Modeling abundance time series through a GLM model

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Outlines

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Relative abundance: proportions of each species in the whole ecosystem. It describes the biodiversity of the ecosystem.

Notations

A relative abundance $y = (y_1, \ldots, y_d)$ is an element of the **simplex**:

$$\mathcal{S}_{d-1} = \left\{ (x_1, \ldots, x_d) \in]0; +\infty[^d \mid \sum_{i=1}^{d} x_i = 1 \right\}.$$

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Furthermore, we denote $\overline{y} = (y_1, \dots, y_{d-1})$.

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➜ It is impossible to apply our favourite time series models...

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Remark

A very popular choice for f is the **additive log-ratio**:

$$\begin{aligned} f :\ \mathcal{S}_{d-1} &\longrightarrow \mathbb{R}^{d-1} \\ (y_1, \ldots, y_d) &\longmapsto \left(\log\left(\frac{y_1}{y_d}\right), \ldots, \log\left(\frac{y_{d-1}}{y_d}\right)\right) \end{aligned}$$

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The interpretation of the model's parameters *(applied to* $(Z_t)_{t\in\mathbb{Z}}$*)* is very difficult, if not impossible.

OUR GOAL:

To propose a model for the time series $(Y_t)_{t\in\mathbb{Z}}$ which is easily interpretable.

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Staying in the simplex

The traditional approach lacks of interpretation due to the transformation of the initial time series.

The idea is thus to propose a model for time series which stays in the simplex:

$$\mathbb{P}(Y_{t+1} \in A \mid Y_t = y_t) = P(A/y_t)$$

where P is a transition kernel with source $\mathcal{S}_{d-1}$ and target $\mathcal{S}_{d-1}$.

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It is obviously possible to consider several lag-values *(even an infinity)*.

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Why ?

Because this distribution allows us to approach almost any kind of distribution on the simplex *(it is the generalization of the Beta distribution)*.

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Actually, for $Y \sim \mathrm{Dir}(\lambda, \varphi)$, then $\mathrm{Cov}(Y_i, Y_j) = -\dfrac{\lambda_i \lambda_j}{\varphi + 1}$ if $i \neq j$ and $\mathrm{Var}(Y_i) = \dfrac{\lambda_i(1-\lambda_i)}{\varphi + 1}$.

Back to the model

We thus propose that:

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Following the GLM framework, we also propose that

$$\eta = (A, B) \in \mathbb{R}^{(d-1)\times(d-1)} \times \mathbb{R}^{d-1} \quad \text{and} \quad \theta = (\theta_1, \theta_2) \in \mathbb{R}^2$$

with the link functions:

$$\mathrm{alr}\left(\lambda(\eta, y_t)\right) = A \cdot \overline{y_t} + B \tag{1}$$

and

$$\varphi(\theta, y_t) = \exp\left(\theta_1 + \theta_2 \cdot I_S(y_t)\right). \tag{2}$$

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A2: η belongs to a compact set H of $\mathbb{R}^{(d-1)\times(d-1)} \times \mathbb{R}^{d-1}$.

Then there exists a unique time series $(Y_t)_{t\in\mathbb{Z}}$ which is strictly stationary and ergodic such that for all $t \in \mathbb{Z}$:

$$\mathcal{L}(Y_{t+1} \mid Y_t = y_t) = \mathrm{Dir}\left(\lambda(\eta, y_t), \varphi(\theta, y_t)\right)$$

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Remark

Under assumptions **A1** and **A2**, the kernel P actually satisfies the **Doeblin's condition**.

Outlines

Interpretation of parameter θ

Recall that the dispersion parameter of our model satisfies:

$$\varphi(\theta, y_t) = \exp(\theta_1 + \theta_2 \cdot I_S(y_t))$$

where the Shannon index $I_S(y_t) > 0$ is a measure of biodiversity in the ecosystem.

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θ_1 corresponds to a variability inherent to the process: the lower it is, the more volatile the time series is.

Interpretation of parameter $\eta = (A, B)$ (1/3)

It is a more tricky explanation, and the mean parameter of our model satisfies:

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$$\begin{aligned} &\lambda(\eta, y_t) \\ &= \mathrm{alr}^{-1}(A \cdot \overline{y_t} + B) \\ &= \left(\frac{\exp(A_{1*} \cdot \overline{y_t} + B_1)}{1 + \sum_{j=1}^{d-1} \exp(A_{j*} \cdot \overline{y_t} + B_j)}, \dots, \frac{1}{1 + \sum_{j=1}^{d-1} \exp(A_{j*} \cdot \overline{y_t} + B_j)} \right) \end{aligned}$$

where A_{j*} denotes the j^{th} line of matrix A.

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In order to interpret A, one can consider the means ratio between species i and j at time $t+1$:

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Assume for example that the abundance is modified at time t: species of reference d increases by p, at the expense of species i and j, resulting in a new abundance:

$$z_t = y_t + \left(0, \dots, 0, -\underset{\substack{\uparrow \\ i}}{\alpha} \cdot p, 0, \dots, 0, (\alpha - \underset{\substack{\uparrow \\ j}}{1}) \cdot p, 0, \dots, 0, \underset{\substack{\uparrow \\ d}}{p}\right)$$

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Considering the impact the means ratio, we get:

$$\frac{MR(i,j,z_t)}{MR(i,j,y_t)} = \exp\left(p\left(\alpha(A_{ij} + A_{ji} - A_{ii} - A_{jj}) + A_{jj} - A_{ij}\right)\right).$$

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Thus, the coefficients in A give us a precise information about how the changes in an abundance would affect the means ratio between two species.

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I. Abundance and compositional data

II. Dirichlet GLM model for time series

III. Estimation
- Maximum of conditional likelihood
- Maximum of conditional pseudo-likelihood

IV. Application of the model

V. Conclusion

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We consider now that we have a sample $(y_t)_{0 \leqslant t \leqslant n}$ of the abundance of an ecosystem along time.

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Furthermore, we consider the couple of parameters (θ, η) under its vectorized form.

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Maximum of conditional likelihood: definition

It is the most natural estimator, and it is defined by

$$\left(\hat{\theta}_n, \hat{\eta}_n\right) = \underset{(\theta,\eta)\in\Theta\times H}{\operatorname{argmin}} \; -\sum_{t=1}^{n} \log\left(p_{(\theta,\eta)}(y_t, y_{t-1})\right)$$

where $p_{(\theta,\eta)}(\cdot, y_{t-1})$ is the density of the kernel $P(\cdot/y_{t-1})$:

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where $p_{(\theta,\eta)}(\cdot, y_{t-1})$ is the density of the kernel $P(\cdot/y_{t-1})$:

$$\begin{aligned} p_{(\theta,\eta)}(y_t, y_{t-1}) = \frac{\Gamma(\varphi(\theta, y_{t-1}))}{\prod_{i=1}^{d} \Gamma(\alpha_i(\theta, \eta, y_{t-1}))} \times \prod_{i=1}^{d-1} y_{t,i}^{\alpha_i(\theta,\eta,y_{t-1})-1} \\ \times \left(1 - \sum_{i=1}^{d-1} y_{t,i}\right)^{\alpha_d(\theta,\eta,y_{t-1})-1} \end{aligned}.$$

Maximum of conditional likelihood: properties

Proposition 1

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$$(\theta, \eta) \longmapsto -\sum_{t=1}^{n} \log\left(p_{(\theta,\eta)}(y_t, y_{t-1})\right)$$

strongly depends on the initial value chosen for (θ, η), and can numerically fail.

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$$\eta \longmapsto -\sum_{t=1}^{n} \sum_{i=1}^{d} y_{t,i} \log\left(\lambda_i(\eta, y_{t-1})\right)$$

is convex.

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It can be a good strategy to initialize the value of η with $\hat{w}_n$ when looking for the maximum of conditional likelihood.

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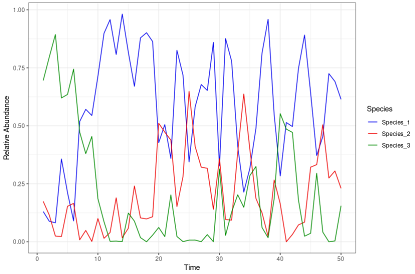

Simulation of an abundance of three species

Estimated results

With the maximum of conditional pseudo-likelihood, the mean of the estimates obtained is given by:

$$\hat{A}_1 = \begin{pmatrix} 4.48 & 2.99 \\ 5.00 & 6.49 \end{pmatrix} \quad \text{and} \quad \hat{B}_1 = \begin{pmatrix} -1.98 \\ -3.99 \end{pmatrix}.$$

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With the maximum of conditional likelihood, we have:

$$\hat{A}_2 = \begin{pmatrix} 4.53 & 3.16 \\ 5.10 & 6.63 \end{pmatrix}, \quad \hat{B}_2 = \begin{pmatrix} -2.03 \\ -4.05 \end{pmatrix} \quad \text{and} \quad \hat{\theta} = \begin{pmatrix} 1.53 \\ 0.02 \end{pmatrix}.$$

Comparison with the true values

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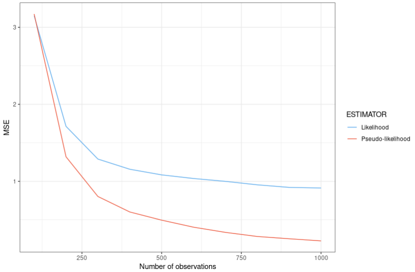
One can find below the MSE of our estimates, depending on the number of observations used.



MSE of both estimators

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For simplification purpose, we will focus on three particular species: Anthus pratensis, Calcarius lapponicus and Oenanthe oenanthe.

(a) Anthus pratensis

(b) Calcarius lapponicus

(c) Oenanthe oenanthe

Scandinavian Birds

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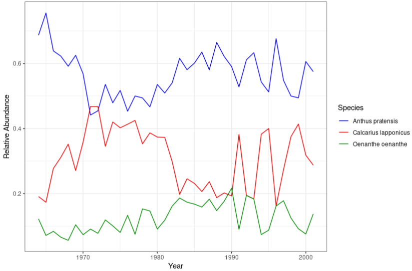
One can find below the graphics of relative abundance for these species.



Abundance of Scandinavian Birds

Estimation results and previsions (1/2)

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$$\hat{A} = \begin{pmatrix} 4.68 & 3.43 \\ 3.83 & 5.13 \end{pmatrix}, \quad \hat{B} = \begin{pmatrix} -2.21 \\ -2.87 \end{pmatrix} \quad \text{and} \quad \hat{\theta} = \begin{pmatrix} 1.34 \\ 0.65 \end{pmatrix}.$$

Estimation results and previsions (2/2)

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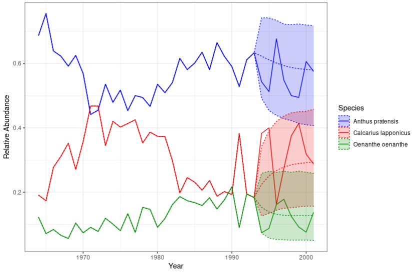

Prevision of the abundance for Scandinavian Birds

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For example, if species 3 increases its abundance by p, at the expense of species 1 and 2:

$$z_t = y_t + (-\alpha \cdot p, (\alpha - 1) \cdot p, p).$$

Interpretation of the results (2/2)

We compute:

$$\frac{MR(1,2,z_t)}{MR(1,2,y_t)} = \exp\left(p\left(\alpha\left(\hat{A}_{12} + \hat{A}_{21} - \hat{A}_{11} - \hat{A}_{22}\right)\right) + \hat{A}_{22} - \hat{A}_{12}\right)$$
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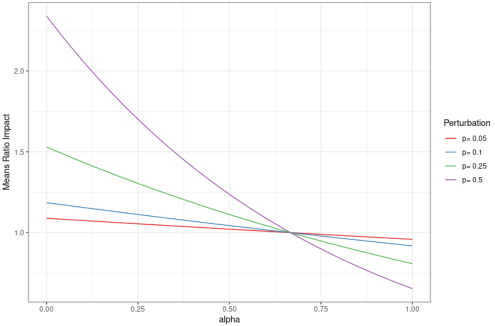

Impacts on the means ratio

Outlines

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  - Infer missing values ?
  - Construction of a model on the simplex, but with a dimension which can vary ?

Thank you !

References

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