# Dynamical Modeling of Abundance Data in Ecology

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# Outlines

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The **relative abundance** of a species in an ecosystem is the proportion of individuals of the species among all individuals from all species.

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| Lions | Zebras | Buffalos | Hyenas | Total |
|---|---|---|---|---|
| 12 | 36 | 48 | 24 | 120 |
| 10 % | 30% | 40% | 20% | 100% |

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|---|---|---|---|---|
| 12 | 36 | 48 | 24 | 120 |
| 10 % | 30% | 40% | 20% | 100% |

The vector $(12, 36, 48, 24)$ is the standard abundance of our ecosystem, while the vector $(0.1, 0.3, 0.4, 0.2)$ is the relative abundance.

### Remark

**Remark**

Relative abundance data are therefore compositional data, i.e. taking values in the simplex:

$$\mathcal{S}_{d-1} = \left\{ (y_1, \ldots, y_d) \in ]0;1[^d \mid \sum_{i=1}^{d} y_i = 1 \right\}.$$

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$\Longrightarrow$ leads to regression problems for compositional data.

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One can immediately guess that the abundance of species in a given ecosystem is a dynamic process, varying along the time.

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In all that follows, we will study the relative abundance along time $t \in \mathbb{Z}$ of $d \geqslant 2$ studies in a given ecosystem, modeled by a sequence $Y^{(t)} = \left( Y_1^{(t)}, \ldots, Y_d^{(t)} \right)$ of random variables, valued in $\mathcal{S}_{d-1}$.

We will assume that we have in our possession a sample $\left(y^{(t)}\right)_{0\leqslant t\leqslant N} \in \mathcal{S}_{d-1}^{N}$ of this abundance, where $y^{(t)}$ is a realization of the random variable $Y^{(t)}$.

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**Example** *Scandinavian birds*

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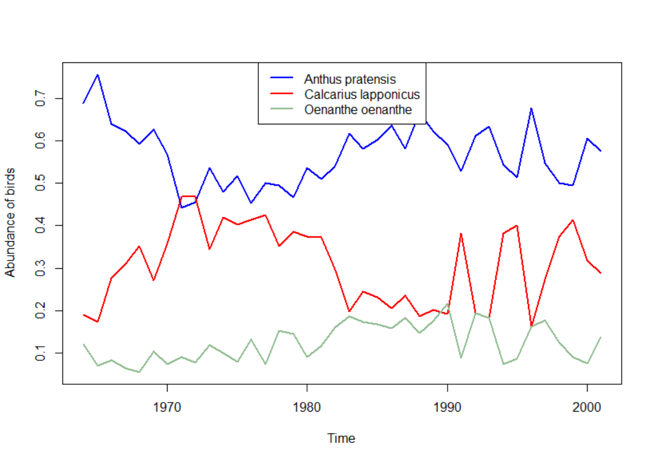
Consider an ecosystem composed by three alpine birds species: «Anthus pratensis», «Calcarius lapponicus» and «Oenanthe oenanthe». The relative abundance of this ecosystem has been registered from 1964 to 2001:

| YEAR | Anthus | Calcarius | Oenanthe |
|---|---|---|---|
| 1964 | 0.69 | 0.19 | 0.12 |
| 1965 | 0.76 | 0.17 | 0.07 |
| 1966 | 0.64 | 0.28 | 0.08 |
| 1967 | 0.62 | 0.31 | 0.07 |

## Example

A graphical representation of the time series is presented below.



# Outlines

I. Abundance Data

II. General framework

III. Data transformation

IV. The «Stay in the simplex approach»

- Some properties about Markov Chains
- Some properties about ergodicity
- Back to the model

As in the static case, the idea is to use a one-to-one mapping:

$$
\begin{aligned}
alr: \quad & \mathcal{S}_{d-1} \longrightarrow \mathbb{R}^{d-1} \\
& y = (y_1, \ldots, y_d) \longmapsto z = \left( \log\left(\frac{y_1}{y_d}\right) \ldots, \log\left(\frac{y_{d-1}}{y_d}\right) \right).
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We thus transform our abundance time series $\left(Y^{(t)}\right)_t$ valued in the simplex into a time series $\left(Z^{(t)}\right)_t$ valued in $\mathbb{R}^{d-1}$ with:

$$\forall t \in \mathbb{Z}, \ Z^{(t)} = alr\left(Y^{(t)}\right).$$

Once we have obtained a fitted time series $\left(\widehat{Z^{(t)}}\right)_t$ on the transformed scale, it is possible to get a fitted time series $\left(\widehat{Y^{(t)}}\right)_t$ on the original scale with:

$$\forall t \in \mathbb{Z}, \ \widehat{Y^{(t)}} = alr^{-1}\left(\widehat{Z^{(t)}}\right).$$

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**Remark**

Let us recall that we have:

$$alr^{-1}: \ \ \mathcal{S}_{d-1} \longrightarrow \mathbb{R}^{d-1}$$
$$z = (z_1, \ldots, z_{d-1}) \longmapsto \left(\frac{\exp(z_1)}{1 + \sum_{j=1}^{d-1} \exp(z_j)}\right)_{1 \leqslant i \leqslant d}.$$

One of the easiest model for the time series $\left(Z^{(t)}\right)$ is the **VAR**$(p)$ model:

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$$\forall t \in \mathbb{Z},\ \ Z^{(t)} = c + \sum_{i=1}^{p} \phi_i \cdot Z^{(t-i)} + \varepsilon_t$$

where $\phi_1, \ldots, \phi_p$ are $(d-1) \times (d-1)$ matrices, $c \in \mathbb{R}^{d-1}$ and $(\varepsilon_t)_{t \in \mathbb{Z}}$ is a gaussian white noise in $\mathbb{R}^{d-1}$.

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If all the solutions of the equation:

$$\det(\phi(z)) = 0$$

have an absolute value strictly larger than 1, then there exists a unique stationary process satisfying equation.

## Example *Scandinavian Birds*

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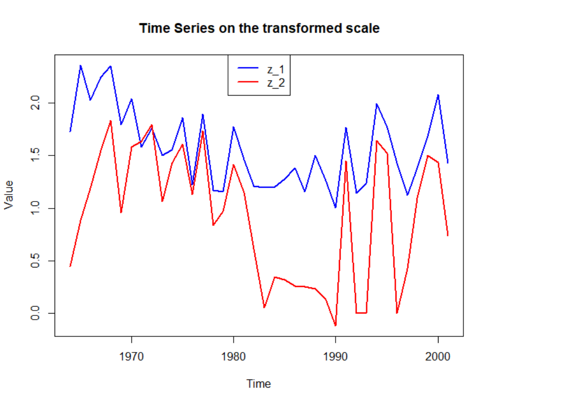
Applying the $alr$ transformation to the time series of Scandinavian birds, we obtain the time series given below.



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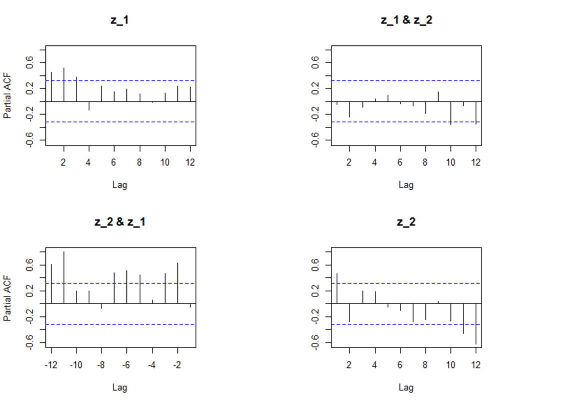

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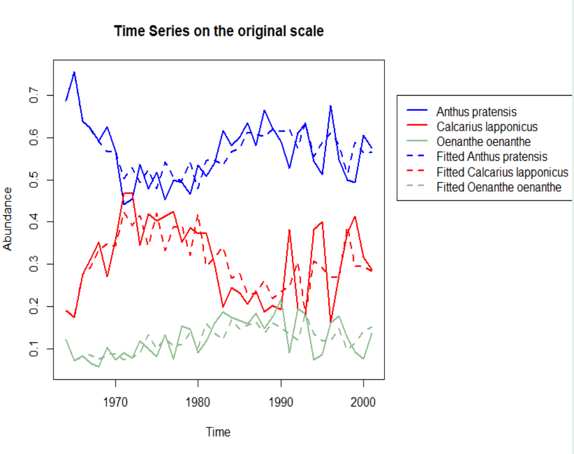
Finally, a backtransformation of those fitted values gives us fitted values on the original scale.



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Some basic ideas of the Dirichlet regression for compositional data:

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The response variable $Y$ follows the Dirichlet distribution of mean $\mu = (\mu_1, \ldots, \mu_d)$ and dispersion parameter $\phi$ with for all $1 \leqslant i \leqslant d - 1$:

$$\mu_i = \frac{\exp\left(\beta^{(i)} \cdot X\right)}{1 + \sum_{j=1}^{d-1} \exp\left(\beta^{(j)} \cdot X\right)}$$

where $X$ is the vector of explanatory variables.

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We thus suggest that for all $t \in \mathbb{Z}$, $Y^{(t)}$ follows the Dirichlet distribution with mean $\mu_t = \left(\mu_{t,1}, \ldots, \mu_{t,d}\right)$ satisfying:

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$$\forall 1 \leqslant i \leqslant d-1,\ \mu_{t,i} = \frac{\exp\left(\beta^{(i)} \cdot Y^{(t-1)}\right)}{1 + \sum_{j=1}^{d-1} \exp\left(\beta^{(j)} \cdot Y^{(t-1)}\right)}$$

and constant dispersion parameter $\phi$.

**Remark**

Observe that we only took the previous value $Y^{(t-1)}$ as covariate. It is of course possible to take several lag-values $Y^{(t-2)}, Y^{(t-3)}, \ldots$ in this expression.

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and:

$$\mathcal{F}_t = \sigma\left(Y^{(t)}\right).$$

The process $Y^{(t)}$ is a **Markov chain** if for any measurable bounded function $f\colon E \longrightarrow \mathbb{R}$:

$$\mathbb{E}\left(f\left(Y^{(t)}\right) \mid \mathcal{F}_{t-1}^-\right) = \mathbb{E}\left(f\left(Y^{(t)}\right) \mid \mathcal{F}_{t-1}\right).$$

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Intuitively, this means that knowing the entire history of the process does not bring more information than knowing the last value.

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A Markov chain $\left(Y^{(t)}\right)_{t\in\mathbb{Z}}$ valued in $(E, \mathcal{E}$ has transition kernel $K$ if for all $t \in \mathbb{Z}$ and all $A \in \mathcal{E}$:

$$\mathbb{P}\left(Y^{(t)} \in A \;\middle|\; Y_{t-1} = y_{t-1}\right) = K(y_{t-1}, A).$$

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In this case, the chain is said to be homogeneous.

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Let us define the shift operator $\sigma : E^{\mathbb{Z}} \longrightarrow E^{\mathbb{Z}}$ by $\tau\left((y_t)_{t\in\mathbb{Z}}\right) = (y_{t+1})_{t\in\mathbb{Z}}$.

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The process $\left(Y^{(t)}\right)_{t\in\mathbb{Z}}$ is **ergodic** if for all $\tau$-invariant event $A \subset E^{\mathbb{Z}}$:

$$\mathbb{P}_Y(A) = 0 \text{ or } 1.$$

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If $(Y_t)_{t\in\mathbb{Z}}$ is an ergodic process, for any measurable function $f : E^{\mathbb{Z}} \longrightarrow \mathbb{R}$ such that $\mathbb{E}\left(|f(Y)|\right) < +\infty$ we have:

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In particular, for any function $g : E \longrightarrow \mathbb{R}$ such that $\mathbb{E}(|g(Y_0)|) < +\infty$:

$$\frac{1}{n}\sum_{k=1}^{n} g(Y_k) \longrightarrow \mathbb{E}(g(Y_0))\ a.s$$

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where:

$$\pi \cdot K(A) = \int K(y, A)\pi(\mathrm{d}y)$$

**Theorem**

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If a transition kernel $K$ admits a unique invariant measure $\pi$, then there exists a unique strongly stationary Markov chain $\left(Y^{(t)}\right)_t$ with transition kernel $K$, and it is ergodic.

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We thus decide to model our abundance times series $\left(Y^{(t)}\right)_{t\in\mathbb{Z}}$ as a Markov chain with Dirichlet transition kernel $K$ with mean $\mu$ and unknown dispersion parameter $\phi$ with:

$$\mu_i = \frac{\exp(\beta^{(i)} \cdot y)}{1 + \sum_{j=1}^{d-1} \exp(\beta^{(j)} \cdot y)}.$$

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**Definition**

A transition kernel $K$ defined on $E \times \mathcal{E}$ satisfies the **Doeblin's condition** if there exists a constant $\eta > 0$ and a probability measure $\lambda$ on $E$ such that:

$$\forall A \in \mathcal{E},\ \forall y \in E,\ K(y, A) \geqslant \eta \cdot \lambda(A).$$

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**Corollary**

There exists a unique strongly stationary Markov chain $\left(Y^{(t)}\right)_t$ with transition kernel $K$, and it is ergodic.

The model parameters $\phi$ and $\beta^{(1)}, \dots, \beta^{(d-1)}$ can be estimated by the maximum of conditional likelihood, The model parameters $\phi$ and $\beta^{(1)}, \ldots, \beta^{(d-1)}$ can be estimated by the maximum of conditional likelihood, and ergodicity is an essential point here, because it ensures the strong consistency of these estimates, as well as their asymptotic normality.

**Example *Scandinavian Birds***

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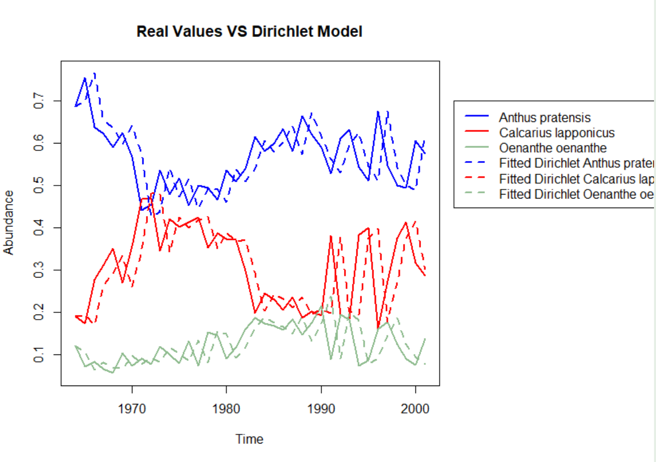
If we try to apply our model to the Scandinavian Birds data, we obtain the following results:

| | $\hat{\phi}$ | $\beta_1^{(1)}$ | $\beta_2^{(1)}$ | $\beta_3^{(1)}$ | $\beta_1^{(2)}$ | $\beta_2^{(2)}$ | $\beta_3^{(2)}$ |
|---|---|---|---|---|---|---|---|
| Estimates | 171.61 | 3.70 | 1.16 | -7.20 | 1.10 | 3.91 | -7.32 |

## Example

We present below the fitted values of abundance according to our model.



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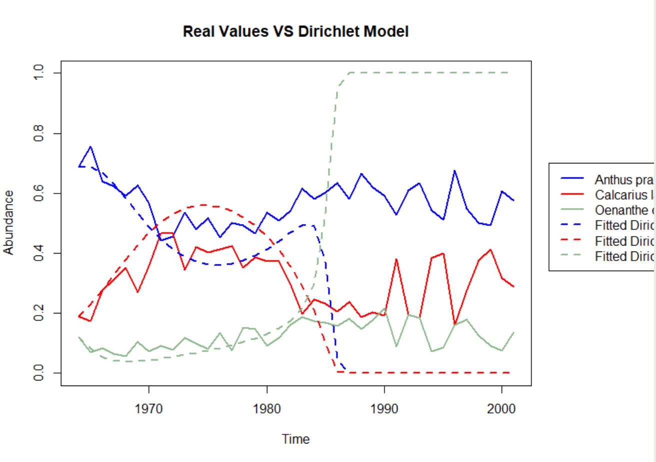

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$$y^{(t+1)} = y^{(t)} + (c, -c, 0).$$

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Assume that between $t$ and $t+1$, the abundance is evolving according to the following equation:

$$y^{(t+1)} = y^{(t)} + (c, -c, 0).$$

Consider the **power balance** between the two species defined by:

$$\frac{\mu_{1,t}}{\mu_{2,t}}.$$

**Remark**

This balance evolves according to:

$$\frac{\frac{\mu_{1,t+1}}{\mu_{2,t+1}}}{\frac{\mu_{1,t}}{\mu_{2,t}}} =$$

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$$\frac{\frac{\mu_{1,t+1}}{\mu_{2,t+1}}}{\frac{\mu_{1,t}}{\mu_{2,t}}} = \exp\left(c \cdot (\beta_1^{(1)} + \beta_2^{(2)} - \beta_2^{(1)} - \beta_1^{(2)})\right).$$