

Report on “Impact of a block structure on the Lotka-Volterra model”
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This paper studies the question of persistence and stability of populations when the species abundances follow a Lotka-Volterra model and the interaction among species is governed by a random matrix. This topic was initiated in seminal work of May and has been developed subsequently by numerous authors, including Allesina, Pascual, Tang and the authors of the present manuscript.

The paper extends previous work on the subject in a significant way: it considers a block structure network representing the inter- and intra-community interactions. This extension is very natural from an ecological standpoint, since the interaction among species is often structured in multiple communities. This extension, is also interesting in that the authors show that it lead to some new phenomena which are not present in the case of a random matrix. The writing is clear and precise.

In view of the above, I believe this paper makes an excellent contribution to the field, and will be of interest to readers interested by in modeling high-dimensional ecosystems. However, I think that there are several aspects in which the paper can be improved, both in terms of its overall structure and presentation, and at particular points. I would therefore suggest that the authors to make some revisions to address these points. General comments are given below, followed by a list of specific remarks and minor corrections.

General comments

1. The Introduction needs improvement to make the paper more accessible and appealing to readers unfamiliar with the topic. The introduction should provide an overview of the aims and the main results and contributions of the paper, and should not immediately launch into technical details. The introduction (see the subsections ‘Model and assumptions’ and ‘Properties of the dynamical system’) mentions some technical aspects (such as existence of a unique equilibrium and its asymptotic stability), some of which could be delayed to a later stage in the paper. It would also be good to provide an explicit biological motivation for the generalized setting investigated in this paper. Perhaps some of the summary statements made in the Discussion section should be moved to the introduction.

2. In May’s work (see the references [May72] and [AT12] of the manuscript), the model is written

$$\frac{dx_k}{dt} = x_k \left(r_k - \theta_k x_k + \sum_{l \neq k} B_{kl} x_l \right), \quad k \in \{1, \dots, n\}$$

where x_k is the density of species k , r_k represents its intrinsic growth rate, θ_k is an intraspecific feedback coefficient (most often denoted $\theta_k = r_k/K_k$, where K_k is the carrying capacity) and B_{kl} is the per capita effect of species $l \neq k$ on species k . The off diagonal coefficients B_{kl} of the random matrix interaction are drawn from a normal distribution. In this paper, see model (1), it is assumed that $\theta_k = 1$, i.e. the carrying capacity is equal to the intrinsic growth rate (what is the biological significance of such an hypothesis ?) and in addition the intraspecific coefficient B_{kk} is not equal to 0 but random. These important

differences between the models that are used in the literature and the model (1) studied by the authors should be discussed.

3. The authors focus on the case with equal growth rates. See the model (3). What is the biological significance of this restriction ?

Specific remarks

1. Page 2: The following sentence is unintelligible

where $\mathcal{I}_1 = [n_1]$ (resp $\mathcal{I}_2 = \{n_1 + 1, \dots, n\}$), the subset of $[n]$ of size $|\mathcal{I}_1| = n_1$ (resp $|\mathcal{I}_2| = n_2$ - here and below $n = n_1 + n_2$) matching the index of species belonging to community 1 (resp community 2) and $\boldsymbol{\beta} = (\beta_1, \beta_2)$ with $\beta_1 = n_1/n$, $\beta_2 = 1 - \beta_1 = n_2/n$. The random matrix A_{ij} is non-Hermitian of size $|\mathcal{I}_i| \times |\mathcal{I}_j|$ with standard Gaussian entries i.e. $\mathcal{N}(0, 1)$.

Indeed, there are no symbols \mathcal{I}_1 , \mathcal{I}_2 or $\boldsymbol{\beta}$ in (2), so the sentence “where $\mathcal{I}_1 \dots \mathcal{I}_2 \dots$ and $\boldsymbol{\beta}$ ” which follows formula (2) is unclear.

I suggest rewording as follows

where A_{ij} is non-Hermitian of size $|\mathcal{I}_i| \times |\mathcal{I}_j|$ with standard Gaussian entries i.e. $\mathcal{N}(0, 1)$. Here $\mathcal{I}_1 = [n_1]$ (resp $\mathcal{I}_2 = \{n_1 + 1, \dots, n\}$), the subset of $[n]$ of size $|\mathcal{I}_1| = n_1$ (resp $|\mathcal{I}_2| = n_2$ - here and below $n = n_1 + n_2$) matching the index of species belonging to community 1 (resp community 2). We define $\boldsymbol{\beta} = (\beta_1, \beta_2)$ by $\beta_1 = n_1/n$, $\beta_2 = 1 - \beta_1 = n_2/n$.

2. Page 2. What do you mean by “The Gaussianity assumption clarifies the explanations, but can be relaxed under certain circumstances (see the corresponding sections for details).” Please specify the sections where this is done.
3. Page 2. The normalization parameter $1/\sqrt{n}$ in the matrix B in (2) deserves further explanation. The sentences “This enables the interaction matrix B to have a macroscopic effect on system (1) . . .” and “From an ecological perspective, an increase in the number of species may not necessarily lead to a corresponding increase in the overall strength of interactions between one species and all others.” on page 2, lines 6 to 10, deserve more detail to make them comprehensible to a reader who is not a specialist in the subject.
4. Page 2. The assumption $r_k = 1$ is very restrictive from an application point of view. Please clarify the footnote “The simplifying assumption $r_k = 1$ allows tractable computations and could be extended to $r_k = c$ with $c > 0$. However, if the growth rate is different for each species, the mathematical development and result may be strongly affected and will be discussed in each section.” Please specify the sections where this is done.