Coexistence of many species in random ecosystems

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Physical Models of Living Systems

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Aim of the project

- First attempt to mathematize the population dynamics of interacting species : **Lotka and Volterra**

- We don’t focus on finding the probability that all initial N species in an ecosystem coexist but, instead, in the **probability to obtain a number k of coexisting species after leaving the system evolve towards equilibrium P(k|n)**.

- We will study the behaviour of ecological models in which the parameters are randomly drawn from fixed distributions (species have not had time to adapt or evolve together). The pioneer in the study of **random ecological communities** was May, using **RMT**.

- **We want to study P(k|n) by varying the parameters of the distributions from which we randomly pick the growth rates and interaction between species.**

Theoretical framework

Problem statement

- Consider n interacting populations of species whose dynamics follow the GLV Equations:

abundance of population i at time t

intrinsic growth rate of species i

$$\frac{\mathrm{d}X_i(t)}{\mathrm{d}t} = X_i(t)\left(r_i + \sum_j A_{ij}X_j(t)\right)$$

per capita effect of species j on the growth rate of species i

- A vector x* is a fixed point of the system if $$0 = x_i^\star\left(r_i + \sum_j A_{ij}x_j^\star\right) \quad \text{for} \quad i = 1, 2, \ldots, n$$

- A fixed point is feasible if $x_i > 0$ for all i.

  If a feasible point exists, it is a solution of $\mathbf{r} = -A\mathbf{x}^*$

  If A is invertible, we obtain the species concentrations at equilibrium through $\mathbf{x}^* = -A^{-1}\mathbf{r}$

Theoretical framework

Global stability

- The **interaction matrix A** is chosen to be **Lyapunov diagonally stable**: we assume A to be negative definite and that $A + A^T$ has only got negative eigenvalues.
- If A is diagonally stable, there exists a solution of the GLV equations that is **globally attractive**.
- This globally stable fixed point has k positive entries and $(n-k)$ equal to 0. Then, we can define:

  $\{S\}_k$: set of the k persistent species ($x_i^* > 0$)

  $\{N\}_{n-k}$: set of $(n-k)$ species with 0 abundance at equilibrium

$$\mathbf{x}^* = \begin{pmatrix} \mathbf{x} \\ \mathbf{0}_{n-k} \end{pmatrix} \qquad A = \left(\begin{array}{c|c} A^{(s)} & A^{(sn)} \\ \hline A^{(ns)} & A^{(n)} \end{array}\right) \qquad \mathbf{r} = \begin{pmatrix} \mathbf{r}^{(s)} \\ \mathbf{r}^{(n)} \end{pmatrix} \longrightarrow$$

The abundance of the k persistent species can then be computed as:

$$A^{(s)}\mathbf{x} = -\mathbf{r}^{(s)}$$

Theoretical framework

Not-invasible fixed point

- Since we are dealing with **diagonally stable matrices**, the **equilibrium point is not invasible** by any of the remaining (n-k) species.

  That is, in the limit of low densities: $\mathbf{r}^{(n)} + A^{(ns)}\mathbf{x} < 0$

- In the case of diagonally stable matrices, the combination of $\{S\}_k$ and x is **unique** (the only one for which the solution has only positive components).

Methods and Results

- **Algorithm to get the feasible fixed point and the number of coexisting species in equilibrium:**

Looping over t trials (each trial yields a sample k; plotting them on an histogram, P(k|n)):

$x = -A^{-1} \cdot r$

$x_{negatives}$ = positions of the x vector with negative concentrations

while $x_{negatives}$ is not empty:

  Update A: delete columns and rows of A corresponding to the species with negative concentration x_i

  Update r: delete r_i entries corresponding to the species with negative concentration x_i

  Update x

  Update $x_{negatives}$

k = length of the resulting x, with all entries positive

Zero-mean case

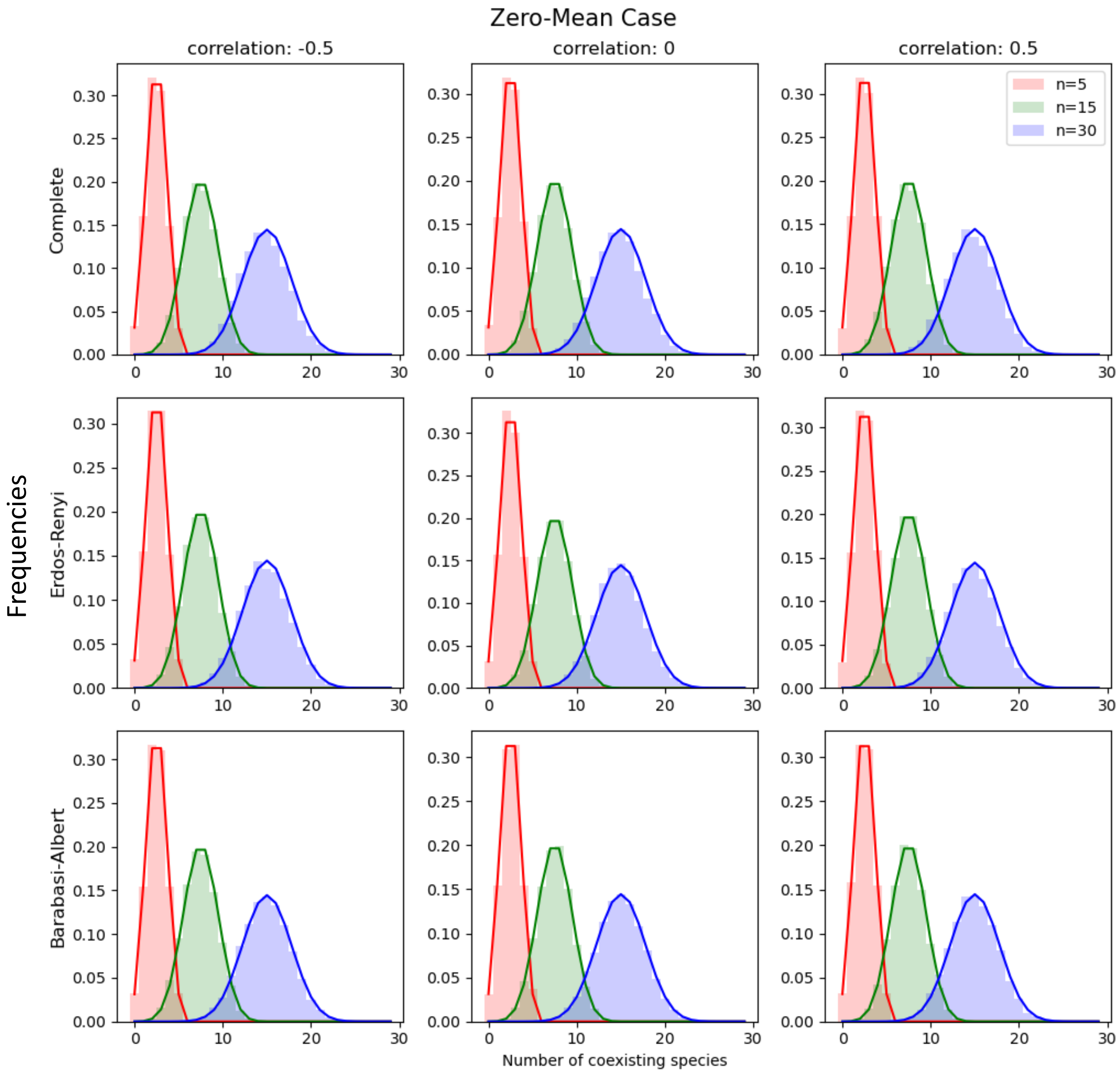
Symmetric mean-0 distributions are used to sample growth rates and inter-specific interactions

A

- $A_{ij} \sim$ symmetric distribution centred around 0
- A_{ii} : mean 0 symmetric random variable + a constant d_i

→ ½ of the species live in isolation and ½ rely in consumption for their survival

r $\quad r_i \sim$ symmetric distribution centred around 0



a) Caricature of a food web

- **Non invasibility** and **feasibility balance** out: each species has probability ½ of being included in the non-invisible solution.
- $P(k|n)$ **follows a binomial distribution** $B(n, 1/2)$.

Given A and r, about **half of the species would coexist no matter** n.

Expected if species did not interact at all.

b) Effect of network structure and correlation in A

- Strong in stability
- What about in coexistence?

Non-zero-mean case

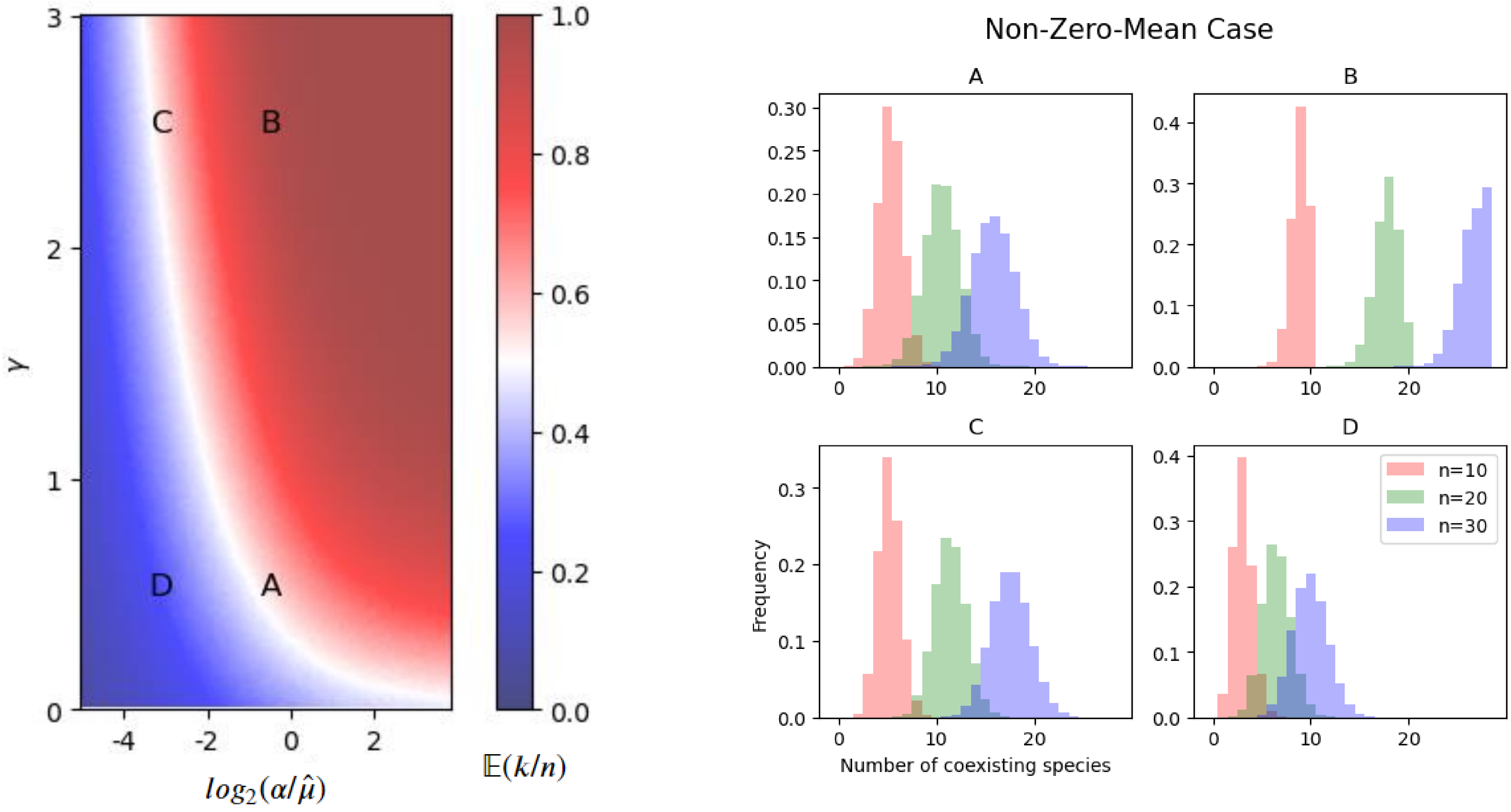
Symmetric NON-0-mean distributions are used to sample growth rates and inter-specific interactions

A_{ii} and A_{ij} are set to be negative (competitive interactions)

$$A \quad \left[\begin{array}{c} A_{ij} = \mu < 0 \\ A_{ii} = d_i = \alpha < 0 \end{array} \right] \longleftarrow \alpha < \mu < 0 \quad \text{(so that A is Lyapunov diagonally stable)}$$

r $\quad r_i \sim$ symmetric distribution centred around $\gamma > 0$ (g.r. need to be positive for species to survive)

This method can yield a larger/smaller number of coexisting species compared to the 0-mean case: $P(k|n)$ not $\sim B(n,\frac{1}{2})$

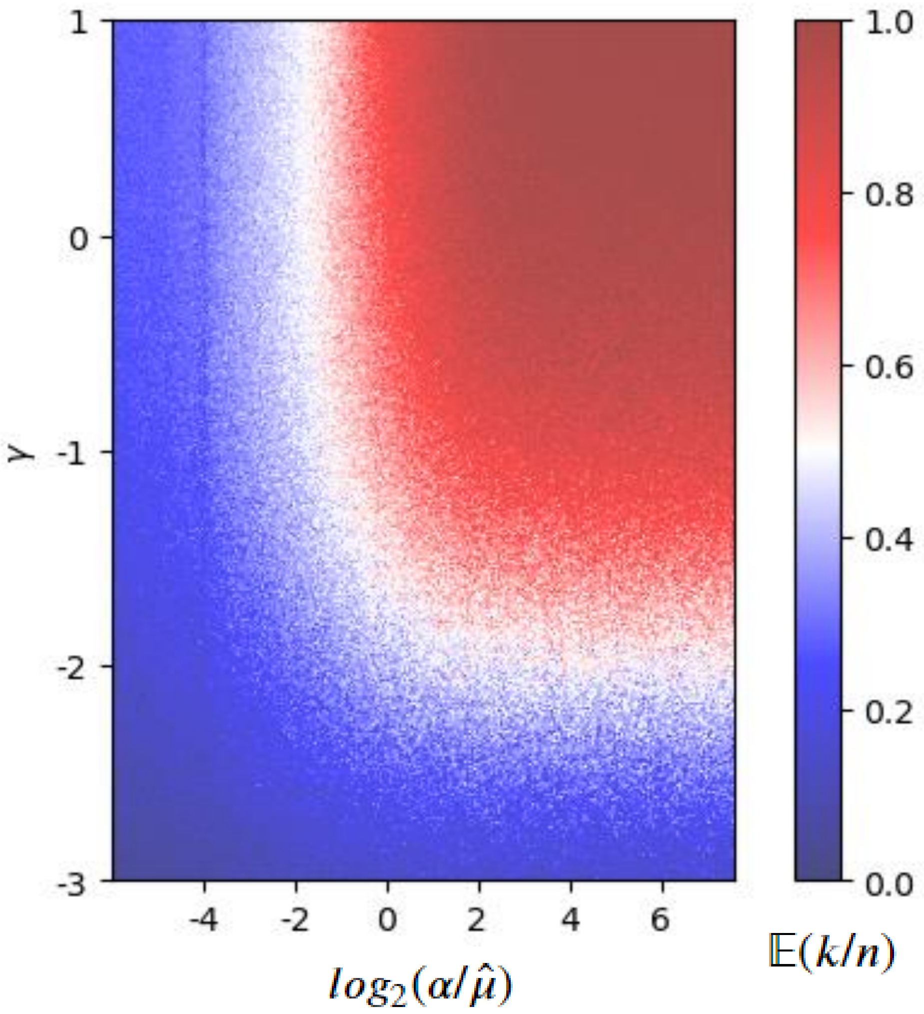


Real Food Web data

What happens if we explore the coexistence for different parameters taking data from a real food web?

- We take μ to be the mean of all the A_{ij}
- We set a value $\alpha < 0$ to fill the diagonal
- Growth rates are still sampled from $N(\gamma, 1)$

Gridsearch on γ and $\frac{\alpha}{\hat{\mu}}$ and compare with previous results.



Data from: *Food-web structure of and fishing impacts on the Gulf of Cadiz ecosystem (South-western Spain)*

References

Serván, C.A., Capitán, J.A., Grilli, J. *et al.*

Coexistence of many species in random ecosystems.

Nat Ecol Evol **2**, 1237–1242 (2018).

https://doi.org/10.1038/s41559-018-0603-6