the fitted model is then an important prerequisite for such applications. At least two of the three considered ordinal models offer this advantage: the PO and the CR model.

The fitted ordinal logistic models are implemented by building a series of formulas, where each model coefficient multiplies its related term. For each predictor, a same coefficient is used, but a different intercept is estimated to predict the different ordinal classes. As a result, there are as many formulas as there are ordinal classes to predict. Predictions from each ordinal equation are first obtained to the scale of the linear predictor (LP_j; see equation 1) so that the inverse logistic transformation

$$\gamma_j = 1 / (1 + \exp(-LP_j)) \qquad (10)$$

is then necessary to obtain probability values between 0 and 1. The values predicted by each formula are stored in separate layers in the GIS.

In the case of the PO model, individual probabilities of each ordinal class are then computed by taking successive differences in the cumulative probabilities. In the case of the CR model conditional probabilities are computed first. Then, cumulative products are calculated to get unconditional probabilities.

Evaluating an ordinal model

Evaluating the prediction of a model can be done in two ways

A. Independent evaluation: Two independent data sets can be used to calibrate and then evaluate the model. For instance, this could be the case when the two data sets originate from distinct sources or experimental design (and should not be mixed) but result from the same measurements. Evaluation is conducted by measuring the concordance between observed and predicted values. Special measures of association are needed to compare ordinal values in a two-way contingency table. Examples of such appropriate measures can be found in Agresti (1990) or Gonzalez & Nelson (1996). They include e.g. Gamma (Goodman & Kruskal 1954), Somers' (1962) d_{yx}, Kim's (1971) $d_{y,x}$ or Wilson's (1974) *e*. A perfect association between two ordinal variables takes value 1 and no agreement takes value 0. Gonzalez & Nelson (1996) discussed more specifically the choice of one or the other of these four measures in situations that contain tied scores. As model predictions are probabilistic, their comparison with observed discrete ordinal values implies either that they are first brought back to the original ordinal scale (Guisan et al. 1998) or that, for any fixed category or by ignoring intercepts altogether, the log-odds are directly related to the ordinal response variable (if the model is not extended).

When the fitted model is intended to be used to estimate not only relative effects (odds ratios) but also probabilities of various events, it is important to ascertain that the predicted probabilities are accurate in terms of agreement with observed proportions of events in a sample not used to develop the model (such accuracy is almost guaranteed when evaluating the model on the same sample used to fit it). As described in Harrell et al. (1998) the bootstrap can be used to estimate the likely predictive accuracy in a new sample by re-sampling from the training sample. One can compare mean predicted probabilities against proportions of events upon stratifying by either the independent variables or by the predicted probability itself. The latter results in a calibration plot. A more precise estimate of the calibration plot may be obtained by using non-parametric regression to smoothly relate predicted probabilities to observed binary events (see e.g. Harrell et al. 1996, 1998).

B. Resampling evaluation: A single data set can be used to calibrate and evaluate the model. In this particular case, the predictive capacity of the model can be evaluated through bootstrap techniques (Harrell et al. 1996, 1998). Through re-sampling (with replacement), the bootstrap allows one to estimate the optimism (bias) in any measure of predictive accuracy and, then, subtract the estimate of optimism from the initial apparent measure to obtain a bias-corrected estimate (Efron & Tibshirani 1993). The bias is the difference between the parameter estimate and the true population value. With GLMs for instance, bias-corrected values of R^2 and Somers' d_{yx} and other statistics can be obtained this way (Table 3). When the difference between apparent and corrected value is too high, what is sometime called the 'optimism from overfitting' (Efron & Gong 1983), the stability of the model should be seriously questioned. A bootstrap evaluation of a PO or CR model can e.g. be performed directly with the tools included in the *S*-Plus' Design library (Harrell 2000; see Harrell et al. 1998 for additional examples).

Case study: modeling the spatial distribution of plant cover

We choose to illustrate the use of ordinal regression models in ecology using examples from a static plant distribution study (see Guisan et al. 1999). The aim here is merely to predict plant distributions as a function of environmental predictors. For this purpose, we had recourse to both ordinal and simple presence-absence logistic models, which then allowed us to compare the results from both models. Ordinal models were fitted in *S*-Plus with a PO model (lrm function, Harrell 1999; see Guisan et al. 1998 for an ecological application) and simple logistic models were fitted with a classical GLM with binomial distribution and logit link (see Nicholls 1989; Guisan et al. 1999).

The data set consists of 215 phytosociological relevés sampled in the Spring Mountains of Nevada, within the framework of a study by The Nature Conservancy (TNC; Nachlinger & Reese 1996; see also Guisan et al. 1999). This inventory included all higher plant species, although we fitted models for tree and shrub species only. Because a subset of observations proved to be sufficient to calibrate models for common species (i.e. they were equivalent to models calibrated with all available observations) and for simplicity, the data set was split into two subsets (In general, however, the bootstrap is far superior to other methods of internal model validation). One set was used for calibrating the models (hereafter called the *calibration data set;* N = 144) whereas the other was used later on to evaluate the quality of the predictions (*evaluation data set*; N = 71). Here, we present the models for four species, namely *Pinus longaeva* (PL), *Coleagyne ramosissima* (CR), *Ephedra viridis* (EV) and *Yucca baccata* (YB).

The response variable in the ordinal models is the abundance of species (percentage cover on the ground) classified in an ordinal fashion. The ordinal abundance scale used is a modified Braun-Blanquet (1964) abundance-dominance scale (the same as used by Guisan et al. 1998). Values are ranked from 0 (absence) to 5 (>50 % of ground cover) with intermediate limits of classes at values of 5 %, 12,5 % and 25 %. Abundance was also transformed into presence/absence, by re-coding all values greater than zero to one, to constitute the binary response for simple logistic models.

The predictor variables used to predict the distribution of species were elevation (*elev*), solar radiation (at summer solstice and spring equinox; *ssol* and *esol*) and several indices of relative topographic position (*tp300, tp1000 and tp2000*). Radiation and topographic position were derived from a 30-m resolution digital elevation model (DEM) of the area (USDA, Forest Service). Details on the respective modeling procedures can be found in Guisan et al. (1999).

Each potential predictor was first checked graphically for its ordinal relationship with the response variable (Fig. 2). Means of each potential predictor were calculated for each ordinal class of the response, and plotted against it (see Harrell et al. 1998).

The combination of predictors, including second order polynomials only and no interactions, reducing the greatest amount of deviance was kept in the final model. We fitted both ordinal and binary (presence-absence) models with the constraint that, for every species, the same subset of predictors had to be used to fit both models. This was necessary as model predictions had later on to be compared. For comparison, ordinal predictions are re-coded into presence-absence and compared to presence-absence prediction from the binary model. An adequate measure to calculate the association between two binary variables is κ (Cohen 1960; see also Monserud & Leemans 1992). In addition, we also provide the estimated generalized R^2 (Nagelkerke 1991) for both models and two specific measures of association between ordinal scales to quantify the quality of ordinal predictions. The two measures of association are *Gamma* (Goodman & Kruskal 1954) and *Somers' d_{yx}* (Somers 1962).

Model results are summarized in Tables 1 and 2. Table 1 provides the final selection of predictors for ordinal models, with their deviance reduction significance. Table 2 show that multiple-R^2 for ordinal models range between 0.628 and 0.727, as compared to those

Table 1. Predictors retained in fitted ordinal models for *Coleogyne ramosissima* (CR), *Ephedra viridis* (EV), *Pinus longaeva* (PL) and *Yucca baccata* (YB), their coefficient and significance. *P(Chi)*: *p*-value of the Likelihood Ratio χ^2-statistics for testing whether the deviance reduction obtained by adding successively each predictor in the model is significant. The α_i below the species names are the different intercept estimated to predict the different ordinal classes.

	Predictor	*Coefficient*	*P(χ)*
Coleogyne ramosissima			
α_1 : 2.97	*Elev*	–6.15	<.0.0001
α_2 : 2.29	*tp2000*	1.26	0.0002
α_3 : 1.53			
Ephedra viridis			
α_1 : 2.31	*Elev*	–0.48	<.0.0001
α_2 : –2.27	*elev²*	–1.27	0.0067
	tp2000	0.82	<.0001
	tp2000²	0.17	0.0047
Pinus longaeva			
α_1 : –47.13	*Elev*	34.42	<.0.0001
α_2 : –48.71	*elev²*	–5.80	<.0.0001
α_3 : –49.52	*Ssol*	–1.60	0.0028
α_4 : –51.47	*ssol²*	–1.47	0.0010
	Esol	–0.38	0.0063
	esol²	0.35	0.0174
Yucca baccata			
α_1 : 1.82	*Elev*	0.45	0.0002
α_2 : –2.82	*elev²*	–2.56	0.0161
	Ssol	–1.99	0.0062
	Esol	1.73	0.0005
	tp1000	0.50	0.0342
	tp1000²	–0.29	0.0213

Table 2. Comparison of model prediction for *Coleogyne ramosissima* (CR), *Ephedra viridis* (EV), *Pinus longaeva* (PL) and *Yucca baccata* (YB). The data set used to evaluate the models is different from the data set used to build the models. O = ordinal abundance model; B = Binary presence-absence model.

Species	R^2 O	R^2 B	γ	d_{yx}	κ O	κ B
Coleogyne ramosissima	0.674	0.812	0.918	0.846	0.785	0.768
Ephedra viridis	0.658	0.531	0.954	0.701	0.746	0.745
Pinus longaeva	0.727	0.716	0.921	0.864	0.696	0.760
Yucca baccata	0.628	0.520	0.996	0.860	0.882	0.852

Table 3. Bootstrap evaluation of some statistics obtained from the model of *Pinus longaeva*, for R =1000 bootstrap samples. The resampling is here stratified by the response variable, to have all ordinal classes at least once represented in every bootstrap sample.

	Original value	Training	Test	Bias (overfitting)	Corrected value
Somers' d_{yx}	0.9052	0.9102	0.89883	0.01136	0.89387
Gen. R^2	0.6541	0.6702	0.64256	0.02765	0.62642
Intercept	0.0000	0.0000	0.02666	– 0.02666	0.02666
Slope	1.0000	1.0000	0.85683	0.14317	0.85683
Emax	0.0000	0.0000	0.03884	0.03884	0.03884

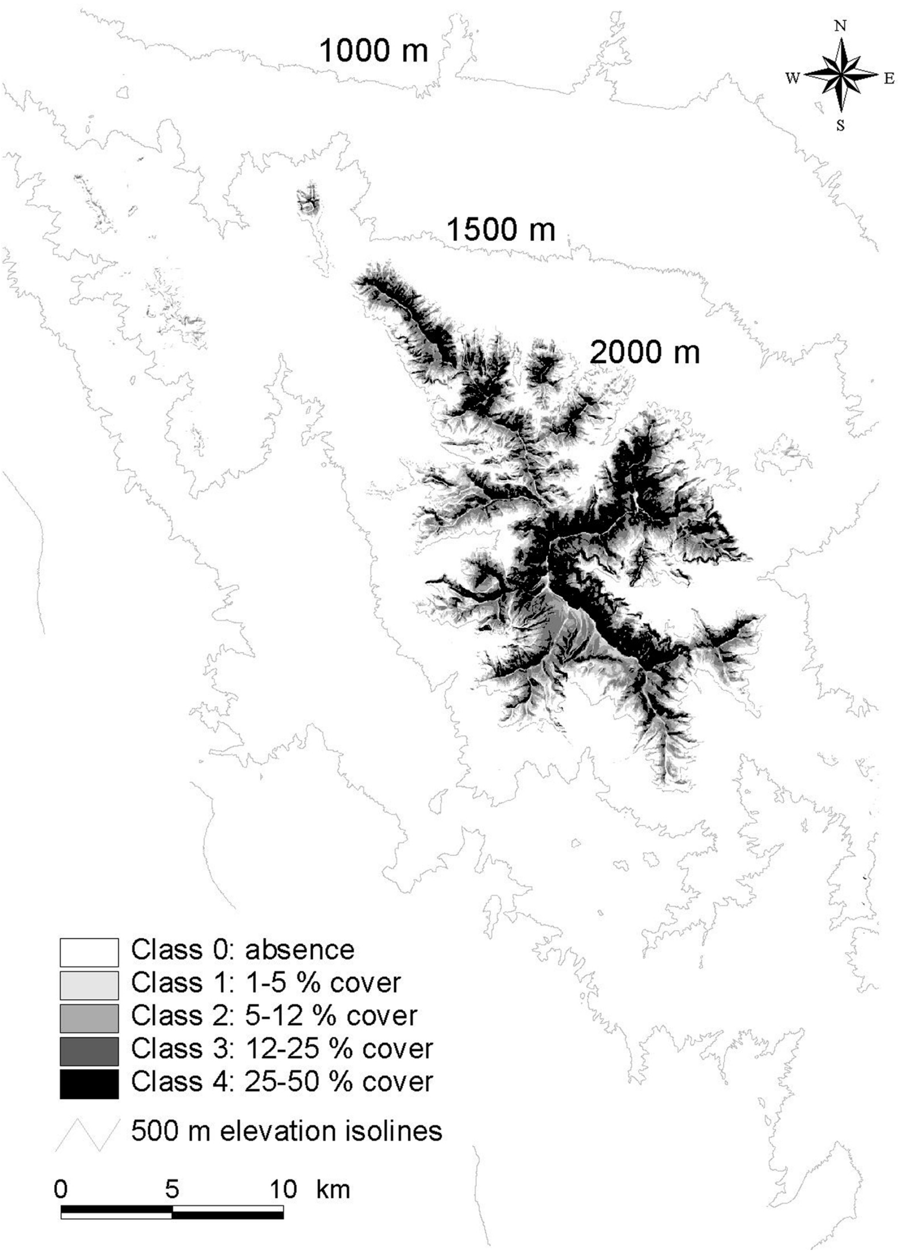

Fig. 3. Predicted distribution map for *Pinus longaeva* in the Spring Mountains of Nevada (USA). The different colours represent the different classes of the plant percent ground cover over regular 20 m× 20m plots.

from binary models that range between 0.520 and 0.812. In both cases, the predictive discrimination ability of models can hence be considered as reasonable (0.628) to rather high (0.812). More satisfying is the fact that all predictions of the ordinal models made on the evaluation data set show a good concordance with observed abundance, as attested by the high values of γ and Somers' d_{yx} (notice that the latter is always smaller than the former). This is generally directly observable in the ordinal contingency tables. Finally, maps generated from implementing the models in a Geographical Information System (GIS) provided a visual confirmation of the coherence of model predictions. An example of such a predicted distribution is given for *Pinus longaeva* in Fig. 3.

Hence, ordinal models *per se* prove to be reasonably good (Tables 1 and 2). It is now interesting to see whether modeling a simple presence-absence by logistic regression would provide better results, by comparing them to the predictions of ordinal models re-coded into presence-absence. This informs us about the power of the model to discriminate locations where the species actually occurs (at one or another abundance) from those where it is absent. Based on the evaluation data set, Table 2 shows that ordinal models are as successful as simple logistic models – or even better as in the case of *Yucca baccata* – for predicting simple presence-absence, but are additionally able to provide realistic estimates of species' abundance. Although κ values of ordinal models are sometimes lower than those of binary models (*Pinus longaeva*), the differences remain generally slight, as usually attested by the comparison of related contingency tables.

Conclusions

We show how valuable it is, in ecology, to recognize a variable as ordinal. In some cases, it might prevent losing important ecological information, when abundance is reduced to presence-absence. In other cases, it might avoid the use of inadequate statistical models, as specific statistical methods have been developed for such semi-quantitative responses. Three ordinal regression models – the Proportional Odds, Continuation Ratio and Stereotype models – are presented, which may apply to different ecological situations. Their originality lies in the fact that they are based on cumulative or conditional probabilities rather than on individual probabilities for each ordinal class. Examples from static modeling of plant distribution show that ordinal response regression models are useful and powerful tools for such applications. Relatively good fits were obtained for the models given as examples, as well as for the quality of their predictions when evaluated with an independent data set. Even when reduced to presence-absence, the quality of their predictions remains comparable to those from simple binary models fitted with the same formulas.

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