Block-structured Random Matrices

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Abstract

Initially, Random Matrix Theory (RMT) was born due to Eugene Wigner in physics. It serves as a powerful statistical model to study large systems with network structure. Biological systems like gene regulatory network, protein-protein interaction network and ecological system network are usually large and complex. Thus RMT can be applied in its full potential to extract important information about them. Block-structured random matrix is a more realistic model to study the ecosystem of modular organization. To study the stability of an ecosystem, it suffices to know the rightmost eigenvalue of the radnom matrix. One naive method is to generate all eigenvalue by brute force and locate the rightmost eigenvalue. But this demands high time complexity ($\mathcal{O}(S^2)$) as S grows. In this project, we will see how random matrix theory and cavity method sheds a light to optimize this problem.

Contents

1 Introduction

1.1 Classical Results in Random Matrix Theory

To study the stability of 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 essential definitions and results in classical random matrix theory. The proof of these results can be found in [1].

Definition 1.1 *Let X be a $S \times S$ Hermitian random matrix of size n. Then, The empirical spectral density 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 of size n. Then, The empirical spectral density 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, 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*

$$\mu(\lambda) = \frac{1}{2\pi}\sqrt{4 - \lambda^2} \tag{1.3}$$

if $\lambda \in [-2, 2]$ and 0 otherwise.

Result 1.2 *(Circular law) Let X be a $S \times S$ nonsymmetic matrix, where X_{ij} are iid are 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*

$$\mu(\lambda) = \frac{1}{\pi} \tag{1.4}$$

if $(\Re(\lambda))^2 + (\Im(\lambda))^2 \leq 1$ and 0 otherwise.

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 0 (vector) 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*

$$\mu(\lambda) = \frac{1}{\pi(1 - \rho^2)} \tag{1.5}$$

if $\frac{(\Re(\lambda))^2}{(1+\rho)^2} + \frac{(\Im(\lambda))^2}{(1-\rho)^2} \leq 1$ and 0 otherwise.

1.2 Motivation

One of the most useful model built using RMT is the community matrix, where it can be used to study the local asymptotic stability of a biological network. To elucidate the idea better, we chose ecological system as our biological background.

The local asymptotic stability of an ecosystem is given by a set of nonlinear differential equations:

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

where X_i is the 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 ecosystem. 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 for which 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 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 slight increase in population of species j affects the growth rate of population i. The rightmost eigenvalue ($\Re(\lambda_1)$) gives the information about the stability of the ecosystem at the equilibrium point. If it has negative real parts, then the equilibrium is stable, else it is unstable, because the directions of the corresponding eigenvectors goes away from the equilibrium point. To determine $\Re(\lambda_1)$ it is required to know exactly the function f_i and the equilibrium $\mathbf{X}^*$, which leads to different community matrix. The main difficulty is that there is no canonical set of equations describing interaction between species, and that even for a specific functional form, 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 using random matrix approach and gave a stability criterion based on the characteristics of the random matrix itself. In his study, May did not specify the details of the distribution except only the mean and variance of the distribution as the general results remain the same in the large S limit (large system). May sets all the diagonal elements $M_{ii} = -d$, the off-diagonal to be 0 with probability $1 - C$ and from a distribution with mean $\mu = 0$ and variance σ^2 with probability C. (C represents the connectivity of the system). By using the circular law [2], we have all eigenvalues approximated by the uniform distribution on a disk with centre $-d$ and radius $\sqrt{SC}$. Thus, the rightmost eigenvalues has a very high probability to have negative real parts if the random matrix satisfies the criterion:

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

The statistical model built by May indeed sheds a light to the study of stability of biological network using random matrix theory. But what May proposed was too simple that it failed to resemble the reality. For instance,

1. In ecological systems it is not necessary that the positive effects of the resource on the consumers precisely offset the negative effects of consumers on resources. Thus it is important to consider a nonzero mean for the off-diagonal entries. In this case [2], one of the eigenvalue (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

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

   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 ecosystem there are different interactions between species like mutualism, commensalism, parasitism, competition, and prey-predator system. 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, all the eigenvalues is approximated by the uniform distribution on a ellipse with centre $-d-E$, horizontal semi-axis $\sqrt{SV}(1+\rho)$, vertical semi-axis $\sqrt{SV}(1-\rho)$ where V is same as the previous one 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 co-variance 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:

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

3. Still, all the above-mentioned modifications and improvements failed to predict the location of the leading eigenvalues in a more realistic case. For example, in a stratified lake, benthic organisms tend to interact with other bottom-dweller organisms, while pelagic species with other organisms that are close to the surface. This means that some species interact more frequently within groups and infrequent among groups, a concept known as modularity (Q). Thus, the community matrix is modelled such that it is divided into "modules" and form a block-structured random matrices. In [4], Jacopo Grilli showed the effects of modularity on the stability of the ecological communities for 2×2 block matrices, i.e two different groups of species.

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The main objective of this thesis is to extend the theory from 2×2 block matrices to $n \times n$ block matrices. We provide an efficient way to determine the rightmost position of eigenvalue of random matrix (ecosystem model) for some important biologically relevant cases. With this rightmost eigenvalue, we can determine its stability ratio and this provides a way to compare the stability between two ecosystem model. The thesis is planned as following: Chapter 2 is devoted to study cavity method in detail. This is an important technique originated from statistical physics and it can be used to prove the main results for $n \times n$ block-structured random matrices in Chapter 3. The readers are encouraged to read Appendix A before proceed to Chapter 2.

2 Cavity Method

In this chapter we discuss cavity method for complex-valued eigenvalues (i.e Non-Hermitian case). Note that this method also holds for Hermitian case by replacing the complex eigenvalues with real eigenvalues. Originally, cavity method is developed to derive the spectral density for sparse random matrices but actually it holds also for densely connected random matrices.

Let $\mathcal{M}$ be an ensemble of $S \times S$ complex, sparse, non-Hermitian random matrices. Then, the 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 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 (2.3) is known as Hermitization. We provide the proof here starting from equation (2.2) and evantually 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

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

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

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

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

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

Also, $\nabla^2 \ln(x^2 + y^2) = \left(\frac{4\epsilon}{x^2+y^2+\epsilon}\right)^2$. For this, if $(x,y) \neq (0,0)$, then $\nabla^2 \ln(x^2 + y^2) \to 0$ as $\epsilon \to 0$. If $(x,y) = (0,0)$, then $\nabla^2 \ln(x^2 + y^2)$ diverge as $\epsilon \to 0$. Thus, $\nabla^2 \ln(x^2 + y^2) \to 4\pi\delta(x)\delta(y)$ as $\epsilon \to 0$. Therefore, 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

$$
\frac{1}{\det H} = \left(\frac{1}{\pi}\right)^{2S} \int \exp\left(-(\boldsymbol{\phi}^\dagger \ \boldsymbol{\chi}^\dagger)H(\boldsymbol{\phi} \ \boldsymbol{\chi})^T\right) d\boldsymbol{\phi}d\boldsymbol{\chi} \tag{2.4}
$$

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

$$
\mathcal{H}(\boldsymbol{\psi}, z, \bar{z}, \epsilon) = \sum_i^S \psi_i^\dagger[\epsilon\mathbf{1}_S + i(x\sigma_x - y\sigma_y)]\psi_i - i\sum_{i,j=1}^S \psi_i^\dagger(A_{ij}^h\sigma_x - A_{ij}^s\sigma_y)\psi_j \tag{2.5}
$$

where σ_x and σ_y are Pauli matrices and $A = A^h + iA^s$, A^h Hermitian, A^s skew-Hermitian. Let

$$
P(\boldsymbol{\psi}) = \frac{1}{\mathcal{Z}}e^{-\mathcal{H}(\boldsymbol{\psi}, z, \bar{z}, \epsilon)} \tag{2.6}
$$

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), (2.4), (2.5), and (2.6), we deduce that

$$p_A(z, \bar{z}) = \lim_{\epsilon \to 0} \frac{1}{\pi N} \sum_{l=1}^{N} -i\partial_{\bar{z}} \left\langle \psi_l^\dagger \sigma^+ \psi_l \right\rangle_P \tag{2.7}$$

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

$$P^{(i)}(\{\psi_l\}_{l \in \partial i}) = \prod_{l \in \partial i} P_l^{(i)}(\psi_l) \tag{2.8}$$

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:

$$P_i^{(j)}(\psi_i) = \frac{e^{-\mathcal{H}_i}}{\mathcal{Z}_i^{(j)}} \int \mathcal{D}(\boldsymbol{\psi}_{\partial i \backslash j}) e^{-\sum_{l \in \partial i \backslash j} \mathcal{H}_{il}} \prod_{l \in \partial i \backslash j} P_l^{(i)}(\psi_l) \tag{2.9}$$

where $\mathcal{Z}_i^{(j)}$ is a normalizing constant, and

$$\mathcal{H}_i = \psi_i^\dagger [\epsilon \mathbf{1}_2 + i(x\sigma_x - y\sigma_y)]\psi_i \tag{2.10}$$

$$\mathcal{H}_{ij} = -i\psi_i^\dagger (A_{ij}^h \sigma_x - A_{ij}^S \sigma_y)\psi_j - i\psi_j^\dagger (A_{ji}^h \sigma_x - A_{ji}^S \sigma_y)\psi_i \tag{2.11}$$

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

$$P_i(\psi_i) = \frac{e^{-\mathcal{H}_i}}{\mathcal{Z}_i} \int \mathcal{D}(\boldsymbol{\psi}_{\partial i}) e^{-\sum_{l \in \partial i} \mathcal{H}_{il}} \prod_{l \in \partial i} P_l^{(i)}(\psi_l) \tag{2.12}$$

Thus, it suffices to know the cavity marginal distribution (2.9). The set of recursive equations in (2.9) can be self-consistently solved by distributions of bivariate Gaussian type. Then for all $i = 1, \cdots, S$ and all $j \in \partial i$ the distribution $P_i^{(j)}$ can be written as

$$P_i^{(j)}(\psi_i) = \frac{1}{\mathcal{Z}_i^{(j)}} e^{-\psi_i^\dagger [C_i^{(j)}]^{-1} \psi_i} \tag{2.13}$$

where $C_i^{(j)}$ is a 2×2 matrix. Substituting this into equation (2.9), we have

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

$$(2.14)$$

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

$$B = A_{il}^h\sigma_x - A_{il}^s\sigma_y$$
$$B' = A_{li}^h\sigma_x - A_{li}^s\sigma_y$$

we can simplify the integral in equation (2.14). By changing the variable $phi_l = U_l^{-1}\psi_l$, equation (2.14) becomes

$$\int \prod_{l\in\partial i\backslash j} \frac{\mathcal{D}\phi_l}{\mathcal{Z}_l^{(i)}} \exp[i\phi_i^\dagger BU_l\phi_l + i\phi_l^\dagger U_l^\dagger B'\psi_i - \phi_l^\dagger U_l^\dagger[C_l^{(i)}]^{-1}U_l\phi_l] \qquad (2.15)$$

$$J_i = \psi_i^\dagger B$$
$$J_i' = B'\psi_i$$

Since $B' = B^\dagger$, we have $J_i' = J_i^\dagger$. Then equation (2.15) can be written (in terms of u_l and v_l) as

$$\int \prod_{l\in\partial i\backslash j} \frac{\mathcal{D}\phi_l}{\mathcal{Z}_l^{(i)}} \exp[\sum_\alpha(iJ_{i\alpha}'^\dagger U_{\alpha l}^l u_l + iJ_{i\alpha}'^\dagger U_{\alpha 2}^l v_l + iu_l^* U_{1\alpha}^{l\dagger} J_{i\alpha}' + iv_l^* U_{2\alpha}^{l\dagger} J_{i\alpha}' - d_{l1}^{(i)}|u_l|^2 - d_{l2}^{(i)}|v_l|^2]$$

$$(2.16)$$

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

$$b^* = [\sum_\alpha U_{1\alpha}^{l\dagger}J_{i\alpha}']^* = \sum_\alpha J_{i\alpha}'^\dagger U_{\alpha 1}^l$$
$$c^* = [\sum_\alpha U_{2\alpha}^{l\dagger}J_{i\alpha}']^* = \sum_\alpha J_{i\alpha}'^\dagger U_{\alpha 2}^l$$

Replacing this and rearranging equation (2.16), we have

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

$$(2.17)$$

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

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

we have

$$\int \prod_{l\in\partial i\backslash j} \frac{du_l^R du_l^I}{4\mathcal{Z}_l^{(i)}} \exp\left(-\frac{d_{l1}^{(i)}}{2}u_l^{lR} + i\frac{b^*}{\sqrt{2}}u_l^R + i\frac{b}{\sqrt{2}}u_l^R\right) \exp\left(-\frac{d_{l1}^{(i)}}{2}u_l^{2I} - \frac{b^*}{\sqrt{2}}u_l^I + \frac{b}{\sqrt{2}}u_l^I\right)$$

$$= \int \prod_{l\in\partial i\backslash j} \frac{du_l^R du_l^I}{4\mathcal{Z}_l^{(i)}} \exp\left(-\frac{d_{l1}^{(i)}}{2}u_l^{2R} + i\sqrt{2}(\Re b)u_l^R - \frac{d_{l1}^{(i)}}{2}u_l^{2I} + i\sqrt{2}(\Im b)u_l^I\right)$$

(2.18)

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 (2.17) finally becomes

$$\prod_{l\in\partial i\backslash j} \frac{1}{4\mathcal{Z}_l^{(i)}} \frac{2\pi}{d_{l1}^{(i)}} \frac{2\pi}{d_{l2}^{(i)}} \exp\left(-\frac{|b|^2}{d_{l1}^{(i)}} - \frac{|c|^2}{d_{l2}^{(i)}}\right) = \prod_{l\in\partial i\backslash j} \exp\left(-\sum_{\alpha,\beta} J_\alpha'^\dagger U_{\alpha 1}^{l\dagger}\frac{1}{d_{l1}^{(i)}}U_{1\beta}^{l\dagger}J_\beta' - \sum_{\gamma,\delta} J_\gamma'^\dagger U_{\gamma 2}^l\frac{1}{d_{l2}^{(i)}}U_{2\delta}^{l\dagger}J_\delta'\right)$$

$$= \prod_{l\in\partial i\backslash j} \exp\left(-J'^\dagger U^l \begin{pmatrix} \frac{1}{d_{l1}^{(i)}} & 0 \\ 0 & \frac{1}{d_{l2}^{(i)}} \end{pmatrix} U^{l\dagger}J'\right)$$

(2.19)

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 (2.19) 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 (2.19) becomes

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

Thus, we have obtained from equation (2.9) a set of recursive equations $\{C_i^{(j)}\}$ (known as cavity equations) given by

$$C_i^{(j)} = [\epsilon\mathbf{1}_2 + i(x\sigma_x - y\sigma_y) + F(C_{\partial i\backslash j}^{(i)}]^{-1}$$

(2.20)

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

$$F(C_{\partial i\backslash j}^{(i)}) = \sum_{l\in\partial i\backslash j} \left(A_{il}^h\sigma_x - A_{il}^s\sigma_y\right) C_l^{(i)} \left(A_{li}^h\sigma_x - A_{li}^s\sigma_y\right)$$

Similarly, we have

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

(2.21)

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for all $i = 1, \cdots, S$ from equation (2.12). 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 $b_i \in \mathbb{C}$.

This form allows to obtain the spectral density in equation (2.7) in terms of b_i as $\left\langle \psi_l^\dagger \sigma^+ \psi_l \right\rangle_P$ can be computed using techniques of Quantum Field Theory [10]. In the end, we have the formula for spectral density given by

$$p_A(z, \bar{z}) = -\frac{1}{\pi S} \lim_{\epsilon \to 0} \sum_{i=1}^{S} \partial_{\bar{z}} b_i(z, \bar{z}, \epsilon) \tag{2.22}$$

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

$$\partial_{\bar{z}} C_i^{(j)} = -C_i^{(j)} \left[\begin{pmatrix} 0 & 0 \\ i & 0 \end{pmatrix} + F(\partial_{\bar{z}} C_{\partial i \backslash j}^{(i)}) \right] C_i^{(j)} \tag{2.23}$$

Using similar argument, we also have

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

To summarise, we iterate equations (2.20) and (2.23) until we reach convergence. Then we can recover equations (2.21) and (2.24) 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 is zero. Thus, short loops are rare and this guarantees the convergence of these equations. Technically, we can remove this assumption but it is necessary to stop the iterations once a pre-determined level of convergence has been reached. So the formula of spectral density obtained using cavity method can be used for densely connected case.

With this formula in hand, we can determine the region where the spectral density vanishes, i.e the region where there is no eigenvalues. As we will show in next chapter, this will help us to efficiently locate the rightmost eigenvalues.

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 terminology. 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,

$$C_b = \frac{L_b}{n_b} = \frac{C\left(\frac{S^2}{2}(1 - Q) - n_w \right)}{n_b}$$

$$= \frac{C\left(\frac{S^2}{2}(1 - Q) - \frac{S^2 \sum_{i=1}^{N} \alpha_i^2}{2} \right)}{S^2\left(\sum_{i<j, i\neq j}^{N} \alpha_i \alpha_j \right)}$$

$$= \frac{C\left(1 - Q - \sum_{i=1}^{N} \alpha_i^2 \right)}{2 \sum_{i<j, i\neq j} \alpha_i \alpha_j}$$

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 $M = W \circ K$ 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 $M_{ii} = 0$ (WLOG) 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

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$1 - C_b$ ($\gamma_i \neq \gamma_j$) 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

$$\mu_w = C_w \mu$$

$$\mu_b = C_b \mu$$

$$\sigma_w^2 = C_w(\sigma^2 + (1 - C_w)\mu^2)$$

$$\sigma_b^2 = C_b(\sigma^2 + (1 - C_b)\mu^2)$$

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

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

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 $\bar{M}$ of our choice with $Q \neq 0$ (modular structure) and compare it with the random community matrix 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 modular structure

Let $\bar{M}$ be a $S \times S$ block-structured random matrix. Using the approach introduced by Allesina et al. [3], we write $\bar{M}$ as the sum of two matrices, $\bar{M} = A + B$, 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 $B = \bar{M} - A$. 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 $\gamma_i \neq \gamma_j$). This parametrization 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.** To determine the rightmost eigenvalues of M, we will need to find:

1. The position of the eigenvalues of A.

2. The region where the eigenvalues of B lies.

3.2.1 Finding eigenvalues of A

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

Figure 1: 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

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

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

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

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

$$(\alpha_1 S\mu_w - \lambda)a_1 + (\alpha_2 S\mu_b)a_2 + \cdots + (\alpha_N S\mu_b)a_N = 0$$
$$(\alpha_1 S\mu_b)a_1 + (\alpha_2 S\mu_w - \lambda)a_2 + \cdots + (\alpha_N S\mu_b)a_N = 0$$
$$\vdots$$
$$(\alpha_1 S\mu_b)a_1 + (\alpha_2 S\mu_b)a_2 + \cdots + (\alpha_N S\mu_w - \lambda)a_N = 0$$

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

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

As a result, we have successfully locate all the outliers of the matrix $\bar{M}$.

3.2.2   Finding eigenvalues of B

First, 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

$$p(x, y) = \frac{1}{S} \sum_{i=1}^{n} \delta(x - \Re(\lambda_i))\delta(y - \Im(\lambda_i)) \tag{3.3}$$

and the resolvent is defined as

$$\mathcal{G}(\boldsymbol{q}) = \frac{1}{S} \sum_i (z_i - \boldsymbol{q})^{-1} \tag{3.4}$$

for which we can rewrite the spectral distribution as

$$p(x, y) = -\frac{1}{\pi} \lim_{\epsilon \to 0^+} \Re \left(\frac{\partial}{\partial \bar{z}} \mathcal{G}(z + \epsilon j) \right) |_{z = x + iy} \tag{3.5}$$

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 [7]. 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 (2.20) and (2.21) using quaternions instead of Pauli matrices using the mapping

$$\boldsymbol{i} \leftrightarrow i\sigma_x$$
$$\boldsymbol{j} \leftrightarrow i\sigma_y$$
$$\boldsymbol{k} \leftrightarrow i\sigma_z$$

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

$$\boldsymbol{B}_{ij} = \begin{pmatrix} B_{ij} & 0 \\ 0 & B_{ji} \end{pmatrix} \tag{3.6}$$

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

$$\mathcal{G}(\boldsymbol{q}) = \frac{1}{S} \sum_i \boldsymbol{G}_{ii}(\boldsymbol{q}) \tag{3.7}$$

Assuming B_{ij} has a tree structure, we can apply cavity method (equation (2.21)) to obtain the recursive equations for the diagonal entries of $\boldsymbol{G}$

$$\boldsymbol{G}_{ii}(\boldsymbol{q}) = - \left(\boldsymbol{q} + \sum_{j \neq i} \boldsymbol{B}_{ij} \boldsymbol{G}_{jj}^{(i)} \boldsymbol{B}_{ji} \right)^{-1} \tag{3.8}$$

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

$$\boldsymbol{G}_{ii}^k(\boldsymbol{q}) = - \left(\boldsymbol{q} + \sum_{j \neq i, k} \boldsymbol{B}_{ij} \boldsymbol{G}_{jj}^{(i)} \boldsymbol{B}_{ji} \right)^{-1} \tag{3.9}$$

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Solving them iteratively, using (3.5), (3.6), (3.7) and substituting them into (3.3), we can find the spectral density. For blocked structured matrices, we can simplify equation (3.6) and (3.7). At the leading order in S, the right side of equation (3.6) 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 $\boldsymbol{G}_{jj}^{(i)} = \boldsymbol{G}_{jj} = \boldsymbol{G}_{\gamma_j}$. This implies that equal (3.6) became closed and thus we can omit equation (3.7). Also, we can use law of large number to approximate the sum of the right hand side of equation (3.6) to obtain, at the leading order in S,

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

To summarize, given N groups of species, we have reformulate the set of equations (3.6) for $i = 1, \cdots, S$ into

$$\boldsymbol{G}_{\gamma_i}(\boldsymbol{q}) = -\left(\boldsymbol{q} + \mathbb{E}\left(\sum_j \boldsymbol{B}_{ij} \boldsymbol{G}_{\gamma_j} \boldsymbol{B}_{ji} \right) \right) \tag{3.10}$$

for $\gamma_i \in (1, \cdots, N)$. Using equation (3.4), we have

$$\boldsymbol{B}_{ij} \boldsymbol{G}_{\gamma_j} \boldsymbol{B}_{ji} = \begin{pmatrix} B_{ij} & 0 \\ 0 & B_{ji} \end{pmatrix} \begin{pmatrix} r_{\gamma_j} & \beta_{\gamma_j} \\ \bar{\beta}_{\gamma_j} & \bar{r}_{\gamma_j} \end{pmatrix} \begin{pmatrix} B_{ji} & 0 \\ 0 & B_{ij} \end{pmatrix} = \begin{pmatrix} B_{ij} r_{\gamma_j} B_{ji} & B_{ij}^2 \beta_{\gamma_j} \\ B_{ji}^2 \bar{\beta}_{\gamma_j} & B_{ij} B_{ji} \bar{r}_{\gamma_j} \end{pmatrix} \tag{3.11}$$

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

$$\mathbb{E}\left(\sum_j B_{ij}^2 z_{\gamma_j} \right) = \sum_j \mathbb{E}(B_{ij}^2) z_{\gamma_j} = \sum_j (\delta_{\gamma_i, \gamma_j} \sigma_w^2 z_{\gamma_j} + (1 - \delta_{\gamma_i, \gamma_j}) \sigma_b^2 z_{\gamma_j}) \tag{3.12}$$

When $\gamma_i = m$, we have

$$\mathbb{E}\left(\sum_j B_{ij}^2 z_{\gamma_j} \right) = S \alpha_m \sigma_w^2 z_m + \sum_{i \neq m} S(\alpha_i) \sigma_b^2 z_i \tag{3.13}$$

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

Using similar argument, we have

$$\mathbb{E}\left(\sum_j B_{ij} B_{ji} z_{\gamma_j} \right) = S \alpha_m \rho_w \sigma_w^2 z_m + \sum_{i \neq m} S(\alpha_i) \rho_b \sigma_b^2 z_i \tag{3.14}$$

Substituting into equation (3.9), we have

$$\mathbb{E}\left(\sum_j \boldsymbol{B}_{ij} \boldsymbol{G}_{\gamma_j} \boldsymbol{B}_{ji} \right) = \begin{pmatrix} \mathbb{E}\left(\sum_j B_{ij} B_{ji} r_{\gamma_j} \right) & \mathbb{E}(\sum_j B_{ij}^2 \beta_{\gamma_j}) \\ \mathbb{E}\left(\sum_j B_{ji}^2 \bar{\beta}_{\gamma_j} \right) & \mathbb{E}\left(\sum_j B_{ij} B_{ji} \bar{r}_{\gamma_j} \right) \end{pmatrix}$$
$$= S \alpha_m \sigma_w^2 \begin{pmatrix} \rho_w r_m & \beta_m \\ \bar{\beta}_m & \rho_w \bar{r}_m \end{pmatrix} + \sum_{i \neq m} S(\alpha_i) \sigma_b^2 \begin{pmatrix} \rho_b r_i & \beta_i \\ \bar{\beta}_i & \rho_b \bar{r}_i \end{pmatrix} \tag{3.15}$$

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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 (3.13) becomes

$$\mathbb{E}(\sum_j \boldsymbol{B_{ij}} \boldsymbol{G_{\gamma_j}} \boldsymbol{B_{ji}}) = \alpha_m \boldsymbol{\Sigma_w} \circ \boldsymbol{G_m} + \sum_{i \neq m} \alpha_i \boldsymbol{\Sigma_b} \circ \boldsymbol{G_i} \qquad (3.16)$$

where $'\circ'$ denotes the element by element matrix product. Substituting this into equation (3.8), we have

$$\boldsymbol{G_m(q)} = - \left(\boldsymbol{q} + \alpha_m \boldsymbol{\Sigma_w} \circ \boldsymbol{G_m} + \sum_{i \neq m} \alpha_i \boldsymbol{\Sigma_b} \circ \boldsymbol{G_i} \right)^{-1} \qquad (3.17)$$

The resolvent from equation (3.5) also becomes

$$\mathcal{G}(\boldsymbol{q}) = \sum_{m=1}^{N} \alpha_m \boldsymbol{G_m(q)} \qquad (3.18)$$

. Thus, the spectral density is

$$p(z, \bar{z}, \epsilon) = -\frac{1}{\pi} \lim_{\epsilon \to 0} \Re \left(\frac{\partial}{\partial \bar{z}} \sum_{m=1}^{N} \alpha_m \boldsymbol{G_m(q)} \right) \qquad (3.19)$$

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

$$p(z, \bar{z}) = -\frac{1}{\pi} \sum_{m=1}^{N} \alpha_m \Re \frac{\partial r_m}{\partial \bar{z}} \qquad (3.20)$$

As we will see later, equation (3.15) and (3.18) 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 $O(N^2)$ instead of $O(S^2)$ which is far more efficient. This is because in a large biological network it is usually that $N << S$. For example, in a stratified lake, there might be millions of number of species, but it is only a three-layered ($N = 3$) ecosystem.
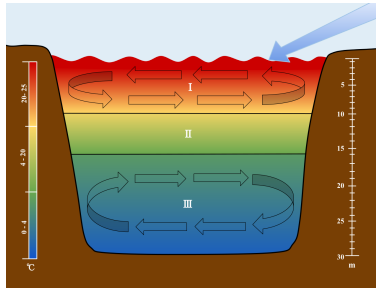

Figure 2: Lakes are stratified into three separate sections: I. The Epilimnion II. The Metalimnion III. The Hypolimnion

Suppose now that $\alpha_1 = \alpha_2 = \cdots = \alpha_N = \frac{1}{N}$. Then the right side of equation (3.17) 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

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

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

Then,

$$\boldsymbol{G} = -\left(\boldsymbol{q} + \tilde{\boldsymbol{\Sigma}} \circ \boldsymbol{G}\right)^{-1} \tag{3.21}$$

where

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

Recalling 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 (3.21), 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

$$r(-rS\tilde{\rho}\tilde{\sigma}^2 - z) + S|\beta|^2\tilde{\sigma}^2 = 1 \tag{3.22}$$

$$\beta(-rS\tilde{\rho}\tilde{\sigma}^2 - z - S\bar{r}\tilde{\sigma}^2) = 0 \tag{3.23}$$

Notice that by equation (3.20), we have

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

If $\beta = 0$, equation (3.22) becomes

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

and thus

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

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 (3.23). Using Mathematica, we have solved r to get

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

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and substituting this into equation 3.23, 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,

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

In summary, we obtain

$$p(z,\bar{z}) = \begin{cases} \frac{1}{\pi S\tilde{\sigma}^2(1-\tilde{\rho})^2} & \text{if } \frac{x^2}{S(1+\tilde{\rho})^2\tilde{\sigma}^2} + \frac{y^2}{S(1-\tilde{\rho})^2\tilde{\sigma}^2} < 1 \\ 0 & \text{otherwise} \end{cases} \tag{3.24}$$

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.

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 indicates the eigenvalues of the community matrix, the red lines indicates the boundary region where the eigenvalues will stay, i.e equation (3.24) and the red cross indicates the predicted outlier eigenvalues of the community matrix. The results showed the rightmost eigenvalue is predicted accurately.
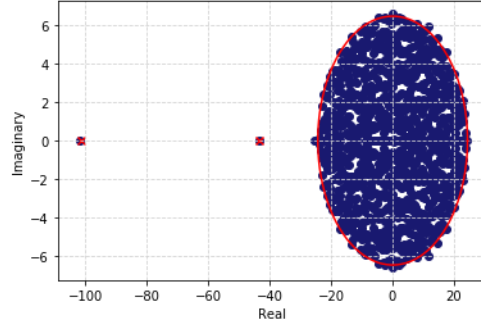
Figure 3: Two equal-sized subsystem community matrix M sampled from normal bivariate distribution with $S = 1000$, $C = 0.2$, $\mu = -0.5$, $\sigma = 1$, $\rho = 0.5$, $Q = 0.2$, $[\alpha_1, \alpha_2] = [0.5, 0.5]$.
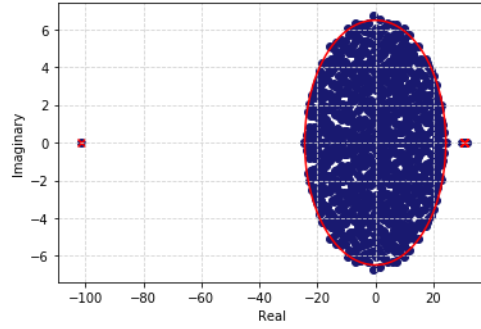

Figure 4: Five equal-sized subsystem community matrix M sampled from normal bivariate distribution with $S = 1000$, $C = 0.2$, $\mu = -0.5$, $\sigma = 1$, $\rho = 0.5$, $Q = -0.2$, $[\alpha_1, \alpha_2, \alpha_3, \alpha_4, \alpha_5] = [0.2, 0.2, 0.2, 0.2, 0.2]$.
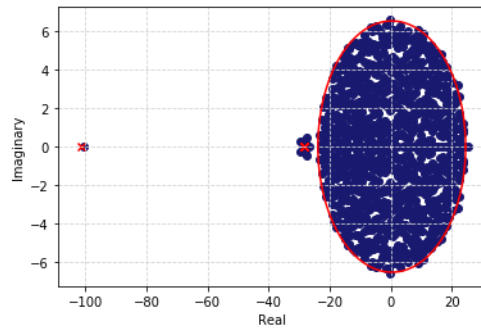

Figure 5: Ten equal-sized subsystem community matrix M sampled from normal bivariate distribution with $S = 1000$, $C = 0.2$, $\mu = -0.5$, $\sigma = 1$, $\rho = 0.5$, $Q = 0.2$, $[\alpha_i]_{i=1}^{10} = [0.1]_{i=1}^{10}$.

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.
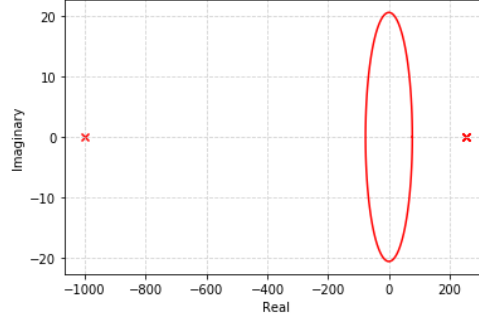

Figure 6: Five equal-sized subsystem community matrix M sampled from normal bivariate distribution with $S = 10000$, $C = 0.2$, $\mu = -0.5$, $\sigma = 1$, $\rho = 0.5$, $Q = -0.2$, $[\alpha_1, \alpha_2, \alpha_3, \alpha_4, \alpha_5] = [0.2, 0.2, 0.2, 0.2, 0.2]$

4 Conclusion

In Chapter 1, we introduce how we study the local stability of huge biological network under the framework of random matrix model. The model is becoming more and more realistic with more features being added. In particular, random matrix with modular structure is the main object of study in this project. Later in Chapter 2, we introduce cavity method, a concept originated from statistical physics that 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 illustrate the effectiveness of this approach to derive a particular case when all subsystem are of equal-sized.

Yet 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 can be arbitrary. The main difficulty is that 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 each r_m using equation (3.17). In fact, it might be not the case that the distribution of eigenvalues will be a combination of region of an ellipse and finitely many outliers. The reason we confidently put this as our conjecture is because we had test many different matrix with adequately large S and it shows that most of the eigenvalues are within an elliptical region and there are finitely many eigenvalues. Thus, we conjecture that this will be the case and hopefully cavity approach sheds a light to solve the most general case in the near future.

A Python code

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

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