

# Analysis of Ontogenetic Spectra of Populations of Plants and Lichens via Ordinal Regression

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**Abstract.** Ontogenetic spectra of plants and lichens tend to vary across the populations. This means that if several subsamples within a sample (or a population) were collected, then the subsamples would not be homogeneous. Consequently, the statistical analysis of the aggregated data would not be correct, which could potentially lead to false biological conclusions. In order to take into account the heterogeneity of the subsamples, we propose to use ordinal regression, which is a type of generalized linear regression. In this paper, we study the populations of cowberry *Vaccinium vitis-idaea* L. and epiphytic lichens *Hypogymnia physodes* (L.) Nyl. and *Pseudevernia furfuracea* (L.) Zopf. We obtain estimates for the proportions of between-sample variability in the total variability of the ontogenetic spectra of the populations.

**Keywords:** ontogenetic spectrum of population, ordinal regression, *Vaccinium vitis-idaea*, *Hypogymnia physodes*, *Pseudevernia furfuracea*

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## INTRODUCTION

Age is one of the characteristics of each individual of any species of living organisms. There can be defined two different types of age: calendar (or chronological) and biological. The calendar age is measured by physical units of time whereas the biological age can be defined by the aggregate of various morphological, physiological and biochemical indicators of an organism [1]. The use of the concept of the biological age appears necessary in the population biology of plants and lichens, especially in cases where the determination of the calendar age may not be possible. In individual development (ontogeny) of species of plants and lichens, the following successive ontogenetic periods can be distinguished: latent, pregenerative, regenerative and postgenerative. In each of these periods, the sequence of discrete ontogenetic states is determined; see Table 1 (for further details, see [2]). Due to particular properties of the formation of morphological structures, some species of plants and lichens have two ontogenetic virginal states:  $v_1$  and  $v_2$  [3, 4].

Thus, a continuous process of ontogenesis of plants and lichens can be described by a sequence of ontogenetic states. Note that each of the ontogenetic states is a qualitative (not quantitative) feature of an individual. Calendar age and biological age are expected to be highly correlated as we have a sequence of ontogenetic states ordered in time. However, individuals that are in the same ontogenetic state may have different calendar age [5]. We can construct the ontogenetic spectrum of a population, considering individuals of the population in the aggregate. In this paper, we use the term “coenopopulation”, which is a set of all individuals of a certain plant species within the same phytocenosis [4, 6, 7].

In order to analyze the ontogenetic spectrum of a population, the data are collected in such a way that each sample consists of several subsamples collected in different parts of the population in different years, etc. For example, herbaceous plants are usually considered on square sites with the area of  $1 \text{ m}^2$ . A researcher determines the ontogenetic state of each plant, the data are aggregated over all sites. For epiphytic lichens, specimens (thalli) of all ontogenetic states are considered on each tree separately, then the data are summarized within the habitat or a phorophyte (substratum). In both cases it allows to obtain the ontogenetic spectrum of the population (or coenopopulation) and the parameters characterizing the ontogenetic spectrum of the population such as the average age [2],  $\Delta = \sum_{i=1}^{11} k_i n_i / \sum_{i=1}^{11} n_i$ , the modified recovery index [8],  $I_1 = \sum_{i=3}^5 n_i / \sum_{i=3}^8 n_i$ , the ageing index [8],  $I_2 = \sum_{i=9}^{11} n_i / \sum_{i=3}^{11} n_i$ , where  $n_i$  is the number of specimens in ontogenetic state  $i$ ,  $k_i$  is the weight coefficient of ontogenetic state  $i$  (see Table 1).

Note that a site (quadrant) is the measurement unit (subsampling) in studies of plants whereas a tree is the measurement unit (subsampling) for epiphytic lichens. The aggregation of the subsamples (sites or trees) in this approach is valid if the distributions of different subsamples do not significantly differ, that is, they can be described by the same multinomial

**TABLE 1.** The discrete description of plant ontogenesis

Period	Ontogenetic state $i$ , its name and notation	Weight coefficient, $k_i$
Latent	1. Seeds, $sm$	0.0025
Pregenerative	2. Seedling, $p$	0.0067
	3. Juvenile, $j$	0.0180
	4. Immature, $im$	0.0474
	5. Virginal, $v$	0.1192
Generative	6. Young generative, $g_1$	0.2700
	7. Mature generative, $g_2$	0.5000
	8. Old generative, $g_3$	0.7310
Postgenerative	9. Subsenile, $ss$	0.8808
	10. Senile, $s$	0.9529
	11. Moribund, $sc$	0.9819

distribution [9]. Thus, if the subsamples are not homogeneous, the statistical analysis of the aggregated data may not be correct. In this paper, we propose to use ordinal regression models in order to take into account the heterogeneity of the subsamples.

## METHODOLOGY

In this section, we describe the methodology of the collection of the data and an ordinal regression model (also known as a cumulative link mixed model), which are a type of generalized linear models [10].

### Data Collection

The data were collected from natural populations of cowberry (*Vaccinium vitis-idaea* L.) and epiphytic lichens *Hypogymnia physodes* (L.) Nyl. and *Pseudevernia furfuracea* (L.) Zopf on the territory of the Republic of Mari El, Russia.

The study of 10 coenopopulations of cowberry (*Vaccinium vitis-idaea* L.) was conducted on the territory of the State Nature Reserve “Bolshaya Kokshaga” (coenopopulations 1, 3, 4, 5 and 6) and in the vicinity of the settlement of Ismentsy, Zvenigovsky district (coenopopulations i1, i2, i3, i4 and i5). Coenopopulation 1 is located in a pine forest recovering from a ground fire in 1995; coenopopulations 3, i1, i4 and i5 are in a pine forest with cowberries; coenopopulations 4, 5 and 6 are in a pine forest with green mosses and cowberries; coenopopulation i2 is in a pine forest with firs and cowberries; coenopopulation i3 is in a pine forest with carex, heath and cowberries. The age of the forest stand in the habitats of different coenopopulations varies from 55 to 85 years, its density is 0.5-1. Geobotanical descriptions were processed using Tsyganov’s ecological scales [11, 12]. In each coenopopulation, 10-30 sites of 1 m<sup>2</sup> were examined, the number of partial cowberry bushes on a site is in the range of 5-778, the number of partial cowberry bushes in different coenopopulations varies from 1498 to 7117 (the diagnostics of partial bushes is described in detail in [13]). The ontogenetic spectrum covers the range of states from  $im$  to  $sc$ , since juvenile individuals cannot be found because partial bushes are of vegetative genesis. There is no doubt that within the same site several (or, possibly, dozens) of the partial bushes belong to the same cowberry specimen [14].

The study of *Hypogymnia physodes* was carried out in two habitats on the territory of forestry Starozhilskoye in Medvedevsky district. The lichens were examined on the trunks (up to 3 m high) of little-leaved lime (linden) (*Tilia cordata* Mill.), Siberian fir (*Abies sibirica* L.) and common pine (*Pinus sylvestris* L.). Two samples were collected in the first habitat that is located in a flood lime-tree forest with firs, ostrich ferns and lilies-of-the-valley in a high-water bed of the Bolshaya Kokshaga River: on 23 little-leaved lime-trees (the number of thalli on a tree in the range of 42-785, the total number of thalli is 3652) and on 7 Siberian firs (the number of thalli on a tree varies from 4 to 1229, the total number of thalli is 3562). The age of the forest stand is 70-80 years; at a height of 1.3, the circumference of the trunk of a lime-tree and a fir is 0.81 m and 0.92 m, respectively. The second habitat is located in a pine tree forest with fescue and bent grass in the settlement of Starozhilsk: 16 *Hypogymnia physodes* were collected (the number of

**TABLE 2.** Nested models,  $M_0 \prec M_1 \prec M_2$ 

Notation	Model
$M_2$	$P(Y_i \leq j) = g(\theta_j - u(\text{Sample}_i) - v(\text{Subsample}_i))$
$M_1$	$P(Y_i \leq j) = g(\theta_j - u(\text{Sample}_i))$
$M_0$	$P(Y_i \leq j) = g(\theta_j)$

thalli on a tree varies from 221 to 691, the total number of thalli is 7651). The age of the forest stand is 75 years, the circumference of the trunk is 1.04 m. Note that the pine forest is subjected to strong anthropogenic impact such as trampling and grazing. For further details on the ontogenetic states of *Hypogymnia physodes* see [15].

The study of *Pseudevernia furfuracea* was conducted in 8 habitats. Two samples were collected in a pine forest with green mosses and birches (*Betula pendula* Roth.) on the territory of the State Nature Reserve ‘‘Bolshaya Kokshaga’’: sample 2a is on pine trees (the age of the trees is 65 years, the circumference of the trunk is 0.6 m) and sample 2b is on birch trees (the age of the trees is 45 years, the circumference of the trunk is 0.46 m). Three samples were collected in forestry Starozhilskoye in Medvedevsky district: sample 3 is on pine trees in a pine forest with blueberry (the age of the trees is 70 years, the circumference of the trunk is 0.54 m); sample 4 is on pine trees in a low bush and a bog moss pine forest (the age of the trees is 110 years, the circumference of the trunk is 0.63 m); sample 5 is on birch trees in a birch forest with carex, calla and bog moss (the age of the trees is 50-60 years, the circumference of the trunk is 0.55 m). Four samples (6, 7, 8 and 9) were collected on pine trees on the territory of forestry Kerebelyakskoye in the National Park ‘‘Mari Chodra’’. The ontogenetic states of *Pseudevernia furfuracea* are described in detail in [16].

Due to a massive collection of data in natural populations of lichens, the ontogenetic spectra can be constructed starting from ontogenetic state  $v_1$ , since the thalli of the initial ontogenetic states are microscopic in size and the species of *im* specimens is sometimes difficult to identify. Note that in natural populations of *Pseudevernia furfuracea*, the frequencies of  $g_3$ ,  $ss$  and  $s$  specimens are very small (about 1%) because they apparently poorly retain on the trunk [17, 18].

## Statistical Models

We consider an ordinal regression model

$$P(Y_i \leq j) = g(\theta_j - u(\text{Sample}_i) - v(\text{Subsample}_i)), \quad i = 1, \dots, n, \quad j = 1, \dots, J - 1,$$

where  $n$  is the total number of individuals in all samples,  $J$  is the number of ontogenetic states,  $g(\cdot)$  is a link function (for example, logit or probit). The ordered logit uses  $g(y) = \exp(y)/(1 + \exp(y))$ , whereas the ordered probit uses  $g(y) = \Phi(y)$ , the cumulative normal distribution function. Note that the variance of the logistic distribution (logit model) is  $\pi^2/3$  and the variance of the standard normal distribution (probit model) is 1.

This is a model for the cumulative probability of the  $i$ th observation falling in the  $j$ th category (ontogenetic state) or below,  $j = 1, \dots, J$ . The  $\theta_j$  are known as threshold parameters or cut-points. We take the sample and the subsample effects to be random, and assume that

$$\begin{aligned} u(\text{Sample}_i) &\sim \text{Normal}(0, \sigma_u^2), \\ v(\text{Subsample}_i) &\sim \text{Normal}(0, \sigma_v^2). \end{aligned}$$

Table 2 shows several nested models that can be constructed using this approach.

## RESULTS AND DISCUSSION

### Cowberry *Vaccinium vitis-idaea* L.

We fit this model with the `clmm` function in R package `ordinal` [19]. Table 3 shows the variances of the random effects for both probit and logit models.

Using the likelihood ratio test, we can show that the random effects (for both probit and logit models) are highly significant, that is, we reject the null hypotheses  $H_0 : \sigma_u^2 = 0$  and  $H_0 : \sigma_v^2 = 0$ . Table 4 and Table 5 show the analysis of

**TABLE 3.** The variances of the random effects of models  $M_2$  (logit and probit) for coenopopulations of cowberry

Random effects	Logit		Probit	
	Variance	Proportion	Variance	Proportion
Sample	0.06367	0.24426	0.01771	0.21322
Subsample	0.19700	0.75574	0.06533	0.78678

**TABLE 4.** Analysis of deviances (number of parameters in the model, AIC, log-likelihood, likelihood ratio test) of nested logit models for coenopopulations of cowberry

Model	no.par	AIC	logLik	LR.stat	df	Pr(>Chisq)
$M_0$	7	135794.15	-67890.08			
$M_2$	9	133907.76	-66944.88	1890.38	2	$< 2.2 \cdot 10^{-16}$
$M_1$	8	135277.46	-67630.73			
$M_2$	9	133907.76	-66944.88	1371.69	1	$< 2.2 \cdot 10^{-16}$
$M_0$	7	135794.15	-67890.08			
$M_1$	8	135277.46	-67630.73	518.69	1	$< 2.2 \cdot 10^{-16}$

variance (or deviance) for the models from Table 2 that use logit and probit link-functions, respectively. The deviance can be used in order to measure the proportion of the variance explained by the model. Using the likelihood ratio statistic (LR.stat in Table 4), we have

$$1 = \frac{1371.69 + 518.69}{1890.38} = 0.72562 + 0.27438.$$

We can obtain a similar decomposition for the probit models (LR.stat in Table 5)

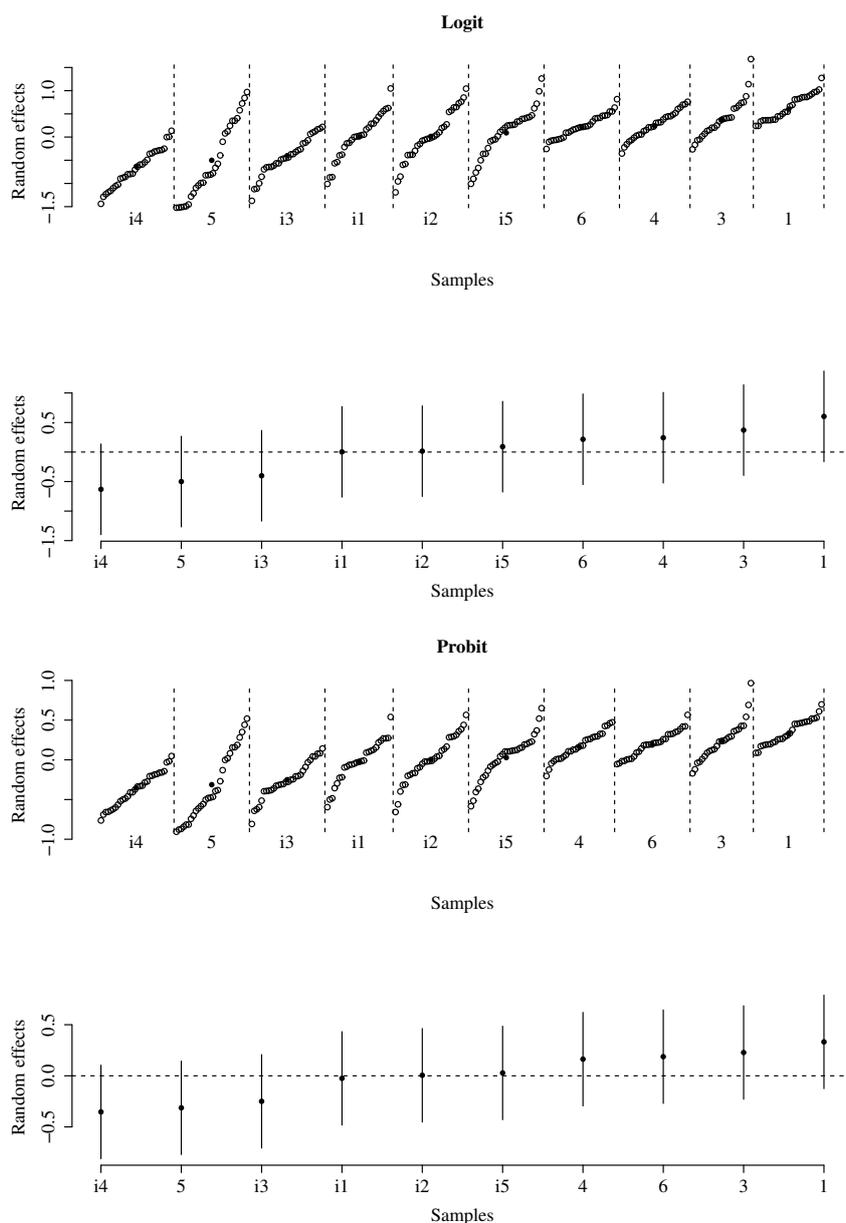
$$1 = \frac{1318.00 + 432.27}{1750.27} = 0.75303 + 0.24697.$$

These results are in concordance with the proportions of the variances of the random effects displayed in Table 3 and, therefore, they can also be used in order to assess the contribution of each predictor (Sample or Subsample). Note that the proportions of the variance of the Sample effect are quite close to each other: 0.244 for the logit model and 0.213 for the probit model.

Figure 1 displays the random effects of models  $M_2$  (logit and probit) for ontogenetic spectra of 10 coenopopulations of cowberry. Here the coenopopulations are ordered by ascending value of the Sample effects (the filled circles), the individual random effects (blank circles) within the samples (coenopopulations) are also arranged in ascending order. It is easy to see that the range of variation of the Sample effects is considerably less than the range of variation of the Subsample (individual) effects. If the value of an effect (Sample or Subsample) is positive (negative), then specimens in the older (younger) ontogenetic states are more likely to be observed.

**TABLE 5.** Analysis of deviances (number of parameters in the model, AIC, log-likelihood, likelihood ratio test) of nested probit models for coenopopulations of cowberry

Model	no.par	AIC	logLik	LR.stat	df	Pr(>Chisq)
$M_0$	7	135794.15	-67890.08			
$M_2$	9	134047.88	-67014.94	1750.27	2	$< 2.2 \cdot 10^{-16}$
$M_1$	8	135363.88	-67673.94			
$M_2$	9	134047.88	-67014.94	1318.00	1	$< 2.2 \cdot 10^{-16}$
$M_0$	7	135794.15	-67890.08			
$M_1$	8	135363.88	-67673.94	432.27	1	$< 2.2 \cdot 10^{-16}$



**FIGURE 1.** The random effects of models  $M_2$  (logit and probit) for ontogenetic spectra of the cenopopulations of cowberry. The filled circles are the random effects for the samples, the blank circles are the individual random effects. The 95% confidence intervals based on the variance of the sample random effect

The proposed approach, which takes into consideration the heterogeneity of coenopopulations of cowberries, identifies significant differences between the ontogenetic spectra of the coenopopulations. Various techniques of assessing the proportion of the effect of coenopopulation give comparable results: from 0.213 to 0.274. This means that the variability between ontogenetic spectra is mainly concentrated within coenopopulations between the sites. This may be because of the species characteristics of cowberry or the fact that the study area (the territory of the Republic of Mari El) is the southern border of the species' habitat and, therefore, the described feature may be typical for populations on the border of the habitat.

**TABLE 6.** The variances of the random effects of models  $M_2$  (logit and probit) for *Hypogymnia physodes*

Random effects	Logit		Probit	
	Variance	Proportion	Variance	Proportion
Sample	0.17439	0.48776	0.05927	0.49446
Subsample	0.18314	0.51224	0.06060	0.50554

**TABLE 7.** Analysis of deviances (number of parameters in the model, AIC, log-likelihood, likelihood ratio test) of nested logit models for *Hypogymnia physodes*

Model	no.par	AIC	logLik	LR.stat	df	Pr(>Chisq)
$M_0$	5	48252.36	-24121.18			
$M_2$	7	47004.79	-23495.40	1251.56	2	$< 2.2 \cdot 10^{-16}$
$M_1$	6	47797.73	-23892.87			
$M_2$	7	47004.79	-23495.40	794.94	1	$< 2.2 \cdot 10^{-16}$
$M_0$	5	48252.36	-24121.18			
$M_1$	6	47797.73	-23892.87	456.62	1	$< 2.2 \cdot 10^{-16}$

### Epiphytic Lichen *Hypogymnia physodes* (L.) Nyl.

Table 6 shows the variances of the random effects for both probit and logit models. Table 7 and Table 8 demonstrate that the differences between the samples are highly significant both for the probit and the logit models.

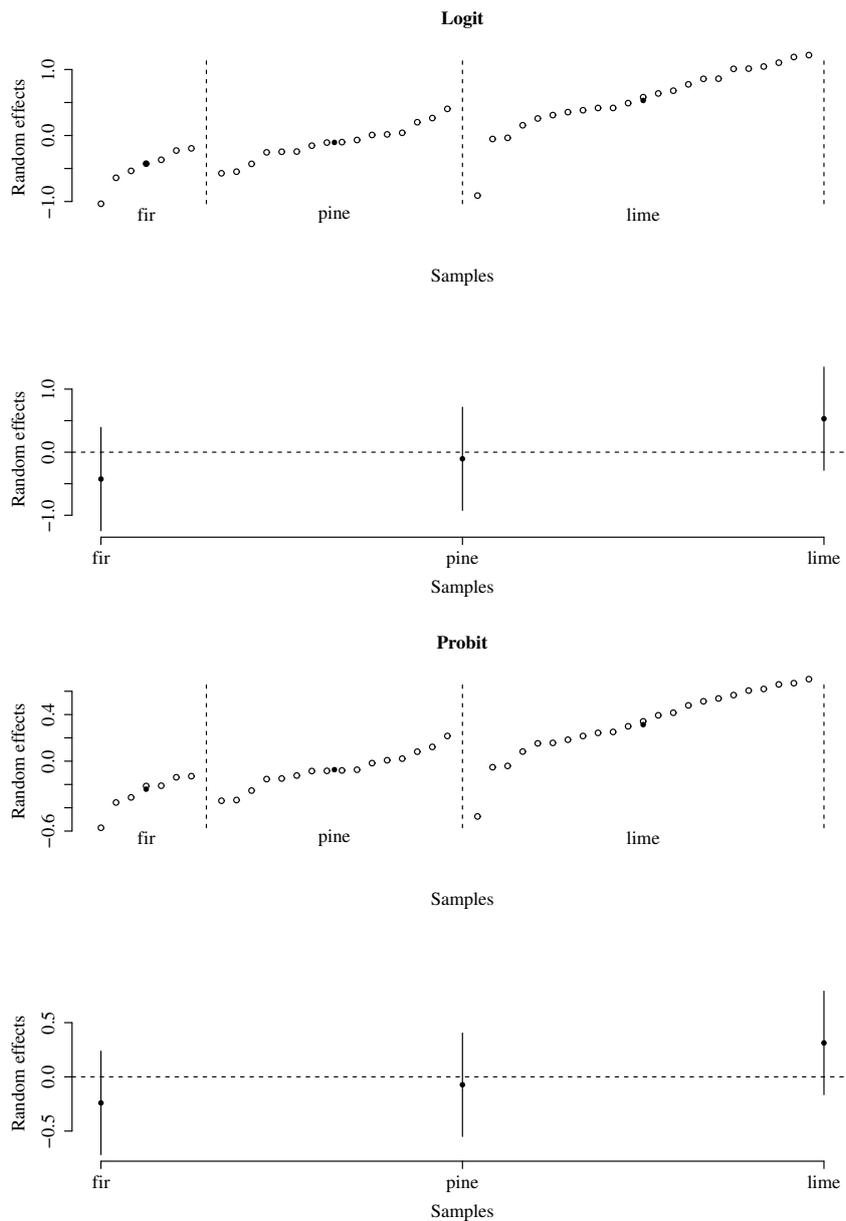
Figure 3 displays the ontogenetic spectra of *H. physodes* on lime-trees, the highlighted ontogenetic spectrum of tree 22 significantly differs from the other spectra. If we exclude tree 22 from the analysis, then the proportion of the sample variance becomes 0.64087 for the logit model and 0.63405 for the probit model, which is higher than similar proportions obtained in the initial analysis presented in Table 6. The distinctive feature of ontogenetic spectrum of thalli *H. physodes* on linden tree 22 may be explained by its position: the tree is located on the edge of the forest at the cliff of high bank of the Bolshaya Kokshaga River. Thus, analyzing ontogenetic spectra (without tree 22) of *H. physodes*, different methods of assessing the proportion of the Sample effect produce consistent results: 0.641 (variance, logit), 0.659 (deviance, logit), 0.634 (variance, probit) and 0.670 (deviance, probit). Unlike for the coenopopulations of cowberry, the effect of between-sample variability for *H. physodes* is much higher.

### Epiphytic Lichen *Pseudevernia furfuracea* (L.) Zopf.

The statistical analysis of *P. furfuracea* follows the ones for cowberry and *H. physodes*. Table 9 shows the variances of the random effects for both probit and logit models.

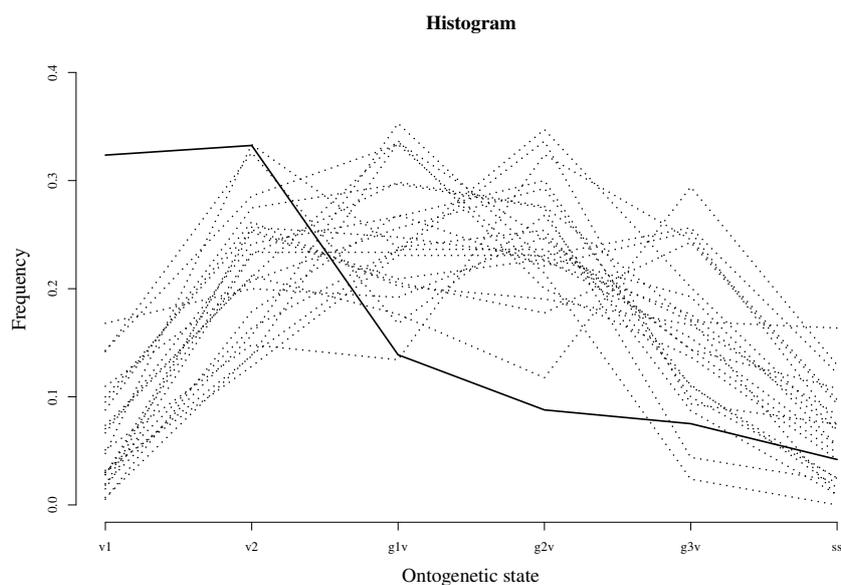
**TABLE 8.** Analysis of deviances (number of parameters in the model, AIC, log-likelihood, likelihood ratio test) of nested probit models for *Hypogymnia physodes*

Model	no.par	AIC	logLik	LR.stat	df	Pr(>Chisq)
$M_0$	5	48252.36	-24121.18			
$M_2$	7	47058.49	-23522.25	1197.86	2	$< 2.2 \cdot 10^{-16}$
$M_1$	6	47811.14	-23899.57			
$M_2$	7	47058.49	-23522.25	754.65	1	$< 2.2 \cdot 10^{-16}$
$M_0$	5	48252.36	-24121.18			
$M_1$	6	47811.14	-23899.57	443.21	1	$< 2.2 \cdot 10^{-16}$



**FIGURE 2.** The random effects of models  $M_2$  (logit and probit) for ontogenetic spectra of *Hypogymnia physodes*. The filled circles are the random effects for the samples (fir, pine and lime-tree), the blank circles are the individual random effects. The first circle in the lime-tree sample (tree 22) appears to be an outlier. The 95% confidence intervals based on the variance of the sample random effect

The analysis reveals significant differences between the ontogenetic spectra of different samples; see Table 10 and 11. The analysis yields similar results for both logit and probit models. The effect of between-sample variability is similar to the one for cowberry and significantly lower than for *H. physodes*: 0.297 (variance, logit) and 0.303 (variance, probit). The results do not totally agree with the results obtained by the analysis of deviance: 0.500 (deviance, logit) and 0.514 (deviance, probit). Such mismatch has not been observed for the data on cowberry and *H. physodes*.



**FIGURE 3.** The ontogenetic spectra of *Hypogymnia physodes* on lime-trees. The black solid line is the ontogenetic spectrum of tree 22

**TABLE 9.** The variances of the random effects of models  $M_2$  (logit and probit) for *Pseudevernia furfuracea*

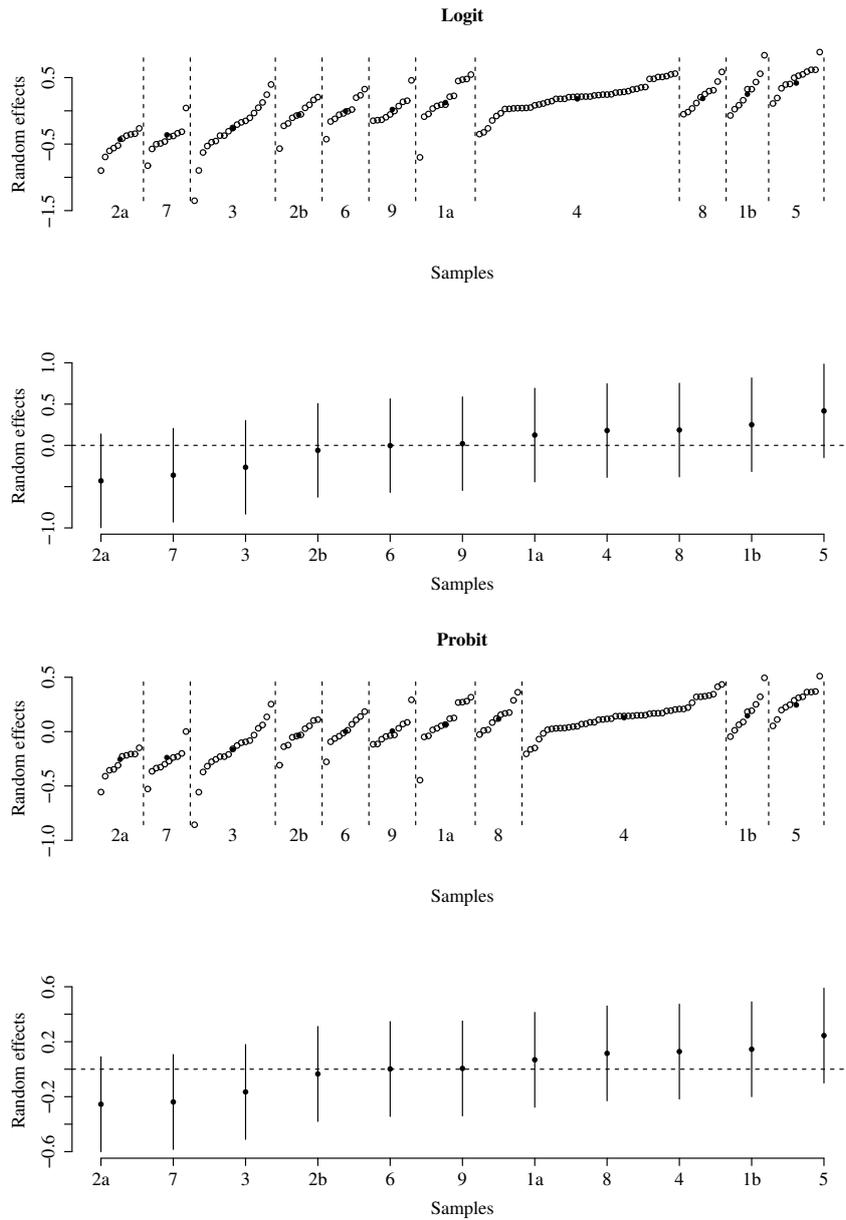
Random effects	Logit		Probit	
	Variance	Proportion	Variance	Proportion
Sample	0.09385	0.29669	0.03368	0.30278
Subsample	0.22248	0.70331	0.07755	0.69722

## CONCLUSION

In this paper, we have analysed ontogenetic spectra of plants and epiphytic lichens. Since several subsamples (either quadrants or trees) within a sample (or a population) are typically collected and the subsamples are not homogeneous, the ontogenetic spectrum varies across the population. Therefore, there is a need for statistical methods that take into account the heterogeneity of the subsamples. The proposed approach based on ordinal regression models allows correct comparisons of ontogenetic spectra of heterogeneous samples from populations of plants and epiphytic lichens.

**TABLE 10.** Analysis of deviances (number of parameters in the model, AIC, log-likelihood, likelihood ratio test) of nested logit models for *Pseudevernia furfuracea*

Model	no.par	AIC	logLik	LR.stat	df	Pr(>Chisq)
$M_0$	6	20351.40	-10169.70			
$M_2$	8	19998.58	-9991.29	356.82	2	$< 2.2 \cdot 10^{-16}$
$M_1$	7	20175.10	-10080.55			
$M_2$	8	19998.58	-9991.29	178.52	1	$< 2.2 \cdot 10^{-16}$
$M_0$	6	20351.40	-10169.70			
$M_1$	7	20175.10	-10080.55	178.30	1	$< 2.2 \cdot 10^{-16}$



**FIGURE 4.** The random effects of models  $M_2$  (logit and probit) for ontogenetic spectra of *Pseudevernia furfuracea*. The filled circles are the random effects for the samples (fir, pine and lime-tree), the blank circles are the individual random effects. The 95% confidence intervals based on the variance of the sample random effect

In addition, the use of the regression model gives us the opportunity to include additional explanatory variables, for example, describing geobotanical characteristics of the habitat. The estimates of between-sample differences are concordant with the results of the principal component analysis [20].

**TABLE 11.** Analysis of deviances (number of parameters in the model, AIC, log-likelihood, likelihood ratio test) of nested probit models for *Pseudevernia furfuracea*

Model	no.par	AIC	logLik	LR.stat	df	Pr(>Chisq)
$M_0$	6	20351.40	-10169.70			
$M_2$	8	19961.33	-9972.67	394.07	2	$< 2.2 \cdot 10^{-16}$
$M_1$	7	20150.83	-10068.42			
$M_2$	8	19961.33	-9972.67	191.50	1	$< 2.2 \cdot 10^{-16}$
$M_0$	6	20351.40	-10169.70			
$M_1$	7	20150.83	-10068.42	202.57	1	$< 2.2 \cdot 10^{-16}$

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## REFERENCES

1. D. Roach, *Genetica* **91**, 53–64 (1993).
2. A. A. Uranov, *Biological Sciences* pp. 7–33 (1975).
3. Y. G. Suetina, *Russian Journal of Ecology* **32**, 185–190 (2001).
4. M. V. Markov, *Population biology of plants*, KMK, 2012.
5. A. A. Uranov, and N. M. Grigorieva, *Bulletin of the Moscow Society of Naturalists: Biological Sciences* **80**, 36–44 (1975).
6. J. White, *The population structure of vegetation*, Springer, 1985.
7. L. B. Zaugolnova, L. A. Zhukova, A. S. Komarov, and O. V. Smirnova, The coenopopulations of plants (essays of plant population biology) (1988).
8. N. V. Glotov, “On the estimation of the parameters of the age structure of plant population,” in *Life populations in heterogeneous environment (Part 1)*, Periodika Mari El, Yoshkar-Ola, 1998, pp. 146–149.
9. R. Sokal, and F. Rohlf, *Biometry*, WH Freeman and company: New York, 1995.
10. J. Hardin, J. Hilbe, and J. Hilbe, *Generalized Linear Models and Extensions*, Stata Press, 2007.
11. D. N. Tsyganov, *Phytoindication of Ecological Regimes in the Coniferous-Broadleaved Forest Subzone*, Nauka, Moscow, 1983.
12. L. B. Zaugolnova, and L. G. Khanina, *Russian Forest Sciences* pp. 76–83 (1996).
13. L. V. Prokopyeva, L. A. Zhukova, and N. V. Glotov, “Ontogenesis of cowberry (*Vaccinium vitis-idaea* L.),” in *Ontogenetic atlas of medicinal plants*, Mari State University, Yoshkar-Ola, 2000, pp. 39–46.
14. N. V. Glotov, V. L. Semerikov, and L. V. Prokopyeva, “Study of the genetic structure of cowberry population (*Vaccinium vitis-idaea* L.) in the reserve,” in *Scientific Papers of the State Nature Reserve “Bolshaya Kokshaga”*, Mari State Technical University, Yoshkar-Ola, 2008, pp. 110–130.
15. Y. G. Suetina, and N. V. Glotov, *Russian Journal of Developmental Biology* **45**, 163–167 (2014).
16. Y. G. Suetina, A. A. Teplyh, and G. A. Bogdanov, “Foliaceous form of the lichen *Pseudevernia furfuracea* (L.),” in *Scientific Papers of the State Nature Reserve “Bolshaya Kokshaga”*, Mari State Technical University, Yoshkar-Ola, 2007, pp. 230–234.
17. Y. G. Suetina, and A. A. Teplyh, “Age-vitality structure of population epiphytic lichen *Pseudevernia furfuracea* (L.) Zopf in lichen-moss pine forest,” in *Principles and methods of biodiversity conservation*, Mari State University, Yoshkar-Ola, 2006, pp. 286–288.
18. A. A. Teplyh, “Spatial and age-vitality population structure of lichen *Pseudevernia furfuracea* (L.) Zopf in upland bog,” in *Scientific Papers of the State Nature Reserve “Bolshaya Kokshaga”*, Mari State Technical University, Yoshkar-Ola, 2008, pp. 143–158.
19. R. H. B. Christensen, ordinal — Regression Models for Ordinal Data (2013), R package version 2013.9-30 <http://www.cran.r-project.org/package=ordinal/>.
20. S. M. Ivanov, G. Y. Sofronov, and N. V. Glotov, “Application of principal component analysis for study of ontogenetic spectrums of populations,” in *Principles and methods of biodiversity conservation*, Mari State University, Yoshkar-Ola, 2013, pp. 197–202.

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