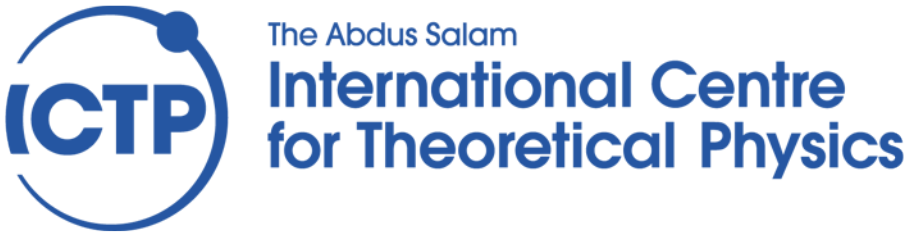

Block-structured Random Matrices

Ling Min Hao

Supervised by: Prof. Jacopo Grilli

Abstract

Random Matrix Theory (RMT) was born due to Eugene Wigner in physics to study the spectrum of large nuclei although origins of RMT could be traced back to works by Wishart and James in the field of multivariate statistics. Initiated by Robert May, it now serves as a powerful statistical model to study large systems with network structures. Biological systems like gene regulatory networks, protein-protein interaction networks, and ecological system networks are large and complex. Thus RMT can be applied to extract important information behind these biological systems. A block-structured random matrix is a more realistic model to study the ecosystem of the modular organization. To study the stability of an ecosystem, it suffices to know the rightmost eigenvalue of the random matrix. One direct method is to generate all eigenvalues by brute force and locate the rightmost eigenvalue. But this demands high time complexity ($\mathcal{O}(S^3)$) when S is large. In this project, we will optimize this problem using RMT.

Contents

1 Introduction

1.1 Classical Results in Random Matrix Theory

To study the stability of the ecosystem, we employ the tools from random matrix theory. The main object of study of random matrix theory is the empirical spectral distribution (ESD). Here we list out some important definitions and results in classical random matrix theory.

Definition 1.1 *Let X be a $S \times S$ Hermitian random matrix. Then, the ESD is defined as*

$$\mu(\lambda) = \frac{1}{S} \sum_{i=1}^{S} \delta(\lambda - \lambda_i) \tag{1.1}$$

where $\{\lambda_1, \cdots, \lambda_n\}$ are eigenvalues of X and δ is Dirac-delta function.

Definition 1.2 *Let X be a $S \times S$ non-Hermitian random matrix. Then, the ESD is defined as*

$$\mu(\lambda) = \frac{1}{S} \sum_{i=1}^{S} \delta(\lambda - \Re\lambda_i)\delta(\lambda - \Im\lambda_i) \tag{1.2}$$

Intuitively, ESD is a counting function that gives the proportion of the eigenvalues in an interval for a matrix X. For examples, if $n = 10$ and $\lambda_1, \lambda_3, \lambda_7 \in (a, b)$, then $\int_a^b \mu(\lambda) = \frac{3}{10}$. Also, it is easy to verify that ESD is indeed a pdf.

Result 1.1 *(Wigner's semicircular law) Let X be a $S \times S$ matrix where all the coefficients X_{ij} in the upper-triangular part are iid random variables, $X_{ij} = X_{ji}$, X_{ii} have zero mean and finite variance, off-diagonal elements have mean zero and unit variance. Then the ESD of $\frac{M}{\sqrt{S}}$ converges almost surely to the Wigner's semicircular distribution as $S \to \infty$, i.e*

$$\mu(\lambda) = \begin{cases} \frac{1}{2\pi}\sqrt{4 - \lambda^2} & \text{if } \lambda \in [-2, 2] \\ 0 & \text{otherwise} \end{cases} \tag{1.3}$$

Result 1.2 *(Circular law) Let X be a $S \times S$ nonsymmetic matrix, where X_{ij} are iid random variables with mean zero and unit variance. Then as $S \to \infty$, the ESD of $\frac{X}{\sqrt{S}}$ converges to the circular law, i.e*

$$\mu(\lambda) = \begin{cases} \frac{1}{\pi} & \text{if } \Re(\lambda)^2 + \Im(\lambda)^2 \leq 1 \\ 0 & \text{otherwise} \end{cases} \tag{1.4}$$

Result 1.3 *(Elliptic law) Let X be a $S \times S$ nonsymmetric matrix, where the pairs of coefficients (X_{ij}, X_{ji}) are sampled independently from a bivariate distribution with mean $\begin{pmatrix} 0 \\ 0 \end{pmatrix}$ and covariance matrix $\begin{pmatrix} 1 & \rho \\ \rho & 1 \end{pmatrix}$. Then the ESD of $\frac{X}{\sqrt{S}}$ converges to the elliptic law, i.e*

$$\mu(\lambda) = \begin{cases} \frac{1}{\pi(1-\rho^2)} & \text{if } \frac{(\Re(\lambda))^2}{(1+\rho)^2} + \frac{(\Im(\lambda))^2}{(1-\rho)^2} \leq 1 \\ 0 & \text{otherwise} \end{cases} \tag{1.5}$$

For a detailed proof, refer to [4] for Result 1.1, [12] for Result 1.2, and [7] for Result 1.3

1.2 Motivation

In this section, we will have a brief overview to see how previous researchers study the local asymptotic stability of a biological network using RMT.

Suppose we have S number of species living under the same ecosystem. The local asymptotic stability of a dynamical system is given by a set of nonlinear differential equations:

$$\frac{dX_i(t)}{dt} = f_i(\mathbf{X}(t))$$

where X_i is the population density of species i at time t, and $\mathbf{X}(t)$ is the vector of the population densities of all species. The function f_i describes how the growth of species i is affected by the abundance of other species. We say $\mathbf{X}^*$ is an equilibrium point if

$$\frac{dX_i(t)}{dt}|_{\mathbf{X}^*} = f_i(\mathbf{X}^*) = 0$$

The equilibrium is said to be locally unstable if the system never goes back to the equilibrium after an infinitesimal perturbation. The main objective is to study the criteria that determines the local asymptotic stability of this system, which is done by the linearization of system at equilibrium point. The analysis is based on Jacobian matrix of $\mathbf{J}$, whose elements are:

$$J_{ij} = \frac{\partial f_i(\mathbf{X})}{\partial X_j}$$

When evaluated at $\mathbf{X}^*$, the $S \times S$ community matrix M is obtained, i.e

$$M_{ij} = J_{ij}|_{\mathbf{X}^*} = \frac{\partial f_i}{\partial X_j}(\mathbf{X}(t))|_{\mathbf{X}^*}$$

Each element in M measures how a slight increase in the population of species j affects the growth rate of population i. Given the set of eigenvalues $\{\lambda_1, \lambda_2, \cdots, \lambda_S\}$ of M such that $\Re\lambda_1 \geq \Re\lambda_2 \geq \cdots \geq \Re\lambda_S$, the rightmost eigenvalue ($\Re(\lambda_1)$) gives the information about the stability of the ecosystem at the equilibrium point. If the sets of eigenvalues are complex-valued, the equilibrium is stable if all of its eigenvalues have negative real parts. Otherwise, the equilibrium is unstable. If the sets of eigenvalues are real-valued, the equilibrium is always unstable.

To determine $\Re(\lambda_1)$ it is required to know exactly the function f_i and the equilibrium point $\mathbf{X}^*$. The main difficulty is that there is no canonical set of equations describing the interaction between species. Even if there exists such a set of equations, measuring empirically all parameters needed to study the dynamics of a large community is unfeasible from a practical point of view.

Instead, Robert May built the community matrix M using the random matrix approach [5] and gave a stability criterion based on the characteristics of the random matrix itself. In his study, May sampled the elements of the community matrix from a distribution. May did not specify the distribution except only its mean and variance as the results remain the same in the large S limit regardless of the choice of distribution, a concept known as universality. Also, the random matrix ensemble are self-averaging, where the relative fluctuations around the average behavior becomes smaller and smaller as the size of the matrix increases. When

this property holds, the spectrum of large matrices converges to the average behavior. With these, it is then safe to use classical results in random matrix theory to obtain the region where all the eigenvalues lie. For convenience, May initialize all the diagonal elements M_{ii} to be $-d$, the off-diagonal elements M_{ij}, $i \neq j$ to be 0 with probability $1 - C$ and from a distribution with mean $\mu = 0$ and variance σ^2 with probability C. Here C represents the connectivity between species in the system. By using the circular law [2], we have all eigenvalues approximated by the uniform distribution on a disk with center $-d$ and radius $\sqrt{SC}$. Thus, the rightmost eigenvalue has negative real parts if the random matrix satisfies the criterion:

$$\sigma\sqrt{SC} < d$$

The statistical model built by May indeed paves the way to the study of local asymptotic stability of biological networks using random matrix theory. But what May proposed is still insufficient to resemble the real-case scenario, for instance:

1. In an ecological system, it is not necessary that the positive effects of the resource on the consumers precisely offset the negative impact of consumers on resources. Thus it is crucial to consider a nonzero mean for the off-diagonal entries. In this case, [2], one of the eigenvalues (outlier) will be the expectation of the row sum, i.e

$$\mathbb{E}(\sum_j M_{ij}) = -d + (S-1)\mathbb{E}(M_{ij}) = -d + (S-1)E$$

where $E = C\mu$. The remaining $S - 1$ eigenvalues are still approximated by the uniform distribution on a disk, where the center of this disk is the mean of these $S-1$ eigenvalues, which is $-(d+E)$ and the radius of this disc is $\sqrt{SV}$, where

$$V = \mathrm{Var}(M_{ij}) = \mathbb{E}(M_{ij}^2) - E^2 = C(\sigma^2 + \mu^2) - C^2\mu^2 = C(\sigma^2 + (1-C)\mu^2)$$

Thus, the stability criterion that considers both eigenvalues corresponding to the outlier and the rightmost eigenvalue on the disk will be:

$$\max\{\sqrt{SV} - E, (S-1)E\} < d$$

2. Also, in an ecosystem, there are different interactions between species like mutualism, commensalism, parasitism, competition, and the prey-predator model. In these cases M_{ij} is not independent from M_{ji}. The way to model this is to sample the symmetric pairs of coefficients from a bivariate distribution. By using the elliptic law [2], all the eigenvalues can be approximated by the uniform distribution on an ellipse with center $-d - E$, horizontal semi-axis $\sqrt{SV}(1+\rho)$, vertical semi-axis $\sqrt{SV}(1-\rho)$ where V is defined the same way as previous and ρ is given by

$$\rho = \frac{\tilde{\rho}\sigma^2 + (1-C)\mu^2}{\sigma^2 + (1-C)\mu^2}$$

where $\tilde{\rho}$ is the correlation from the bivariate distribution of mean $\boldsymbol{\mu} = \begin{bmatrix}\mu \\ \mu\end{bmatrix}$ and covariance matrix $\boldsymbol{\Sigma} = \begin{bmatrix}\sigma^2 & \tilde{\rho}\sigma^2 \\ \tilde{\rho}\sigma^2 & \sigma^2\end{bmatrix}$. Combining with the first statement, we have the following stability criterion:

$$\max\{\sqrt{SV}(1+\rho) - E, (S-1)E\} < d$$

Despite some improvements of the model, it is still insufficient to resemble the real-case scenario. In a stratified lake, benthic organisms living at the lowest level of a body of the lake tend to interact with other bottom-dweller organisms, while pelagic species living from the surface to the bottom of the lake interact with other organisms that are close to the surface. Here, some species interact more frequently within groups and infrequently among groups. Modularity (Q) is a concept used to quantify this phenomenon. The more frequent the interaction within groups and infrequent among groups, the higher is the value of Q. Thus, the community matrix is modeled such that it is divided into "modules" and eventually form block-structured random matrices. In [3], the author showed the effects of modularity on the stability of the ecological communities for 2×2 block matrices, i.e species divided into two groups.

The main objective of this thesis is to extend the theory from 2×2 block matrices to $n \times n$ block matrices. From the previous discussion, we shall realize that the rightmost position of the eigenvalue of the random matrix plays a key role to determine the local asymptotic stability of an ecosystem. To find this eigenvalue, empirical spectral distribution is an important tool to locate all the eigenvalues on the complex plane, and thus deriving an useful explicit formula for empirical spectral distribution becomes the main component of this project. Together with results from random matrix theory, empirical spectral distribution provides an efficient way to determine the rightmost position of the eigenvalue of the random matrix for systems with modular structure. For example, in a stratified lake, there might be millions of number of species, but it is only a three-layered groups ecosystem.

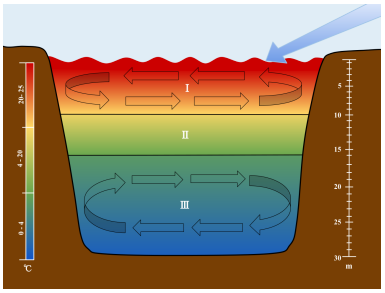

Figure 1: Lakes are stratified into three separate sections: I. The Epilimnion II. The Metalimnion III. The Hypolimnion

The thesis is planned as followed: Chapter 2 is devoted to studying the cavity method in detail. The cavity method is an important technique that originated from statistical physics and it can be used to prove the main results for $S \times S$ block-structured random matrices in Chapter 3. Chapter 4 ends with a brief discussion on the future possibility of extending the theory of $S \times S$ block-structured matrices to the most general form, i.e without the assumption of equal-sized subsystems.

2 Cavity Method

In this chapter we discuss cavity method, an approach that originated from statistical physics. This method can be used to derive the spectral density for sparse random matrices and densely connected random matrices as we shall see later in this chapter.

Let $\mathcal{M}$ be an ensemble of $S \times S$ complex, sparse, non-Hermitian random matrices. Then, the empirical spectral density of $A \in \mathcal{C}$ at $z = x + iy$ is given by

$$p_A(z, \bar{z}) = \frac{1}{S} \sum_{i=1}^{N} \delta(x - \Re\lambda_i^A)\delta(y - \Im\lambda_i^A) \tag{2.1}$$

The empirical spectral density can be rewritten as

$$p_A(z, \bar{z}) = \frac{1}{\pi S} \lim_{\epsilon \to 0} \partial_{\bar{z}} \partial_z \ln \det H' \tag{2.2}$$

where H' is a $2S \times 2S$ Hermitian matrix given by

$$H' \equiv H'(z, \bar{z}, \epsilon) = \begin{pmatrix} \epsilon \mathbf{1}_S & A - z\mathbf{1}_S \\ A^\dagger - \bar{z}\mathbf{1}_S & \epsilon \mathbf{1}_S \end{pmatrix}$$

and

$$\partial_{\bar{z}} = \frac{1}{2}\left(\frac{\partial}{\partial x} - i\frac{\partial}{\partial y}\right), \partial_{\bar{z}} = \frac{1}{2}\left(\frac{\partial}{\partial x} + i\frac{\partial}{\partial y}\right)$$

The process of rewritting equation (2.1) to (2.2) is known as Hermitization. We provide the proof here starting from equation (2.2) and eventually derive equation (2.1). Equation (2.2) can be reformulated as

$$\begin{aligned} p_A(x, y) &= \frac{1}{\pi S} \lim_{\epsilon \to 0} \frac{1}{4} \left(\frac{\partial}{\partial x} + i\frac{\partial}{\partial y}\right)\left(\frac{\partial}{\partial x} - i\frac{\partial}{\partial y}\right) \ln \det H' \\ &= \frac{1}{4\pi S} \lim_{\epsilon \to 0} \nabla^2 \ln \det H' \end{aligned} \tag{2.3}$$

where

$$\begin{aligned} \det H' &= \det(\epsilon \mathbf{1}_S - (A - z\mathbf{1}_S)(\epsilon \mathbf{1}_S)^{-1}(A^\dagger - \bar{z}\mathbf{1}_S)) \det(\epsilon \mathbf{1}_S) \\ &= (-1)^S \det((A - z\mathbf{1}_S)(A^\dagger - \bar{z}\mathbf{1}_S)) \end{aligned}$$

as $\epsilon \to 0$.

Also, given $H = \begin{pmatrix} \epsilon \mathbf{1}_S & i(z\mathbf{1}_S - A) \\ i(z\mathbf{1}_S - A)^\dagger & \epsilon \mathbf{1}_S \end{pmatrix}$, we can show that

$$\ln \det H' = \ln(-1)^S + \ln \det H = i\pi S + \ln \det H$$

as $\epsilon \to 0$. Thus, by (2.3), we have

$$
\begin{aligned}
p_A(x,y) &= \frac{1}{4\pi S}\nabla^2 \ln\det H \\
&= \frac{-1}{4\pi S}\nabla^2(\ln\det H - i\pi S) \\
&= \frac{1}{4\pi S}\nabla^2 \ln\det((A - z\mathbf{1}_S)(A^\dagger - \bar{z}\mathbf{1}_S)) \\
&= \frac{1}{4\pi S}\nabla^2 \operatorname{Tr}\ln((A - z\mathbf{1}_S)(A^\dagger - \bar{z}\mathbf{1}_S)) \\
&= \frac{1}{4\pi S}\nabla^2 \sum_i^S [\ln(\lambda_i^A - z) + \ln(\bar{\lambda_i}^A - \bar{z})] \\
&= \frac{1}{4\pi S}\nabla^2 \sum_i^S \ln|\lambda_i^A - z|^2 \\
&= \frac{1}{4\pi S}\nabla^2 \sum_i^S \ln[(\Re\lambda_i^A - x)^2 + (\Im\lambda_i^A - y)^2]
\end{aligned}
\tag{2.4}
$$

Notice that $\nabla^2 \ln(x^2+y^2+\epsilon) = \frac{4\epsilon}{(x^2+y^2+\epsilon)^2}$. For any continuous function g with compact support, we have

$$\lim_{\epsilon\to 0}\int_S \nabla^2 \ln(r^2+\epsilon)g(r)dS = 0$$

where $r^2 = x^2 + y^2$ and S is any circular region that does not include the origin. Suppose that the region S includes the origin. Then we have

$$
\begin{aligned}
\lim_{\epsilon\to 0}\int_S \nabla^2 \ln(r^2+\epsilon)g(r)dS &= \lim_{\epsilon\to 0}\int_{S-S_\delta} \frac{4\epsilon}{(r^2+\epsilon)^2}g(r)dS + \lim_{\epsilon\to 0}\int_{S_\delta} \frac{4\epsilon}{(r^2+\epsilon)^2}g(r)dS \\
&= \lim_{\epsilon\to 0}\int_{S_\delta} \frac{4\epsilon}{(r^2+\epsilon)^2}g(r)dS
\end{aligned}
$$

where S_δ is the circular region centered at origin with radius δ. Then for any $\epsilon > 0$, choose $\delta > 0$ such that $|g(r) - g(0)| \le \frac{\epsilon}{4\pi}$ whenever $0 < |r| < \delta$. Then,

$$
\begin{aligned}
\lim_{\epsilon\to 0}\left|\int_S \nabla^2 \ln(x^2+y^2+\epsilon)(g(r)-g(0))dS\right| &\le \lim_{\epsilon\to 0}\int_{S_\delta} |g(r)-g(0)|\frac{4\epsilon}{(r^2+\epsilon)^2}dS \\
&\le \frac{\epsilon}{4\pi}2\pi\lim_{\epsilon\to 0}\int_0^\infty \frac{4\epsilon}{(r^2+\epsilon)^2}rdr \\
&\le \epsilon
\end{aligned}
$$

Therefore, we have for any continuous function g with compact support,

$$\lim_{\epsilon\to 0}\int_S \nabla^2 \ln(r^2+\epsilon)g(r)dS = 4\pi g(0)$$

Hence, we have, in the sense of distribution,

$$\lim_{\epsilon\to 0}\nabla^2\ln(x^2+y^2+\epsilon)=4\pi\delta(x)\delta(y)$$

Using this result into equation (2.4), we have

$$p_A(x,y)=\frac{1}{S}\sum_i^S\delta(x-\Re\lambda_i^A)\delta(y-\Im\lambda_i^A)$$

which is equation (2.1).

Next, notice that if ϵ is positive, all the eigenvalues of H have strictly positive real part. By introducing $2S$ complex integration variables into vectors $\boldsymbol{\phi}=(\phi_1,\cdots,\phi_S)$ and $\boldsymbol{\chi}=(\chi_1,\cdots,\chi_S)$, we can write $(\det H)^{-1}$ as a convergent Fresnel integral, i.e

$$\frac{1}{\det H}=\left(\frac{1}{\pi}\right)^{2S}\int\exp\left(-(\boldsymbol{\phi}^\dagger\ \boldsymbol{\chi}^\dagger)H(\boldsymbol{\phi}\ \boldsymbol{\chi})^T\right)d\boldsymbol{\phi}d\boldsymbol{\chi} \tag{2.5}$$

Then, we rearrange the bilinear form $2S\times 2S$ in the exponential term as a sum of S terms by rearranging all variables into N pairs of complex variables:

$$\psi_i=\begin{pmatrix}\phi_i\\ \chi_i\end{pmatrix},i=1,\cdots,S$$

Then define the Hamiltonian to be

$$\mathcal{H}(\boldsymbol{\psi},z,\bar{z},\epsilon)=\sum_i^S\psi_i^\dagger[\epsilon\mathbf{1}_S+i(x\sigma_x-y\sigma_y)]\psi_i-i\sum_{i,j=1}^S\psi_i^\dagger(A_{ij}^h\sigma_x-A_{ij}^s\sigma_y)\psi_j \tag{2.6}$$

where σ_x and σ_y are Pauli matrices defined by

$$\sigma_x=\begin{pmatrix}0&1\\1&0\end{pmatrix},\sigma_y=\begin{pmatrix}0&-i\\i&0\end{pmatrix}$$

and $A=A^h+iA^s$, A^h Hermitian, A^s skew-Hermitian. Let

$$P(\boldsymbol{\psi})=\frac{1}{\mathcal{Z}}e^{-\mathcal{H}(\boldsymbol{\psi},z,\bar{z},\epsilon)} \tag{2.7}$$

be a probability distribution, where $\mathcal{Z}$ is the normalizing constant. Here, the problem to obtain the spectral density can be converted into a statistical mechanics problem of S interacting particles $\boldsymbol{\psi}=(\psi_1,\cdots,\psi_S)$ on a treelike sparse (assumption) graph $\mathcal{G}_A$ associated with matrix A with effective Hamiltonian defined above. The interaction of variables ψ_i and ψ_j are linked with an edge between nodes i and j. If the elements A_{ij} or A_{ji} of the matrix A is not zero, then the pair of vertices (i,j) are neighbors. So A_{ij} or A_{ji} is the weight of interaction between the particles i and j. We define ∂_i is the set of neighbors of i, k_i is the number of neighbors of i and $c=\frac{\sum_i k_i}{N}$ is the average number of neighbors of each node.

By using equation (2.2), (2.5), (2.6), and (2.7), we deduce that

$$p_A(z,\bar{z})=\lim_{\epsilon\to 0}\frac{1}{\pi N}\sum_{l=1}^N-i\partial_{\bar{z}}\left\langle\psi_l^\dagger\sigma^+\psi_l\right\rangle_P \tag{2.8}$$

where $\sigma^+ = \frac{\sigma_x + i\sigma_y}{2}$ and $\langle ... \rangle_P$ is the average over the probability distribution P. Thus, to find the spectral density, it is equivalent to evaluate these averages. To do this it is sufficient to find the marginal distribution $P_i(\psi_i)$. The marginal distribution of ψ_i is the probability distribution P integrated over the other $S-1$ variables.

If A is **treelike**, the removal of one vertex forms $k_i's$ disjoint components. This graph is known as cavity graph. So, we can write the joint distribution of the neighbors of the vertex as

$$P^{(i)}(\{\psi_l\}_{l\in\partial i}) = \prod_{l\in\partial i} P_l^{(i)}(\psi_l) \tag{2.9}$$

the distribution of each neighbour vertex of i is independent to one another. Then, the cavity marginals $\{P_i^{(j)}\}$ is given by the following recursive relations:

$$P_i^{(j)}(\psi_i) = \frac{e^{-\mathcal{H}_i}}{\mathcal{Z}_i^{(j)}} \int \mathcal{D}(\boldsymbol{\psi}_{\partial i\setminus j}) e^{-\sum_{l\in\partial i\setminus j}\mathcal{H}_{il}} \prod_{l\in\partial i\setminus j} P_l^{(i)}(\psi_l) \tag{2.10}$$

where $\mathcal{Z}_i^{(j)}$ is a normalizing constant, $\mathcal{D}(\boldsymbol{\psi}_{\partial i\setminus j}) = \prod_{k\in\partial i\setminus j} d\psi_k$, and

$$\mathcal{H}_i = \psi_i^\dagger[\epsilon \mathbf{1}_2 + i(x\sigma_x - y\sigma_y)]\psi_i \tag{2.11}$$

$$\mathcal{H}_{ij} = -i\psi_i^\dagger(A_{ij}^h\sigma_x - A_{ij}^S\sigma_y)\psi_j - i\psi_j^\dagger(A_{ji}^h\sigma_x - A_{ji}^S\sigma_y)\psi_i \tag{2.12}$$

Once they are known, the actual marginal distribution of vertex i can be recovered by merging the contributions of the neighbors vertex, i.e

$$P_i(\psi_i) = \frac{e^{-\mathcal{H}_i}}{\mathcal{Z}_i} \int \mathcal{D}(\boldsymbol{\psi}_{\partial i}) e^{-\sum_{l\in\partial i}\mathcal{H}_{il}} \prod_{l\in\partial i} P_l^{(i)}(\psi_l) \tag{2.13}$$

Thus, it suffices to know the cavity marginal distribution (2.10). The set of recursive equations in (2.10) can be self-consistently solved by distributions of bivariate Gaussian type because the convolution of Gaussian distributions is Gaussian. Then for all $i = 1, \cdots, S$ and all $j \in \partial i$ the distribution $P_i^{(j)}$ can be written as

$$P_i^{(j)}(\psi_i) = \frac{1}{\mathcal{Z}_i^{(j)}} e^{-\psi_i^\dagger[C_i^{(j)}]^{-1}\psi_i} \tag{2.14}$$

where $C_i^{(j)}$ is a 2×2 matrix. Substituting this into equation (2.10), we have

$$\begin{aligned} e^{-\psi_i^\dagger[C_i^{(j)}]^{-1}\psi_i} = e^{-\mathcal{H}_i} \int \mathcal{D}(\boldsymbol{\psi}_{\partial i\setminus j}) \exp\left(-\sum_{l\in\partial i\setminus j} [-i\psi_i^\dagger(A_{il}^h\sigma_x - A_{il}^s\sigma_y)\psi_l - i\psi_l^\dagger(A_{li}^h\sigma_x - A_{li}^s\sigma_y)\psi_i] \right) \\ \prod_{l\in\partial i\setminus j} \frac{1}{\mathcal{Z}_l^{(i)}} e^{-\sum_{l\in\partial i\setminus j}\psi_l^\dagger[C_l^{(i)}]^{-1}\psi_l} \end{aligned} \tag{2.15}$$

Then, we diagonalize the matrix $[C_l^{(i)}]^{-1}$ by $D_l^{(i)} = U_l^\dagger[C_l^{(i)}]^{-1}U_l$. By defining

$$
\begin{aligned}
B &= A^h_{il}\sigma_x - A^s_{il}\sigma_y \\
B' &= A^h_{li}\sigma_x - A^s_{li}\sigma_y
\end{aligned}
$$

we can simplify the integral in equation (2.15). By changing the variable $\phi_l = U_l^{-1}\psi_l$, equation (2.15) becomes

$$
\int \prod_{l\in\partial i\setminus j} \frac{\mathcal{D}\phi_l}{\mathcal{Z}_l^{(i)}} \exp[i\phi_i^\dagger B U_l \phi_l + i\phi_l^\dagger U_l^\dagger B'\psi_i - \phi_l^\dagger U_l^\dagger [C_l^{(i)}]^{-1} U_l \phi_l] \tag{2.16}
$$

$$
\begin{aligned}
J_i &= \psi_i^\dagger B \\
J_i' &= B'\psi_i
\end{aligned}
$$

Since $B' = B^\dagger$, we have $J_i' = J_i^\dagger$. Then equation (2.16) can be written (in terms of u_l and v_l) as

$$
\int \prod_{l\in\partial i\setminus j} \frac{\mathcal{D}\phi_l}{\mathcal{Z}_l^{(i)}} \exp[\sum_\alpha (iJ'^\dagger_{i\alpha}U^l_{\alpha l}u_l + iJ'^\dagger_{i\alpha}U^l_{\alpha 2}v_l + iu_l^* U^{l\dagger}_{1\alpha}J'_{i\alpha} + iv_l^* U^{l\dagger}_{2\alpha}J'_{i\alpha} - d^{(i)}_{l1}|u_l|^2 - d^{(i)}_{12}|v_l|^2] \tag{2.17}
$$

where $d^{(i)}_{l1}$ and $d^{(i)}_{l2}$ are the diagonal entries of $D_l^{(i)}$. By defining

$$
\begin{aligned}
b^* &= [\sum_\alpha U^{l\dagger}_{1\alpha}J'_{i\alpha}]^* = \sum_\alpha J'^\dagger_{i\alpha}U^l_{\alpha 1} \\
c^* &= [\sum_\alpha U^{l\dagger}_{2\alpha}J'_{i\alpha}]^* = \sum_\alpha J'^\dagger_{i\alpha}U^l_{\alpha 2}
\end{aligned}
$$

Replacing this and rearranging equation (2.17), we have

$$
\int \prod_{l\in\partial i\setminus j} \frac{du_l dv_l du_l^* dv_l^*}{4\mathcal{Z}_l^{(i)}} \exp\left[-d^{(i)}_{l1}\left(|u_l|^2 - i\frac{b^*}{d^{(i)}_{l1}}u_l - i\frac{b}{d^{(i)}_{l1}}u_l^*\right) - d^{(i)}_{l2}\left(|v_l|^2 - i\frac{c^*}{d^{(i)}_{l2}}v_l - i\frac{c^*}{d^{(i)}_{l2}}v_l - i\frac{c}{d^{(i)}_{l2}}v_l^*\right)\right] \tag{2.18}
$$

Since the integrals of (u_l, u_l^*) and (v_l, v_l^*) are in the same form, we restrict the analysis to one of them. By defining

$$
\begin{aligned}
u_l^R &= \frac{1}{\sqrt{2}}(u_l + u_l^*) \\
u_l^I &= \frac{-i}{\sqrt{2}}(u_l - u_l^*)
\end{aligned}
$$

we have

$$
\begin{aligned}
&\int \prod_{l\in\partial i\setminus j} \frac{du_l^R du_l^I}{4\mathcal{Z}_l^{(i)}} \exp\left(-\frac{d^{(i)}_{l1}}{2}u_l^{lR} + i\frac{b^*}{\sqrt{2}}u_l^R + i\frac{b}{\sqrt{2}}u_l^R\right)\exp\left(-\frac{d^{(i)}_{l1}}{2}u_l^{2I} - \frac{b^*}{\sqrt{2}}u_l^I + \frac{b}{\sqrt{2}}u_l^I\right) \\
&\quad = \int \prod_{l\in\partial i\setminus j} \frac{du_l^R du_l^I}{4\mathcal{Z}_l^{(i)}} \exp\left(-\frac{d^{(i)}_{l1}}{2}u_l^{2R} + i\sqrt{2}(\Re b)u_l^R - \frac{d^{(i)}_{l1}}{2}u_l^{2I} + i\sqrt{2}(\Im b)u_l^I\right)
\end{aligned} \tag{2.19}
$$

A similar equation can also be obtained for (v_l, v_l^*). Together with Hubbard-Stratonovich formula:

$$\int_{-\infty}^{\infty} e^{-\frac{1}{2}ax^2+iJx}dx = \left(\frac{2\pi}{a}\right)^{\frac{1}{2}} e^{-\frac{J^2}{2a}}$$

Equation (2.18) finally becomes

$$\begin{aligned}\prod_{l\in\partial i\setminus j} \frac{1}{4\mathcal{Z}_l^{(i)}} \frac{2\pi}{d_{l1}^{(i)}} \frac{2\pi}{d_{l2}^{(i)}} \exp\left(-\frac{|b|^2}{d_{l1}^{(i)}} - \frac{|c|^2}{d_{l2}^{(i)}}\right) &= \prod_{l\in\partial i\setminus j} \exp\left(-\sum_{\alpha,\beta} J'^{\dagger}_{\alpha} U^{l\dagger}_{\alpha 1} \frac{1}{d_{l1}^{(i)}} U^{l\dagger}_{1\beta} J'_{\beta} - \sum_{\gamma,\delta} J'^{\dagger}_{\gamma} U^{l}_{\gamma 2} \frac{1}{d_{l2}^{(i)}} U^{l\dagger}_{2\delta} J'_{\delta}\right) \\ &= \prod_{l\in\partial i\setminus j} \exp\left(-J'^{\dagger} U^{l} \begin{pmatrix} \frac{1}{d_{l1}^{(i)}} & 0 \\ 0 & \frac{1}{d_{l2}^{(i)}} \end{pmatrix} U^{l\dagger} J'\right)\end{aligned} \tag{2.20}$$

where we have used

$$\mathcal{Z}_l^{(i)} = \frac{\pi^2}{\det[C_l^{(i)}]^{-1}}$$

Notice that the matrix in the exponential in equation (2.20) is the inverse matrix of $D_l^{(i)}$, we have

$$[D_l^{(i)}]^{-1} = [U_l^{\dagger}(C_l^{(i)})^{-1}U_l]^{-1}$$

Using this, equation (2.20) becomes

$$\prod_{l\in\partial i\setminus j} e^{J'^{\dagger}_{\alpha} U^{l}_{\alpha\beta} U^{\dagger}_{\beta\sigma} [C_l^{(i)}]_{\sigma\lambda} U^{l}_{\lambda\delta} U^{l\dagger}_{\delta\gamma} J'_{\gamma}} = \prod_{l\in\partial i\setminus j} e^{J'^{\dagger}_{\sigma} [C_l^{(i)}]_{\sigma\lambda} J'_{\lambda}}$$

Thus, we have obtained from equation (2.10) a set of recursive equations $\{C_i^{(j)}\}$ (known as cavity equations) given by

$$C_i^{(j)} = [\epsilon \mathbf{1}_2 + i(x\sigma_x - y\sigma_y) + F(C^{(i)}_{\partial i\setminus j}]^{-1} \tag{2.21}$$

for all $i = 1, \cdots, S$ and all $j \in \partial i$, where F is the matrix field:

$$F(C^{(i)}_{\partial i\setminus j}) = \sum_{l\in\partial i\setminus j} \left(A^h_{il}\sigma_x - A^s_{il}\sigma_y\right) C_l^{(i)} \left(A^h_{li}\sigma_x - A^s_{li}\sigma_y\right)$$

Similarly, we have

$$C_i = [\epsilon \mathbf{1}_2 + i(x\sigma_x - y\sigma_y) + F(C^{(i)}_{\partial i}]^{-1} \tag{2.22}$$

for all $i = 1, \cdots, S$ from equation (2.13). By performing the inverse of H in block form, it reveals enough information to allow us to write generally

$$C_i^{(j)} \equiv \begin{pmatrix} a_i^{(j)} & i\bar{b}_i^{(j)} \\ ib_i^{(j)} & d_i^{(j)} \end{pmatrix}$$

where $a_i^{(j)}, d_i^{(j)} \in \mathbb{R}^+$, $b_i^{(j)} \in \mathbb{C}$ and similarly

$$C_i \equiv \begin{pmatrix} a_i & i\bar{b}_i \\ ib_i & d_i \end{pmatrix}$$

where $a_i, d_i \in \mathbb{R}^+$ and $b_i \in \mathbb{C}$.

With equation (2.21), we can recover the marginal distribution $P_i(\phi_i)$ from equation (2.22). Since $\{C_i^j\}$ and $\{C_i\}$ depends upon z and ϵ, $\left\langle \psi_l^\dagger \sigma^+ \psi_l \right\rangle_P$ can be expressed as a function b_i in terms of z and ϵ. In the end, we have the formula for spectral density given by

$$p_A(z, \bar{z}) = -\frac{1}{\pi S} \lim_{\epsilon \to 0} \sum_{i=1}^{S} \partial_{\bar{z}} b_i(z, \bar{z}, \epsilon) \tag{2.23}$$

So, to compute the spectral density, it suffices to know what is $\partial_{\bar{z}} C_i$. Using the relation

$$\partial_{\bar{z}}(A^{-1}) = -A^{-1}(\partial_{\bar{z}} A)A^{-1}$$

we have

$$\partial_{\bar{z}} C_i^{(j)} = -C_i^{(j)} \left[\begin{pmatrix} 0 & 0 \\ i & 0 \end{pmatrix} + F(\partial_{\bar{z}} C_{\partial i \setminus j}^{(i)}) \right] C_i^{(j)} \tag{2.24}$$

Using similar argument, we also have

$$\partial_{\bar{z}} C_i = -C_i \left[\begin{pmatrix} 0 & 0 \\ i & 0 \end{pmatrix} + F(\partial_{\bar{z}} C_{\partial i}^{(i)}) \right] C_i \tag{2.25}$$

To summarise, we iterate equations (2.21) and (2.24) until we reach convergence. Then we can recover equations (2.22) and (2.25) and thus obtain the spectral density. Notice that we use the assumption of treelike structure to start with the derivation, where many entries of the matrix A are zero. When this occurs, the graph is sparse and thus the existence of loops in the graph (tree) are rare. The absence of loops guarantees the convergence of these equations in a finite step of iterations of the above equations, where the iteration stops at the leaves of the tree (node of degree 1). Technically, we can remove this assumption but it is necessary to stop the iterations once a pre-determined level of convergence has been reached, which means we should stop the iterations once the cavity covariance matrices and their derivatives for each node in the loop are known to avoid infinite looping of the iterations. So the formula of spectral density obtained using the cavity method can be used for the densely connected case.

With this formula in hand, we can derive an explicit formula of empirical spectral distribution which we will use to determine the region where the eigenvalues lie. This will help us to efficiently locate the rightmost eigenvalues.

Before deriving the formula of empirical spectral distribution, we introduce some operations about quaternions that are important. A quaternion $\boldsymbol{q}$ is given by $\boldsymbol{q} = a + b\boldsymbol{i} + c\boldsymbol{j} + d\boldsymbol{k}$, $a, b, c \in \mathbb{R}$ with the properties $\boldsymbol{k} = \boldsymbol{ij}$. By rewriting $\boldsymbol{k}$ in terms of $\boldsymbol{ij}$ and then rearranging it, we see $\boldsymbol{q}$ can be written in two form, i.e

$$\boldsymbol{q} = z + wj = \begin{pmatrix} z & w \\ \bar{w} & \bar{z} \end{pmatrix}$$

The sum of two quaternions is

$$(z + wj) + (\alpha + \beta j) = (z + \alpha) + (w + \beta)j$$

and their products are

$$(z + wj)(\alpha + \beta j) = (z\alpha - w\bar{\beta}) + (z\beta + w\bar{\alpha})j$$

Also, $wj \neq jw$. Instead, we have $wj = j\bar{w}$.

The spectral distribution for a non-Hermitian random matrix is defined as

$$p(x, y) = \frac{1}{S} \sum_{i=1}^{n} \delta(x - \Re(\lambda_i))\delta(y - \Im(\lambda_i)) \tag{2.26}$$

and the resolvent is defined as

$$\mathcal{G}(\boldsymbol{q}) = \frac{1}{S} \sum_{i} (z_i - \boldsymbol{q})^{-1} \tag{2.27}$$

for which we can rewrite the spectral distribution as

$$p(x, y) = -\frac{1}{\pi} \lim_{\epsilon \to 0^+} \Re \left(\frac{\partial}{\partial \bar{z}} \mathcal{G}(z + \epsilon j) \right) |_{z=x+iy} \tag{2.28}$$

where $\frac{\partial}{\partial \bar{z}} := \frac{1}{2} \left(\frac{\partial}{\partial x} + i \frac{\partial}{\partial y} \right)$. For the proof, refer to [9]. So, determining the location of the eigenvalues of the random matrix reduces to the problem of determining the region where $p(x, y)$ does not vanish. The main part of this chapter is to derive an useful expression for $\mathcal{G}(z + \epsilon j)$ using cavity method so that we can find this region.

Next, we rewrite equation (2.21) and (2.22) using quaternions instead of Pauli matrices using the mapping

$$\begin{aligned} \boldsymbol{i} &\leftrightarrow i\sigma_x \\ \boldsymbol{j} &\leftrightarrow i\sigma_y \\ \boldsymbol{k} &\leftrightarrow i\sigma_z \end{aligned}$$

into

$$\epsilon \mathbf{1}_2 + i(x\sigma_x - y\sigma_y) = \begin{pmatrix} \epsilon & i\lambda \\ i\bar{\lambda} & \epsilon \end{pmatrix} \equiv \epsilon + \lambda j$$

Let B be our intended matrix formed form $\bar{M} - A$. We introduce the resolvent matrix $\boldsymbol{G} = (\boldsymbol{B} - \boldsymbol{q})^{-1}$ where $\boldsymbol{q}$ is the quaternion

$$\boldsymbol{q} = z + \epsilon j = \begin{pmatrix} z & \epsilon \\ \epsilon & \bar{z} \end{pmatrix}$$

and $\boldsymbol{B}$ is a $2S \times 2S$ block matrix with

$$\boldsymbol{B}_{ij} = \begin{pmatrix} B_{ij} & 0 \\ 0 & B_{ji} \end{pmatrix} \tag{2.29}$$

with B_{ij} and B_{ji} are entries from B. Then the resolvent becomes

$$\mathcal{G}(\boldsymbol{q}) = \frac{1}{S} \sum_{i} \boldsymbol{G}_{ii}(\boldsymbol{q}) \tag{2.30}$$

Assuming B_{ij} has a tree structure, we can apply cavity method (equation (2.22)) to obtain the recursive equations for the diagonal entries of $\boldsymbol{G}$

$$\boldsymbol{G}_{ii}(\boldsymbol{q}) = -\left(\boldsymbol{q} + \sum_{j\neq i} \boldsymbol{B}_{ij}\boldsymbol{G}^{(i)}_{jj}\boldsymbol{B}_{ji}\right)^{-1} \tag{2.31}$$

where $\boldsymbol{G}^{(i)}$ is the resolvent of the matrix obtained by removing row and column i from B. (removing nodes i). Similarly, we have

$$\boldsymbol{G}^{k}_{ii}(\boldsymbol{q}) = -\left(\boldsymbol{q} + \sum_{j\neq i,k} \boldsymbol{B}_{ij}\boldsymbol{G}^{(i)}_{jj}\boldsymbol{B}_{ji}\right)^{-1} \tag{2.32}$$

Solving them iteratively, using (2.30), (2.31), (2.32) and substituting them into (2.28), we can find the spectral density.

3 Main Results

3.1 Formulation of problem

Species tend to live among themselves in groups, where this is known as modular organization in ecology. It is important to study how modular organization affect the (local) stability of ecological communities. It turns out that block-structured random matrices serves as an important model to tackle this problem. Let M be a $S \times S$ community matrix with S species. M is the element-by-element multiplication between interaction strength matrix W and adjacency matrix K, where entries in W represents the influence of species j on species i around the equilibrium. We can assume the diagonal elements of matrix M to be zero since the degree of self interactions do not affect the general results.

The pairs (W_{ij}, W_{ji}) are taken from bivariate distributions with mean $\mu = \mathbb{E}[W_{ij}] = \mathbb{E}[W_{ji}]$, variance $\sigma^2 = \mathbb{E}[(W_{ij} - \mu)^2] = \mathbb{E}[(W_{ji} - \mu)^2]$ and correlation $\rho = \frac{\mathbb{E}[W_{ij}W_{ji}] - \mu^2}{\sigma^2}$. All these parameters can be modified to model all possible type of interactions in real life. Thus, the matrix W is fully characterized by the parameters μ, ρ and σ^2.

The elements (K_{ij}) in K equals to 1 if there is an interaction and equals to 0 if there is no interaction between species i and j. The density of interactions in matrix K, i.e porpotion of nonzero entries of K is known as the overall connectance, also denoted as C. For a modular organization, K will be a block-structured matrix, where there are N subsystems, which means S species are partitioned into N groups represented by $\gamma_1, \cdots, \gamma_N$, each of size $\alpha_1 S, \cdots, \alpha_N S$. The species within the same subsystem interact with probability C_w and the species which are in different subsystems interact with probability C_b. For example, if $C_w = 0$, there will be no interactions within systems and thus there is no modular structure in the organization. If $C_w = C_b = C$, this falls into the well-studied case of random ecological community (no block structure) solved by May before.

It is convenient to define a parameter which describes the degree of modularity in an ecological community as follow:

$$Q = \frac{L_w - \mathbb{E}(L_w)}{L_w + L_b}$$

where L_w is the number of observed interactions within subsystem, L_b is the number of observed interactions between subsystem and $\mathbb{E}(L_w)$ is the expected number of interactions within subsystem, of a random ecological community. Thus, $Q > 0$ means there is more observed interactions than expected, i.e resembling modular structure and vice versa. Also, the case $Q = 0$ represents the case for a random community matrix without block structure.

Also, C_w and C_b can also be expressed in terms of C, Q and $[\alpha_1, \cdots, \alpha_N]$. The overall connectance is

$$C = \frac{2L}{S(S-1)} = \frac{2(L_w + L_b)}{S(S-1)}$$

The type of random graph in which the number of vertices (S) is fixed and the number of edges (L) is indicated by $G(S, L)$. The random graph model used to describe random matrix with $Q = 0$ is the Erdos-Renyi random graph known as $G(S, p)$. In this graph, the probability p is fixed rather than the number of edges between vertices. Now there are S vertices, but now we place an edge between pair of vertices with fixed probability p. As

$S \to \infty$, the two types of graphs are the same if $p = \frac{2L}{S(S-1)} = C \to \frac{2L}{S^2}$. Letting n_w be the total number of species that can interact within the same group and n_b be the number of species that can interact among groups. In this limit, we have

$$n_w = \frac{S^2(\alpha_1^2 + \cdots + \alpha_N^2)}{2}$$
$$n_b = S^2 \left(\sum_{i<j, i\neq j}^{N} \alpha_i \alpha_j \right)$$

Also, $\mathbb{E}(L_w) = Cn_w$ and $\mathbb{E}(L_b) = Cn_b$. So, we have

$$L_w = \mathbb{E}(L_w) + LQ = Cn_w + C\frac{QS^2}{2} = C\left(\frac{QS^2}{2} + n_w\right)$$

which implies

$$C_w = \frac{L_w}{n_w} = \frac{C\left(\frac{QS^2}{2} + n_w\right)}{n_w} = C\left(1 + \frac{Q}{\sum_{i=1}^{N} \alpha_i^2}\right)$$

Also,

$$\begin{aligned} C_b = \frac{L_b}{n_b} &= \frac{C\left(\frac{S^2}{2}(1-Q) - n_w\right)}{n_b} \\ &= \frac{C\left(\frac{S^2}{2}(1-Q) - \frac{S^2 \sum_{i=1}^{N} \alpha_i^2}{2}\right)}{S^2\left(\sum_{i<j, i\neq j}^{N} \alpha_i \alpha_j\right)} \\ &= \frac{C\left(1 - Q - \sum_{i=1}^{N} \alpha_i^2\right)}{2\sum_{i<j, i\neq j} \alpha_i \alpha_j} \end{aligned}$$

Thus, we can see matrix K is fully characterized by the parameters $[\alpha_1, \cdots, \alpha_N], C$ and Q. In short, we have modelled an ecosystem with modular structure using community matrix $M = W \circ K$ with parameters $\mu, \sigma^2, \rho, [\alpha_1, \cdots, \alpha_N], C$ and Q.

Writing the community matrix into $M = W \circ K$, where $\circ$ is element by element matrix multiplication is a way to model the ecosystem. But we can also model M in a more general way. We build the community matrix M such that the diagonal coefficients $M_{ii} = 0$ (without loss of generality) and off-diagonal coefficients independently sampled in pairs as

$$(M_{ij}, M_{ji}) \begin{cases} \mathcal{Z}_w \left(\begin{pmatrix} \mu_w \\ \mu_w \end{pmatrix}, \sigma_w^2 \begin{pmatrix} 1 & \rho_w \\ \rho_w & 1 \end{pmatrix} \right) & \text{if } \gamma_i = \gamma_j \\ \mathcal{Z}_b \left(\begin{pmatrix} \mu_b \\ \mu_b \end{pmatrix}, \sigma_b^2 \begin{pmatrix} 1 & \rho_b \\ \rho_b & 1 \end{pmatrix} \right) & \text{if } \gamma_i \neq \gamma_j \end{cases}$$

This means when the species belonged to the same group, they are sampled from distribution $\mathcal{Z}_w$ while they are sampled from distribution $\mathcal{Z}_b$ if they belonged to different group instead of considering the pairs (M_{ij}, M_{ji}) are zero with probability $1 - C_w$ $(\gamma_i = \gamma_j)$ or

$1 - C_b$ ($\gamma_i \neq \gamma_j$) and the nonzero pairs are sampled from bivariate distribution using parameters μ, σ^2 and ρ. Despite the model is different, but they resembles the same biological scenario. Thus, we have the following set of equations

$$\begin{aligned}
\mu_w &= C_w \mu \\
\mu_b &= C_b \mu \\
\sigma_w^2 &= C_w(\sigma^2 + (1 - C_w)\mu^2) \\
\sigma_b^2 &= C_b(\sigma^2 + (1 - C_b)\mu^2) \\
\rho_w &= \frac{\rho\sigma^2 + (1 - C_w)\mu^2}{\sigma^2 + (1 - C_w)\mu^2} \\
\rho_b &= \frac{\rho\sigma^2 + (1 - C_b)\mu^2}{\sigma^2 + (1 - C_b)\mu^2}
\end{aligned}$$

Later on, we will use the parameters $\mu_w, \mu_b, \sigma_w, \sigma_b$ to perform the derivations and then convert them back in terms of our required parameters $\mu, \sigma^2, \rho, [\alpha_1, \cdots, \alpha_N], C$ and Q.

To study the effect of block structure (modularity) on local stability of ecosystem, we will need a community matrix M of our choice with $Q \neq 0$ (modular structure) and compare it with the random unstructured community matrix $\bar{M}$ with $Q = 0$ (unstructured). As we know earlier, the rightmost eigenvalue determines the local stability of an ecosystem. Denote the rightmost eigenvalue of $\bar{M}$ as $\Re(\lambda_{\bar{M}})$ and rightmost eigenvalue of M as $\Re(\lambda_M)$. The effect of modularity Q on community stability can be measured as the ratio

$$\Gamma = \frac{\Re(\lambda_M)}{\Re(\lambda_{\bar{M}})}$$

for a given choice of $\mu, [\alpha_1, \cdots, \alpha_N], \rho, \sigma^2$ and C. We can know the rightmost eigenvalue of M by using the results done by previous studies using classical random matrix theory as described in Appendix A because M is a random matrix without modular structure. Thus, it remains to find the rightmost eigenvalues of a community matrix with equal-sized modular subsystem, which is what we wish to achieve in this project. If the number of species is small, we can use computer to generate all eigenvalues by brute force and locate the rightmost eigenvalue. But this requires high complexity as S gets larger ($\mathcal{O}(S^2)$). So we will need a better way to solve this problem.

3.2 Finding the rightmost eigenvalue of community matrix with equal-sized subsystems

Let M be a $S \times S$ random matrix. We can decompose M as the sum of two matrices, $M = A + B$, where A is a block structure whose elements are

$$A_{ij} = \begin{cases} \mu_w & \text{if } \gamma_i = \gamma_j \\ \mu_b & \text{if } \gamma_i \neq \gamma_j \end{cases}$$

and $B = M - A$. This decomposition is convenient because the spectrum of B describes the bulk of eigenvalues of M, and the outliers of M are given by the nonzero eigenvalues of A, **modified by a small correction**[8]. Thus, the diagonal elements of $B_{ii} = -\mu_w$, while the off-diagonal $\mathbb{E}(B_{ij}) = 0$, and $\mathbb{E}(B_{ij}B_{ji}) = \rho_w\sigma_w^2$ (when $\gamma_i = \gamma_j$) or $\mathbb{E}(B_{ij}B_{ji}) = \rho_b\sigma_b^2$ (when $\gamma_i \neq \gamma_j$).

It is important to note that this decomposition is not true in general unless A has low rank with few nonzero eigenvalues that are sufficiently larger than those in B and B is a large random matrix whose follows the elliptic law. We shall see later that these assumptions hold when M is a block-structured matrices with equal-sized subsystems.

3.2.1 Finding eigenvalues of A

Suppose we partition the matrix A into $\alpha_1 S, \cdots, \alpha_N S$ as shown in figure below.

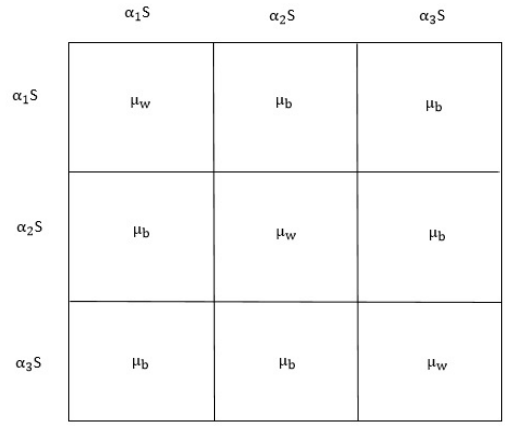

Figure 2: Example of Block matrix with $N = 3$

Let $\vec{v_i} = (0, \cdots, 0, \underbrace{0, \cdots, 0}_{\alpha_{i-1}S}, \underbrace{1, \cdots, 1}_{\alpha_i S}, \underbrace{0, \cdots, 0}_{\alpha_{i+1}S}, 0, \cdots, 0)$. Any vector Φ orthogonal to the vector space spanned by $\{v_1, \cdots, v_N\}$ gives $A(\Phi) = 0$. This implies that there are $S - 3$ zero eigenvalues. So it remains only to find N nonzero eigenvalues (w.r.t its eigenvectors $\vec{\phi}$) of this matrix from the space formed by the linear combination

$$\vec{\phi} = a_1\vec{v_1} + a_2\vec{v_2} + a_3\vec{v_3}$$

which is

$$A\vec{\phi} = a_1 A\vec{v_1} + a_2 A\vec{v_2} + a_3 A\vec{v_3}$$

Evaluating $A\vec{v_i}$, we have

$$A\vec{v_i} = \alpha_i S\mu_b\vec{v_1} + \alpha_i S\mu_b\vec{v_2} + \cdots + \alpha_i S\mu_w\vec{v_i} + \cdots + \alpha_i S\mu_b\vec{v_{N-1}} + \alpha_i S\mu_b\vec{v_N}$$

Thus,

$$A\vec{\phi} = \sum_{i=1}^{N} a_i \left(\sum_{j=1, j\neq i}^{N} \alpha_i S\mu_b\vec{v_j} + \alpha_i S\mu_w\vec{v_i} \right) \tag{3.1}$$

Since $\vec{\phi}$ is eigenvector, we have also

$$A\vec{\phi} = \sum_{i=1}^{N} a_i \lambda \vec{v_i} \tag{3.2}$$

where λ is the eigenvalues with respect to $\vec{\phi}$. Combining (3.1) and (3.2), we have a system of equations

$$\begin{aligned}
(\alpha_1 S\mu_w - \lambda)a_1 + (\alpha_2 S\mu_b)a_2 + \cdots + (\alpha_N S\mu_b)a_N &= 0 \\
(\alpha_1 S\mu_b)a_1 + (\alpha_2 S\mu_w - \lambda)a_2 + \cdots + (\alpha_N S\mu_b)a_N &= 0 \\
&\vdots \\
(\alpha_1 S\mu_b)a_1 + (\alpha_2 S\mu_b)a_2 + \cdots + (\alpha_N S\mu_w - \lambda)a_N &= 0
\end{aligned}$$

which leads to solution for $a_1, \cdots, a_N$ when

$$\begin{vmatrix}
\alpha_1 S\mu_w - \lambda & \alpha_2 S\mu_b & \alpha_3 S\mu_b & \cdots & \alpha_N S\mu_b \\
\alpha_1 S\mu_b & \alpha_2 S\mu_w - \lambda & \alpha_3 S\mu_b & \cdots & \alpha_N S\mu_b \\
\vdots & \vdots & \vdots & \ddots & \vdots \\
\alpha_1 S\mu_b & \alpha_2 S\mu_b & \alpha_3 S\mu_b & \cdots & \alpha_N S\mu_w - \lambda
\end{vmatrix} = 0$$

Thus, to find all possible candidates for λ, it suffices to find the eigenvalues of the matrix

$$A' = \begin{bmatrix}
\alpha_1 S\mu_w & \alpha_2 S\mu_b & \alpha_3 S\mu_b & \cdots & \alpha_N S\mu_b \\
\alpha_1 S\mu_b & \alpha_2 S\mu_w & \alpha_3 S\mu_b & \cdots & \alpha_N S\mu_b \\
\vdots & \vdots & \vdots & \ddots & \vdots \\
\alpha_1 S\mu_b & \alpha_2 S\mu_b & \alpha_3 S\mu_b & \cdots & \alpha_N S\mu_w
\end{bmatrix}$$

3.2.2 Finding eigenvalues of B

For blocked structured matrices, we can simplify equation (2.31) and (2.32). At the leading order in S, the right side of equation (2.31) is identical for all i in the same group, so we can write $\boldsymbol{G}_{jj} = \boldsymbol{G}_{\gamma_j}$. Since S is assumed to be large, omitting a single node do not effect the overall behaviour of the system, so we can claim that $\boldsymbol{G}^{(i)}_{jj} = \boldsymbol{G}_{jj} = \boldsymbol{G}_{\gamma_j}$. This implies that equation (2.31) became closed and thus we can omit equation (2.32). Also, we can use law of large number to approximate the sum of the right hand side of equation (2.31) to obtain, at the leading order in S,

$$\sum_{j \neq i,k} \boldsymbol{B}_{ij} \boldsymbol{G}^{(i)}_{jj} \boldsymbol{B}_{ji} \approx \mathbb{E}\left(\sum_j \boldsymbol{B}_{ij} \boldsymbol{G}_{\gamma_j} \boldsymbol{B}_{ji} \right)$$

To summarize, given N groups of species, we have reformulate the set of equations (2.31) for $i = 1, \cdots, S$ into

$$\boldsymbol{G}_{\gamma_i}(\boldsymbol{q}) = -\left(\boldsymbol{q} + \mathbb{E}\left(\sum_j \boldsymbol{B}_{ij} \boldsymbol{G}_{\gamma_j} \boldsymbol{B}_{ji} \right) \right) \tag{3.3}$$

for $\gamma_i \in (1, \cdots, N)$. Using equation (2.29), we have

$$\boldsymbol{B}_{ij}\boldsymbol{G}_{\gamma_j}\boldsymbol{B}_{ji} = \begin{pmatrix} B_{ij} & 0 \\ 0 & B_{ji} \end{pmatrix}\begin{pmatrix} r_{\gamma_j} & \beta_{\gamma_j} \\ \bar{\beta}_{\gamma_j} & \bar{r}_{\gamma_j} \end{pmatrix}\begin{pmatrix} B_{ji} & 0 \\ 0 & B_{ij} \end{pmatrix} = \begin{pmatrix} B_{ij}r_{\gamma_j}B_{ji} & B_{ij}^2\beta_{\gamma_j} \\ B_{ji}^2\bar{\beta}_{\gamma_j} & B_{ij}B_{ji}\bar{r}_{\gamma_j} \end{pmatrix} \tag{3.4}$$

where we denote $\boldsymbol{G}_\gamma = r_\gamma + \beta_\gamma j$. In the case of N blocks, for arbitrary vector with component z_{γ_j}, we have

$$\mathbb{E}\left(\sum_j B_{ij}^2 z_{\gamma_j}\right) = \sum_j \mathbb{E}(B_{ij}^2) z_{\gamma_j} = \sum_j (\delta_{\gamma_i,\gamma_j}\sigma_w^2 z_{\gamma_j} + (1-\delta_{\gamma_i,\gamma_j})\sigma_b^2 z_{\gamma_j}) \tag{3.5}$$

When $\gamma_i = m$, we have

$$\mathbb{E}\left(\sum_j B_{ij}^2 z_{\gamma_j}\right) = S\alpha_m\sigma_w^2 z_m + \sum_{i\neq m} S(\alpha_i)\sigma_b^2 z_i \tag{3.6}$$

where α_m is the fraction of elements belonging to block m.

Using similar argument, we have

$$\mathbb{E}\left(\sum_j B_{ij}B_{ji} z_{\gamma_j}\right) = S\alpha_m\rho_w\sigma_w^2 z_m + \sum_{i\neq m} S(\alpha_i)\rho_b\sigma_b^2 z_i \tag{3.7}$$

Then, we have

$$\begin{aligned} \mathbb{E}\left(\sum_j \boldsymbol{B}_{ij}\boldsymbol{G}_{\gamma_j}\boldsymbol{B}_{ji}\right) &= \begin{pmatrix} \mathbb{E}\left(\sum_j B_{ij}B_{ji}r_{\gamma_j}\right) & \mathbb{E}(\sum_j B_{ij}^2\beta_{\gamma_j}) \\ \mathbb{E}\left(\sum_j B_{ji}^2\bar{\beta}_{\gamma_j}\right) & \mathbb{E}\left(\sum_j B_{ij}B_{ji}\bar{r}_{\gamma_j}\right) \end{pmatrix} \\ &= S\alpha_m\sigma_w^2\begin{pmatrix} \rho_w r_m & \beta_m \\ \bar{\beta}_m & \rho_w\bar{r}_m \end{pmatrix} + \sum_{i\neq m} S(\alpha_i)\sigma_b^2\begin{pmatrix} \rho_b r_i & \beta_i \\ \bar{\beta}_i & \rho_b\bar{r}_i \end{pmatrix} \end{aligned} \tag{3.8}$$

By defining $\boldsymbol{\Sigma_w} = S\sigma_w^2\begin{pmatrix} \rho_w & 1 \\ 1 & \rho_w \end{pmatrix}$ and $\boldsymbol{\Sigma_b} = S\sigma_b^2\begin{pmatrix} \rho_b & 1 \\ 1 & \rho_b \end{pmatrix}$, we have for $\gamma_i = m$, equation (3.8) becomes

$$\mathbb{E}(\sum_j \boldsymbol{B_{ij}}\boldsymbol{G_{\gamma_j}}\boldsymbol{B_{ji}}) = \alpha_m\boldsymbol{\Sigma_w}\circ\boldsymbol{G_m} + \sum_{i\neq m}\alpha_i\boldsymbol{\Sigma_b}\circ\boldsymbol{G_i} \tag{3.9}$$

where $'\circ'$ denotes the element by element matrix product. Substituting this into equation (3.3), we have

$$\boldsymbol{G_m}(\boldsymbol{q}) = -\left(\boldsymbol{q} + \alpha_m\boldsymbol{\Sigma_w}\circ\boldsymbol{G_m} + \sum_{i\neq m}\alpha_i\boldsymbol{\Sigma}_b\circ\boldsymbol{G}_i\right)^{-1} \tag{3.10}$$

The resolvent from equation (2.30) also becomes

$$\mathcal{G}(\boldsymbol{q}) = \sum_{m=1}^{N}\alpha_m\boldsymbol{G_m}(\boldsymbol{q}) \tag{3.11}$$

Thus, the spectral density is

$$p(z,\bar{z},\epsilon) = -\frac{1}{\pi}\lim_{\epsilon\to 0}\Re\left(\frac{\partial}{\partial\bar{z}}\sum_{m=1}^{N}\alpha_m \boldsymbol{G_m}(\boldsymbol{q})\right) \tag{3.12}$$

If we let $\boldsymbol{G_m}(\boldsymbol{q}) = r_m + \beta_m j$, then as $\epsilon \to 0$, we have the simplified spectral density given by

$$p(z,\bar{z}) = -\frac{1}{\pi}\sum_{m=1}^{N}\alpha_m \Re\frac{\partial r_m}{\partial\bar{z}} \tag{3.13}$$

As we will see later, equation (3.10) and (3.13) plays fundamental role to determine the region where the spectral density completely vanishes. With this, we can determine the rightmost eigenvalues of matrix B analytically. Together with the eigenvalues of matrix A determined by brute force, the problem of computing the eigenvalues of matrix M reduces to $O(N^3)$ instead of $O(S^3)$ which is far more efficient. This is because in a large biological network it is usually that $N << S$.

Suppose now that $\alpha_1 = \alpha_2 = \cdots = \alpha_N = \frac{1}{N}$. Then the right side of equation (3.10) becomes equal for all $m = 1\cdots, N$ and thus $\boldsymbol{G}_1 = \boldsymbol{G}_2 = \cdots = \boldsymbol{G}_N = \boldsymbol{G} := r + \beta j$. Therefore, we have

$$\begin{aligned}\boldsymbol{G}(\boldsymbol{q}) &= -\left(\boldsymbol{q} + \frac{\boldsymbol{\Sigma}_w \circ \boldsymbol{G} + (N-1)\boldsymbol{\Sigma}_b \circ \boldsymbol{G}}{N}\right)^{-1} \\ &= -\left(\boldsymbol{q} + \frac{\boldsymbol{\Sigma}_w + (N-1)\boldsymbol{\Sigma}_b}{N} \circ \boldsymbol{G}\right)^{-1}\end{aligned}$$

Then,

$$\boldsymbol{G} = -\left(\boldsymbol{q} + \tilde{\boldsymbol{\Sigma}} \circ \boldsymbol{G}\right)^{-1} \tag{3.14}$$

where

$$\tilde{\boldsymbol{\Sigma}} = \frac{\boldsymbol{\Sigma}_w + (N-1)\boldsymbol{\Sigma}_b}{N}$$

Using the definition of $\boldsymbol{\Sigma}_w$ and $\boldsymbol{\Sigma}_b$, we then have

$$\tilde{\boldsymbol{\Sigma}} = S\tilde{\sigma^2}(\tilde{\rho} + j)$$

where

$$\tilde{\sigma}^2 = \frac{\sigma_w^2 + (N-1)\sigma_b^2}{N},\ \tilde{\rho} = \frac{\rho_w\sigma_w^2 + (N-1)\rho_b\sigma_b^2}{\sigma_w^2 + (N-1)\sigma_b^2}$$

Expanding equation (3.14), we have

$$(r+\beta j)(-z - S\tilde{\sigma^2}(\tilde{\rho}+j) \circ (r+\beta j)) = 1$$

By comparing the j part and non-j part, we have

$$r(-rS\tilde{\rho}\tilde{\sigma}^2 - z) + S|\beta|^2\tilde{\sigma}^2 = 1 \tag{3.15}$$

$$\beta(-rS\tilde{\rho}\tilde{\sigma}^2 - z - S\bar{r}\tilde{\sigma}^2) = 0 \tag{3.16}$$

Notice that by equation (3.13), we have

$$p(z,\bar{z}) = -\frac{1}{\pi}\Re\frac{\partial r}{\partial\bar{z}}$$

If $\beta = 0$, equation (3.15) becomes

$$-r^2 S\tilde{\rho}\tilde{\sigma}^2 - rz = 1$$

and thus

$$\frac{\partial r}{\partial \bar{z}}(-2rS\tilde{\rho}\tilde{\sigma}^2 - z) = 0$$

which implies $\frac{\partial r}{\partial \bar{z}} = 0$. Therefore, $p(z, \bar{z}) = 0$. If $\beta \neq 0$, we have

$$-rS\tilde{\rho}\tilde{\sigma}^2 - z - S\tilde{r}\tilde{\sigma}^2 = 0$$

from equation (3.16). Using Mathematica, we have solved r to get

$$r = \frac{1}{S\tilde{\sigma}^2}\left(-\frac{x}{1+\tilde{\rho}} + \frac{iy}{1-\tilde{\rho}}\right)$$

and substituting this into equation 3.15, we have

$$0 < |\beta|^2 = \frac{1}{S\tilde{\sigma}^2}\left(1 - \frac{x^2}{S(1+\tilde{\rho})^2\tilde{\sigma}^2} - \frac{y^2}{S(1-\tilde{\rho})^2\tilde{\sigma}^2}\right)$$

Also,

$$\begin{aligned}\frac{\partial r}{\partial \overline{\lambda}} &= \frac{1}{2}\left(\frac{\partial r}{\partial x} + i\frac{\partial r}{\partial y}\right) \\ &= \frac{1}{2}\left[\frac{1}{S\tilde{\sigma}^2}\left(-\frac{1}{1+\tilde{\rho}} + i\frac{i}{1-\tilde{\rho}}\right)\right] \\ &= -\frac{1}{(1-\tilde{\rho}^2)S\tilde{\sigma}^2}\end{aligned}$$

In summary, we obtain

$$p(z, \bar{z}) = \begin{cases} \frac{1}{\pi S\tilde{\sigma}^2(1-\tilde{\rho})^2} & \text{if } \frac{x^2}{S(1+\tilde{\rho})^2\tilde{\sigma}^2} + \frac{y^2}{S(1-\tilde{\rho})^2\tilde{\sigma}^2} < 1 \\ 0 & \text{otherwise} \end{cases} \tag{3.17}$$

So, the spectral density is constant inside the ellipse with $r_x = \sqrt{S}\tilde{\sigma}(1+\tilde{\rho})$ and $r_y = \sqrt{S}\tilde{\sigma}(1-\tilde{\rho})$ with

$$\tilde{\rho} = \frac{\rho_w\sigma_w^2 + (N-1)\rho_b\sigma_b^2}{\sigma_w^2 + (N-1)\sigma_b^2}$$

$$\tilde{\sigma}^2 = \frac{\sigma_w^2 + (N-1)\sigma_b^2}{N}$$

Using the set of equations from, we obtain

$$\tilde{\rho} = \frac{\rho A\sigma^2 + B\mu^2}{A\sigma^2 + B\mu^2}$$

$$\tilde{\sigma}^2 = -\frac{C}{N}(A\sigma^2 + B\mu^2)$$

where $A = -4Q + N(2Q - 1$ and $B = 4Q(2C-1) + N(2Q-1)(2CQ - C + 1)$ in terms of μ, σ, C, Q and ρ. Using this approach, we successfully locate the eigenvalues of B.

3.2.3 Finding eigenvalues of M

We are now ready to combine the results to determine the eigenvalues of M. According to the study by O'Rourke and Renfrew [8], the bulk of eigenvalues of M are actually eigenvalues of B that follows the ellipse law. The outlier of eigenvalues of M are actually eigenvalues of A, but modified with a small correction. Using Theorem 2.4 from [8], the correction for the outliers of matrix $M/\sqrt{S} = (A+B)/\sqrt{S}$ is given by

$$\lambda_{M/\sqrt{S},i} = \lambda_{(A+B)/\sqrt{S},i} = \lambda_{A,i}/\sqrt{S} + \frac{\rho}{\lambda_{A,i}/\sqrt{S}} + o(1)$$

With this, we can locate all the eigenvalues of M accurately.

3.2.4 Verification of result

To verify the result we obtained, we used Python to compute the positions of eigenvalues for a 1000×1000 community matrix with different choices of parameter. The blue dots indicate the eigenvalues of the community matrix, the red line indicates the predicted boundary region where the eigenvalues will stay and the red cross indicates the predicted outlier eigenvalues of the community matrix. The results showed the rightmost eigenvalue is predicted accurately using our approach.

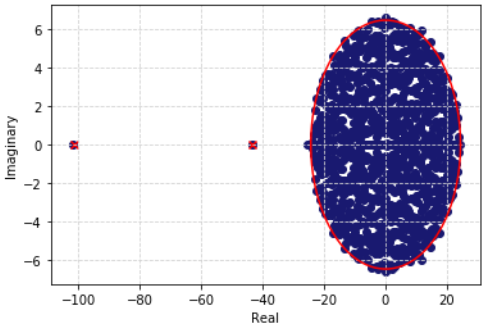

Figure 3: Two equal-sized subsystem community matrix M sampled from normal bivariate distribution with $S = 1000$, $C = 0.2$, $\mu = -0.5$, $\sigma = 1$, $\rho = 0.5$, $Q = 0.2$, $[\alpha_1, \alpha_2] = [0.5, 0.5]$

.

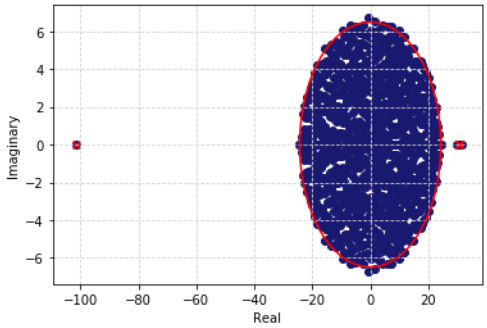

Figure 4: Five equal-sized subsystem community matrix M sampled from normal bivariate distribution with $S = 1000$, $C = 0.2$, $\mu = -0.5$, $\sigma = 1$, $\rho = 0.5$, $Q = -0.2$, $[\alpha_1, \alpha_2, \alpha_3, \alpha_4, \alpha_5] = [0.2, 0.2, 0.2, 0.2, 0.2]$

.

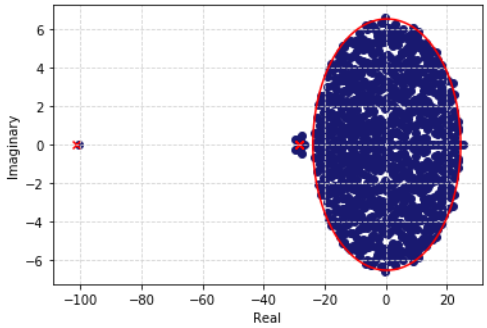

Figure 5: Ten equal-sized subsystem community matrix M sampled from normal bivariate distribution with $S = 1000$, $C = 0.2$, $\mu = -0.5$, $\sigma = 1$, $\rho = 0.5$, $Q = 0.2$, $[\alpha_i]_{i=1}^{10} = [0.1]_{i=1}^{10}$

.

Our ultimate goal is to use this scheme to locate the rightmost eigenvalues of a very huge but equally-sized subsystem ecosystem. For instance, when $S = 10000$, the example below predicts the rightmost eigenvalues of this community matrix to be 255.5.

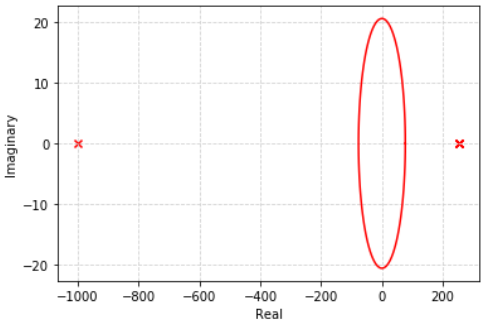

Figure 6: Five equal-sized subsystem community matrix M sampled from normal bivariate distribution with $S = 10000$, $C = 0.2$, $\mu = -0.5$, $\sigma = 1$, $\rho = 0.5$, $Q = -0.2$, $[\alpha_1, \alpha_2, \alpha_3, \alpha_4, \alpha_5] = [0.2, 0.2, 0.2, 0.2, 0.2]$

4 Conclusion

In Chapter 1, we studied the local stability of a huge biological network under the framework of the random matrix model. The model is becoming more and more realistic as we add more features. In particular, a random matrix with a modular structure is the main object of study in this project. Later in Chapter 2, we introduced the cavity method, a concept that originated from statistical physics. This approach helps us to obtain a simplified formula of the spectral distribution of the eigenvalues of the random matrix, which we had shown in Chapter 3. We illustrated the effectiveness of this approach to determine the rightmost eigenvalue when all subsystems are equal-sized.

The theory is far from complete as we haven't shown for the most general case of the modular structure, where the size of each subsystem is arbitrary. The main difficulty to solve this problem using the approach introduced here is, when the partition is unequal, i.e $\alpha_i's$ are not all equal, the formula in (3.20) remains complicated as we still have to evaluate every r_m using equation (3.13). In fact, it might be not be clear at all that the distribution of eigenvalues are located inside region of an ellipse except for finitely many outliers in the most general case. We confidently conjecture this because many different matrix had been tested using Python code mentioned in Appendix A with adequately large S and the results are shown to be consistent with the conjecture.

For future study, one of the possible approaches to solve this problem is to approximate the general block-structured matrices C to the block matrices with equal-sized subsystems D. If the size of each subsystem of C does not deviate too far from one another, it might be possible to define a loss function that minimizes the differences between C and D. With this, we can use C to predict the elliptic regions of D. Combining this with the outliers of D, we might be able to approximate fairly well the rightmost eigenvalues of D. Hopefully, this idea sheds a light that can solve this problem for the most general case of block-structured random matrices in the future.

A Python code

The Python code to generate Figure 3 - Figure 6 is available at `https://github.com/lingminhao/Block-structured-random-matrices`.

References

[1] Stefano Allesina and Jacopo Grilli. "Models for large ecological communities—a random matrix approach". In: *Theoretical Ecology*. Oxford University Press, pp. 74–92.

[2] Stefano Allesina and Si Tang. "The stability–complexity relationship at age 40: a random matrix perspective". In: *Population Ecology* 57.1 (2015), pp. 63–75.

[3] Jacopo Grilli, Tim Rogers, and Stefano Allesina. "Modularity and stability in ecological communities". In: *Nature communications* 7.1 (2016), pp. 1–10.

[4] Giacomo Livan, Marcel Novaes, and Pierpaolo Vivo. *Introduction to random matrices: theory and practice*. Vol. 26. Springer, 2018.

[5] Robert M May. "Will a large complex system be stable?" In: *Nature* 238.5364 (1972), pp. 413–414.

[6] Fernando Lucas Metz, Izaak Neri, and Tim Rogers. "Spectral theory of sparse non-Hermitian random matrices". In: *Journal of Physics A: Mathematical and Theoretical* 52.43 (2019), p. 434003.

[7] Hoi H Nguyen and Sean O'Rourke. "The elliptic law". In: *International Mathematics Research Notices* 2015.17 (2015), pp. 7620–7689.

[8] Sean O'Rourke and David Renfrew. "Low rank perturbations of large elliptic random matrices". In: *Electronic Journal of Probability* 19 (2014), pp. 1–65.

[9] Tim Rogers. "Universal sum and product rules for random matrices". In: *Journal of mathematical physics* 51.9 (2010), p. 093304.

[10] Tim Rogers and Isaac Pérez Castillo. "Cavity approach to the spectral density of non-Hermitian sparse matrices". In: *Physical Review E* 79.1 (2009), p. 012101.

[11] Tim Rogers et al. "Cavity approach to the spectral density of sparse symmetric random matrices". In: *Physical Review E* 78.3 (2008), p. 031116.

[12] Terence Tao, Van Vu, and Manjunath Krishnapur. "Random matrices: Universality of ESDs and the circular law". In: *The Annals of Probability* 38.5 (2010), pp. 2023–2065.