Ranking Problems Arising from ODE Models on Networks

by

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Abstract

The use of ordinary differential equations modelled on networks has become an increasingly important technique in many areas of research. The local behaviour of the system is modelled with differential equations and interactions between members or nodes are described using weighted digraphs. For instance, in public health nodes can represent different groups of people affected by an infectious disease, while edges in the network represent the cross-infection between the groups. The local behaviours of the disease in each group are described with ODE dynamics. In ecology, the spatial dispersal of one or more species considers the habitation patches as nodes and the edges between nodes describe the movement of the species between patches.

This thesis develops a method of ranking the nodes of an ODE network at a positive equilibrium $\mathbf{x}^* = (x_1^*, \ldots, x_n^*)^T$. Such a ranking is called an *equilibrium ranking*. More specifically, assuming an ODE system modelled on a network $(\mathcal{G}, B)$ has a positive equilibrium $\mathbf{x}^*$, we associate x_i^* to node i of the network. These positive equilibrium values x_i^* are used to rate, and hence rank, the individual nodes of the network. Such an equilibrium ranking reflects both the graph structure and the local ODE parameters of the model.

In my dissertation I investigate equilibrium ranking for several ODE networks including SIR epidemiology models with n different groups or spatial regions, single or multiple species ecological models, and coupled oscillator models from engineering. For an SIR model the equilibrium ranking can be obtained using the equilibrium values of the disease prevalence vector $\mathbf{I}^* = (I_1^*, \ldots, I_n^*)^T$. This will indicate which of the n groups or patches has the highest number of infected individuals per capita. In the single species

ecology model an equilibrium ranking vector comes from the species density vector $\mathbf{x}^* = (x_1^*, \ldots, x_n^*)^T$, and reflects overpopulation or extinction on different patches or in different groups.

The dependence of equilibrium ranking on both graph structure and local parameters is also investigated. In particular, the dependence of the equilibrium ranking is considered for several digraph structures including rooted trees, loop digraphs, unicyclic and multi-cyclic digraphs. This will allow researchers to fix the network structure $(\mathcal{G}, B)$ of the system and focus on how the dynamics play a role in the importance of nodes in a network.

DEDICATION

To my family and friends for their unconditional support over the years. Without your help this would not have been possible;

To my beautiful daughter Mabel Lea, for whom this entire endeavour has been done.

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Contents

KEY WORDS AND PHRASES

Weighted Digraphs, Strongly Connected Digraphs, Graph Metrics, Networks, ODE Models on Networks, Relative Importance and Centrality, Eigenvector Centrality, Ranking Vector, Rating Vector, Nonnegative Irreducible Matrices, The Perron-Fröbenius Theorem, Ranking, Equilibrium Ranking Vector, Approximate Equilibrium Ranking.

FIGURES

Chapter 1

Introduction

The use of ordinary differential equations modelled on networks has become an increasingly important technique in many areas of research. The local behaviour of a system is modelled with differential equations and interactions between members or nodes are described using weighted digraphs. For instance, in public health the nodes can represent different groups of people affected by an infectious disease, while edges in the network represent the cross-infection between the groups. The local behaviours of the disease in each group are described with ODE dynamics. In ecology, the spatial dispersal of one or more species considers the habitation patches as nodes and the edges between nodes describe the movement of the species between patches.

Considering an ODE system modelled on a network $(\mathcal{G}, B)$ at a positive steady state $\mathbf{x}^* = (x_1^*, \ldots, x_n^*)^T$, one can ask the question of which node has the most relative importance. In other words, we want to rank a network's nodes at equilibrium. In an epidemiology model the node with the highest rank can be interpreted as the group with the highest disease prevalence given an endemic outbreak. In an ecology system modelling the density of a species over a range

of habitation patches the most important node represents the species with the highest population density. A ranking in this case would allow researchers to predict which areas a species is thriving and which patches the species is in danger of going extinct (patches having a relatively low population density).

Given a ranking of the members of an ODE network, we would like to know how effective this ranking is and how it relates to other network ranking methods established in literature. Another important aspect of a given network ranking is how it depends on both the dispersal connections of the network and the local ODE parameter values. Answering this question of dependence can give insight into how network structure and local dynamics influences which node will be the most important.

Mathematically, a network is defined using a *digraph* $\mathcal{G} = (V, E)$ consisting of a set V of nodes and a set E of directed edges representing the connections between vertices. For example, in epidemiology, depending on the situation the nodes of a digraph can represent the different groups of a host population, different spatial regions such as countries, cities or even individual cells. The directed edges then represent the cross-infection between the individual components of the disease network. A digraph $\mathcal{G}$ is *weighted* if each arc from node i to node j, denoted by (i, j), is assigned a positive real number $\omega(i, j) \in \mathbb{R}_+$. For a disease model these weights can represent the disease transmission rates from group to group.

An $n \times n$ matrix B is associated to a digraph $\mathcal{G}$ by defining the the ij^{th} entry b_{ij} of B to be equal to the weight of directed arc (j, i) if it exists, and zero otherwise. Thus, if an edge (j, i) exists in the digraph $\mathcal{G}$, then $b_{ij} = \omega(j, i)$. The matrix B is called the *weight matrix* or *dispersal matrix* of the network $\mathcal{G}$.

Therefore, it is often useful to represent a network as the ordered pair $(\mathcal{G}, B)$, where $\mathcal{G}$ is the digraph and B is the weight matrix associated to $\mathcal{G}$.

The local dynamics at each node i of the system are described using ordinary differential equations of the form

$$\dot{x}_i = f_i(x_i), \qquad i = 1, \ldots, n, \tag{1.1}$$

where f_i is a nonlinear function of x_i. The x_i of the system can represent individuals in a population infected with a disease, to the density of a species in an ecology system. Hence, combining the local ODE equations with the dispersal connections described by $(\mathcal{G}, B)$ gives a coupled ODE system of the form

$$\dot{x}_i = f_i(x_i) + \sum_{j=1}^{n} b_{ij} g_{ij}(x_i, x_j), \qquad i = 1, \ldots, n, \tag{1.2}$$

where $B = (b_{ij})_{n \times n}$ is the weight matrix of the network, and g_{ij} describes the influence among the nodes depending on the situation. Given an ODE model of the kind described by (1.2), we make the following assumption

(A1) System (1.2) has a unique positive equilibrium $\mathbf{x}^* = (x_1^*, \ldots, x_n^*)^T > \mathbf{0}$.

In such a case, we would like to know which node of the network has the most relative importance. Therefore, the equilibrium $\mathbf{x}^*$ is defined as the *equilibrium ranking vector* for the ODE network, and the entry $x_i^* > 0$ is associated to node i of the network and the nodes are ranked from most to least important based on the x_i^* values. A ranking of an ODE network obtained in this way will be called an *equilibrium ranking* of the ODE network. Therefore, this thesis is structured to investigate three important aspects of

the equilibrium ranking.

The second chapter is used to state preliminary definitions and results needed for the thesis and to give a review of literary works on network ranking.

Chapter 3 addresses the issue of how equilibrium ranking relates to other network ranking methods. I investigate a multigroup SIR epidemiology model with positive equilibrium $\mathbf{x}^* = (S_1^*, I_1^*, R_1^* \ldots, S_n^*, I_n^*, R_n^*)^T$. I derive a matrix equation containing a disease prevalence equilibrium vector $\mathbf{I}^* = (I_1^*, \ldots, I_n^*)^T$. Therefore, $\mathbf{I}^*$ is the unique positive eigenvector of a matrix. This establishes a link between equilibrium ranking and the well known method of eigenvector centrality ranking. The benefit of this new equilibrium ranking is that it takes into account not only the network structure but also the local parameter values of the system. The last section of this chapter gives implications that an equilibrium ranking can have for the control of an infectious disease.

Chapter 4 considers defining a ranking for a more general class of nonlinear ODE networks. In particular, we consider several engineering and ecology examples and then state results for two particular forms of (1.2). In each case we use the equilibrium equations to derive a matrix equation of the form

$$M(\mathbf{x}^*)\mathbf{x}^* = \mathbf{x}^*. \tag{1.3}$$

Then we can show that $\mathbf{x}^*$ is the Perron eigenvector of $M(\mathbf{x}^*)$ associated to the spectral radius $\rho(M(\mathbf{x}^*)) = 1$.

As in Chapter 3, this establishes a link between eigenvector ranking of a network and our equilibrium ranking vector. Moreover, the equilibrium ranking vector depends not only on the networks weight matrix B, but also

the local parameter values of the ODE system.

Chapter 5 deals with how an equilibrium ranking vector $\mathbf{x}^*$ depends on both the structure of the network $(\mathcal{G}, B)$ and the local ODE parameter values. In many cases, an equilibrium ranking vector $\mathbf{x}^*$ is obtained from a matrix equation $M\mathbf{x}^* = \mathbf{x}^*$, where M is the product of a diagonal matrix D and the irreducible weight matrix B of the system. Therefore, to answer the question of how an equilibrium ranking vector depends on network structure and local dynamics, we investigate the structure of the unique positive Perron eigenvector $\mathbf{p}$ of a matrix $M = D \cdot B$.

Suppressing the local parameter values encoded in the diagonal matrix D allows for the investigation of how the entries of a nonnegative eigenvector $\mathbf{p}$ depend on the weight matrix B of a network $(\mathcal{G}, B)$. More specifically, several typical network structures including cycle, rooted tree, and unicyclic digraphs are considered. Analysis of the unique nonnegative eigenvector gives insight into how the structure of a digraph affects the importance of the individual nodes of the network. Then, fixing a network $(\mathcal{G}, B)$, we consider how the entries of the Perron eigenvector change when B is multiplied by a diagonal matrix D containing the local ODE parameter values. This will allow for the investigation of how the local dynamics play a role in equilibrium ranking given a fixed network structure.

Chapter 2

Preliminaries and Literature Review

This chapter will be used to state the basic definitions and notions required throughout the thesis. The first section covers results on positive and nonnegative matrices and the Perron-Fröbenius Theorem (See [6], [17], [52], and [74]). Section two states the necessary definitions and results about graph theory. For a more detailed discussion of graph theory see [40], [47], [48], [77], [110], and [111]. The third section is used for a review of related literature. The results of this section originate from the works of [8], [9], [10], [15], [27], [63], [75], [80], and [101].

2.1 The Perron-Fröbenius theorem

This section will consist of three subsections that develop the so-called Perron-Fröbenius Theorem. The first states basic results about eigenvalues and eigenvectors of a real $n \times n$ matrix A. The second and third subsections list results about positive and nonnegative matrices respectively.

In what follows, we assume that the reader is familiar with linear algebra. By a matrix in $\mathcal{M}_{m\times n}(\mathbb{R})$ we mean a matrix with m rows, n columns, and real entries. In particular $\mathcal{M}_n(\mathbb{R})$ is the set of all square matrices of size n with real coefficients. A matrix $A \in \mathcal{M}_{m\times n}(\mathbb{R})$ will be identified with a linear transformation $A : \mathbb{R}^n \to \mathbb{R}^m$, so that A can be thought of both as a matrix and a linear transformation. We will also denote by $I := I_n$, the $n \times n$ identity matrix.

2.1.1 Eigenvectors and Their Properties

Let $A \in \mathcal{M}_n(\mathbb{R})$ be a matrix. Then $\lambda \in \mathbb{C}$ is called an *eigenvalue* of A, if there is some nonzero vector $\mathbf{x} \in \mathbb{R}^n$, such that $A\mathbf{x} = \lambda\mathbf{x}$. We call $\mathbf{x}$ an *eigenvector* associated with λ. In such a case, $(\lambda, \mathbf{x})$ is called an *eigenpair* of A. The *characteristic equation* of A is given by

$$\det(A - \lambda \cdot I) = 0,$$

and the left-hand-side is called the *characteristic polynomial* of A, and is denoted by $p_A(\lambda)$.

Definition 2.1.1. Let $A \in \mathcal{M}_n(\mathbb{R})$. Then the *spectrum* $\sigma(A)$, of A is the set of all eigenvalues of A, i.e., we have

$$\sigma(A) := \{\lambda \in \mathbb{C} \ : \ \det(A - \lambda I) = 0\} = \{\lambda_1, \ldots, \lambda_k\},$$

where for every $i = 1, \ldots, k$, $A\mathbf{v_i} = \lambda_i\mathbf{v_i}$ for some $\mathbf{0} \neq \mathbf{v_i} \in \mathbb{R}^n$.

Recall that given an $n\times n$ matrix A, an $r\times r$ *principal submatrix* is obtained from A by deleting the same set of $n - r$ rows and columns from A, and an

$r \times r$ *principal minor* is the determinant of an $r \times r$ principal submatrix. Also note that there are $\binom{n}{r}$ such principal minors. Moreover, the 1×1 principal minors are the n diagonal entries $a_{ii},\ i = 1, \ldots, n$ of A and the $n \times n$ principal minor is the determinant of A (delete $n - n = 0$ row and columns).

Theorem 2.1.1. *Let A be an $n \times n$ matrix, and let $M_k^r,\ k = 1, \ldots, \binom{n}{r}$ denote the $r \times r$ principal minors of A. Then the characteristic polynomial of A is given by*

$$p_A(\lambda) = \lambda^n - Tr(A)\lambda^{n-1} + c_2\lambda^{n-2} + \cdots + c_{n-1}\lambda + (-1)^n \det(A) \tag{2.1}$$

where $c_r = (-1)^r \sum_{k=1}^{\binom{n}{r}} M_k^r$ *for all* $r = 2, \ldots, n-1$.

Definition 2.1.2. Let $A \in \mathcal{M}_n(\mathbb{R})$. If $\lambda_i \in \mathbb{C}$ is an eigenvalue of A, then the *algebraic multiplicity* $a_i := \text{alg}(\lambda_i)$ of λ_i is the largest integer such that $(\lambda - \lambda_i)^{a_i}$ divides the characteristic polynomial $p_A(\lambda)$.

Definition 2.1.3. Let $A \in \mathcal{M}_n(\mathbb{R})$, and let λ be an eigenvalue of A with associated linearly independent eigenvectors $\mathbf{x}_1, \ldots, \mathbf{x}_r$ $(r \leq n)$. Then the *eigenspace* E_λ associated with λ, is given by the subspace

$$E_\lambda := \text{span}\{\mathbf{x}_1, \ldots, \mathbf{x}_r\}.$$

Definition 2.1.4. Let $A \in \mathcal{M}_n(\mathbb{R})$. If $\lambda_i \in \mathbb{C}$ is an eigenvalue of A, define the *geometric multiplicity* $g_i := geo(\lambda_i)$ of λ_i to be the number of linearly independent eigenvectors associated with λ_i, i.e., $g_i = \dim(E_{\lambda_i})$.

Remark 2.1.1. Therefore, given an $n \times n$ matrix A with an eigenvalue λ, the

eigenspace of λ is nothing more than the span of the null space of $\lambda I - A$, i.e.,

$$E_\lambda := \text{span}(\text{null}(\lambda I - A)),$$

and hence $\text{geo}(\lambda) = \dim(\text{span}(\text{null}(\lambda I - A)))$.

Definition 2.1.5. Let A be an $n \times n$ matrix and let λ be an eigenvalue of A. If $\text{alg}_A(\lambda) = 1$, then λ is called a *simple eigenvalue* of A. If $\text{alg}_A(\lambda) = geo_A(\lambda)$ then λ is called *semisimple*.

Theorem 2.1.2. *Let $A \in \mathcal{M}_n(\mathbb{R})$. If λ_i is an eigenvalue of algebraic multiplicity a_i, then the geometric multiplicity g_i of λ_i satisfies*

$$1 \leq g_i = n - rank(\lambda_i I - A) \leq a_i.$$

Corollary 2.1.1. *Let $A \in \mathcal{M}_n(\mathbb{R})$. If λ_i is simple, then λ_i has a unique eigenvector up to a scalar.*

Proof: If λ_i is simple, then the theorem tells us that there are at most $1 \leq g_i \leq 1$ linearly independent eigenvectors, i.e., $g_i = 1$ and there is only one linearly independent eigenvector associated to λ_i. □

Definition 2.1.6. Let $A \in \mathcal{M}_n(\mathbb{R})$. The *spectral radius* $\rho(A)$, of A is defined as

$$\rho(A) := \max\{\ |\lambda|\ :\ \lambda \in \sigma(A)\ \}$$

Definition 2.1.7. Let $A \in \mathcal{M}_n(\mathbb{R})$. The *spectral circle* $S_{\rho(A)}(0)$, of A is defined as

$$S_{\rho(A)}(0) := \{\ \lambda \in \sigma(A)\ :\ |\lambda| = \rho(A)\}.$$

2.1.2 Positive Matrices

We first focus on a matrix $0 < A \in \mathcal{M}_n(\mathbb{R})$, and the so-called Perron Theorem about the spectral radius of a positive matrix A. The proof can be found in Appendix A.

The lemma below lists several useful properties when working with positive and nonnegative matrices.

Lemma 2.1.1. *Let $A \in \mathcal{M}_n(\mathbb{R})$, $\mathbf{x} \in \mathbb{R}^n$, and let $\rho(A)$ be the spectral radius of A. Then*

(a) $A > 0 \;\Leftrightarrow\; \frac{A}{\rho(A)} > 0$,

(b) $0 < \alpha \in \mathbb{R} \;\Rightarrow\; \rho(\alpha A) = \alpha\rho(A)$,

(c) $A > 0$, $\mathbf{x} \geq \mathbf{0}$, $\mathbf{x} \neq \mathbf{0} \;\Rightarrow\; A\mathbf{x} > \mathbf{0}$,

(d) $A \geq 0$, $\mathbf{u} \geq \mathbf{v} \geq \mathbf{0} \;\Rightarrow\; A\mathbf{u} \geq A\mathbf{v}$,

(e) $A \geq 0$, $\mathbf{x} > \mathbf{0}$, $A\mathbf{x} = \mathbf{0} \;\Rightarrow\; A = 0$,

(f) $A \geq 0$, $A \neq 0$, $\mathbf{x} > \mathbf{y} > \mathbf{0} \;\Rightarrow\; A\mathbf{x} > A\mathbf{y}$.

Proof: See R. Horn and C. Johnson; [52]. □

We can now state the so-called Perron Theorem about positive matrices.

Theorem 2.1.3 (Perron)**.** *Let $0 < A \in \mathcal{M}_n(\mathbb{R})$, and let $\rho(A)$ be the spectral radius of A. Then*

(a) $0 < \rho(A) \in \sigma(A)$,

(b) $\text{alg}(\rho(A)) = 1$,

(c) $\exists\,!\,\mathbf{p} > \mathbf{0}$ $A\mathbf{p} = \rho(A)\mathbf{p}$, *and* $\|\mathbf{p}\|_1 = 1$,

(d) *if* $\rho(A) \neq \mu \in \sigma(A)$*, then* $|\mu| < \rho(A)$*,*

(e) $\mathbf{x} \geq \mathbf{0}$ *an eigenvector of* A *implies* $\mathbf{x} = \alpha\mathbf{p}$*,* $\alpha > 0$*.*

Proof: We outline the proof here. For complete details see Appendix A.

(a) This is Lemma A.0.2, and Theorem A.0.3.

(b) This is Theorem A.0.5.

(c) From part (b) and Theorem A.0.3, we know that $\mathbf{0} < |\mathbf{x}|$ is an eigenvector of A associated to $\rho(A)$. Therefore, note that $\text{null}(\rho(A)I - A) = E_{\rho(A)}$ implies that $\dim(E_{\rho(A)}) = 1$ from part (b). Hence, there exists an eigenvector $\mathbf{x}$ of $\rho(A)$ such that $|\mathbf{x}| > \mathbf{0}$ and $E_{\rho(A)} = \text{span}\{|\mathbf{x}|\}$. Therefore, by normalizing $\mathbf{v} := |\mathbf{x}|$ with norm $\|\cdot\|_1$, we obtain $\mathbf{p} = \frac{\mathbf{v}}{\|\mathbf{v}\|_1}$ such that

$$\mathbf{p} \in E_{\rho(A)}, \qquad \mathbf{p} > \mathbf{0}, \qquad \text{and} \qquad \sum_{j=1}^{n} p_j = 1.$$

We call $\mathbf{p}$ the *Perron vector* of $A > 0$, and the associated eigenvalue $\rho(A)$ the *Perron root* of A. Moreover, $(\rho(A), \mathbf{p})$ is called the *Perron eigenpair* of A.

(d) This follows from Theorem A.0.4.

(e) This is Theorem Theorem A.0.6.

□

2.1.3 Nonnegative and Irreducible Matrices

Now consider the case where $A \in \mathcal{M}_n(\mathbb{R})$ has nonnegative entries, and see what happens to the conclusions of Perron's theorem. In order to do this lets look at some examples of 2×2 matrices with at least one zero entry.

Example 2.1.1. Consider the matrices $A = \begin{bmatrix} 0 & a \\ 0 & 0 \end{bmatrix}$, $B = \begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix}$, and $C = \begin{bmatrix} 1 & 0 \\ 0 & 2 \end{bmatrix}$. Then, for the matrix A

$$\det(\lambda I - A) = \begin{vmatrix} \lambda & -a \\ 0 & \lambda \end{vmatrix} = \lambda^2.$$

Thus, we see that $\lambda_1 = \lambda_2 = 0$ so $\text{alg}_A(0) = 2 > 1$ and $\rho(A) = \max\{|\lambda| \ : \ \lambda \in \sigma(A)\} = |0| = 0$. Also note that for $\lambda = 0$ we have the eigenvector $\mathbf{v} = (1, 0)^T$, which is not positive. Moreover, this gives

$$\text{null}(A - \rho(A)I) = \text{null}(A) = \text{span}\{(1, 0)^T\}.$$

Hence, there is no positive eigenvector in the eigenspace E_0 of $\rho(A) = 0$. Furthermore, note that

$$(A - \lambda I)^2 = \begin{bmatrix} \lambda^2 & -2a\lambda \\ 0 & \lambda^2 \end{bmatrix} \quad \text{and} \quad (A - \lambda I)^3 = \begin{bmatrix} -\lambda^3 & a\lambda^2(1 + 2a\lambda) \\ 0 & -\lambda^3 \end{bmatrix}.$$

Therefore, when $\lambda = 0$ we get $\text{null}((A - \lambda I)^2) = \text{null}((A - \lambda I)^3) = \mathbb{R}^2$. Thus, the index of $\lambda = 0$ is equal to $2 > 1$, i.e., $\text{index}(\rho(A)) \neq 1$ if and only if $\rho(A) = 0$ is not semisimple. Hence, matrix A, properties (a), (b), (c), and (d) all fail to hold.

Next, the characteristic polynomial of B is given by,

$$\det(\lambda I - A) = \begin{vmatrix} \lambda & -1 \\ -1 & \lambda \end{vmatrix} = \lambda^2 - 1 = (\lambda + 1)(\lambda - 1).$$

Hence, $\rho(B) = 1$. However, $-1 \in \sigma(B)$, but $|-1| = 1 = \rho(B)$, so that $\rho(B) = 1$ is not the only eigenvalue of B on the spectral circle. Therefore, property (d) fails for matrix B.

Finally, for C we obtain

$$\det(\lambda I - C) = \begin{vmatrix} \lambda - 1 & 1 \\ 1 & \lambda - 2 \end{vmatrix} = \lambda^2 - 1 = (\lambda - 1)(\lambda - 2).$$

However, the eigenvector corresponding to $\rho(C) = 2$ is $\mathbf{v}_\rho = (0, 1)^T = \mathbf{e}_2$ and to $\mu = 1$ is $\mathbf{v}_1 = (1, 0)^T = \mathbf{e}_1$. Therefore, there is an eigenvector $\mathbf{v}_1 \geq \mathbf{0}$ of C that is not a positive multiple of $\mathbf{v}_\rho$. Hence, property (e) fails for C.

This example shows that relaxing the condition of $A > 0$ to $A \geq 0$ implies that most of the results from Perron's theorem fail to hold in general. The next result highlights the properties that remain true for nonnegative matrices. Essentially it states that the spectral radius is an eigenvalue but can now be zero, and has an associated nonnegative eigenvector.

Theorem 2.1.4. *Let $0 \leq A \in \mathcal{M}_n(\mathbb{R})$, and $r := \rho(A)$ be the spectral radius of A. Then*

(a) $0 \leq \rho(A) \in \sigma(A)$, (b) $\exists\, \mathbf{x} \geq \mathbf{0} \;:\; A\mathbf{x} = \rho(A)\mathbf{x}$.

Proof: Consider the sequence $\{A_k\}_{k=1}^{\infty}$ defined by $A_k := A + \frac{1}{k}E$, where $E = [e_{ij}]$ is the $n \times n$ matrix with all entries equal to 1, i.e., $e_{ij} = 1$ for

all i, j. Then $A_k > 0$ for all $k \geq 1$, and we can let $r_k > 0$ and $\mathbf{p}_k > \mathbf{0}$ be the associated Perron root and eigenvector of A_k respectively. Note that $\{\mathbf{p}_k\}_{k=1}^{\infty}$ is bounded, since $\|\mathbf{p}_k\|_1 = 1 < \infty$ for all $k \geq 1$. Therefore, from the Bolzano-Weierstrass Theorem in $\mathbb{R}^n$, the sequence $\{\mathbf{p}_k\}_{k=1}^{\infty}$ has a convergent subsequence, say $\{\mathbf{p}_{k_i}\}_{i=1}^{\infty}$ converging to $\mathbf{z} \geq \mathbf{0}$ and $\mathbf{z} \neq \mathbf{0}$.

Now, since $A_1 > A_2 > \cdots > A$ we have that $r_1 \geq r_2 \geq \cdots \geq r$. Hence, $\{r_k\}_{k=1}^{\infty}$ is monotonically decreasing and bounded below by r. Therefore, the Monotone Convergence Theorem implies that there is an $0 \leq r_0 \in \mathbb{R}$ such that $\lim_{k\to\infty} r_k = r_0$. In particular, we note that $\lim_{i\to\infty} r_{k_i} = r_0 \geq r$.

On the other hand, $\lim_{i\to\infty} A_{k_i} = A$, and so we obtain

$$A\mathbf{z} = \lim_{i\to\infty} A_{k_i}\mathbf{p}_{k_i} = \lim_{i\to\infty} r_{k_i}\mathbf{p}_{k_i} = \lim_{i\to\infty} r_{k_i} \cdot \lim_{i\to\infty} \mathbf{p}_{k_i} = r_0\mathbf{z}.$$

Thus, $r_0 \in \sigma(A)$ and so $r_0 \leq r$. Hence, $0 \leq r_0 = r$, $\mathbf{z} \geq \mathbf{0}$ and $A\mathbf{z} = r\mathbf{z}$. □

This will be as far as the properties of positive matrices can be extend to nonnegative matrices without the introduction of some additional assumptions on a matrix A. To find an appropriate condition that will guarantee the same results of Perron's theorem, Fröbenius noticed that it was not simply the fact the A had zero entries that made the conditions fail, but rather the position of the zeros in A. Therefore, the set of all $n \times n$ nonnegative matrices is divided into two subsets via the following definition.

Definition 2.1.8. Let $A \in \mathcal{M}_n(\mathbb{R})$ be nonnegative. Then A is called *reducible*,

if there is a symmetric permutation matrix P (i.e., $P^{-1} = P^T$) such that

$$P^T A P = \begin{bmatrix} X & Y \\ 0 & Z \end{bmatrix},$$

where X and Z are both square submatrices. Otherwise, A is called *irreducible*.

Remark 2.1.2. The property of a nonnegative matrix $A \in \mathcal{M}_n(\mathbb{R})$ being irreducible will be of interest to us here and there are two equivalent definitions for an irreducible nonnegative matrix. They are stated in the theorem below.

Theorem 2.1.5. *Let $A \in \mathcal{M}_n(\mathbb{R})$. Then the following are equivalent.*

(1) *A is irreducible;*

(2) *$A\mathbf{x} \geq 0$, for any nonnegative vector $\mathbf{x} \in \mathbb{R}^n$;*

(3) *for any two indices i and j, there is an integer $s \geq 0$ and a sequence of integers $k_1, \ldots, k_s$ such that the product $a_{ik_1} a_{k_1 k_2} \cdots a_{k_s j}$ is nonzero.*

Proof: See Carl D. Meyer [74]. □

The next result is know as the Perron-Fröbenius Theorem, and it is the extension of Perron's Theorem to the set of irreducible nonnegative square matrices.

Theorem 2.1.6 (Perron-Fröbenius)**.** *Let $A \in \mathcal{M}_n(\mathbb{R})$ be a nonnegative, irreducible matrix, and let $\rho(A)$ be the spectral radius of A. Then we have the following:*

(a) $0 < \rho(A) \in \sigma(A)$,

(b) $\text{alg}(\rho(A)) = 1$,

(c) $\exists\,!\,\mathbf{p} > \mathbf{0}$ $A\mathbf{p} = \rho(A)\mathbf{p}$, *and* $\|\mathbf{p}\|_1 = 1$,

(d) *if* $\mu \in \sigma(A)$, *then* $|\mu| \leq \rho(A)$,

(e) $\mathbf{x} \geq \mathbf{0}$ *an eigenvector of* A *implies* $\mathbf{x} = \alpha\mathbf{p}$, $\alpha > 0$.

Proof: For part (a), we see that $\rho(A) > 0$ or else $A\mathbf{x} = \mathbf{0}$, which is impossible if $A \geq 0$ and $\mathbf{x} > \mathbf{0}$. Part (b) follows from Perron's Theorem. For (c), let $B = (I + A)^{n-1} > 0$. Then $\lambda \in \sigma(A) \Leftrightarrow (1 + \lambda)^{n-1} \in \sigma(B)$, and $\text{alg}(\lambda) = \text{alg}((1 + \lambda)^{n-1})$. Therefore, letting $s = \rho(B)$,

$$s = \max_{\lambda \in \sigma(A)} \{|(1 + \lambda)|^{n-1}\} = \max_{\lambda \in \sigma(A)} \{|1 + \lambda|\}^{n-1} = (1 + r)^{n-1}.$$

Now, if the disk $|z| \leq s$ is translated to the right by 1, then $|z + 1| \leq s$ has a maximum modulus of $1 + s$, i.e., $|z + 1| \leq 1 + s$. Thus, if $\text{alg}_A(r) = k > 1$, then $\text{alg}_B(s) > 1$, which is a contradiction as $B > 0$. Therefore, $\text{alg}(r) = 1$. Parts (d) and (e) are proved the same way as in Perron's Theorem (see Appendix A for details).

□

Remark 2.1.3. The Perron-Fröbenius Theorem says that for an irreducible nonnegative matrix A, up to a positive scalar, there exists a unique eigenvector associated to the spectral radius of A. The unique eigenvector $\mathbf{p} > \mathbf{0}$ associated to $\rho(A)$ with $\|\mathbf{p}\|_1 = 1$ is often called the *Perron eigenvector* of A. Throughout this thesis, I will refer to any positive eigenvector associated to $\rho(A)$ a Perron eigenvector of A. This is because multiplying an eigenvector by a positive scalar will not change the which entry is the largest.

Remark 2.1.4. Note that there is one remaining property that nonnegative irreducible matrices do not share with positive matrices. Namely, property

(d), stating that $\rho(A)$ is the unique eigenvalue with modulus on the spectral circle of A. Indeed, the matrix given by

$$B = \begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix},$$

is nonnegative and irreducible. However, Example 2.1.1 shows that $\sigma(B) = \{-1, 1\}$, and so $\lambda = -1$ is such that $|-1| = 1 = \rho(B)$.

Therefore, the notion of an irreducible nonnegative matrix A having exactly one eigenvalue on the spectral circle of A, splits these matrices into two new classes of matrices.

Definition 2.1.9. Let $A \geq 0$ be irreducible. Then A is called *primitive* if A has exactly one eigenvalue, $\rho(A)$ on the spectral circle of A. Otherwise, A is called *imprimitive*, and the number $i > 1$ of eigenvalues on the spectral circle is called the *index of imprimitivity*.

Remark 2.1.5. The notion of primitive matrices is important when using the power method (see the subsection below) for computing the Perron eigenvector $\mathbf{p}$ of a matrix A. This is due to the fact that starting with an arbitrary vector in $\mathbb{R}^n$, if there is at least one eigenvalue $\lambda \neq \rho(A)$ on the spectral circle, then the power method described below may converge to eigenvectors in E_λ instead of to the Perron eigenvector $\mathbf{p}$.

If a matrix A is imprimitive, then a primitive matrix B can be constructed from A by adding a matrix E to A, where E is a scalar multiple of the identity matrix, i.e., the matrix

$$B := A + \varepsilon I,$$

where $\varepsilon > 0$ can be made arbitrarily small.

2.1.4 The Power Method Algorithm

This subsection outlines a method for finding the Perron eigenvector $\mathbf{p}$ and associated Perron eigenvalue $\rho(A)$, of a nonnegative and irreducible real matrix A. This will give a practical method of finding the Perron eigenvector of a large matrix A using computers. In what follows, " $\bullet$ " stands for the usual dot product of two vectors in $\mathbb{R}^n$, and $\|\cdot\|_2$ represents the standard Euclidean norm on $\mathbb{R}^n$.

The first theorem below will allow for an iterative method for the computation of the dominant Perron eigenvector of a matrix A.

Theorem 2.1.7. *Let $A \in \mathcal{M}_n(\mathbb{R})$ and $\lambda_1, \ldots, \lambda_m$ be the $m \leq n$ distinct eigenvalues of A with corresponding eigenvectors $\mathbf{x}_1, \ldots, \mathbf{x}_m$ such that $\|\mathbf{x}_1\|_2 = 1$. Let λ_1 be the dominant eigenvalue of A, and assume that $|\lambda_1| > |\lambda_2| \geq \cdots \geq |\lambda_m|$. Let $\mathbf{x}_0 \in \operatorname{span}\{\mathbf{x}_1, \ldots, \mathbf{x}_m\}$ be such that $\mathbf{x}_0 = c_1\mathbf{x}_1 + \cdots + c_m\mathbf{x}_m$, with $c_1 \neq 0$. Then the sequence $\{x_k\}_{k=1}^{\infty}$ given by $x_k = \frac{A^k\mathbf{x}_0}{\|A^k\mathbf{x}_0\|_2}$ converges to $\mathbf{x}_1$.*

Proof: Let $\mathbf{x}_0 \in \operatorname{span}\{\mathbf{x}_1, \ldots, \mathbf{x}_m\}$ be such that $\mathbf{x}_0 = c_1\mathbf{x}_1 + \cdots + c_m\mathbf{x}_m$, with $c_1 \neq 0$. Then

$$A^k\mathbf{x}_0 = A^k \sum_{j=1}^{m} c_j\mathbf{x}_j = \sum_{j=1}^{m} c_j A^k\mathbf{x}_j = \sum_{j=1}^{m} c_j\lambda^k\mathbf{x}_j = c_1\lambda_1^k\left(\mathbf{x}_1 + \sum_{j=2}^{m}\frac{c_j}{c_1}\left(\frac{\lambda_j}{\lambda_1}\right)^k\mathbf{x}_j\right).$$

Now, for all $j = 2, \ldots, m$ we have that $\left|\frac{\lambda_j}{\lambda_1}\right| < 1$ (λ_1 is dominant). Thus, for all $j = 2, \ldots, m$

$$\lim_{k\to\infty}\frac{c_j}{c_1}\left(\frac{\lambda_j}{\lambda_1}\right)^k\mathbf{x}_j = \frac{c_j}{c_1}\mathbf{x}_j\lim_{k\to\infty}\left(\frac{\lambda_j}{\lambda_1}\right)^k = \frac{c_j}{c_1}\mathbf{x}_j\cdot 0 = \mathbf{0}.$$

Therefore, we obtain

$$\lim_{k\to\infty} A^k\mathbf{x}_0 = \lim_{k\to\infty} c_1\lambda_1^k\left(\mathbf{x}_1 + \sum_{j=2}^{m}\frac{c_j}{c_1}\left(\frac{\lambda_j}{\lambda_1}\right)^k\mathbf{x}_j\right) = \lim_{k\to\infty} c_1\lambda_1^k\mathbf{x}_1.$$

Hence, as $\|A^k\mathbf{x}_0\|_2 \geq c_1\lambda_1^k$, we have that $\frac{A^k\mathbf{x}_0}{\|A^k\mathbf{x}_0\|_2} \leq \frac{A^k\mathbf{x}_0}{c_1\lambda_1^k} \to \mathbf{x}_1$ as $k \to \infty$. □

Remark 2.1.6. The sequence $\left\{\frac{A^k\mathbf{x}_0}{\|A^k\mathbf{x}_0\|_2}\right\}_{k=1}^{\infty}$ converges to $\mathbf{x}_1$ geometrically, with geometric ratio given by $|\frac{\lambda_2}{\lambda_1}|$. Thus, if the modulus of the next largest eigenvalue is close to that of the dominant eigenvalue, this convergence is slow.

Theorem 2.1.8 (Rayleigh)**.** *Let $A \in \mathcal{M}_n(\mathbb{R})$, $\mathbf{x}$ be an eigenvector of A, and let $\mathbf{x}^*$ is the conjugate transpose of $\mathbf{x}$. Then the eigenvalue λ associated to $\mathbf{x}$ is given by*

$$\lambda = \frac{\mathbf{x}^* \bullet A\mathbf{x}}{\mathbf{x}^* \bullet \mathbf{x}}.$$

Proof: Let $\mathbf{x}$ be an eigenvector of A. Then there exists a $\lambda \in \mathbb{C}$ such that $A\mathbf{x} = \lambda\mathbf{x}$. Thus,

$$\frac{\mathbf{x}^* \bullet A\mathbf{x}}{\mathbf{x}^* \bullet \mathbf{x}} = \frac{\mathbf{x}^* \bullet \lambda\mathbf{x}}{\mathbf{x}^* \bullet \mathbf{x}} = \lambda \bullet \frac{\mathbf{x}^* \bullet \mathbf{x}}{\mathbf{x}^* \bullet \mathbf{x}} = \lambda \bullet 1 = \lambda.$$

□

Remark 2.1.7. Rayleigh's theorem tells us that since the Perron eigenvalue $\rho(A)$ of a nonnegative irreducible matrix A is a positive real number, we have that $\mathbf{p}^* = \mathbf{p}^T$, and hence

$$\rho(A) = \frac{\mathbf{p}^T \bullet A\mathbf{p}}{\mathbf{p}^T \bullet \mathbf{p}}.$$

Therefore, if we can find the Perron eigenvector $\mathbf{p}$, then we can also obtain $\rho(A)$ from $\mathbf{p}$ and A.

These two results above give a method for finding the dominant eigenvector and eigenvalue of a nonnegative irreducible matrix A.

The Power Method Algorithm. Let $0 \leq A \in \mathcal{M}_n(\mathbb{R})$ be irreducible and let $\mathbf{x}_0$ be a random vector. Choose an accuracy tolerance, say ε, and a maximum number of iterations N. Then to compute the Perron eigenvector of A to within an accuracy of ε use the following set of commands.

set $k = 1$;

while $k \leq N$;

set $\mathbf{y}_k = A\mathbf{x}_{k-1}$;

set $n_k = \|\mathbf{y}_k\|_2$;

set $\mathbf{x}_k = \mathbf{y}_k / n_k$

if $|n_k - n_{k-1}| \leq \varepsilon$, then $k = N + 1$; else, set $k = k + 1$;

end.

Display the Perron eigenvector $\mathbf{p} \approx \mathbf{x}_k$ and the associated Perron eigenvalue $\lambda = \rho(A) \approx \frac{\mathbf{x}_k^T \bullet A\mathbf{x}_k}{\mathbf{x}_k^T \bullet \mathbf{x}_k}$.

Remark 2.1.8. This method will fail to produce the dominant eigenvector $\mathbf{p}$ of A if the initial guess $\mathbf{x}_0$ does not contain any components of the dominant eigenvector $\mathbf{p}$. Instead, the power method will converge to the largest eigenvector contained in the decomposition of $\mathbf{x}_0$. Now if there are two eigenvalues with the same modulus and their eigenvectors are in the decomposition of $\mathbf{x}_0$, then the method need not converge.

To help avoid this rare possibility, the entries of the starting vector $\mathbf{x}_0$ can

be randomly chosen. Then run the method for several different random initial vectors to guarantee convergence to the largest eigenvalue and eigenvector of the given matrix A using a comparison of the results.

2.2 Graph theory and networks

This section states the basic graph theoretical results needed throughout the thesis. For a more detailed discussion on these topics please see, for instance [40], [110], and [111].

2.2.1 Basic Definitions

The mathematical description of a network is defined via weighted digraphs $\mathcal{G}$. A nonnegative matrix B is then associated to a given digraph, thus allowing for the connection between the mathematical analysis of the matrix B and the structure of the digraph $\mathcal{G}$.

A network is described by defining individual members or items of a given real world model and then, how they interact, gives rise to the connections between members. The connections of a network are weighted if each directed edge from node i to node j is assigned a positive weight, which can represent the strength of interaction or influence between individuals of the network. For instance, in epidemiology the nodes of a network can be viewed as different groups of people in a given population (age, gender, social, religious, etc), and the edges represent which groups have cross-infection, while the weights of the edges become the transmission rates from group to group. Similarly, in a single species migration model, the nodes represent patches of habitation, the directed edges are the migration routes or movement between patches and the

weights of the edges become the dispersal rates between the patches. Below is the mathematical definition of a digraph.

Definition 2.2.1. A *directed graph* $\mathcal{G} = (V, E)$ is an ordered pair consisting of a set of nodes $V = \{1, \ldots, n\}$ and a set of directed edges $E \subseteq \{(i, j) \mid i, j \in V\}$. We call a digraph $\mathcal{G}$ *weighted*, if each directed edge from node i to node j, denoted by (i, j), is assigned a positive real number $\omega(i, j) \in \mathbb{R}_+$.

Definition 2.2.2. Let $\mathcal{G} = (V, E)$ be a digraph. Then a *directed path* $\mathcal{P}$ in $\mathcal{G}$ is a subgraph consisting of distinct vertices and edges $\{(i_k, i_{k+1}) \mid k = 1, \ldots, m-1\}$. We may also call this the *directed path from node* i_1 *to node* i_m. Moreover, if we allow for $i_m = i_1$, then $\mathcal{P}$ is called a *directed cycle*. The *length* of a directed path $\mathcal{P}$ is the number of directed edges in $\mathcal{P}$.

Definition 2.2.3. Let $\mathcal{G} = (V, E)$ be a digraph. Then a *geodesic* $d(i, j)$ from node i to node j is a directed path of minimal length. If there is no directed path from i to j then we set $d(i, j) := \infty$.

The next definition associates an $n \times n$ matrix to a given digraph $\mathcal{G}$.

Definition 2.2.4. The *weight matrix* B of a digraph $\mathcal{G} = (V, E)$ is the $n \times n$ matrix with ij^{th} entry equal to $b_{ij} = \omega(j, i)$ if edge $(j, i) \in E$, and zero otherwise.

The weight matrix B is also called the dispersal matrix of the network G. It is often useful to represent a network as the ordered pair $(\mathcal{G}, B)$, where $\mathcal{G}$ is the digraph and B is the weighted dispersal matrix associated to $\mathcal{G}$.

2.2.2 Strongly Connected Digraphs and Irreducibility

The connection between the connectedness of a digraph $\mathcal{G}$ and the irreducibility of its associated nonnegative weight matrix B is given below.

Definition 2.2.5. A digraph $(\mathcal{G}, B)$ is called *strongly connected* if for every pair of vertices $i \neq j$, there is a directed path from node i to node j and vice versa.

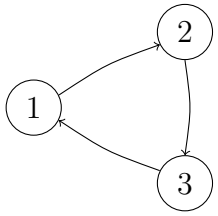
The next result is well-known in literature and the proof can be found in [77]. It relates the connectedness of a graph $\mathcal{G}$ to the irreducibility of its associated nonnegative weight matrix B.

Theorem 2.2.1. *Let $\mathcal{G}$ be a digraph, and let $B \in \mathcal{M}_n(\mathbb{R})$ be its associated weight matrix. Then B is irreducible if and only if $\mathcal{G}$ is strongly connected.*

Therefore, to ensure the irreducibility of the weight matrix B of a digraph $\mathcal{G}$, it suffices to ensure that $\mathcal{G}$ is strongly connected. The following two basic examples help to illustrate the result of Theorem 2.2.1.

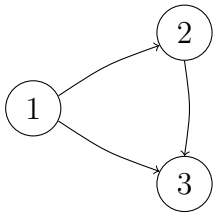
Example 2.2.1. A strongly connected digraph $\mathcal{G}$ and its irreducible weight matrix B.

$$B = \begin{bmatrix} 0 & 0 & b_{13} \\ b_{21} & 0 & 0 \\ 0 & b_{32} & 0 \end{bmatrix}$$



Example 2.2.2. A digraph $\mathcal{G}$ that is not strongly connected and its associated reducible weight matrix B.

$$B = \begin{bmatrix} 0 & 0 & 0 \\ b_{21} & 0 & 0 \\ b_{31} & b_{32} & 0 \end{bmatrix}$$



Remark 2.2.1. The Perron Theorem and Perron-Fröbenius Theorem tell us that if $\mathcal{G}$ is a network with weight matrix $B \geq 0$, then

- The spectral radius $\rho(B)$ is an eigenvalue of B with a nonnegative eigenvector $\mathbf{p} = (p_1, \ldots, p_n)^T$.
- If $\mathcal{G}$ is strongly connected and hence B is irreducible, then $\rho(B)$ is simple and $\mathbf{p} > \mathbf{0}$.
- $\mathbf{p}$ is the only positive eigenvector up to a scalar multiple.

Therefore, considering a strongly connected network $(\mathcal{G}, B)$, the positive entries of $\mathbf{p} = (p_1, \ldots, p_n)^T$ can be used to rate the nodes of the network by associating p_i to node i for all $i = 1, \ldots, n$. This is the basic idea behind eigenvector centrality ranking of a network (see the section below).

One other matrix that may arise in the study of a network $(\mathcal{G}, B)$ is the Laplacian matrix L_B of a weight matrix B. The definition is given below for completeness.

Definition 2.2.6. Let $(\mathcal{G}, B)$ be a directed network. The *Laplacian matrix* of the network is given by

$$L_B = \text{diag}(\sum_{j \neq 1} b_{1j}, \ldots, \sum_{j \neq 1} b_{nj}) - B.$$

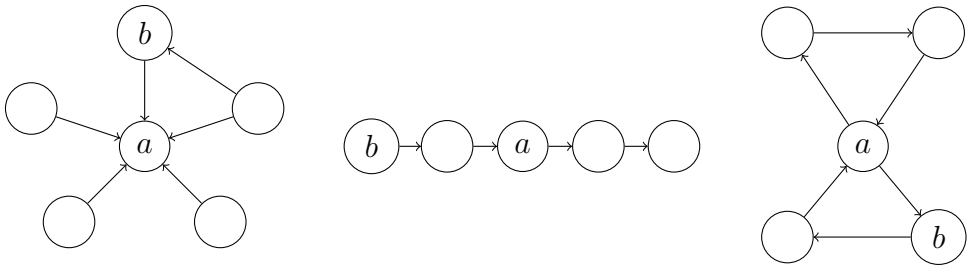
2.2.3 Graph structure and metrics for ranking

Next, consider the structure of a given network. Many real world network models have quantitative features in common and the study of the structure of these networks is ever present in more recent mathematical research papers. This is primarily due to the fact that the structure of a given network always affects how it functions. For example, such network structures include transitivity or clustering, degree distribution and maximum degree, network

resilience, average path length, centrality and centralization. These are often referred to as *graph metrics*.

Recently, many research papers have been devoted to using centrality metrics to answer the so-called *ranking problem*, i.e., who is the most important or highest ranked individual of a network, relative to the other members (See [1], [11], [12], [13], [14], [58], [63], [82], [95], [101], and [109]). Moreover, centralization of a network can be used to describe how much variation there is between the centrality scores of the nodes in a network. There are many ways to rate and/or rank the items of a network in terms of importance or centrality. Consequently, there are several different types of centrality including degree centrality, closeness, stress and betweenness centrality based on the notion of shortest paths, and eigenvector centrality.

This is due to the fact that the definition of most *central* or important individual can vary depending on the context of what the model is describing. For example, local centrality can be described using degree (in or out degree) centrality, whereas centrality based on the entire network structure uses notions like closeness, betweenness and eigenvector centrality. Given in Figure 2.1 below is an example of three different types of centrality metrics. In each of the networks, node a has a higher centrality score than b according to the indicated centrality metric.



Indegree Closeness Betweenness

Figure 2.1: Different Centrality Metrics.

Described below are some of the frequently used centrality metrics in more detail below. Note that these metrics can be defined for both undirected and directed graphs, but we focus on the case of directed networks. For more details on centrality metrics see [9], [10], [80], and [95]. In each case the idea of centrality ranking is to give each node i of a network $(\mathcal{G}, B)$ a *centrality score* of some kind, and then to use these values to rank the nodes from most to least important relative the the structure of the network.

A: Degree Centrality.

Given a network $(\mathcal{G}, B)$ consisting of n nodes, the indegree centrality of node i is a measure of how many directed edges leading from other nodes $j \neq i$ to node i. Similarly, the outdegree centrality of node i is the number of directed edges from i leading into $j \neq i$. Moreover, we can normalize these degree centralities by dividing by $n - 1$, i.e., the total number of possible directed edges to or from node i.

The number of connections that a node i has is a good measure of centrality when considering networks that describe friendship or business relationships, article or paper citations or those describing nominations or elections where people vote for n individuals.

However, degree centrality may be an insufficient measure of centrality when considering the ability for information, a given species or an infectious disease to reach node i, regardless of where it originates from. Degree centrality can also be inadequate if local connections are not as important as knowing which nodes are connected by a directed path, and given a fixed node i, which

paths from node $j \neq k$ contain i.

B: Closeness Centrality.

Now consider a measure of centrality based not only on direct connections, but also indirect connections among the network vertices. Closeness centrality of a node i is based on an average of the shortest paths between i and all other nodes $j \neq i$ of the network.

Also note that if the graph $\mathcal{G}$ is not strongly connected, only reachable nodes are taken into consideration, and then the result is weighted with the number of reachable nodes. Thus, this indegree closeness centrality tells us how close the selected node i is to all other nodes of the network.

The outdegree closeness centrality is defined in a similar manner and measures how close all other nodes of the network are to node i.

C: Betweenness Centrality.

In other network models, we may be interested not just in how close a node is to others, but rather how many pairs of nodes j, k have a geodesic path that contain a given node i. In other words, the betweenness centrality of node i is equal to the number of pairs of individuals $j \neq k$ that would have to go through i in order to reach or contact one other.

D: Eigenvector Centrality.

Eigenvector centrality is one of the more beneficial quantitative measures of centrality because it is based on the graph structure as well as the weights of the connections between individuals.

Indeed, consider a network $(\mathcal{G}, B)$ where B is the associated nonnegative weight matrix. Then from Theorem 2.1.4, B has a unique (up to a positive scalar multiple) nonnegative *Perron* eigenvector $\mathbf{p} = (p_1, \ldots, p_n)^T$ associated to the largest real eigenvalue of B, which is equal to the spectral radius $\rho(B)$ of B. Moreover, if the digraph $\mathcal{G}$ is strongly connected, and hence B is irreducible, then $\mathbf{p}$ is strictly positive and the entries of this Perron vector $\mathbf{p}$ can be used to associate the value $p_i > 0$ to each node i of the network. This then gives a numerical rating to the n nodes of the network based on the weighted connections. Then, using this Perron vector rating, the nodes of the network can be ranked from first to least important. This is known in literature as the so-called *eigenvector centrality* ranking of a given network. In Chapter 3 we make a connection between equilibrium ranking and eigenvector centrality ranking. Therefore, the concept of eigenvector centrality is made precise with the following definition.

Definition 2.2.7. Let $(\mathcal{G}, B)$ be a network consisting of n nodes and having associated weight matrix $B \geq 0$. The *eigenvector centrality* of node $k \in V = \{1, \cdots, n\}$ is defined as $p_k \geq 0$, where $\mathbf{p} = (p_1, \ldots, p_n)^T$ is the Perron eigenvector of B.

The idea of eigenvector centrality ranking has been used to rank football (and other sports) teams within a given league. For a detailed discussion of the ranking of sports teams see [56]. Social groups of all kinds can also be ranked using eigenvector centrality giving a quantitative method of who is the most central member of a social network that is based not only on how individuals interact within the network but also on strength of these interactions.

Recently, many research articles have been written on the subject of information retrieval on the internet and the search algorithms used for these

purposes. Some of the more notable search engines are HITS, SALSA, and Google's PageRank (see [15], [16], [28], [61]-[64] for more details). These search algorithms use a version of eigenvector centrality to rank the relative importance of the pages of the internet to return the most relevent pages given a users query into a given topic.

2.3 Literature review

There are many areas of research that benefit from the use of network modelling. For example, M. Golubitsky, *et. al.*, (see [29] - [36]), study *coupled cell* networks, and the stability of equilibria in such models. This section gives a demographic of the fields of research using network models and the main idea behind using network structure to rank individual members. Some of the more common fields can be divided into four main categories, namely biological networks, knowledge or information networks, technological or engineering networks, and social networks. For a more detailed survey of networks in the sciences and a more in-depth discussion of the different graph types used to describe networks and different graph metrics see, for instance [26], [27], [47], [48], [82], [85], [86], [87], [90], and [101].

2.3.1 Examples of networks

Consider the four main types of networks in more detail.

A. Biological Networks.

Many different biological processes can be modelled using networks. One of the first large scale biological network studies considered gene expression.

In particular, a genome itself forms a network with vertices representing the proteins and directed edges representing dependence of protein production on the proteins at other vertices. Another biological process modelled with a network is the spread of an infections disease through a host population ([39], [49], [50], [55], [66], [67], [68], [106]). Here, the population groups or spatial regions become the vertices and transmission of the disease between groups or regions become the directed edges. Ecological food webs and migration patterns of a species over several spatial habitats are also modelled using networks ([41], [66], [103], [104], [105]). In this context, problems such as overpopulation and extinction can be addressed. In the study of the interaction of neurons and the structure of neural pathways in the brain ([51]) individual neurons become the nodes and edge (i, j) exists in the network if neuron i is connected to neuron j. Extensive research has also been done on blood vessel interactions and vascular networks of the human body, and a cells metabolic processes.

B. Information Networks.

The two main types of information networks are citation networks between academic research papers and information retrieval on the world wide web or internet. The more classical of the two is citation networks which date back to the 1920's. Citation networks are formed by individual research papers citing related articles, so that the vertices are articles and a directed edge from article i to article j indicates that i cites j. The added benefit to studying citation networks is the large quantitative data bases accumulated over the past several decades (see, for instance [93], [94], and [97]). The other important type of information network is the World Wide Web or internet. Here the pages on the internet represent nodes, and the hyperlinks between web pages become

the directed edges. Unlike citation networks, the World Wide Web is cyclic in nature since there is no specific ordering of sites and no constraints that would prevent closed loops in the graph. Hence, the structure of the internet is much more complex than that of a citation network.

C. Technological Networks.

Technological networks are usually man-made and are designed to distribute resources or commodities of some kind. Electricity networks have been studied extensively ([102], and [109]). For example the structure of power grids used for the distribution of high-voltage electricity throughout a city or country. Another popular example of a distribution network are postal services such as Canada Post, Fedex, and UPS. Airline, railway, bus and public transportation routes are also well studied examples of technological networks. Infrastructure networks such as sewer or cable systems are studied by municipalities and government bodies. Taking into consideration geography, the study of village and town accessibility has been studied based on the network of roads between them, [100]. Finally, an example of naturally occurring distribution networks are those of river and lake systems. These types of networks have been used extensively throughout history to transport commodities of all kinds, and many important civilizations have thrived based on their location along such routes.

D. Social Networks.

A social network, roughly speaking, is a group or population of people that have some kind of interaction or contact pattern between them. Social networks including business relationships, friendship networks, family trees,

intermarriage relationships and patterns of sexual contact have been studied extensively. Other interesting social networks considered by researchers are those studying the so-called small world problem and the famous notion of six degrees of separation, coauthorship networks amount academics, the interaction and ranking of sports teams ([56]), and in archaeology, networks are used to determine the relationship between artifacts found in different layers in the ground. Furthermore, social science is one of the longest studied academic disciplines (see [7], [8], [53], [75], [76], [79], [80]-[84]).

Chapter 3

Equilibrium Ranking

This chapter introduces the notion of equilibrium ranking for a nonlinear ODE modelled on a network. The first section is used to give the setting for our problem and motivation for its use. The idea of equilibrium ranking is then applied to different epidemiological models on networks in section 2 and 3. Section 2 considers an SIR model with n groups, and Section 3 looks at an SIR model on a patchy network. Section 4 considers the implications of equilibrium ranking on disease control methods. For further details about epidemiological models see for instance [2], [39], [49], [50], [55], [67], [68], [106], [107], and [108].

3.1 Introduction to equilibrium ranking

Consider a system of coupled ODE model on a network $(\mathcal{G}, B)$ consisting of n nodes given by equations of the form

$$\dot{x}_i = f_i(x_i) + \sum_{j=1}^{n} b_{ij} g_{ij}(x_i, x_j), \qquad i = 1, \ldots, n, \quad (3.1)$$

where $f_i(x_i)$ describes the local dynamics at each node i, $B = (b_{ij})_{n\times n}$ is the weight matrix of the network, and g_{ij} describes the influence among the nodes. These quantities x_i represent useful information about a system. For instance x_i can represent the number of infected individuals at node i in epidemiology models to population density of a species in ecological models with spatial dispersal.

Therefore, at a steady state $\mathbf{x}^* = (x_1^*, \ldots, x_n^*)^T$ of system (3.1) knowing the individual equilibrium values x_i^* gives insight into which node has the largest (or smallest) quantity of the network. For an epidemiology model, the largest x_i^* can represent the node with the highest disease prevalence, while for an ecological models, x_i^* can be interpreted as species density at patch i. Hence, we make the following assumption:

A1: System (3.1) has a unique positive equilibrium that is globally asymptotically stable in its associated feasible region.

Many papers have already been published stating that such unique equilibria exist. For example, see [39], [66], and [67]. The following definition gives a quantitative method of answering the question of how to rank which node of an ODE network has the most relative importance. Moreover, this ranking method is based on both the structure of the network, and the local ODE dynamics.

Definition 3.1.1. A positive equilibrium $\mathbf{x}^* = (x_1^*, \ldots, x_n^*)^T$ of system (3.1) will be called an *equilibrium ranking vector* of the system. The entries x_i^* rate the relative importance of nodes. The nodes are then ranked according to the rating. A ranking of an ODE system obtained in this way will be called an

equilibrium ranking for the network.

Thus, the equilibrium ranking vector $\mathbf{x}^*$ can be used to determine the relative importance of the nodes of a given ODE network by associating the positive value x_i^* to node i. Unlike a graph metric such as eigenvector centrality, which uses graph structure alone to determine relative importance, the equilibrium ranking considers the importance of a node with respect to both the network structure and the dynamic process that is defined on the network.

The next two sections consider specific ODE models on networks to investigate how equilibrium ranking compares to other rankings of networks.

3.2 Equilibrium ranking for an epidemiology model on a network

Consider the Kermack-McKendrick epidemiological model of a disease spreading through a multi-group network with nonlinear ODE dynamics given by

$$\begin{cases} S_k' = b_k N_k - \displaystyle\sum_{j=1}^{n} \beta_{kj} \frac{S_k I_j}{N_j} - d_k S_k \\ I_k' = \displaystyle\sum_{j=1}^{n} \beta_{kj} \frac{S_k I_j}{N_j} - (\gamma_k + d_k) I_k \qquad\qquad k = 1, \ldots, n, \\ R_k' = \gamma_k I_k - d_k R_k \end{cases} \tag{3.2}$$

with S_k, I_k, and R_k representing the number of susceptible, infectious, and

recovered individuals of the k-th group of the population respectively, and $N_k = S_k + I_k + R_k$ is the total population of the k-th group. The parameter $b_k > 0$ is the proportion of new individuals in the k-th group, $\gamma_k > 0$ is the recovery rate of infectious individuals in group k, and d_k is the death rate of group k. $B = (\beta_{kj})_{n\times n}$ is the networks nonnegative and irreducible weight or *transmission* matrix (for details see [66]).

For an epidemiological model of this form researchers are interested in which node or group has the highest disease prevalence, i.e., the highest number of infected individuals per capita. Hence, the relative importance of individual nodes for these ODE networks is phrased in terms of disease prevalence.

First, divide each of the populations S_k, I_k, and R_k, by the total population N_k to give a system modelling the fractions of the population that are infected. Note that the rate of change of the total population N_k is equal to $(b_k - d_k)N_k$. Indeed,

$$\begin{aligned} N_k'(t) &= \frac{d}{dt}(S_k(t) + I_k(t) + R_k(t)) = S_k'(t) + I_k'(t) + R_k'(t) \\ &= \left(b_k N_k - \sum_{j=1}^{n} \beta_{kj}\frac{S_k I_j}{N_j} - d_k S_k\right) + \left(\sum_{j=1}^{n} \beta_{kj}\frac{S_k I_j}{N_j} - (\gamma_k + d_k)I_k\right) + (\gamma_k I_k - d_k R_k) \\ &= b_k N_k - d_k(S_k + I_k + R_k) = (b_k - d_k)N_k. \end{aligned}$$

Thus, setting $\bar{S}_k = \frac{S_k}{N_k}$, $\bar{I}_k = \frac{I_k}{N_k}$, and $\bar{R}_k = \frac{R_k}{N_k}$, gives

$$\begin{aligned}\frac{d}{dt}(\bar{S}_k) &= \frac{d}{dt}\left(\frac{S_k}{N_k}\right) = \frac{S_k'}{N_k} - \frac{S_k N_k'}{N_k^2} \\ &= \frac{1}{N_k}\left(b_k N_k - \sum_{j=1}^{n} \beta_{kj}\frac{S_k I_j}{N_j} - d_k S_k\right) - \frac{S_k}{N_k^2}((b_k - d_k)N_k)\end{aligned}$$

$$= \frac{b_k N_k}{N_k} - \sum_{j=1}^{n} \beta_{kj}\frac{S_k}{N_k}\frac{I_j}{N_j} - d_k\frac{S_k}{N_k} - \frac{S_k}{N_k}\frac{b_k N_k}{N_k} + d_k\frac{S_k}{N_k}$$

$$\begin{aligned}&= b_k - \sum_{j=1}^{n} \beta_{kj}\frac{S_k}{N_k}\frac{I_j}{N_j} - b_k\frac{S_k}{N_k} \\ &= b_k - \sum_{j=1}^{n} \beta_{kj}\bar{S}_k\bar{I}_j - b_k\bar{S}_k\end{aligned}$$

Similar equations can be derived for $\bar{I}_k$ and $\bar{R}_k$. Therefore, we obtain the following system for the fractional variables $\bar{S}_k = \frac{S_k}{N_k}$, $\bar{I}_k = \frac{I_k}{N_k}$, and $\bar{R}_k = \frac{R_k}{N_k}$

$$\begin{cases} \bar{S}_k' = b_k - \sum_{j=1}^{n} \beta_{kj}\bar{S}_k\bar{I}_j - b_k\bar{S}_k \\ \bar{I}_k' = \sum_{j=1}^{n} \beta_{kj}\bar{S}_k\bar{I}_j - (\gamma_k + b_k)\bar{I}_k \qquad k = 1, \ldots, n. \\ \bar{R}_k' = \gamma_k\bar{I}_k - b_k\bar{R}_k \end{cases} \tag{3.3}$$

Note that $\bar{S}_k + \bar{I}_k + \bar{R}_k = 1$. In particular, $\bar{I}_k$ indicates the disease prevalence in the k-th group. Assuming the existence of a unique positive equilibrium $P^* = (\bar{S}_1^*, \bar{I}_1^*, \bar{R}_1^*, \ldots, \bar{S}_n^*, \bar{I}_n^*, \bar{R}_n^*)^T$ for system (3.3), we would like to know which

of the subpopulations has the highest disease prevalence $\bar{I}_k^*$ or largest number of infected individuals per capita.

Since there is no $\bar{R}_k$ appearing in the first two equations of system (3.3), consider a reduced system where we have removed the bar for simplicity of notation.

$$\begin{cases} S_k' = b_k - \sum_{j=1}^{n} \beta_{kj} S_k I_j - b_k S_k \\ \\ \\ I_k' = \sum_{j=1}^{n} \beta_{kj} S_k I_j - (\gamma_k + b_k) I_k \end{cases} \qquad k = 1, \ldots, n. \tag{3.4}$$

Results in this thesis stated for system (3.4) can be translated to the original system (3.3) in a straightforward manner.

From van den Driessche and Watmough (see [106]), the *reproduction number* of this system is given by $R_0 = \rho(M(\mathbf{S}^0))$, where $M(\mathbf{S}) = \left(\frac{S_k \cdot \beta_{kj}}{\gamma_k + b_k}\right)$ is called the *reproduction matrix* and $\mathbf{S}^0$ is the vector of equilibrium value of the susceptible populations when there is no disease. The following result, due to M. Li *et. al.*, states when system (3.4) has a positive endemic equilibrium and can be found in [39].

Theorem 3.2.1 (Guo-Li-Shuai)**.** *Consider system* (3.4)*, and assume the weight matrix* $B = (\beta_{ij})$ *is irreducible. If the basic reproduction number* $R_0 > 1$*, then there is a unique positive endemic equilibrium* $\mathbf{P}^* = (S_1^*, I_1^*, R_1^*, \ldots, S_n^*, I_n^*, R_n^*)^T$*, and* $\mathbf{P}^*$ *is globally asymptotically stable in the feasible region* Γ*.*

Under the assumptions of Theorem 3.2.1 system (3.4) has a unique equilibrium in its associated feasible region. Note that because the n groups where

further subdivided into three groups, we only use a subset of the equilibrium values to define the equilibrium ranking in this case. Therefore, the *disease prevalence vector* $\mathbf{I}^* = (I_1^*, \ldots, I_n^*)^T$ will be used as the equilibrium ranking vector. Setting the right hand side of (3.4) equal to zero gives

$$\begin{cases} 0 = b_k - \sum_{j=1}^{n} \beta_{kj} S_k^* I_j^* - b_k S_k^* \\ 0 = \sum_{j=1}^{n} \beta_{kj} S_k^* I_j^* - (\gamma_k + b_k) I_k^* \end{cases} \qquad k = 1, \ldots, n. \tag{3.5}$$

Hence, solving the second equation above explicitly for I_k^* gives

$$(\gamma_k + b_k) I_k^* = \sum_{j=1}^{n} \beta_{kj} S_k^* I_j^* \qquad\qquad k = 1, \ldots, n.$$

Solving these equations simultaneously gives the matrix equation

$$\operatorname{diag}(\gamma_k + b_k)\mathbf{I}^* = \operatorname{diag}(S_k^* \cdot B \cdot \mathbf{I}^*) \;\; \Leftrightarrow \;\; \mathbf{I}^* = \operatorname{diag}\left(\frac{S_k^*}{\gamma_k + b_k}\right) \cdot B \cdot \mathbf{I}^*$$

We give the following definition.

Definition 3.2.1. Let $\mathbf{S} = (S_1, \ldots, S_n)^T \in \mathbb{R}_+^n$, $0 < \gamma_k, b_k$ for all $k = 1, \ldots, n$, and let $B = (\beta_{kj})$ be an irreducible transmission matrix. Define the *generalized reproduction matrix* by

$$M(\mathbf{S}) := \operatorname{diag}\left(\frac{S_k}{\gamma_k + b_k}\right) \cdot B = \left(\frac{S_k \cdot \beta_{kj}}{\gamma_k + b_k}\right)_{n \times n} \tag{3.6}$$

Thus, the equilibrium equations give rise to the following matrix equation.

$$M(\mathbf{S}^*) \cdot \mathbf{I}^* = \mathbf{I}^* \tag{3.7}$$

Therefore, $\mathbf{I}^*$ can be found by solving this eigenvalue problem. If $R_0 > 1$,

then Theorem 3.2.1 says that $\mathbf{I}^*$ is an eigenvector of $M(\mathbf{S}^*)$ associated to eigenvalue 1. The result below states that the spectral radius of $M(\mathbf{S}^*)$ is equal to 1, and therefore the disease prevalence equilibrium vector $\mathbf{I}^*$ is the Perron eigenvector of $M(\mathbf{S}^*)$.

Theorem 3.2.2. *Assume that $R_0 > 1$. Let $M(\mathbf{S})$ be the generalized reproduction matrix given by* (3.6)*, and $\mathbf{S}^0$ be the equilibrium value of the susceptible populations when there is no disease. Then*

(1) $\rho(M(\mathbf{S}^0)) = R_0$ *(van den Driessche and Watmough),*

(2) $\rho(M(\mathbf{S}^*)) = 1$,

(3) $\mathbf{I}^* = (I_1^*, \ldots, I_n^*)^T$ *is the Perron vector of $M(\mathbf{S}^*)$.*

Proof: For the details about part (1) see [106]. Therefore, we prove statements (2) and (3).

First, note that the dispersal matrix B is irreducible and so the matrix $M(\mathbf{S}^*) = \left(\frac{S_k^* \cdot \beta_{kj}}{r}\right)$ is also irreducible.

Now, since $R_0 = \rho(M(\mathbf{S}^0)) > 1$, an endemic equilibrium $\mathbf{I}^* = (I_1, \ldots, I_n) > \vec{0}$ exists in the positive feasible region Γ. Therefore, there is a nontrivial solution to the equation

$$M(\mathbf{S}^*) \cdot \mathbf{I}^* = \mathbf{I}^*.$$

Hence, $1 \in \sigma(M(\mathbf{S}^*))$, i.e., 1 is an eigenvalue of $M(\mathbf{S}^*)$, and so $1 \leq \rho(M(\mathbf{S}^*))$. Therefore, it remains to show that $\rho(M(\mathbf{S}^*)) = 1$. Indeed, assume that $\rho(M(\mathbf{S}^*)) > 1$. Then from the Perron-Fröbenius theorem, that there is an eigenvector $\mathbf{p} > \mathbf{0}$, associated to $\rho(M(\mathbf{S}^*)) > 1$. Moreover, any other eigenvector, from any other eigenvalue, must have at least one negative entry. But this

is a contradiction, since we know there is some $\mathbf{I}^* > \mathbf{0}$ such that $M(\mathbf{S}^*)\cdot\mathbf{I}^* = \mathbf{I}^*$. Therefore, $\rho(M(\mathbf{S}^*)) = 1$. □

This result establishes a relationship between equilibrium ranking $\mathbf{I}^*$ and the Perron vector of $M(\mathbf{S}^*)$. Therefore, the unique Perron eigenvector can be used to assign a rating (and therefore a ranking) to the n nodes of the original system. This will show which node (and therefore which group) k has the highest disease prevalence given an endemic outbreak for the system. Moreover, unlike eigenvector centrality ranking, this disease prevalence equilibrium ranking vector $\mathbf{I}^*$ depends on both the network structure contained in the weight matrix B, and the local ODE parameter values γ_k and b_k, contained in the diagonal matrix $D = \text{diag}(\frac{S_k^*}{\gamma_k + b_k})$.

3.3 Equilibrium ranking for an SIR model on a patchy network

Consider the SIR epidemiological model with bilinear incidence in a patchy environment given by

$$\begin{cases} S_k' = \Lambda_k - \beta_k S_k I_k - d_k^S S_k + \sum_{j=1}^{n} a_{kj} S_j - \sum_{j=1}^{n} a_{jk} S_k \\ I_k' = \beta_k S_k I_k - (\gamma_k + d_k^I) I_k + \sum_{j=1}^{n} b_{kj} I_j - \sum_{j=1}^{n} b_{jk} I_k \qquad k = 1, \ldots, n, \\ R_k' = \gamma_k I_k - d_k^R R_k + \sum_{j=1}^{n} c_{kj} R_j - \sum_{j=1}^{n} c_{jk} R_k \end{cases} \tag{3.8}$$

with S_k, I_k, and R_k representing the number of susceptible, infectious, and removed individuals in the k-th patch, respectively, Λ_k is the influx of individuals

into the k-th patch, and β_k is the transmission coefficient between susceptible and infectious individuals in the k-th patch, d_k^S, d_k^I and d_k^R represent death rates of S, I and R populations in the k-th patch, respectively, and γ_k is the recovery rate of infectious individuals in the k-th patch. The travel rates of susceptible, infectious, and removed individuals from the j-th patch to the k-th patch are given by a_{kj}, b_{kj} and c_{kj}, respectively. For a more detailed discussion of epidemic models on patches, we refer to [2, 67, 107].

As in Section 3.2, since the variable R_k does not appear in the first two equations of (3.8), we can study the following reduced system.

$$\begin{cases} S_k' = \Lambda_k - \beta_k S_k I_k - d_k^S S_k + \sum_{j=1}^{n} a_{kj} S_j - \sum_{j=1}^{n} a_{jk} S_k \\ I_k' = \beta_k S_k I_k - (\gamma_k + d_k^I) I_k + \sum_{j=1}^{n} b_{kj} I_j - \sum_{j=1}^{n} b_{jk} I_k \end{cases} \qquad k = 1, \ldots, n, \quad (3.9)$$

with the initial conditions $S_k(0) \geq 0$ and $I_k(0) \geq 0$. The behaviour of R_k can then be determined from equation three of (3.8). Hence, the results stated here are for system (3.9), and can be extended to the original SIR model (3.8) in a straightforward manner.

To define the basic reproduction number R_0 of system (3.9), we first define the following matrices

$$F = \begin{bmatrix} \beta_1 S_1^0 & 0 & \cdots & 0 \\ 0 & \beta_2 S_2^0 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \beta_n S_n^0 \end{bmatrix} \qquad (3.10)$$

where $\mathbf{S}^0 = (S_1^{)}, \ldots, S_n^0)^T$ is the equilibrium value of the susceptible populations when there is no disease, and

$$V = \begin{bmatrix} d_1^I + \gamma_1 + \sum_{j\neq 1} b_{1j} & -b_{12} & \cdots & -b_{1n} \\ -b_{21} & d_2^I + \gamma_2 + \sum_{j\neq 2} b_{2j} & \cdots & -b_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ -b_{n1} & -b_{2n} & \cdots & d_n^I + \gamma_n + \sum_{j\neq n} b_{nj} \end{bmatrix} \tag{3.11}$$

The next definition and the theorem that follows are about M-matrices. They are mentioned here only to guarantee that V above, is invertible. In particular, I do not give the proof of the properties of an M-matrix. For details, see [38].

Definition 3.3.1. A matrix $B_{n\times n}$ is called an *M-matrix* if

(1) the off-diagonal entries of B are non-positive, and

(2) B is positively stable, i.e., all eigenvalues of B have positive real parts.

In particular, a matrix B with non-positive off-diagonal entries that is also *diagonally dominant*, i.e., for all rows of B we have $|b_{ii}| \geq \sum_{j\neq i} |b_{ij}|$, is an M-matrix (See [6]).

Theorem 3.3.1. *Properties of M-matrices.*

(1) *B is nonsingular and $B^{-1} \geq 0$.*

(2) *There exists $\beta > 0$ such that $B^{-1}\mathbf{x} \geq \beta\mathbf{x}$, for all $\mathbf{x} \geq \mathbf{0}$.*

Therefore, V has non-positive off-diagonal entries and is diagonally dominant, and is hence an M-matrix. Thus, it has an inverse V^{-1}, and R_0 of this

system can be calculated as $R_0 = \rho(FV^{-1})$, where ρ is the spectral radius of a matrix and FV^{-1} is called the next generation matrix (see [106] for details). The next result is from [67].

Theorem 3.3.2 (Li-Shuai)**.** *Assume that $R_0 > 1$ and suppose that one of the following assumptions is true.*

(1) *$A = 0$ and B is irreducible;*

(2) *A and B are irreducible, and there exists $\lambda > 0$ such that $a_{kj}S_k^* = \lambda b_{kj}I_k^*$ for all $1 \leq k, j \leq n$.*

Then a unique endemic equilibrium $P^* = (S_1^*, I_1^*, \ldots, S_n^*, I_n^*)^T > \mathbf{0}$ exists and is globally asymptotically stable in the feasible region $\overset{\circ}{\Gamma}$.

Therefore, the equilibrium ranking vector of network (3.9) is given by $\mathbf{I}^* = (I_1^*, \ldots, I_n^*)^T$. At equilibrium, the second equation of (3.9) gives the following matrix equation

$$V \cdot \mathbf{I}^* = \operatorname{diag}(\beta_k S_k^*) \cdot \mathbf{I}^*, \tag{3.12}$$

where V is given in (3.11). For $\mathbf{S} \in \mathbb{R}_+^n$ let $M(\mathbf{S}) = V^{-1} \cdot \operatorname{diag}(\beta_k S_k)$. Then equation (3.12) can be written as

$$M(\mathbf{S}^*) \cdot \mathbf{I}^* = \mathbf{I}^*. \tag{3.13}$$

The following result is an analogue to Theorem 3.2.2, and can be proved in a similar manner, noting that $\rho(FV^{-1}) = \rho(V(V^{-1}F)V^{-1}) = \rho(V^{-1}F)$.

Theorem 3.3.3. *Let $M(\mathbf{S}^*)$ be defined as in* (3.13)*. Then*

(1) $\rho(M(\mathbf{S}^0)) = R_0$,

(2) $\rho(M(\mathbf{S}^*)) = 1$,

(3) $\mathbf{I}^*$ *is the Perron vector of* $M(\mathbf{S}^*)$.

Thus, similar to Section 3.2, the theorem above establishes a link between the infected individual vector $\mathbf{I}^*$ and the Perron eigenvector of the matrix $M(\mathbf{S}^*)$ defined in (3.13).

3.4 Implications for disease control

Given an SIR model of the form (3.4), Theorem 3.2.2 says that the relative disease prevalence of the system is given by the Perron eigenvector $\mathbf{I}^*$ of the nonnegative and irreducible matrix

$$M(\mathbf{S}^*) = D \cdot B,$$

where $D = \text{diag}(\frac{S_k^*}{\gamma_k + b_k})$ is a diagonal matrix containing local ODE parameter values and B is the networks weight matrix. Similarly, Theorem 3.3.3 tells us that system (3.9) has equilibrium ranking vector given by the Perron vector of $M(\mathbf{S}^*)$ defined by (3.13).

In the context of an n-group epidemiology model, using the equilibrium ranking vector $\mathbf{I}^* = (I_1^*, \ldots, I_n^*)^T$ to rank some node k as the most important means that the k-th group has the highest disease prevalence or infected individuals. In an n-patch SIR model ranking node k as the most important means that the environmental patch k has the highest disease prevalence. In either case, attention can be focused on this specific node k and what it is about the local dynamics and the network structure that makes I_k^* the largest entry of the disease prevalence equilibrium ranking vector.

In both of the SIR network model of Section 3.2 and 3.3, because $M(\mathbf{S}^*)$

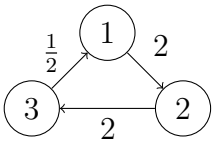
contains information about the local ODE parameters in a diagonal matrix D and the networks structure in B, we can base prevention methods such as quarantine and immunization on both of these aforementioned aspects of the system.

If the interest of researchers is to investigate how the systems network structure affects importance they can consider the network $(\mathcal{G}, B)$ alone and use the Perron eigenvector $\mathbf{p}$ of B. This is essentially the idea of *eigenvector centrality ranking*. This includes investigating which specific weighted connections of the network, described by B, conspire to make a certain entry p_k of the $\mathbf{p}$ the largest. Then, the weights b_{ij} of the edges (j, i) can be altered, in order to reduce the ranking value of I_k^*. This can be done by reducing the value of some of the weights b_{kj} or making some equal to zero (and hence severing the connection from node j to node k). In terms of epidemiology, reducing the weights b_{ij} amounts to reducing the cross transmission rate from group (or patch) j to group i, on the travel rate from patch j to patch i. This is crucial information if public health authorities are considering a strategy of quarantine to control the outbreak of a given disease.

On the other hand, given a fixed network structure described by $(\mathcal{G}, B)$, unlike eigenvector centrality ranking of a network, focus can be turned to the local ODE dynamics (described by the diagonal matrix D) and how they affect the disease prevalence at each node k of the network. This allows for the study of how specific parameter values of the system are contributing to the disease prevalence vector $\mathbf{I}^*$. Thus, changing certain parameter values of the system, will allow us to reduce the largest value I_k^*, hence reducing the disease prevalence of node k. In particular, if immunization techniques are

employed in a given model using a parameter β say, we can consider changing the importance of nodes in the network by changing the values of β.

Example 3.4.1. Consider a 3-group SIR model as described by (3.2) and having directed network given below. The Perron eigenvector of the weight matrix B, we obtain $p_1 \approx 0.39$, $p_2 \approx 0.63$, and $p_3 = 1$. Hence, using only the network structure, eigenvector centrality says node 3 is the most important.



$$\begin{bmatrix} 0 & 0 & \frac{1}{2} \\ 2 & 0 & 0 \\ 0 & 2 & 0 \end{bmatrix} \qquad \mathbf{p} = \begin{bmatrix} 0.39 \\ 0.63 \\ 1.00 \end{bmatrix}$$

Now consider the diagonal matrix $D = \text{diag}(\frac{3}{2}, \frac{2}{3}, 2)$, which represents the part of $M = D \cdot B$ containing the local ODE parameter values. Then M is given by

$$M = D \cdot B = \begin{bmatrix} 0 & 0 & 3 \\ \frac{4}{3} & 0 & 0 \\ 0 & 4 & 0 \end{bmatrix}.$$

Therefore, $\rho(M) = \sqrt[3]{16} \approx 2.5198$, and noting that $m_{13} = 3 > \rho(M)$, we have

$$\mathbf{v} = \begin{bmatrix} v_1 \\ v_2 \\ v_3 \end{bmatrix} = \begin{bmatrix} 2.38 \\ 2.52 \\ 1.00 \end{bmatrix}.$$

Hence, by adding the local dynamical information the ranking changes, and the most important node of the network according to the equilibrium ranking is node 2.

Moreover, a combination of the two techniques above can be employed to take advantage of both aspects of the equilibrium ranking in order to better control an endemic outbreak.

Chapter 4

Equilibrium Ranking for ODE Networks

In this chapter we extend the idea of equilibrium ranking to more general nonlinear ODE networks that have equilibrium equations giving rise to nonlinear vector equations. Section 4.1 introduces equilibrium ranking in a more general setting. The remaining sections consider equilibrium ranking for specific nonlinear ODE models on networks. In particular, Section 4.2 investigates coupled oscillator models, Section 4.3 ecological models with dispersal of a single species, Section 4.4 considers biodiversity models on spatially structured habitats, and Section 4.5 considers equilibrium ranking for some general forms of nonlinear ODEs. Finally, Section 4.6 is used to consider the implications of such an equilibrium ranking for these models.

4.1 Equilibrium ranking for ODE systems on networks

Consider the nonlinear ODE system on a network where the local dynamics of the network are given by the equations

$$\dot{\mathbf{x}} = F(\mathbf{x}), \qquad \mathbf{x} \in \mathbb{R}^n. \tag{4.1}$$

We will make the following assumption when considering a system of the form (4.1).

A1: System (4.1) has a unique positive equilibrium $\mathbf{x}^*$.

More specifically, consider the ODE system on a network given by

$$\dot{x}_i = f_i(x_i) + \sum_{j=1}^{n} b_{ij} g_{ij}(x_i, x_j), \qquad i = 1, \ldots, n, \tag{4.2}$$

where $f_i(x_i)$ describes the local dynamics at each node i, $B = (b_{ij})_{n\times n}$ is the weight matrix of the network, and g_{ij} describes the influence among the nodes. Similar to Chapter 3, under assumption **A1**, the unique solution $\mathbf{x}^* > \mathbf{0}$ can be defined as the equilibrium ranking vector for the network. Thus, we associate the value $x_i^* > 0$ to node i for all $i = 1, 2, \ldots, n$, and then rank the importance of the nodes from these values.

Solving equations (4.2) for the equilibrium $\mathbf{x}^*$, we obtain a nonlinear equation of the form

$$G(\mathbf{x}^*) = B\mathbf{x}^* \tag{4.3}$$

where G is a nonlinear function and B is the weight matrix of the network (see the examples in the next few sections below). Solving equation (4.3) gives no insight into how the entries of $\mathbf{x}^*$ depend on the network structure or the local ODE dynamics. Therefore, we instead follow the ideas in Chapter 3 and rewrite (4.3) in the following matrix form

$$M(\mathbf{x}^*)\mathbf{x}^* = \mathbf{x}^*,$$

where $M(\mathbf{x}^*) = D(\mathbf{x}^*) \cdot B$ is the product of a diagonal matrix $D(\mathbf{x}^*)$ and the system's weight matrix B. This again establishes the link between the idea of using a positive eigenvector of a Matrix, as with centrality ranking, to define an equilibrium ranking vector for an ODE network.

This matrix $M(\mathbf{x}^*)$ contains both the entries of the weight matrix B and information about the local parameter values of the system. Hence, the equilibrium ranking is again based on both the network structure and local ODE dynamics as in Chapter 3.

4.2 A coupled oscillator model of n moving components

A coupled system of nonlinear oscillators can be built on a weighted digraph $(\mathcal{G}, B)$ with $n \geq 2$ vertices and $B = (b_{ij})$, as follows: assign to each vertex i a nonlinear oscillator described by the equations

$$x_i'' + \alpha_i x_i' + f_i(x_i) + \sum_{j=1}^{n} b_{ij}(x_i - x_j) = 0, \qquad i = 1, \ldots, n \tag{4.4}$$

where $\alpha_i \geq 0$ is the damping coefficient, $f_i : \mathbb{R} \to \mathbb{R}$ is the non-linear restoring force, and the influence from vertex j to vertex i is given by $b_{ij}(x_i - x_j)$. In first order form, for every i

$$\begin{cases} \dot{x}_i = y_i \\ \dot{y}_i = -\alpha_i y_i - f_i(x_i) - \sum_{j=1}^{n} b_{ij}(x_i - x_j) \end{cases} \tag{4.5}$$

An equilibrium $(\mathbf{x}^*, \mathbf{y}^*)$ of equation (4.5) satisfies

$$\begin{cases} 0 = y_i^* \\ 0 = -\alpha_i y_i^* - f_i(x_i^*) - \sum_{j=1}^{n} b_{ij}(x_i^* - x_j^*), \end{cases} \tag{4.6}$$

and therefore $y_i^* = 0$ and the second equation of (4.6) gives

$$f_i(x_i^*) + x_i^* \sum_{j=1}^{n} b_{ij} = \sum_{j=1}^{n} b_{ij} x_j^*, \tag{4.7}$$

which can be written in the form

$$G(\mathbf{x}^*) = B\mathbf{x}^*, \tag{4.8}$$

with $B = (b_{ij})$ an irreducible weight matrix and $G_i(\mathbf{x}^*) := f_i(x_i^*) + \beta_i x_i^*$, where $\beta_i = \sum_{j=1}^{n} b_{ij}$.

Instead of considering the unique solution to this nonlinear vector equation, we reformulate equation (4.8) into a matrix equation of the form $M(\mathbf{x}^*)\mathbf{x}^* = \mathbf{x}^*$, where $M(\mathbf{x}^*) = D \cdot B$, is the product of a diagonal matrix and the systems

weight matrix B. Note that $f_i(x_i)$ is usually assumed to be an odd function, and hence $f_i(x_i)$ has the form $f_i(x_i) = x_i g(x_i)$, with $g_i(x_i)$ even. Therefore, the equilibrium equations give

$$f_i(x_i^*) + \beta_i x_i^* = \sum_{j=1}^{n} b_{ij} x_j^* \;\Leftrightarrow\; x_i^*(g_i(x_i^*) + \beta_i) = \sum_{j=1}^{n} b_{ij} x_j^*.$$

Solving simultaneously, gives the matrix equation:

$$M(\mathbf{x}^*) \cdot \mathbf{x}^* = \mathbf{x}^*, \tag{4.9}$$

where $M(\mathbf{x}^*) = \operatorname{diag}\left(\frac{1}{\beta_i + g_i(x_i^*)}\right) B$. This essentially proves part (2) of the following result. Part (1) is due to M. Li and Z. Shuai (see [66]).

Theorem 4.2.1. *Given the system* (4.4),

(1) *There is a positive equilibrium* $\mathbf{x}^* = (x_1^*, \ldots, x_n^*)^T$. *(M. Li & Z. Shuai)*

(2) $\mathbf{x}^*$ *satisfies the matrix equation*

$$M(\mathbf{x}^*)\mathbf{x}^* = \mathbf{x}^*.$$

where $M(\mathbf{x}^*) = \operatorname{diag}\left(\frac{1}{\beta_i + g_i(x_i^*)}\right) B$, $\beta_i = \sum_{j=1}^{n} b_{ij}$, *and* $B = (b_{ij})$ *is the weight matrix of system* (4.4).

(3) *The spectral radius* $\rho(M(\mathbf{x}^*))$ *of* $M(\mathbf{x}^*)$ *equals* 1.

(4) $\mathbf{x}^*$ *is a Perron vector of matrix* $M(\mathbf{x}^*)$.

Proof:

(1) The existence and global stability of $\mathbf{x}^* > \mathbf{0}$ is due to M. Li and Z. Shuai.

(2) $M(\mathbf{x}^*)$ is derived above in equation (4.9).

(3) / (4) Since $\mathbf{x}^*$ exists, we know that $\mathbf{x}^*$ is a positive eigenvector of $M(\mathbf{x}^*)$ associated to eigenvalue 1. Therefore, the Perron-Fröbenius Theorem says that the only eigenvector with all positive entries is a positive multiple of the dominant Perron eigenvector $\mathbf{p}$ associated to the spectral radius $\rho(M(\mathbf{x}^*))$. Therefore, 1 must be the spectral radius $\rho(M(\mathbf{x}^*))$ of $M(\mathbf{x}^*)$, and $\mathbf{x}^*$ is a Perron vector of $M(\mathbf{x}^*)$.

□

4.3 An ecological model on a network

Consider the single species dispersal model on n patches described by the differential equations

$$\dot{x}_i = x_i g_i(x_i) + \sum_{j=1}^{n} b_{ij}(x_j - \alpha_{ij} x_i), \quad i = 1, \ldots, n. \tag{4.10}$$

Here, $x_i \in \mathbb{R}_+$ represents the population density of the given species in patch i, and $g_i \in C^1(\mathbb{R}_+, \mathbb{R})$ is the density dependent growth rate in patch i. Also assume there is a constant dispersal rate from patch j to patch i which is given by $b_{ij} \geq 0$ so that $B = (b_{ij})$ is a nonnegative weight matrix for the network. The $\alpha_{ij} \geq 0$ represent different boundary conditions in the case of continuous diffusion.

Assuming that (4.10) has a unique, globally asymptotically stable equilibrium implies that for all $i = 1, \ldots, n$

$$0 = x_i^* g_i(x_i^*) + \sum_{j=1}^{n} b_{ij}(x_j^* - \alpha_{ij} x_i^*) \;\Rightarrow\; \sum_{j=1}^{n} b_{ij} x_j^* = x_i^* \left(\sum_{j=1}^{n} b_{ij} \alpha_{ij} - g_i(x_i^*) \right).$$

Now, let $\beta_i = \sum_{j=1}^{n} b_{ij}$ and for simplicity let $\alpha_{ij} = 1$ for all i and j. Therefore,

the equation becomes

$$\sum_{j=1}^{n} b_{ij}x_j^* = x_i^*(\beta_i - g_i(x_i^*)) \quad \Rightarrow \quad \frac{1}{\beta_i - g_i(x_i^*)} \sum_{j=1}^{n} b_{ij}x_j^* = x_i^*.$$

Thus, solving the equations simultaneously, gives

$$M(\mathbf{x}^*)\mathbf{x}^* = \mathbf{x}^*, \tag{4.11}$$

where $M(\mathbf{x}) = \text{diag}\left(\frac{1}{\beta_i - g_i(x_i)}\right) B$.

Theorem 4.3.1. *Given the system* (4.10)

(1) *There is a positive equilibrium* $\mathbf{x}^* = (x_1^*, \ldots, x_n^*)^T$ *(M. Li et. al.)*

(2) $\mathbf{x}^*$ *satisfies the matrix equation*

$$M(\mathbf{x}^*)\mathbf{x}^* = \mathbf{x}^*,$$

where $M(\mathbf{x}^*) = \text{diag}\left(\frac{1}{\beta_i - g_i(x_i^*)}\right) B$, $\beta_i = \sum_{j=1}^{n} b_{ij}$, *and* $B = (b_{ij})$ *is the weight matrix of system* (4.10).

(3) *The spectral radius* $\rho(M(\mathbf{x}^*))$ *of* $M(\mathbf{x}^*)$ *equals* 1.

(4) $\mathbf{x}^*$ *is a Perron vector of matrix* $M(\mathbf{x}^*)$.

Proof:

(1) The existence of $\mathbf{x}^* > \mathbf{0}$ is due to M. Li et. al.

(2) $M(\mathbf{x}^*)$ is derived above in equation (4.11).

(3) / (4) Since $\mathbf{x}^*$ exists, we know that $\mathbf{x}^*$ is a positive eigenvector of $M(\mathbf{x}^*)$ associated to eigenvalue 1. Therefore, the Perron-Fröbenius Theorem

says that 1 must be the spectral radius $\rho(M(\mathbf{x}^*))$ of $M(\mathbf{x}^*)$ and $\mathbf{x}^*$ is a Perron vector of $M(\mathbf{x}^*)$.

□

4.4 Biodiversity models on n spatially structured habitats

Consider the ODE model of the biodiversity of n sessile species competing in a spatially structured habitat where the interactions are structured to give a competitive hierarchy. The species are indexed such that species x_1 is the most superior to x_n the least superior. Then make the following assumptions.

A1: When two species x_i and x_j with $i < j$ both occur at the same site then the dominant species x_i displaces the inferior species x_j.

A2: If $i < j$ then species x_j can never displace x_i and can never invade sites occupied by x_i.

Let p_i be the fraction of habitat sites occupied by species i, called the *abundance* of species i. Let $m_i > 0$ be the mortality rate and $c_i > 0$ the colonization rate of species x_i. The colonization rate or rate of propagule production by sites occupied by species x_i is $c_i p_i$, and the proportion of sites not yet occupied by species i is $(1-\sum_{j=1}^{i} p_i)$. Therefore, the rate of production of newly colonized sites by species i is given by $c_i p_i(1 - \sum_{j=1}^{i} p_i))$. Also, $m_i p_i$ is the rate at which sites that species i occupies become vacant (the individual dies). More dominant species can also invade inferior species sites, so that the equation for species i has the term $-p_i \sum_{j=1}^{i-1} c_j p_j$. Therefore, the equation for the i^{th} species is given by

$$\frac{dp_i}{dt} = c_i p_i \left(1 - \sum_{j=1}^{i} p_j\right) - m_i p_i - p_i \sum_{j=1}^{i-1} c_j p_j \tag{4.12}$$

Assuming system (4.12) has a unique positive equilibrium, setting the left hand side equal to zero implies

$$c_i p_i^* = p_i^* \left(\sum_{j=1}^{i-1} (c_i + c_j) p_j^* + m_i + c_i p_i^*\right) \Rightarrow$$

$$p_i^* = p_i^* \left(\sum_{j=1}^{i-1} \left(1 + \frac{c_j}{c_i}\right) p_j^* + \frac{m_i}{c_i} + p_i^*\right).$$

Solving simultaneously gives the following matrix equation:

$$M(\mathbf{p}^*)\mathbf{p}^* = \mathbf{p}^*, \tag{4.13}$$

where $M(\mathbf{p}^*) = D(\mathbf{p}^*) + C$, with $D(\mathbf{p}^*) = \text{diag}\left(\frac{m_i}{c_i} + p_i^*\right)$ and

$$C = \begin{bmatrix} 0 & 0 & 0 & \cdots & 0 \\ 1 + \frac{c_1}{c_2} & 0 & \cdots & 0 & 0 \\ 1 + \frac{c_1}{c_3} & 1 + \frac{c_2}{c_3} & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 1 + \frac{c_1}{c_n} & 1 + \frac{c_2}{c_n} & \cdots & 1 + \frac{c_{n-1}}{c_n} & 0 \end{bmatrix}.$$

Theorem 4.4.1. *Given the system* (4.12)

(1) *There is a positive equilibrium* $\mathbf{p}^* = (p_1^*, \ldots, p_n^*)^T$ *(Tilman et. al.),*

(2) $\mathbf{p}^*$ *satisfies the matrix equation*

$$M(\mathbf{p}^*)\mathbf{p}^* = \mathbf{p}^*,$$

where $M(\mathbf{p}^*) = D(\mathbf{p}^*) + C$ *is given in* (4.13).

(3) *The spectral radius* $\rho(M(\mathbf{p}^*))$ *of* $M(\mathbf{p}^*)$ *equals* 1.

(4) $\mathbf{p}^*$ *is a Perron vector of matrix* $M(\mathbf{p}^*)$.

Proof: The proof of (1), *i.e.*, the existence of a positive equilibrium $\mathbf{p}^* = (p_1^*, \ldots, p_n^*)^T$ is due to Tilman et. al. (see [104] and [105]), and the matrix in statement (2) is derived above in equation (4.13). Finally, for (3) and (4) we again note that $\mathbf{p}^* > \mathbf{0}$ being a positive equilibrium of system (4.12) implies that $\mathbf{p}^*$ is a positive eigenvector associated to the eigenvalue 1. Therefore, the Perron-Fröbenius Theorem says that 1 must be the spectral radius $\rho(M(\mathbf{x}^*))$ of $M(\mathbf{x}^*)$ and $\mathbf{x}^*$ is a Perron vector. □

Now consider a slightly altered model from the one above. We consider the scenario where the species are all allowed to displace one another. To incorporate this into model (4.12) we let the first sum on the right hand side to run from 1 to n instead of i. The new system is given by

$$\frac{dp_i}{dt} = c_i p_i \left(1 - \sum_{j=1}^{n} p_j\right) - m_i p_i - p_i \sum_{j=1}^{i-1} c_j p_j \tag{4.14}$$

Assuming system (4.14) has a unique positive equilibrium, setting the left hand side equal to zero implies

$$c_i p_i^* = p_i^* \left(\sum_{j=1}^{i-1} (c_i + c_j) p_j^* + m_i + c_i p_i^*\right) \Rightarrow$$

$$p_i^* = p_i^* \left(\sum_{j=1}^{i-1} \left(1 + \frac{c_j}{c_i} \right) p_j^* + \frac{m_i}{c_i} + \sum_{k=i}^{n} p_k^* \right).$$

Solving simultaneously gives the following matrix equation:

$$M(\mathbf{p}^*)\mathbf{p}^* = \mathbf{p}^*, \tag{4.15}$$

where $M(\mathbf{p}^*) = D(\mathbf{p}^*) + C$, with $D(\mathbf{p}^*) = \text{diag}\left(\frac{m_i}{c_i} + \sum_{k=i}^{n} p_k^* \right)$ and

$$C = \begin{bmatrix} 0 & 0 & 0 & \cdots & 0 \\ 1 + \frac{c_1}{c_2} & 0 & \cdots & 0 & 0 \\ 1 + \frac{c_1}{c_3} & 1 + \frac{c_2}{c_3} & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 1 + \frac{c_1}{c_n} & 1 + \frac{c_2}{c_n} & \cdots & 1 + \frac{c_{n-1}}{c_n} & 0 \end{bmatrix}.$$

Theorem 4.4.2. *Given the system* (4.14)

(1) *There is a positive equilibrium* $\mathbf{p}^* = (p_1^*, \ldots, p_n^*)^T$ *(Tilman et. al.),*

(2) $\mathbf{p}^*$ *satisfies the matrix equation*

$$M(\mathbf{p}^*)\mathbf{p}^* = \mathbf{p}^*,$$

where $M(\mathbf{p}^*) = D(\mathbf{p}^*) + C$ *is given in* (4.15).

(3) *The spectral radius* $\rho(M(\mathbf{p}^*))$ *of* $M(\mathbf{p}^*)$ *equals* 1.

(4) $\mathbf{p}^*$ *is a Perron vector of matrix* $M(\mathbf{p}^*)$.

Proof: The proof is similar in detail to the proof of Theorem 4.4.1, and is therefore omitted. □

4.5 Equilibrium ranking for general ODE forms

Consider the general nonlinear system of ODE's of the form

$$\dot{x}_i = x_i h_i(x_i) + \sum_{j=1}^{n} b_{ij} g_{ij}(x_i, x_j), \quad i = 1, \ldots, n, \tag{4.16}$$

where B is the weight matrix of the network, $h_i(x_i)$ is a $C^1(\mathbb{R})$ function, and we will assume that $g_{ij}(x_i, x_j)$ consists only of linear and/or bilinear terms in x_i and x_j (see the cases below).

Case 1: $g_{ij}(x_i, x_j) = a_j x_j - a_i x_i$, for some $a_i, a_j \in \mathbb{R}_+$. Therefore, equation (4.16) becomes

$$\dot{x}_i = x_i h_i(x_i) - a_i x_i \sum_{j=1}^{n} b_{ij} + \sum_{j=1}^{n} b_{ij} a_j x_j, \quad i = 1, \ldots, n. \tag{4.17}$$

Thus, letting $\beta_i = \sum_{j=1}^{n} b_{ij}$, the equilibrium equations imply

$$x_i^*(a_i \beta_i) - h_i(x_i^*) = \sum_{j=1}^{n} b_{ij} a_j x_j^*, \quad i = 1, \ldots, n. \tag{4.18}$$

Solving simultaneously, gives

$$M(\mathbf{x}^*)\mathbf{x}^* = \mathbf{x}^*, \tag{4.19}$$

where $M(\mathbf{x}^*) = \operatorname{diag}\left(\frac{a_i}{a_i\beta_i - h_i(x_i^*)}\right) \cdot B$.

Theorem 4.5.1. *Given the system* (4.17) *and assuming there exists a positive equilibrium* $\mathbf{x}^* = (x_1^*, \ldots, x_n^*)^T$,

(1) $\mathbf{x}^*$ *satisfies the matrix equation*

$$M(\mathbf{x}^*)\mathbf{x}^* = \mathbf{x}^*,$$

where $M(\mathbf{x}^*)$ *is given in* (4.19).

(2) *The spectral radius* $\rho(M(\mathbf{x}^*))$ *of* $M(\mathbf{x}^*)$ *equals* 1.

(3) $\mathbf{x}^*$ *is a Perron vector of matrix* $M(\mathbf{x}^*)$.

Proof:

(1) $M(\mathbf{x}^*)$ is derived above in equation (4.19) directly from the equilibrium equations (4.17) by solving them simultaneously.

(2) / (3) Since $\mathbf{x}^*$ exists, we know that $\mathbf{x}^*$ is a positive eigenvector of $M(\mathbf{x}^*)$ associated to eigenvalue 1. Therefore, the Perron-Fröbenius Theorem says that the only eigenvector with all positive entries is a positive multiple of the dominant Perron eigenvector $\mathbf{p}$ associated to the spectral radius $\rho(M(\mathbf{x}^*))$. Therefore, 1 must be the spectral radius $\rho(M(\mathbf{x}^*))$ of $M(\mathbf{x}^*)$ and $\mathbf{x}^*$ is a Perron vector of $M(\mathbf{x}^*)$..

□

Case 2: $g_{ij}(x_i, x_j) = -c_{ij}x_i x_j$, for $c_{ij} \in \mathbb{R}_+$. Then, equation (4.16) becomes

$$\dot{x}_i = x_i h_i(x_i) - x_i \sum_{j=1}^{n} b_{ij}c_{ij}x_j, \quad i = 1, \ldots, n. \tag{4.20}$$

Hence, the equilibrium equations imply

$$x_i^* h_i(x_i^*) = x_i^* \sum_{j=1}^{n} b_{ij}c_{ij}x_j^*, \quad i = 1, \ldots, n. \tag{4.21}$$

Solving simultaneously, gives

$$M(\mathbf{x}^*)\mathbf{x}^* = \mathbf{x}^*, \tag{4.22}$$

where $M(\mathbf{x}^*) = \text{diag}\left(\frac{x_i^*}{h_i(x_i^*)}\right) \cdot R$, with $R = (r_{ij}) = (b_{ij}c_{ij})$.

Theorem 4.5.2. *Given the system* (4.20) *and assuming there exists a positive equilibrium* $\mathbf{x}^* = (x_1^*, \ldots, x_n^*)^T$,

(1) $\mathbf{x}^*$ *satisfies the matrix equation*

$$M(\mathbf{x}^*)\mathbf{x}^* = \mathbf{x}^*,$$

where $M(\mathbf{x}^*)$ *is given in* (4.22).

(2) *The spectral radius* $\rho(M(\mathbf{x}^*))$ *of* $M(\mathbf{x}^*)$ *equals* 1.

(3) $\mathbf{x}^*$ *is a Perron vector of matrix* $M(\mathbf{x}^*)$.

Proof: The proof is similar in detail to the proof of Theorem 4.5.1, and is therefore omitted. □

4.6 Implications for ecological models

For an ecological model of the form (4.10), describing the movement of a single species on multiple spatial environments, an equilibrium ranking vector $\mathbf{x}^* = (x_1^*, \ldots, x_n^*)^T$ can give insight into which regions the species is thriving (the largest entries of $\mathbf{x}^*$), and where this species runs the risk of going extinct (x_i values near zero). Thus, we can consider using the equilibrium rating vector $\mathbf{x}^*$ in a different manner. Instead of using the largest entry x_i^* of $\mathbf{x}^*$ to conclude the most important species is that which has the highest x_i^* value, we use the smallest entry x_k^* of $\mathbf{x}^*$ to conclude that the most important node is the one in which the species has the lowest population density x_k^*. This

will indicate in which patch the species is most likely to go extinct (*i.e.*, has a population density x_k^* near zero).

Similarly, for models like system (4.12) and (4.14), describing several sessile species competing for one or more natural resource, an equilibrium ranking $\mathbf{x}^*$ can allow for the prediction of which species will become dominant over the others. We can again turn this rating vector on it's head and use the smallest entry x_k^* of $\mathbf{x}^*$ to rank node (*i.e.* species) i as the most important. This, in turn, means that instead of being the most dominant species, this ranking indicates which species is most likely to go extinct.

Furthermore, regardless of the model taken into consideration, this equilibrium ranking vector $\mathbf{x}^*$ is the eigenvector of a nonnegative irreducible matrix $M(\mathbf{x}^*) = D(\mathbf{x}^*) \cdot B$. Hence, $\mathbf{x}^*$ depends on both the network structure of the system encapsulated in the weight matrix B and the local ODE parameter values contained in a diagonal matrix $D(\mathbf{x}^*)$. Therefore, we can for the first time, fix the network structure $(\mathcal{G}, B)$ and isolate what it is about the local dynamics that are leading to a species being dominant in certain spatial regions or dominating the other species involved.

Chapter 5

Rank Dependence on Network Structure and ODE Dynamics

This chapter considers ODE models on a network $(\mathcal{G}, B)$ where the existence of a positive equilibrium is assumed. Then from Chapter 3 and 4, the equilibrium equations of either the system or the associated linearized system can be use to construct a matrix $M = D \cdot B$, where B is the weight matrix and $D = \text{diag}(d_i)$ is a diagonal matrix containing local ODE parameter values. We then ask the question of how the entries of the Perron eigenvector $\mathbf{p} = (p_1, \ldots, p_n)^T$ of M depend on the digraph structure described by B and the local dynamics of the network given in D.

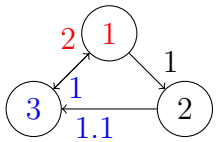
Therefore, Section 1 first investigates how the Perron vector $\mathbf{p}$ of a network $(\mathcal{G}, B)$ depends on the entries of B for several simple but typical network structures. For a detailed analysis of the spectra of graphs see [18], [23], [54], and [69]. In particular, rooted trees, cycles, unicyclic and multi-cyclic digraphs are considered. Results guaranteeing which entry of $\mathbf{p}$ will be the largest based on the entries of B can then be derived. Section 2 considers the network structures of Section 1, but investigates how the entries of a Perron

vector $\mathbf{v}$ depend on the entries of the matrix $M = D \cdot B$. This will isolate the effects of both the local ODE dynamics and the network structure on the entries of the equilibrium ranking vector $\mathbf{v}$.

5.1 Perron Eigenvectors and Graph Structure

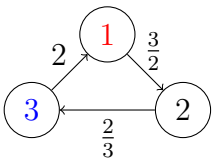
We begin the section by emphasizing the benefit of using eigenvector ranking over some other commonly used measures of importance for a network.

Example 5.1.1. The directed network below has weighted indegrees given by indeg(1) = 2, indeg(2) = 1, and indeg(3) = 2.1. Therefore, using indegree as a relative importance rating, node 3 is the most important. However, using the Perron eigenvector of the weight matrix B, we obtain $p_1 \approx 1.8$, $p_2 = 1.0$, and $p_3 \approx 1.64$. Hence, using eigenvector centrality, node 1 is the most important.



$$\begin{bmatrix} 0 & 0 & 2 \\ 1 & 0 & 0 \\ 1 & 1.1 & 0 \end{bmatrix} \qquad \mathbf{p} = \begin{bmatrix} 1.80 \\ 1.00 \\ 1.64 \end{bmatrix}$$

Example 5.1.2. In this directed network if we consider the most important node that which has the largest "inweight", then node 1 is the most important node of the network. Again, using the Perron eigenvector of B, we see that node 2 is chosen as the most important.



$$\begin{bmatrix} 0 & 0 & 2 \\ \frac{3}{2} & 0 & 0 \\ 0 & \frac{2}{3} & 0 \end{bmatrix} \qquad \mathbf{p} = \begin{bmatrix} 1.58 \\ 1.88 \\ 1.00 \end{bmatrix}$$

These two examples show that considering the node with the largest indegree or weight does not always give the same relative importance ranking for the nodes as eigenvector centrality. Moreover, eigenvector centrality ranking seems most relevent for our purposes because it depends on both the number of connections a node has and the weights of those connections.

In general, given a digraph $(\mathcal{G}, B)$ with associated weight matrix B, the relationship between the Perron eigenvector $\mathbf{p}$ and the entries of B is complex. Therefore, this section considers an increasingly complex demographic of networks $(\mathcal{G}, B)$ and how the Perron vector $\mathbf{p}$ of $B = (b_{ij})$ depends on the entries b_{ij} and the spectral radius $\rho(B)$ of B. This survey includes rooted trees, cycle digraphs, unicyclic and multi-cyclic digraphs.

5.1.1 Rooted trees

Consider the digraph $(\mathcal{G}, B)$ that is a directed tree rooted at a single node, namely node 1. By a directed tree rooted at node 1 we mean that 1 is a sink node, and all other nodes have directed edges leading towards node 1. An example of such a tree is given in the Figure 5.1.1. For a directed tree $(\mathcal{G}, B)$ rooted at node 1 we have the following result about the characteristic polynomial and Perron eigenvector of the non-negative weight matrix B.

Theorem 5.1.1. *Let $(\mathcal{G}, B)$ be a directed tree consisting of n nodes rooted at node 1. Then we have*

(1) *the characteristic polynomial of B is $p_B(\lambda) = \lambda^n$,*

(2) *the unique nonnegative Perron eigenvector associated to the spectral radius $\rho(B) = 0$ is given by $\mathbf{p} = (1, 0, \ldots, 0)^T$.*

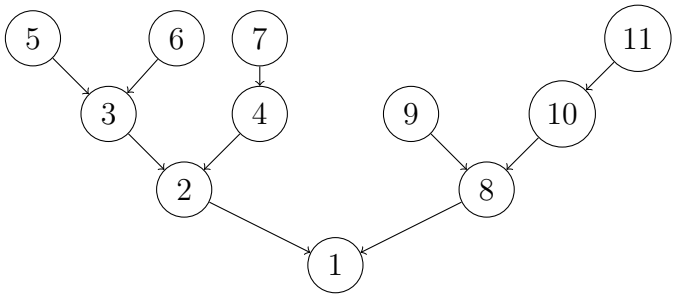


Figure 5.1: A Directed Tree rooted at node 1.

Proof:

We first show that $p_B(\lambda) = \lambda^n$. If $\mathcal{G} = (V, E)$ is a tree rooted at node $1 \in V = \{1, 2, \ldots, n\}$, then there are three types of nodes in $\mathcal{G}$. Namely, the sink node 1, source nodes at the top of the tree, and the nodes in between. We show that regardless of the node type, there are nonzero entries only above the main diagonal in B. Therefore, we have an upper triangular matrix with all diagonal entries equal to zero, and the first statement follows immediately.

Note that if an edge (i, j) exists in $\mathcal{G}$, then $b_{ji} \neq 0$ in the weight matrix B. Therefore we cannot have $b_{ij} \neq 0$, otherwise edge (j, i) exists in $\mathcal{G}$ and hence there is a 2-cycle, which is impossible as $\mathcal{G}$ is a tree. Moreover, there are no loops (i, i) in $\mathcal{G}$, so that $b_{ii} = 0$ for all $i = 1, 2, \ldots, n$.

We make the convention of labelling the nodes of the tree $\mathcal{G}$ by starting with an arbitrary branch and label the node connected to the sink 1 as node 2. Labelling the rest of the branch we work away from the sink to the top of the branch to the source nodes, labelling left to right at each level in the tree. We then move clockwise until all branches are labelled. See Figure 5.1, for example.

Case 1. The sink node 1 is such that $\text{outdeg}(1) = 0$ and $\text{indeg}(1) \geq 1$.

Then, there exist nodes $l_1 = 2, l_2, \ldots, l_m \in V$ with directed edges $(2,1)$, $(l_2,1), \ldots, (l_m,1)$ in the edge set E. Then by our convention, $b_{12}, b_{1l_2}, \ldots, b_{1l_m}$ are nonzero in B, and these all lie above the main diagonal.

Case 2. $j \in V$ is a source, *i.e.*, node j is such that outdeg$(1) = 1$ and indeg$(1) = 0$.

In this case the j-th row of B consists of all zeros, *i.e.*, $b_{jk} = 0$, $k = 1, \ldots, n$. Moreover, there exists a single node $l < j$ such that $(j,l) \in E$. Hence $b_{lj} \neq 0$ is above the main diagonal in matrix B.

Case 3. $j \in V$ is such that outdeg$(1) = 1$ and indeg$(1) \geq 1$.

Then outdeg$(j) = 1$ implies the is a node $l \in V$ such that $l < j$ and $b_{lj} \neq 0$. Similar to case 1, there are also nodes $k_1, \ldots, k_s \in V$ with $k_i > j$ for all $i = 1, \ldots, s$ and $(k_1, j), \ldots, (k_s, j) \in E$. Therefore, $b_{jk_i} \neq 0$ for all $= 1, \ldots, s$, which are all entries above the main diagonal in B.

Therefore, the weight matrix B is upper-triangular with all diagonal entries equal to zero. Hence, $p_B(\lambda) = \lambda^n$. This means that $\rho(B) = 0$, with algebraic multiplicity n.

For statement (2) we must solve the equation

$$(\lambda I - B)\mathbf{v} = \mathbf{0},$$

where $\lambda = \rho(B) = 0$. Therefore, $-B\mathbf{v} = \mathbf{0}$ or just $B\mathbf{v} = \mathbf{0}$. The j-th row of B is either all zeros, or has nonzero entries b_{jl_i} for $i = 1, \ldots, s$. Moreover, column 1 is all zeros, and every other column has exactly one nonzero entry b_{kj} with $k < j$. Hence, moving the zero rows to the bottom if necessary, B is in

reduced echelon form. The number r of free variables is equal to the number of source nodes in $\mathcal{G}$, and $r \geq 1$, since $\mathcal{G}$ is a rooted tree.

Therefore, when solving for the entries of $\mathbf{v}$ there are three cases:

Case (i). In row 1, the only nonzero entries are $b_{12}, b_{1l_2} \ldots, b_{1l_m}$, where $m = \text{indeg}(1) \geq 1$. Then let $v_1 = t_1$, $v_2 = t_2, \ldots, v_{l_{m-1}} = t_{m-1}$ be free variables, and solve for v_m to obtain

$$v_m = -\frac{1}{b_{1m}} \left(b_{12}t_2 + \cdots + b_{1(m-1)}t_{m-1} \right). \tag{5.1}$$

Case (ii). In row j, where node j is not a source, the only nonzero entries are $b_{jl_1}, \ldots, b_{jl_s}$, where $s = \text{indeg}(j)$. Again, let $v_{l_1}, \ldots, v_{l_{s-1}}$ be free variables, and hence

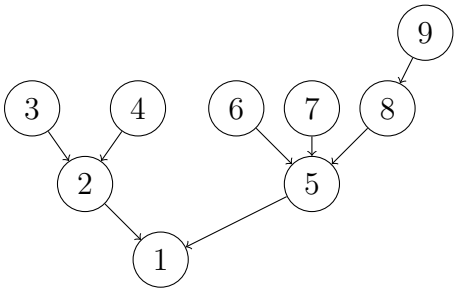
$$v_{l_s} = -\frac{1}{b_{jl_s}} \left(b_{jl_1}v_{l_1} + \cdots + b_{jl_{s-1}}v_{s-1} \right). \tag{5.2}$$

Case (iii). If node j is a source and is the only node connected to some node $k < j$, then the only nonzero entry in row k is b_{kj}, and hence $v_j = 0$.

This produces an eigenvector $\mathbf{v}$ in the span of r linearly independent vectors. Other than the eigenvector $\mathbf{p} = (1, 0, \ldots, 0)^T$, all of these eigenvectors have at least one negative entry by equations (5.1) and (5.2). Therefore, statement (2) of the theorem is proved. □

Thus, regardless of the weights of the directed edges, p_1 is the only nonzero value of the Perron eigenvector $\mathbf{p}$ of B. Therefore, the node of a rooted tree with the most relative importance is the root node, *i.e.*, node 1.

Example 5.1.3. Consider the rooted tree given below with its associated weight matrix B.



$$\begin{bmatrix} 0 & b_{12} & 0 & 0 & b_{15} & 0 & 0 & 0 & 0 \\ 0 & 0 & b_{23} & b_{24} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & b_{56} & b_{57} & b_{58} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & b_{89} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Then with eigenvalue $\lambda = \rho(B) = 0$, solving the equation $(\rho(B)I - B)\mathbf{v} = \mathbf{0}$ or just $B\mathbf{v} = \mathbf{0}$, we see that the number of free variables is equal to $r = 5$; the number of source nodes in the tree $\mathcal{G}$. Moreover, $v_1 = t_1$, $v_2 = t_2$, $v_5 = -\frac{b_{12}}{b_{15}}t_2$, $v_3 = t_3$, $v_4 = -\frac{b_{23}}{b_{24}}t_3$, $v_6 = t_4$, $v_7 = t_5$, $v_8 = -\frac{1}{b_{58}}(b_{56}t_4 + b_{57}t_5)$, and $v_9 = 0$. This gives a basis for the five dimensional eigenspace E_0 of the spectral radius $\rho(B) = 0$.

$$\mathbf{v} = \begin{bmatrix} 1 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} t_1 + \begin{bmatrix} 0 \\ 1 \\ 0 \\ 0 \\ -\frac{b_{12}}{b_{15}} \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} t_2 + \begin{bmatrix} 0 \\ 0 \\ 1 \\ -\frac{b_{23}}{b_{24}} \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} t_3 + \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 1 \\ 0 \\ -\frac{b_{56}}{b_{58}} \\ 0 \end{bmatrix} t_4 + \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 1 \\ -\frac{b_{57}}{b_{58}} \\ 0 \end{bmatrix} t_5 \quad (5.3)$$

Note that four of the five basis eigenvectors contain a negative entry. Hence, the nonnegative Perron eigenvector is given by $\mathbf{p} = (1, 0, 0, 0, 0, 0, 0, 0, 0)^T$.

5.1.2 Directed cycles

Next, consider a directed cycle, *i.e.*, the digraph $(\mathcal{G}, B)$ consisting of n nodes, and the n edges $(1,2),(2,3),\ldots,(n-1,n)$. Thus, $\mathcal{G}$ is just a directed cycle with n nodes (see Figure 5.2). Also note that in this case, $\mathcal{G}$ is strongly connected, so by Theorem 2.2.1, the weight matrix B is irreducible and is given by

$$B = \begin{bmatrix} 0 & 0 & \cdots & 0 & b_{1n} \\ b_{21} & 0 & \cdots & 0 & 0 \\ 0 & b_{32} & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & \cdots & b_{n(n-1)} & 0 \end{bmatrix}. \tag{5.4}$$

Note that there is exactly one nonzero entry in every row and column of B. The following result gives the spectral radius and Perron eigenvector of B.

Theorem 5.1.2. *Let $(\mathcal{G}, B)$ be a directed cycle consisting of n nodes the n edges $(1,2),(2,3),\ldots,(n-1,n)$. Then*

(1) *the characteristic polynomial of B is $p_B(\lambda) = \lambda^n - b_{21}b_{32}\cdots b_{1n}$,*

(2) *the unique positive Perron eigenvector associated to the spectral radius $\rho := \rho(B) = \sqrt[n]{b_{21}b_{32}\cdots b_{1n}}$ is given by*

$$\mathbf{p} = \begin{bmatrix} \frac{b_{1n}}{\rho} \\ \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho} \\ \vdots \\ \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho}\cdots\frac{b_{(n-1)(n-2)}}{\rho} \\ 1 \end{bmatrix}. \tag{5.5}$$

Proof: By Theorem 2.1.1 the characteristic polynomial of B is

$$p_B(\lambda) = \lambda^n - \mathrm{tr}(B)\lambda^{n-1} + c_2\lambda^{n-2} + \cdots + c_{n-1}\lambda + (-1)^n \det(B),$$

where $c_r = (-1)^r \sum_{k=1}^{t} M_k^r$ for all $r = 2, \ldots, n-1$, $t = \binom{n}{r}$, and M_k^r, for all $k = 1, \ldots, \binom{n}{r}$ denote the $r \times r$ principal minors of B. Then, since $b_{11}, \ldots, b_{nn}$ are all zero, the trace of B is zero. Similarly, for all $r = 2, \ldots, n-1$ any $r \times r$ principal minor is obtained by deleting at least one of the same row and column from B. Thus, all of these minors are zero and

$$p_B(\lambda) = \lambda^n + (-1)^n \det(B).$$

Now, for the determinant of B, cofactor expansion along the first column gives

$$\det \begin{bmatrix} 0 & 0 & \cdots & 0 & b_{1n} \\ b_{21} & 0 & \cdots & 0 & 0 \\ 0 & b_{32} & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & \cdots & b_{n(n-1)} & 0 \end{bmatrix} = -b_{21} \begin{vmatrix} 0 & \cdots & 0 & b_{1n} \\ b_{32} & \cdots & 0 & 0 \\ \vdots & \ddots & \vdots & \vdots \\ 0 & \cdots & b_{n(n-1)} & 0 \end{vmatrix}.$$

Continuing in this manner, and expanding along the first column of each new minor of B gives

$$\det(B) = (-1)^{n-2} b_{21} \cdots b_{(n-1)(n-2)} \begin{vmatrix} 0 & b_{1n} \\ b_{n(n-1)} & 0 \end{vmatrix} = (-1)^{n-1} b_{21} \cdots b_{n1}.$$

There, $p_B(\lambda) = \lambda^n - b_{21} \cdots b_{n1}$, and statement (1) holds. For statement

(2), $p_B(\lambda) = 0 \Leftrightarrow \lambda = \sqrt[n]{b_{21}b_{32}\cdots b_{1n}}$. Therefore, regardless of whether n is even or odd, the unique positive real eigenvalue of B is $\rho(B) = \sqrt[n]{b_{21}b_{32}\cdots b_{1n}}$.

Finally, for the unique (up to a positive scalar) Perron eigenvector $\mathbf{p}$ associated to the spectrum $\rho := \rho(B) = \sqrt[n]{b_{21}b_{32}\cdots b_{1n}}$ solve the system

$$(\rho I - B)\mathbf{p} = \mathbf{0}.$$

Without loss of generality, make the last row zero and so

$$\begin{bmatrix} \rho & 0 & \cdots & 0 & -b_{1n} \\ -b_{21} & \rho & \cdots & 0 & 0 \\ 0 & -b_{32} & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & \cdots & 0 & 0 \end{bmatrix} \sim \begin{bmatrix} 1 & 0 & 0 & \cdots & -\frac{b_{1n}}{\rho} \\ -\frac{b_{21}}{\rho} & 1 & 0 & \cdots & 0 \\ 0 & -\frac{b_{32}}{\rho} & 1 & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \cdots & 0 \end{bmatrix}.$$

Hence, let $p_n = t$. This gives one free variable and solving in terms of $p_n = t$ gives $p_1 = \frac{b_{1n}}{\rho}t$, $p_2 = \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho}t$, $\ldots$, $p_{n-1} = \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho}\cdots\frac{b_{(n-1)(n-2)}}{\rho}t$. Therefore, the Perron eigenvector is $\mathbf{p} = (\frac{b_{1n}}{\rho}, \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho}, \ldots, \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho}\cdots\frac{b_{(n-1)(n-2)}}{\rho}, 1)^T$ and statement (2) is proved. □

Therefore, given a network $(\mathcal{G}, B)$ consisting of a single directed cycle, the Perron eigenvector $\mathbf{p} = (p_1, \ldots, p_n)^T$ has entries depending on the entries of B and the spectral radius $\rho(B)$ of B. Thus, in the case of a single directed loop graph, we have the following two statements which are both direct corollaries of Theorem 5.1.2. The first is a sufficient condition for p_n to be the largest entry of the Perron eigenvector $\mathbf{p}$.

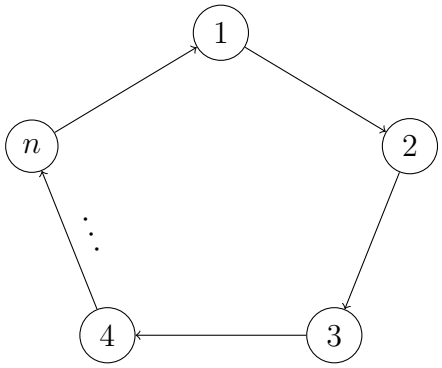


Figure 5.2: The Single Directed Loop Digraph.

Theorem 5.1.3. *Given a matrix B of the form* (5.4)*, if we have that*

$$b_{1n}, b_{21}, b_{32}, \ldots, b_{(n-1)(n-2)} < \rho(B), \tag{5.6}$$

then p_n is the largest entry of the Perron eigenvector $\mathbf{p} = (p_1, \ldots, p_n)^T$ of B.

Proof: From Theorem 5.1.2, we know that

$$\mathbf{p} = \begin{bmatrix} p_1 \\ p_2 \\ \vdots \\ p_{n-1} \\ p_n \end{bmatrix} = \begin{bmatrix} \frac{b_{1n}}{\rho} \\ \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho} \\ \vdots \\ \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho}\cdots\frac{b_{(n-1)(n-2)}}{\rho} \\ 1 \end{bmatrix}. \tag{5.7}$$

Therefore, $p_n = 1$ and if we assume $b_{1n}, b_{21}, b_{32}, \ldots, b_{(n-1)(n-2)} < \rho(B)$, then $p_1, p_2, \ldots, p_{n-1} < 1$. Thus, p_n is the largest entry of $\mathbf{p}$. □

Note that by permuting the entries in the result above, sufficient conditions for any entry p_k, $k = 1, \ldots, n$ to be the largest value in $\mathbf{p}$ can be derived. Therefore, this sufficiently guarantees which node of the network will be ranked as having the most relative importance. The next result gives a necessary

condition for p_n to be the largest entry of the weight matrix B of the network in Figure 5.1.2.

Theorem 5.1.4. *Let B be the matrix given by* (5.4), $\rho := \rho(B) = \sqrt[n]{b_{21}b_{32}\cdots b_{1n}}$, *and let* $\mathbf{p}$ *be given by* (5.5). *Then p_n is the largest entry of* $\mathbf{p}$, *if and only if*

$$\begin{aligned} b_{1n} &< \rho \\ b_{1n}b_{21} &< \rho^2 \\ &\vdots \\ b_{1n}b_{21}\cdots b_{n(n-1)} &< \rho^{n-1}. \end{aligned}$$

Proof: Assume that $1 = p_n > p_k$ for all $k = 1\ldots, n-1$. Theorem 5.1.2 states that the Perron eigenvector is given by

$$\mathbf{p} = \begin{bmatrix} \frac{b_{1n}}{\rho} \\ \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho} \\ \vdots \\ \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho}\cdots\frac{b_{(n-1)(n-2)}}{\rho} \\ 1 \end{bmatrix}.$$

Hence, $\frac{b_{1n}}{\rho} < 1, \ldots, \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho}\cdots\frac{b_{(n-1)(n-2)}}{\rho} < 1$.

Conversely, if we have

$$\begin{aligned} b_{1n} &< \rho \\ b_{1n}b_{21} &< \rho^2 \\ &\vdots \\ b_{1n}b_{21}\cdots b_{(n-1)(n-2)} &< \rho^{n-1}, \end{aligned}$$

then we have that $p_1 = \frac{b_{1n}}{\rho} < 1, \ldots, p_{n-1} = \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho}\cdots\frac{b_{(n-1)(n-2)}}{\rho} < 1$, and $p_3 = 1$, so that p_n is the largest entry of $\mathbf{p}$ and the result is shown. □

Results similar to Theorem 5.1.4 can also be stated for the entries $p_1, \ldots, p_{n-1}$ of $\mathbf{p}$. We now consider several examples that illustrate the results of Theorem 5.1.3 and Theorem 5.1.4 above.

Remark 5.1.1. The necessary direction of Theorem 5.1.4 is best stated in its contrapositive form. If the conditions

$$b_{1n} < \rho$$

$$b_{1n}b_{21} < \rho^2$$

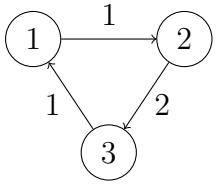
$$\vdots$$

$$b_{1n}b_{21}\cdots b_{(n-1)(n-2)} < \rho^{n-1}.$$

are not satisfied , then p_n is not the largest entry of $\mathbf{p}$.

Example 5.1.4. The following directed cycle $(\mathcal{G}, B)$ consisting of the three nodes $V = \{1, 2, 3\}$, directed edge set $E = \{(1, 2), (2, 3), (3, 1)\}$, and weights $b_{21} = \omega(1, 2) = 1,\ b_{32} = \omega(2, 3) = 2,\ b_{13} = \omega(3, 1) = 1$ is given by

$$B = \begin{bmatrix} 0 & 0 & 1 \\ 1 & 0 & 0 \\ 0 & 2 & 0 \end{bmatrix}$$



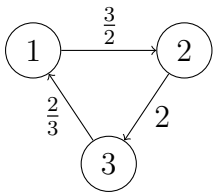
Note that in this case $b_{13} = b_{21} = 1 < \rho(B) = \sqrt[3]{2} \approx 1.2599$. Therefore, the sufficient conditions of Theorem 5.1.3 are satisfied and

$$\mathbf{p} = \begin{bmatrix} \frac{1}{\sqrt[3]{2}} \\ \frac{1}{\sqrt[3]{2}}\frac{1}{\sqrt[3]{2}} \\ 1 \end{bmatrix} \approx \begin{bmatrix} 0.79 \\ 0.63 \\ 1.00 \end{bmatrix}.$$

Hence, p_3 is the largest entry of the Perron vector $\mathbf{p}$.

Example 5.1.5. Next, consider the directed cycle consisting of three nodes, but change the weights slightly. Then $\rho(B) = \sqrt[3]{2} \approx 1.2599$.

$$B = \begin{bmatrix} 0 & 0 & \frac{2}{3} \\ \frac{3}{2} & 0 & 0 \\ 0 & 2 & 0 \end{bmatrix}$$



The Perron eigenvector is

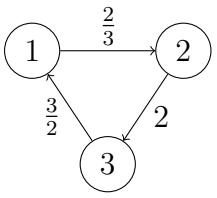
$$\mathbf{p} = \begin{bmatrix} \frac{2}{3\sqrt[3]{2}} \\ \frac{2}{3\sqrt[3]{2}}\frac{3}{2\sqrt[3]{2}} \\ 1 \end{bmatrix} \approx \begin{bmatrix} 0.53 \\ 0.63 \\ 1.00 \end{bmatrix}.$$

Note that $b_{21} = \frac{3}{2} > 1$, and so it is not necessary to have $b_{13} < \rho(B)$, and $b_{21} < \rho(B)$ for p_3 to be the largest entry of the Perron vector $\mathbf{p}$. However, the necessary conditions of Theorem 5.1.4 are satisfied. Indeed, p_3 is the largest entry of $\mathbf{p}$ and

$$b_{13} = \frac{2}{3} < \sqrt[3]{2} = \rho(B),$$
$$b_{13}b_{21} = \frac{2}{3} \cdot \frac{3}{2} = 1 < \sqrt[3]{4} = \rho(B)^2.$$

Example 5.1.6. Again, consider the directed cycle consisting of three nodes, but switch the weights of the previous example slightly. Then $\rho(B) = \sqrt[3]{2} \approx 1.2599$.

$$B = \begin{bmatrix} 0 & 0 & \frac{3}{2} \\ \frac{2}{3} & 0 & 0 \\ 0 & 2 & 0 \end{bmatrix}$$



The Perron eigenvector is

$$\mathbf{p} = \begin{bmatrix} \frac{3}{2\sqrt[3]{2}} \\ \frac{2}{3\sqrt[3]{2}} \frac{3}{2\sqrt[3]{2}} \\ 1 \end{bmatrix} \approx \begin{bmatrix} 1.19 \\ 1.58 \\ 1.00 \end{bmatrix}.$$

Therefore, using the contrapositive of Theorem 5.1.4, we see that $b_{13} = \frac{3}{2} > \rho \approx 1.2599$, implies p_3 is not the largest entry of $\mathbf{p}$.

5.1.3 Unicyclic digraphs

Consider the unicyclic digraph $(\mathcal{G}, B)$ consisting of a central cycle of n nodes, and each of these nodes $1, 2, \ldots, n$ having directed trees leading into them. Then $\mathcal{G} = (V, E)$ has nodes $1, 2, \ldots, n, n+1, \ldots, N$, where V can be split into the "cycle node" set $V_1 = \{1, 2, \ldots, n\}$ and the "tree node" set $V_2 = \{n+1, \ldots, N\}$. (For an example of such a unicyclic digraph see Figure 5.3.)

Theorem 5.1.5. *Let $(\mathcal{G}, B)$ be a unicyclic digraph, $p_B(\lambda)$ the characteristic polynomial of the weight matrix B, and $\rho := \rho(B)$ the spectral radius of B. Then we have the following*

(1) $p_B(\lambda) = \lambda^{N-n}(\lambda^n - b_{21}b_{32}\cdots b_{1n})$,

(2) $\rho = \sqrt[n]{b_{21}b_{32}\cdots b_{1n}}$, *and the Perron eigenvector is given by*

$$\mathbf{p} = \begin{bmatrix} \frac{b_{1n}}{\rho} \\ \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho} \\ \vdots \\ \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho}\cdots\frac{b_{(n-1)(n-2)}}{\rho} \\ 1 \\ 0 \\ \vdots \\ 0 \end{bmatrix}. \tag{5.8}$$

Proof: As with the case of a directed tree rooted at node 1, we label the cycle nodes as $1, 2, \ldots, n$, and then label the tree nodes $n+1, \ldots, N$. To prove statement (1), consider the determinant of $\lambda I - B$ which has the form

$$\begin{bmatrix} \lambda & 0 & 0 & \cdots & 0 & -b_{1n} & -b_{1(n+1)} & * & \cdots & * \\ -b_{21} & \lambda & 0 & \cdots & 0 & 0 & 0 & * & \cdots & * \\ 0 & -b_{32} & \lambda & \cdots & 0 & 0 & 0 & * & \cdots & * \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \vdots & \cdots & \vdots \\ 0 & 0 & 0 & \cdots & \lambda & 0 & 0 & * & \cdots & * \\ 0 & 0 & 0 & \cdots & -b_{n(n-1)} & \lambda & 0 & * & \cdots & * \\ 0 & 0 & 0 & \cdots & 0 & 0 & \lambda & * & \cdots & * \\ 0 & 0 & 0 & \cdots & 0 & 0 & 0 & \lambda & \cdots & * \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \cdots & 0 & 0 & 0 & 0 & 0 & \lambda \end{bmatrix}. \tag{5.9}$$

Here, an asterix "$*$" represents either zero or $-b_{jk}$ depending on whether or not the directed edge (k, j) exists in $\mathcal{G}$.

Then note that $\lambda I - B$ contains of two square diagonal blocks B_1 and B_2 given by

$$B_1 = \begin{bmatrix} \lambda & 0 & 0 & \cdots & 0 & -b_{1n} \\ -b_{21} & \lambda & 0 & \cdots & 0 & 0 \\ 0 & -b_{32} & \lambda & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & \lambda & 0 \\ 0 & 0 & 0 & \cdots & -b_{n(n-1)} & \lambda \end{bmatrix}_{n\times n},$$

and

$$B_2 = \begin{bmatrix} \lambda & * & \cdots & * \\ 0 & \lambda & \cdots & * \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \lambda \end{bmatrix}_{(N-n)\times(N-n)}.$$

Therefore, since $\lambda I - B$ has all zero entries below these B_1, the determinant is the product of $\det(B_1)$ and $\det(B_2)$. By Theorem 5.1.2, we know that $\det(B_1) = \lambda^n - b_{21}\cdots b_{1n}$, and B_2 is upper-triangular, so that $\det(B_2) = \lambda^{N-n}$. Thus,

$$p_B(\lambda) = \det(\lambda I - B) = \det(B_1)\cdot\det(B_2) = \lambda^{N-n}(\lambda^n - b_{21}\cdots b_{1n}).$$

This shows that statement (1) is true. For the spectral radius $\rho(B)$ of B, note that (regardless of whether n is even or odd) the only real and positive solution to $p_B(\lambda) = 0$ is the eigenvalue $+\sqrt[n]{b_{21}b_{32}\cdots b_{1n}}$, and this implies $\rho(B) = \sqrt[n]{b_{21}b_{32}\cdots b_{1n}}$. For the second part of statement (2), we must find the

Perron eigenvector $\mathbf{p}$ associated to $\rho := \rho(B)$.

From (5.9), any nonzero entry $-b_{jk}$ where $j < k$ can be eliminated using λ in position (k, k) and $(\rho I - B)$ is equivalent to a matrix

$$M = \begin{bmatrix} M_1 & 0 \\ 0 & M_2 \end{bmatrix},$$

where

$$M_1 = \begin{bmatrix} \rho & 0 & \cdots & 0 & -b_{1n} \\ -b_{21} & \rho & \cdots & 0 & 0 \\ 0 & -b_{32} & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & \cdots & -b_{n(n-1)} & \rho \end{bmatrix},$$

and

$$M_2 = \begin{bmatrix} \rho & 0 & \cdots & 0 \\ 0 & \rho & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \rho \end{bmatrix}.$$

Note that M_1 is an $n \times n$ matrix and M_2 is $(N-n) \times (N-n)$, and therefore $p_k = 0$ for all $k = n+1, \ldots, N$ and by Theorem 5.1.2, $p_1, \ldots, p_n$ are as desired. □

Hence, all entries p_i of the Perron eigenvector $\mathbf{p}$ are zero except for p_1, $p_2, \ldots, p_n$, and therefore the most important node will be one of these cycle nodes $1, 2, \ldots, n$.

Thus, as a corollary, the following result reduces the importance of the nodes of the entire unicyclic digraph to those of the directed cycle.

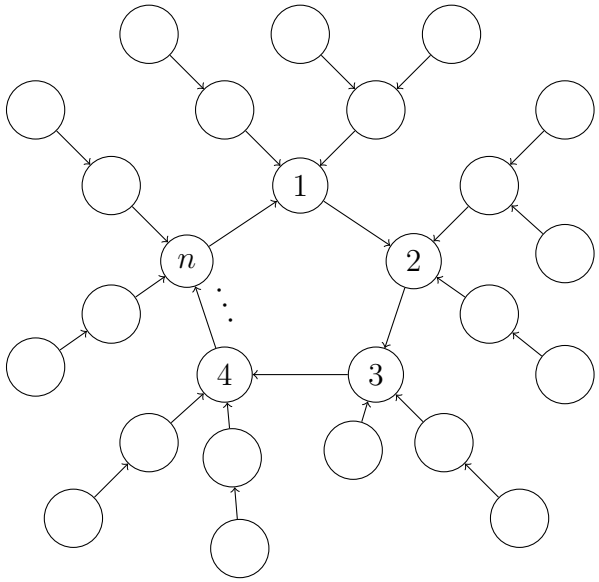


Figure 5.3: A Unicyclic Digraph.

Theorem 5.1.6. *Let $(\mathcal{G}, B)$ be a unicyclic digraph with N nodes, $\rho := \rho(B)$ be the spectral radius of B, and let $\mathbf{p} = (p_1, \ldots, p_N)^T$ be the Perron eigenvector of B associated to ρ. If we let $1, \ldots, n$ be the nodes of the cycle, then $p_k = 0$, for all $k = n+1, \ldots, N$, and*

(1) *$b_{1n}, b_{21}, \ldots, b_{(n-1)(n-2)} < \rho(B)$, then p_n is the largest entry of the Perron eigenvector $\mathbf{p} = (p_1, \ldots, p_n, p_{n+1}, \ldots, p_N)^T$ of B;*

(2) *p_n is the largest entry of $\mathbf{p}$, if and only if*

$$b_{1n}b_{21}b_{32}\cdots b_{n(n-1)} < \rho^{n-1}$$
$$b_{1n}b_{21}\cdots b_{(n-1)(n-2)} < \rho^{n-2}$$
$$\vdots$$
$$b_{1n} < \rho.$$

Proof: From Theorem 5.1.5, the Perron eigenvector $\mathbf{p}$ of a unicyclic graph

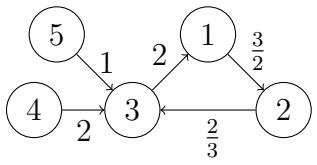
is given by

$$\mathbf{p} = \begin{bmatrix} \frac{b_{1n}}{\rho} \\ \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho} \\ \vdots \\ \frac{b_{1n}}{\rho}\frac{b_{21}}{\rho}\cdots\frac{b_{(n-1)(n-2)}}{\rho} \\ 1 \\ 0 \\ \vdots \\ 0 \end{bmatrix}.$$

Therefore, see Theorem 5.1.4 and Theorem 5.1.3 for the necessary and sufficient conditions, respectively, for the entries of $\mathbf{p}$ for a directed cycle graph.

□

Example 5.1.7. In the network $(\mathcal{G}, B)$ below the spectral radius is $\rho(B) = \sqrt[3]{2}$ and since $b_{21} = \frac{3}{2} > \sqrt[3]{2}$, the weights of the digraph conspire to make $p_2 \approx 1.88$ the largest entry of the Perron eigenvector. Thus, node 2 and not node 3 is ranked the most important node of the network.



$$\rho(B) = \sqrt[3]{2}$$
$$b_{32} < \rho(B) < b_{21} < b_{13}$$
$$\mathbf{p} = (1.56, 1.88, 1, 0, 0)^T$$
$$p_3 < p_1 < p_2$$

Also note that regardless of the weights of the edges in the tree rooted at node 3, node 2 is rated the highest, and therefore ranked as most important.

5.1.4 Multi-cyclic digraphs

Consider a digraph $(\mathcal{G}, B)$ consisting of m unicyclic digraphs leading into a single node 1. More specifically, let the first cycles consist of the nodes $2, \ldots, s_1$,

cycle two have nodes $s_1 + 1, \ldots, s_2$, and so on until the m-th cycle contains nodes $s_{m-1}+1, \ldots, s_m$, where $s_1 = n_1+1$ and for all $k = 2, \ldots, m$ $s_k = s_{k-1}+n_k$ are the actual values of the nodes in $\mathcal{G}$ and n_k is the number of nodes in the k-th cycle.

Then $\mathcal{G} = (V, E)$, with vertex set V given by

$$V = \{1\} \cup \{2, \ldots, s_1\} \cup \{s_1 + 1, \ldots, s_2\} \cup \cdots \cup \{s_{m-1} + 1, \ldots, s_m\} \cup W,$$

where W is the set of all other nodes, *i.e.*, the "tree nodes" of $\mathcal{G}$.

This means that all entries of the weight matrix B are zero below the main diagonal except for the entries $b_{k(k-1)}$ in one of the m cycles of $\mathcal{G}$. Therefore, B can be viewed as a block diagonal matrix, and therefore the determinant of $\lambda I - B = p_B(\lambda)$ can be computed. This, together with the Perron eigenvector of B are given in the result below.

Theorem 5.1.7. *Let $(\mathcal{G}, B)$ consist of m unicyclic digraphs leading into a single node 1, and $\rho := \rho(B)$ be the spectral radius of B. Then*

(1) $p_B(\lambda) = \lambda^{N-(n_1+\cdots+n_m)} p_1(\lambda) \cdots p_m(\lambda)$, *where* $p_1(\lambda) = \lambda^{n_1} - b_{32} \cdots b_{2s_1}, \ldots$
$p_m(\lambda) = \lambda^{n_m} - b_{(s_{m-1}+2)(s_{m-1}+1)} \cdots b_{(s_{m-1}+1)s_m}$,

(2) *if* $\rho = max\{ \sqrt[n_1]{b_{32} \cdots b_{2s_1}}, \ldots, \sqrt[n_m]{b_{(s_{m-1}+2)(s_{m-1}+1)} \cdots b_{(s_{m-1}+1)s_m}} \}$ *is unique, the Perron eigenvector is given by*

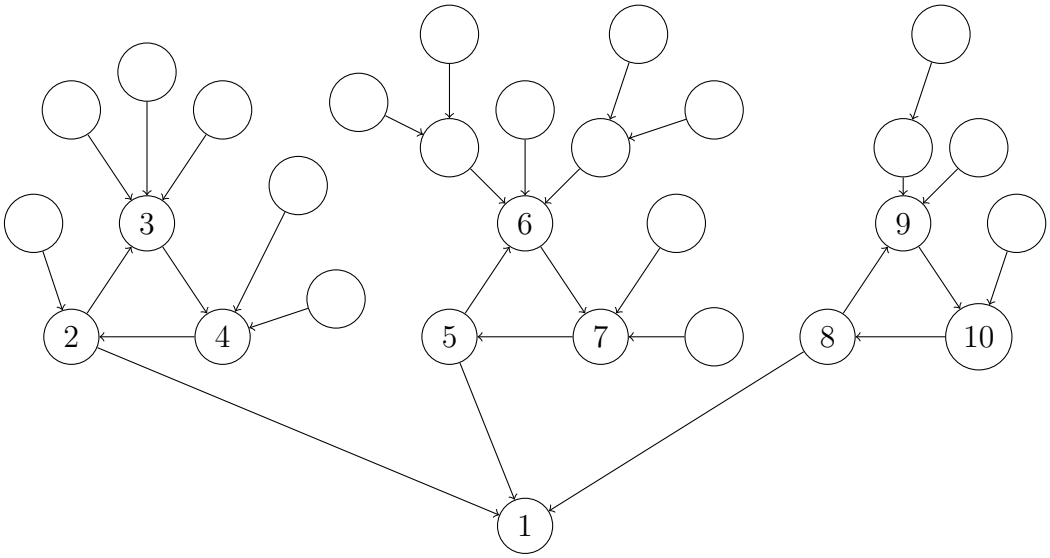


Figure 5.4: A Multi-cyclic Digraph leading to node 1.

$$\mathbf{p} = \begin{bmatrix} \frac{b_{1(s_k+1)}}{\rho} \frac{b_{(s_{k-1}+1)s_k}}{\rho} \\ 0 \\ \vdots \\ 0 \\ \frac{b_{(s_{k-1}+1)s_k}}{\rho} \\ \vdots \\ \frac{b_{(s_{k-1}+2)(s_{k-1}+1)}}{\rho} \cdots \frac{b_{(s_{k-1}+1)s_k}}{\rho} \\ 1 \\ 0 \\ \vdots \\ 0 \end{bmatrix}, \tag{5.10}$$

where $\rho = \sqrt[n_k]{b_{(s_{k-1}+2)(s_{k-1}+1)} \cdots b_{(s_{k-1}+1)s_k}}$*, and* k *is the index where the maximum occurs for* ρ*.*

Proof: As mentioned in the paragraph above the theorem, $\lambda I - B$ can be written in block form as follows

$$B = \begin{bmatrix} \lambda & * & \cdots & * & * \\ 0 & B_1 & \cdots & * & * \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & \cdots & B_m & * \\ 0 & 0 & \cdots & 0 & B_{m+1} \end{bmatrix},$$

where

$$B_k = \begin{bmatrix} \lambda & 0 & \cdots & 0 & -b_{(s_{k-1}+1)s_k} \\ -b_{(s_{k-1}+2)(s_{k-1}+1)} & \lambda & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & \cdots & -b_{s_k(s_k-1)} & \lambda \end{bmatrix},$$

for all $k = 1, \ldots, m$ and

$$B_{m+1} = \begin{bmatrix} \lambda & * & \cdots & * \\ 0 & \lambda & \cdots & * \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \lambda \end{bmatrix}.$$

By Theorem 5.1.2, $\det(B_k) = \lambda^{n_k} - b_{(s_{k-1}+2)(s_{k-1}+1)} \cdots b_{(s_{k-1}+1)s_k}$, for all $k = 1 \ldots, m$, and $\det(B_{m+1}) = \lambda^{N-1-n_1-\cdots-n_m}$ since it is upper-triangular and square of size $N - 1 - (n_1 + \cdots + n_m)$. Thus,

$$p_B(\lambda) = \lambda^{N-(n_1+\cdots+n_m)}(\lambda^{n_1} - b_{32} \cdots b_{2s_1}) \cdots (\lambda^{n_m} - b_{(s_{m-1}+2)(s_{m-1}+1)} \cdots b_{(s_{m-1}+1)s_m}).$$

Hence, $\rho(B)$ is the largest real root of $p_B(\lambda)$, .i.e,

$$\rho = \max\{\sqrt[n_1]{b_{32}\cdots b_{2s_1}}, \ldots, \sqrt[n_m]{b_{(s_{m-1}+2)(s_{m-1}+1)}\cdots b_{(s_{m-1}+1)s_m}}\}.$$

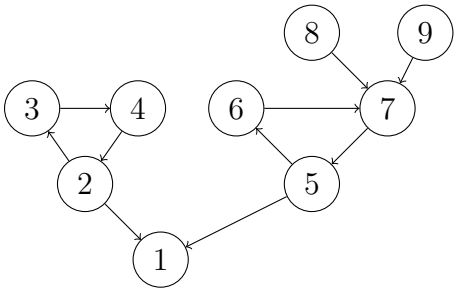
Finally, for the Perron eigenvector associated to ρ, note that if we let $\rho = \max\{\rho_1, \ldots, \rho_m\}$, then there is some k such that $\rho = \rho_k$ (we need $\rho_k \neq \rho_j$ for all $k \neq j$). Therefore, solving $(\rho_k I - B)\mathbf{p} = \mathbf{0}$, we see that any nonzero entry $-b_{jk}$ where $j < k$ can be eliminated using ρ_k in the (k,k)-th position in B. Thus, for any $j \neq k$, $j = 1, \ldots, m$, the block B_j is equivalent to a diagonal matrix. Hence, we see that for all $j \neq 1, s_{k-1}+1, \ldots, s_k$ it follows that $p_j = 0$ in the eigenvector $\mathbf{p}$. Thus, using Theorem 5.1.2, $\mathbf{p}$ is given by

$$\mathbf{p} = \left(\frac{b_{1(s_k+1)}}{\rho}\frac{b_{(s_{k-1}+1)s_k}}{\rho}, 0\ldots, 0, \frac{b_{(s_{k-1}+1)s_k}}{\rho}, \ldots, 1, 0, \ldots, 0\right)^T,$$

as desired. □

Note that depending on which of the cycles ends up having the maximum attained for the spectral radius there may be no zeros between p_1 and the next positive entry in the expression for the Perron eigenvector.

Example 5.1.8. Consider the dicyclic digraph rooted at 1 given below with its associated weight matrix B.



$$\begin{bmatrix} 0 & b_{12} & 0 & 0 & b_{15} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & b_{24} & 0 & 0 & 0 & 0 & 0 \\ 0 & b_{32} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & b_{43} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & b_{57} & 0 & 0 \\ 0 & 0 & 0 & 0 & b_{65} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & b_{76} & 0 & b_{78} & b_{79} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Therefore $p_B(\lambda) = \lambda^3(\lambda^3 - b_{24}b_{32}b_{43})(\lambda^3 - b_{57}b_{65}b_{76})$, so that the spectral radius is $\rho(B) = \max\{\sqrt[3]{b_{24}b_{32}b_{43}},\ \sqrt[3]{b_{57}b_{65}b_{76}}\}$. Suppose $\rho = \sqrt[3]{b_{24}b_{32}b_{43}}$, then the Perron eigenvector is given by

$$\mathbf{p} = \left[\frac{b_{12}}{\rho}\frac{b_{24}}{\rho}, \frac{b_{24}}{\rho}, \frac{b_{43}}{\rho}\frac{b_{24}}{\rho}, 1, 0, 0, 0, 0, 0\right]^T.$$

5.2 The Perron Vector of $M = \mathbf{diag}(d_i) \cdot B$

This section investigates what happens to the Perron vector entries if we multiply the weight matrix B of a network $(\mathcal{G}, B)$ by a diagonal matrix $D = \mathrm{diag}(d_i)$, where $d_i > 0$ for all i. Then, for ODE models on networks like the SIR model of Chapter 3, insight can be gained into how the local dynamics affect equilibrium ranking. This is due to the fact that the equilibrium ranking vector $\mathbf{p}$ is the Perron vector of a matrix $M = D \cdot B$, where $D = \mathrm{diag}(\frac{S_k^*}{\gamma_k + b_k})$ is a diagonal matrix containing local ODE parameter values. Similarly, in Chapter 4, an approximate equilibrium ranking is considered, that also uses the Perron eigenvector of a matrix of the form $M = D \cdot B$, with D diagonal.

The same digraph structures $(\mathcal{G}, B)$ as in Section 5.1 are considered. Multiplying the weight matrix B by a diagonal matrix $D = \mathrm{diag}(d_i)$, allows for the analysis of the effects on the entries of the Perron eigenvector, and hence the ranking order, in each case.

5.2.1 Directed tree rooted at a single node

For a directed tree $(\mathcal{G}, B)$, rooted at node 1, the Perron eigenvector $\mathbf{p} = (p_1, \ldots, p_n)^T$ of the weight matrix B has all entries p_i equal to zero except for $p_1 = 1$. Therefore, multiplying B by a diagonal matrix D still gives $p_i = 0$, for

$i = 2, \ldots, n$ and $p_1 = 1$. Hence, as long as $d_{nn} \neq 0$, the Perron vector remains unchanged in this case. This essentially proves the following statement.

Theorem 5.2.1. *Let $(\mathcal{G}, B)$ be a directed tree with n nodes rooted at node 1, $D = diag(d_i)$ be a diagonal matrix such that $d_i > 0$ for all $i = 1, \ldots, n$, and let $M = D \cdot B$. Then*

(1) *the characteristic polynomial of M is $p_M(\lambda) = \lambda^n$,*

(2) *the Perron eigenvector associated to the spectral radius $\rho(M) = 0$ is given by $\mathbf{v} = (1, 0, \ldots, 0)^T$.*

Proof: $M = D \cdot B$ is also upper-triangular with all diagonal entries equal to zero. Hence, $p_M(\lambda) = \lambda^n$ and therefore $\rho(M) = 0$. Solving $M\mathbf{x} = \mathbf{0}$ for the basis of the eigenspace E_0, as in the proof of Theorem 5.1.1 gives the Perron vector as $\mathbf{v} = (1, 0, \ldots, 0)^T$. □

Therefore, in the case of a directed tree rooted at node 1, the largest entry of the Perron ranking vector $\mathbf{v}$ of the matrix $M = D \cdot B$ remains entry v_1, and hence the root, node 1, is the most important node of the network.

Example 5.2.1. If $(\mathcal{G}, B)$ is the directed tree rooted 1 such that $\mathcal{G} = (V, E)$, where $|V| = 5$, and $E = \{(2,1), (3,1), (4,3), (5,3)\}$. Then, considering the diagonal matrix $D = \mathrm{diag}(d_i)$, we obtain

$$M = D \cdot B = \begin{bmatrix} 0 & d_{11}b_{12} & d_{11}b_{13} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & d_{33}b_{34} & d_{33}b_{35} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}.$$

Thus, $p_M(\lambda) = \lambda^5$, and if we solve $M\mathbf{x} = \mathbf{0}$, we get

$$\mathbf{x} = \begin{bmatrix} t_1 \\ -\frac{b_{13}}{b_{12}} t_2 \\ t_2 \\ -\frac{b_{35}}{b_{34}} t_3 \\ t_3 \end{bmatrix} = \begin{bmatrix} 1 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} t_1 + \begin{bmatrix} 0 \\ -\frac{b_{13}}{b_{12}} \\ 1 \\ 0 \\ 0 \end{bmatrix} t_2 + \begin{bmatrix} 0 \\ 0 \\ 0 \\ -\frac{b_{35}}{b_{34}} \\ 1 \end{bmatrix} t_3.$$

Therefore, $\mathbf{v} = (1, 0, 0, 0, 0)^T$ is the Perron eigenvector of $M = D \cdot B$.

5.2.2 Cycle digraphs with n nodes

Next, consider the directed cycle graph $(\mathcal{G}, B)$ with n nodes (see Figure 5.2). Since $\mathcal{G}$ is strongly connected, B is irreducible. Therefore, if $D = \mathrm{diag}(d_i)$, where $d_i > 0$ for all i, then the matrix $M = D \cdot B$ is also irreducible and is given by

$$M = D \cdot B = \begin{bmatrix} 0 & 0 & \cdots & 0 & d_1 b_{1n} \\ d_2 b_{21} & 0 & \cdots & 0 & 0 \\ 0 & d_3 b_{32} & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & \cdots & d_n b_{n(n-1)} & 0 \end{bmatrix} \tag{5.11}$$

Theorem 5.2.2. *Let $(\mathcal{G}, B)$ be a directed cycle with node set $V = \{1, 2, \ldots, n\}$ and edge set $E = \{(1,2), (2,3), \ldots, (n-1, n)\}$, and let $D = diag(d_i)$, where $d_i > 0$ for $i = 1, 2, \ldots, n$. If $M = D \cdot B$, then*

(1) $p_M(\lambda) = \lambda^n - (d_1 \cdots d_n)(b_{21} b_{32} \cdots b_{1n})$,

(2) *the Perron vector associated to* $\rho := \rho(M) = \sqrt[n]{(d_1 \cdots d_n)(b_{21} b_{32} \cdots b_{1n})} =$

$\sqrt[n]{d_1 \cdots d_n} \cdot \rho(B)$ is given by

$$\mathbf{v} = \begin{bmatrix} d_1 \frac{b_{1n}}{\rho} \\ d_1 d_2 \frac{b_{1n}}{\rho} \frac{b_{21}}{\rho} \\ \vdots \\ d_1 \cdots d_{n-1} \frac{b_{1n}}{\rho} \cdots \frac{b_{(n-1)(n-2)}}{\rho} \\ 1 \end{bmatrix}. \tag{5.12}$$

Proof:

(1) $M = D \cdot B$ in (5.11) has the same nonzero entries as B given by (5.4). Therefore, using an argument similar to that of Theorem 5.1.2 part (1), the determinant of M is the product of the nonzero entries, the trace of M and all other principal $r \times r$ minors of M are zero so that

$$p_M(\lambda) = \lambda^n - (d_1 \cdots d_n)(b_{21} b_{32} \cdots b_{1n}).$$

(2) Again, similar to the arguments used in Theorem 5.1.2 part (2), the only positive real root of $p_M(\lambda)$ is $\sqrt[n]{(d_1 \cdots d_n)(b_{21} b_{32} \cdots b_{1n})}$ which is equal to $\rho(M)$ by the Perron-Fröbenius Theorem (see section 2.1.3). Solving $(\rho I - M)\mathbf{v} = \mathbf{0}$, gives $\mathbf{v}$ as described by (5.12).

□

Theorem 5.2.3. *Let $(\mathcal{G}, B)$ be as in Theorem 5.2.2, $D = diag(d_i)$, where $d_i > 0$ for $i = 1, 2, \ldots, n$, $M = D \cdot B$, and set $d := \sqrt[n]{d_1 \cdots d_n}$ and $\rho := \rho(M)$. Assume that $(\mathcal{G}, B)$ satisfies Theorem 5.1.3, i.e., $b_{1n}, b_{21}, \ldots, b_{(n-1)(n-2)} < \rho(B)$ so that the largest entry of the Perron vector $\mathbf{p}$ of B is p_n. Let $\mathbf{v}$ be the Perron eigenvector of M associated to $\rho = d \cdot \rho(B)$. If $d_1, d_2, \ldots, d_{n-1} < d$, then v_n is*

the largest entry of the Perron eigenvector $\mathbf{v}$ *of* M*.*

Proof: Theorem 5.2.2 gives the Perron eigenvector as

$$\mathbf{v} = \begin{bmatrix} d_1 \frac{b_{1n}}{\rho} \\ d_1 d_2 \frac{b_{1n}}{\rho} \frac{b_{21}}{\rho} \\ \vdots \\ d_1 \cdots d_{n-1} \frac{b_{1n}}{\rho} \cdots \frac{b_{(n-1)(n-2)}}{\rho} \\ 1 \end{bmatrix} = \begin{bmatrix} \frac{d_1}{d} \frac{b_{1n}}{\rho(B)} \\ \frac{d_1}{d} \frac{d_2}{d} \frac{b_{1n}}{\rho(B)} \frac{b_{21}}{\rho(B)} \\ \vdots \\ d_1 \cdots d_{n-1} \frac{b_{1n}}{\rho} \cdots \frac{b_{(n-1)(n-2)}}{\rho} \\ 1 \end{bmatrix}.$$

Therefore, since $b_{1n}, b_{21}, \ldots, b_{(n-1)(n-2)} < \rho(B)$, and if we are also assuming that $d_1, d_2, \ldots, d_{n-1} < d$ then every entry $v_k < 1$, for $k = 1, \ldots, n-1$. Thus, since $v_n = 1$, it is the largest entry of $\mathbf{v}$. □

Theorem 5.2.4. *Let* $(\mathcal{G}, B)$ *be as in Theorem* 5.2.2*,* $D = diag(d_i)$*, where* $d_i > 0$ *for* $i = 1, 2, \ldots, n$*,* $M = D \cdot B$*, and set* $d := \sqrt[n]{d_1 \cdots d_n}$ *and* $\rho := \rho(B)$*. Assume that* $(\mathcal{G}, B)$ *satisfies Theorem* 5.1.4*. If*

$$\begin{gathered} d_1 d_2 \cdots d_{n-1} < d^{n-1} \\ d_1 d_2 \cdots d_{n-2} < d^{n-2} \\ \vdots \\ d_1 < d, \end{gathered}$$

then v_n *is the largest entry of* $\mathbf{v}$*.*

Proof: If

$$\left\{ \begin{array}{c} b_{1n}b_{21}\cdots b_{(n-1)(n-2)} < \rho^{n-1} \\ \vdots \\ b_{1n}b_{21} < \rho^2 \\ b_{1n} < \rho \end{array} \right\} \quad \text{and} \quad \left\{ \begin{array}{c} d_1 \cdots d_{n-1} < d^{n-1} \\ \vdots \\ d_1 d_2 < d^2 \\ d_1 < d \end{array} \right\},$$

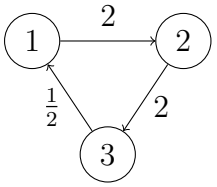
then by Theorem 5.2.2, for all $k = 1, \ldots, n-1$ entry v_k of $\mathbf{v}$ is given by

$$v_k = \left(\frac{d_1}{d} \cdots \frac{d_k}{d}\right) \cdot \left(\frac{b_{1n}}{\rho} \cdots \frac{b_{k(k-1)}}{\rho}\right) < 1 \cdot 1 = 1.$$

On the other hand $v_n = 1$, and hence is the largest entry of $\mathbf{v}$. □

Example 5.2.2. Consider the following directed cycle $(\mathcal{G}, B)$ consisting of the three nodes $V = \{1, 2, 3\}$, directed edge set $E = \{(1,2), (2,3), (3,1)\}$, and fixed weights $b_{21} = \omega(1,2) = 2,\ b_{32} = \omega(2,3) = 2,\ b_{13} = \omega(3,1) = \frac{1}{2}$, given by

$$B = \begin{bmatrix} 0 & 0 & \frac{1}{2} \\ 2 & 0 & 0 \\ 0 & 2 & 0 \end{bmatrix}$$



Then the Perron eigenvector of the weight matrix B alone is given by

$$\mathbf{p} = \begin{bmatrix} p_1 \\ p_2 \\ p_3 \end{bmatrix} \approx \begin{bmatrix} 0.40 \\ 0.63 \\ 1.00 \end{bmatrix}.$$

Thus, p_3 is the largest entry of $\mathbf{p}$ and hence node 1 is ranked as the most important node based on the network's structure alone.

To illustrate Theorem 5.2.3, consider multiplying B by two different diagonal matrices D_1 and D_2 given by

$$D_1 = \begin{bmatrix} \frac{2}{3} & 0 & 0 \\ 0 & \frac{3}{2} & 0 \\ 0 & 0 & 2 \end{bmatrix} \quad \text{and} \quad D_2 = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 2 \end{bmatrix}.$$

This gives the matrices

$$M_1 = D_1 \cdot B = \begin{bmatrix} 0 & 0 & \frac{1}{3} \\ 3 & 0 & 0 \\ 0 & 4 & 0 \end{bmatrix} \quad \text{and} \quad M_2 = D_2 \cdot B = \begin{bmatrix} 0 & 0 & \frac{1}{2} \\ 2 & 0 & 0 \\ 0 & 4 & 0 \end{bmatrix}.$$

Therefore, the eigenvectors $\mathbf{v}$ of M_1 and $\mathbf{w}$ of M_2 respectively, are

$$\mathbf{v} \approx \begin{bmatrix} 0.21 \\ 0.39 \\ 1.00 \end{bmatrix} \quad \text{and} \quad \mathbf{w} \approx \begin{bmatrix} 0.31 \\ 0.40 \\ 1.00 \end{bmatrix}$$

Then D_1 does not satisfy Theorem 5.2.3, but v_3 is still the largest entry of $\mathbf{v}$. The matrix D_2 does satisfy the sufficient conditions of Theorem 5.2.3, and so we must have w_3 the largest entry of $\mathbf{w}$.

To illustrate Theorem 5.2.4, consider multiplying B by the diagonal matrix

$$D_3 = \begin{bmatrix} 4 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}, \text{ which gives } M_3 = \begin{bmatrix} 0 & 0 & 2 \\ 2 & 0 & 0 \\ 0 & 2 & 0 \end{bmatrix}.$$

Therefore, since $d_1 = 4 > d = \sqrt[3]{4}$, u_3 is not larger than the other two

entries of the eigenvector $\mathbf{u} = (1, 1, 1)^T$ of M_3.

5.2.3 Unicyclic digraphs

Consider the unicyclic digraph $(\mathcal{G}, B)$ from Section 5.1.3. Then after multiplying B by a diagonal matrix D with $d_i > 0$ for all i, we can formulate a result similar to Theorem 5.1.5. This result gives the spectral radius and associated Perron eigenvector $\mathbf{v}$ of a matrix $M = D \cdot B$.

Theorem 5.2.5. *Let $(\mathcal{G}, B)$ be a unicyclic digraph, and let $D = diag(d_i)$, where $d_i > 0$ for $i = 1, 2, \ldots, n$. If $M = D \cdot B$, and $\rho := \rho(M)$ the spectral radius of M, then*

(1) $p_M(\lambda) = \lambda^{N-n}(\lambda^n - (d_1 \cdots d_n)(b_{21} b_{32} \cdots b_{1n}))$,

(2) $\rho = \sqrt[n]{(d_1 \cdots d_n)(b_{21} b_{32} \cdots b_{1n})}$, *and the Perron eigenvector is given by*

$$\mathbf{v} = \begin{bmatrix} d_1 \frac{b_{1n}}{\rho} \\ d_1 d_2 \frac{b_{1n}}{\rho} \frac{b_{21}}{\rho} \\ \vdots \\ d_1 \cdots d_{n-1} \frac{b_{1n}}{\rho} \frac{b_{21}}{\rho} \cdots \frac{b_{(n-1)(n-2)}}{\rho} \\ 1 \\ 0 \\ \vdots \\ 0 \end{bmatrix}. \tag{5.13}$$

Proof: $M = D \cdot B$ has the same structure and nonzero entries as B. In particular, the nonzero entries of M are $m_{21} = d_2 \cdot b_{21}, \ldots, m_{1n} = d_1 \cdot b_{1n}$. Therefore, arguments similar to those in the proof of Theorem 5.1.5 show that $p_M(\lambda) = \lambda^{N-n}(\lambda^n - m_{21} m_{32} \cdots m_{1n})$, thus proving part (1).

The only real positive root of $p_M(\lambda)$ is $+\sqrt[n]{m_{21}m_{32}\cdots m_{1n}}$, and hence it follows that $\rho(M) = \sqrt[n]{(d_1\cdots d_n)(b_{21}b_{32}\cdots b_{1n})}$. Therefore, solving the equation $(\rho I - M)\mathbf{x} = \mathbf{0}$, the Perron eigenvector $\mathbf{v}$ associated to $\rho := \rho(M)$ is

$$\mathbf{v} = \begin{bmatrix} \frac{m_{1n}}{\rho} \\ \frac{m_{1n}}{\rho}\frac{m_{21}}{\rho} \\ \vdots \\ \frac{m_{1n}}{\rho}\frac{m_{21}}{\rho}\cdots\frac{m_{(n-1)(n-2)}}{\rho} \\ 1 \\ 0 \\ \vdots \\ 0 \end{bmatrix} = \begin{bmatrix} d_1\frac{b_{1n}}{\rho} \\ d_1d_2\frac{b_{1n}}{\rho}\frac{b_{21}}{\rho} \\ \vdots \\ d_1\cdots d_{n-1}\frac{b_{1n}}{\rho}\frac{b_{21}}{\rho}\cdots\frac{b_{(n-1)(n-2)}}{\rho} \\ 1 \\ 0 \\ \vdots \\ 0 \end{bmatrix}.$$

□

Theorem 5.2.6. *Let $(\mathcal{G}, B)$ be a unicyclic digraph with N nodes, and $M = D \cdot B$, where D is a diagonal matrix with $d_i > 0$ for $i = 1, \ldots, N$. Let $\mathbf{v} = (v_1, \ldots, v_N)^T$ be the Perron eigenvector of M associated to $\rho(M)$. Assume that $(\mathcal{G}, B)$ satisfies Theorem* 5.1.6*, i.e., p_n is the largest entry of the Perron vector $\mathbf{p}$ of B. Then*

(1) *If $d_1, d_2, \ldots, d_{n-1} < d$, then v_n is the largest entry of the Perron eigenvector $\mathbf{v}$ of M.*

(2) *If*

$$\begin{aligned} d_1 d_2 \cdots d_{n-1} &< d^{n-1} \\ d_1 d_2 \cdots d_{n-2} &< d^{n-2} \\ &\vdots \\ d_1 &< d, \end{aligned}$$

then v_n is the largest entry of $\mathbf{v}$.

Proof: Since Theorem 5.2.7 gives

$$\mathbf{v} = \begin{bmatrix} d_1 \frac{b_{1n}}{\rho} \\ d_1 d_2 \frac{b_{1n}}{\rho} \frac{b_{21}}{\rho} \\ \vdots \\ d_1 \cdots d_{n-1} \frac{b_{1n}}{\rho} \frac{b_{21}}{\rho} \cdots \frac{b_{(n-1)(n-2)}}{\rho} \\ 1 \\ 0 \\ \vdots \\ 0 \end{bmatrix},$$

the proof of statements (1) and (2) above are proved with arguments analogous to Theorems 5.2.3 and 5.2.4, respectively. □

5.2.4 Multi-cyclic digraphs

Consider the multi-cyclic digraph $(\mathcal{G}, B)$ from Section 5.1.4. Then after multiplying B by a diagonal matrix D with $d_i > 0$ for all i, we can again formulate a result similar to that of Theorem 5.1.5.

Theorem 5.2.7. *Let $(\mathcal{G}, B)$ be a multi-cyclic digraph rooted at node 1, and let $D = diag(d_i)$, where $d_i > 0$ for $i = 1, 2, \ldots, n$. If $M = D \cdot B$, and $\rho := \rho(M)$ the spectral radius of M, then*

(1) $p_M(\lambda) = \lambda^{N-(n_1+\cdots+n_m)} p_1(\lambda) \cdots p_m(\lambda)$, *where* $p_1(\lambda) = \lambda^{n_1} - b_{32} \cdots b_{2s_1}, \ldots$ $p_m(\lambda) = \lambda^{n_m} - b_{(s_{m-1}+2)(s_{m-1}+1)} \cdots b_{(s_{m-1}+1)s_m}$,

(2) *if* $\rho = max\{ \sqrt[n_1]{b_{32} \cdots b_{2s_1}}, \ldots, \sqrt[n_m]{b_{(s_{m-1}+2)(s_{m-1}+1)} \cdots b_{(s_{m-1}+1)s_m}} \}$ *is unique, the Perron eigenvector of M is*

$$\mathbf{v} = \begin{bmatrix} d_1 d_{s_{k-1}+1} \frac{b_{1(s_k+1)}}{\rho} \frac{b_{(s_{k-1}+1)s_k}}{\rho} \\ 0 \\ \vdots \\ 0 \\ d_{s_{k-1}+1} \frac{b_{(s_{k-1}+1)s_k}}{\rho} \\ \vdots \\ d_{s_{k-1}+2} \cdots d_{s_{k-1}+1} \frac{b_{(s_{k-1}+2)(s_{k-1}+1)}}{\rho} \cdots \frac{b_{(s_{k-1}+1)s_k}}{\rho} \\ 1 \\ 0 \\ \vdots \\ 0 \end{bmatrix}, \tag{5.14}$$

where $\rho = \sqrt[n_k]{d_{s_{k-1}+2} \cdots d_{s_{k-1}+1} \cdot b_{(s_{k-1}+2)(s_{k-1}+1)} \cdots b_{(s_{k-1}+1)s_k}}$, *and k is the index where the maximum is obtained for ρ.*

Proof: $M = D \cdot B$ has the same nonzero entries as B. Therefore, the arguments are the same as in Theorem 5.1.5. □

In the future I would like to continue to investigate different types more

complicated digraph structures $(\mathcal{G}, B)$ and how the entries of the Perron eigenvector of B and $M = \mathrm{diag}(d_i) \cdot B$ depend on B, $\rho(B)$, and $d_1, \ldots, d_n$.

Chapter 6

Conclusions

This chapter is used to summarize the results of my thesis and state my ideas for further research.

6.1 Thesis Summary

In summary, my thesis investigates ODE systems defined on a network with n nodes. A network is defined using a weighted digraph $(\mathcal{G}, B)$. The local dynamics at node i of the system are described using ordinary differential equations $x_i = f_i(x_i)$, where f_i is a nonlinear function of x_i. Introducing coupling between the nodes gives an ODE system of the form

$$\dot{x}_i = f_i(x_i) + \sum_{j=1}^{n} b_{ij} g_{ij}(x_i, x_j), \qquad i = 1, \ldots, n, \quad (6.1)$$

where $B = (b_{ij})_{n\times n}$ is the weight matrix of the network, and the coupling term g_{ij} describes the influence among the nodes.

The main assumption of my dissertation is that system (6.1) has a unique positive equilibrium $\mathbf{x}^* = (x_1^*, \ldots, x_n^*)^T$. We use $\mathbf{x}^*$ to obtain an *equilibrium*

ranking for the nodes of the network. In particular, this equilibrium ranking indicates which node has the most relative importance in the network. My dissertation investigates three important aspects of the equilibrium ranking.

The first aspect addresses the issue of how equilibrium ranking relates to other network ranking methods. I investigate a multigroup SIR epidemiology model with positive steady state $\mathbf{x}^* = (S_1^*, I_1^*, R_1^* \ldots, S_n^*, I_n^*, R_n^*)^T$. I derive a matrix equation $M(\mathbf{S}^*)\mathbf{I}^* = \mathbf{I}^*$ containing a disease prevalence equilibrium vector $\mathbf{I}^* = (I_1^*, \ldots, I_n^*)^T$, and $\mathbf{I}^*$ is the unique positive eigenvector of a matrix. This establishes a link between equilibrium ranking and the well known method of eigenvector centrality ranking. The advantage of this new equilibrium ranking over eigenvector centrality ranking, is that it takes into account not only the network structure but also the local parameter values of the system.

The second aspect considers relating equilibrium ranking to eigenvector ranking for a more general class of nonlinear ODE networks. I consider a more general class of coupling terms described by the functions g_{ij}. Again, a matrix equation $M(\mathbf{x}^*)\mathbf{x}^* = \mathbf{x}^*$ is derived, and $M(\mathbf{x}^*)$ involves both the network structure and local dynamic parameter values. The unique solution of this matrix equation can be used to rank the nodes of the system. I conclude this investigation by applying this technique to different models including a coupled oscillators model, a single species ecology model with spatial dispersal, and an extinction model involving several competing species.

The third aspect deals with how the equilibrium-ranking vector depends on network structure and the local ODE parameters. An equilibrium ranking vector $\mathbf{x}^*$ is obtained from a matrix equation $M\mathbf{x}^* = \mathbf{x}^*$, where $M = D \cdot B$ is

the product of a diagonal matrix D and the irreducible weight matrix B of the system. Therefore, we investigate the structure of the unique positive Perron eigenvector $\mathbf{p}$ of a matrix $M = D \cdot B$ in two stages.

First, by suppressing the local parameter values encoded in the diagonal matrix D I investigate how the entries of a nonnegative eigenvector $\mathbf{p}$ depend on the weight matrix B of a network $(\mathcal{G}, B)$. Several typical network structures including cycle, rooted tree, and unicyclic digraphs are considered. Analysis of the unique nonnegative eigenvector gives insight into how the digraph structure affects the importance of the individual nodes of the network. Then, fixing a network $(\mathcal{G}, B)$, we consider how the order of the entries of the Perron eigenvector change when B is multiplied by a diagonal matrix D containing the local ODE parameter values. We can then investigate how the local dynamics play a role in equilibrium ranking given a fixed network structure. This also allows for the investigation of the impact on ranking combining the changes in model parameters and network structures.

6.2 Future Research

The research in this thesis leads to several future research directions.

The work of chapter 3 investigates equilibrium ranking for epidemiology models. One of the ways I would like to continue investigating SIR models is to combine the n-group model and the patchy model to obtain an equilibrium ranking for an n-group model in a patchy environment. A thorough investigation into the practical implications of equilibrium ranking on disease control is needed. Using equilibrium ranking we can focus on the group and/or patch with the highest disease prevalence. This can provide new quarantine and/or

vaccination methods.

For chapter 4, I would like to continue the investigation into defining equilibrium ranking for a more general class of nonlinear ODE network. In particular, I will consider more network models from engineering, ecology, and many other disciplines including neural networks, and cell interactions, to see if they have a similar structure to those models discussed in my thesis. If some systems have different dispersal terms we would like to know if a similar equilibrium ranking can be obtained.

The work of chapter 5 is ongoing and I intend on continuing the process of investigating different types of digraph networks and how the entries of the Perron eigenvector depend on the weight matrix B. Then consider the case where we fix the network structure described by B, and consider ranking network with a matrix $M = \text{diag}(d_i) \cdot B$, in order to investigate how the local ODE parameters are influencing the ranking eigenvector.

Furthermore, the primary assumption of my thesis is that the systems that I consider have a unique positive equilibrium. However, many researchers investigate systems with two or more positive equilibria. I would like to consider such models in the future and define *local* equilibrium ranking at each positive equilibrium. For example if a disease like cholera has two seasonal endemic outbreaks, importance in the network may be different depending on which outbreak is being considered.

As another aspect of my research in the future I would like to consider what happens to the system and who becomes the most important after the removal of the most important node. This makes sense in the context of quarantine

interventions in an epidemic model, for example. The most important node in this case is the group or patch with the highest disease prevalence. Therefore, one way to try and prevent further spreading of the disease is to quarantine that group or patch with the highest disease prevalence. Once this is done we would like to know how the new, reduced system behaves and who becomes the new number one in the equilibrium ranking.

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Appendix A

Nonnegative Matrix Results

This appendix states classical results from nonnegative matrix theory. For further details see for instance, [6], [17], [52], and [74].

Lets start by defining an partial-order relation on the set $\mathcal{M}_{m\times n}(\mathbb{R})$ of all $m \times n$ matrices with real coefficients.

Definition A.0.1. Let $A, B \in \mathcal{M}_{m\times n}(\mathbb{R})$ be matrices. Then

(a) $A \geq B$ to mean $a_{ij} \geq b_{ij}$ for all i, j, and

(b) $A > B$ to mean $a_{ij} > b_{ij}$ for all i, j.

Definition A.0.2. Let $A \in \mathcal{M}_{m\times n}(\mathbb{R})$ and let $0 \in \mathcal{M}_{m\times n}(\mathbb{R})$ be the zero matrix. Then we say that A is *nonnegative* if $A \geq 0$, and A is *positive* if $A > 0$.

Next, we define the Jordan normal form (JNF) of a matrix and state some of their basic results.

Definition A.0.3. Let $A \in \mathcal{M}_{n\times n}(\mathbb{C})$. Then the *Jordan normal form* (JNF) of A is given by

$$J = B^{-1}AB$$

with B invertible, and the matrix J is given by

$$J = \begin{bmatrix} J_{m_1}(\lambda_1) & 0 & 0 & \cdots & 0 \\ 0 & J_{m_2}(\lambda_2) & 0 & \ddots & 0 \\ 0 & 0 & J_{m_3}(\lambda_3) & \ddots & \vdots \\ \vdots & \vdots & \vdots & \ddots & 0 \\ 0 & 0 & 0 & \cdots & J_{m_s}(\lambda_s) \end{bmatrix} \tag{A.1}$$

where each $J_{m_i}(\lambda_i)$, called a *Jordan block* of A, is given by

$$J_{m_i}(\lambda_i) = \begin{bmatrix} \lambda_i & 1 & 0 & \cdots & 0 \\ 0 & \lambda_i & 1 & \ddots & \vdots \\ 0 & 0 & \lambda_i & \ddots & 0 \\ \vdots & \vdots & \vdots & \ddots & 1 \\ 0 & 0 & 0 & \cdots & \lambda_i \end{bmatrix} \tag{A.2}$$

Theorem A.0.1 (Jordan Normal Form)**.** *Let $A \in \mathcal{M}_{n\times n}(\mathbb{C})$. Then there exists a matrix B in $GL_n(\mathbb{C})$ such that*

$$J = B^{-1}AB$$

is in Jordan normal form, i.e., A is similar to a matrix J in JNF.

Lemma A.0.1. *Let A and B be similar matrices, i.e., $A = PBP^{-1}$. Then for every $n \geq 1$, we have*

$$A^n = PB^nP^{-1}.$$

Proof: Proceed by induction on the power n of A.

Base Step. $n = 1$. Then $A^1 = PB^1P^{-1}$ by the definition of similarity.

I.H. Assume that $A^n = PB^nP^{-1}$ for some n. Then we have that

$$\begin{aligned} A^{n+1} &= (PBP^{-1})^{n+1} = (PBP^{-1})^n(PBP^{-1}) \\ &= (PB^nP^{-1})(PBP^{-1}) \\ &= (PB^nP^{-1})(PBP^{-1}) \\ &= PB^{n+1}(P^{-1}P)BP^{-1} \\ &= PB^{n+1}P^{-1} \end{aligned}$$

□

Proposition A.0.1. *Let $A \in \mathcal{M}_{n\times n}(\mathbb{C})$, and let $J = B^{-1}AB$ be the Jordan normal form of A. Then for every $k \in \mathbb{Z}^+$, we have that $A^k = BJ^kB^{-1}$, where*

$$J^k = \begin{bmatrix} J^k_{m_1}(\lambda_1) & 0 & 0 & \cdots & 0 \\ 0 & J^k_{m_2}(\lambda_2) & 0 & \ddots & 0 \\ 0 & 0 & J^k_{m_3}(\lambda_3) & \ddots & \vdots \\ \vdots & \vdots & \vdots & \ddots & 0 \\ 0 & 0 & 0 & \cdots & J^k_{m_s}(\lambda_s) \end{bmatrix} \tag{A.3}$$

and each $J^k_{m_i}(\lambda_i)$ is given by

$$J^k_{m_i}(\lambda_i) = \begin{bmatrix} \lambda_i^k & \binom{k}{1}\lambda_i^{k-1} & \binom{k}{2}\lambda_i^{k-2} & \cdots & \binom{k}{m_i-1}\lambda_i^{k-m_i+1} \\ 0 & \lambda_i^k & \binom{k}{1}\lambda_i^{k-1} & \ddots & \binom{k}{m_i-2}\lambda_i^{k-m_i+2} \\ 0 & 0 & \lambda_i^k & \ddots & \vdots \\ \vdots & \vdots & \vdots & \ddots & \binom{k}{1}\lambda_i^{k-1} \\ 0 & 0 & 0 & \cdots & \lambda_i^k \end{bmatrix} \tag{A.4}$$

We now state and prove the results used for the Perron-Fröbenius Theorem. The first result simply states that if A is a positive matrix, then so is its spectral

radius $\rho(A)$ and hence, A must have a nonzero eigenvalue λ.

Lemma A.0.2. *Let $A \in \mathcal{M}_n(\mathbb{R})$. If $A > 0$, then $\rho(A) > 0$.*

Proof: Assume that $A > 0$, but that $\rho(A) = \max\{|\lambda| \ : \ \lambda \in \sigma(A)\} = 0$. Then $\lambda_1 = 0$ is an eigenvalue of algebraic multiplicity n (since $|\lambda| \geq 0$ for every $\lambda \in \mathbb{C}$). Thus, by Theorem A.0.1, there exists a matrix B such that $A = BJB^{-1}$, where the matrix J is given by

$$J = \begin{bmatrix} \lambda_1 & 1 & 0 & \cdots & 0 \\ 0 & \lambda_1 & 1 & \ddots & \vdots \\ 0 & 0 & \lambda_1 & \ddots & 0 \\ \vdots & \vdots & \vdots & \ddots & 1 \\ 0 & 0 & 0 & \cdots & \lambda_1 \end{bmatrix} = \begin{bmatrix} 0 & 1 & 0 & \cdots & 0 \\ 0 & 0 & 1 & \ddots & \vdots \\ 0 & 0 & 0 & \ddots & 0 \\ \vdots & \vdots & \vdots & \ddots & 1 \\ 0 & 0 & 0 & \cdots & 0 \end{bmatrix}$$

so that J and therefore A is nilpotent, i.e., there is a $k \in \mathbb{Z}$ such that $A^k = 0$ (Proposition A.0.1). But this is a contradiction since $a_{ij} > 0$ for all i, j. $\square$

Theorem A.0.2. *Let $A \in \mathcal{M}_{n\times n}(\mathbb{R})$, and let $\rho(A)$ be its spectral radius. Then*

$$\lim_{k\to\infty} A^k = 0 \quad \Leftrightarrow \quad \rho(A) < 1.$$

Proof: ($\Rightarrow$) Let $(\lambda, \mathbf{x})$ be an eigenpair of A. Then, since $A^k\mathbf{x} = \lambda^k\mathbf{x}$, it follows that

$$0 = (\lim_{k\to\infty} A^k)\mathbf{x} = \lim_{k\to\infty} (A^k\mathbf{x}) = \lim_{k\to\infty} \lambda^k\mathbf{x} = \mathbf{x} \lim_{k\to\infty} \lambda^k.$$

And, $\mathbf{x} \neq 0$ implies that $\lim_{k\to\infty} \lambda^k = 0$. This means that $|\lambda| < 1$, and as $\lambda \in \sigma(A)$ was arbitrary, it follows that $\rho(A) < 1$.

($\Leftarrow$) Conversely, assume that $\rho(A) < 1$. From the Jordan Normal Form Theorem, there exist matrices J and B such that $A = BJB^{-1}$ and J is in Jordan normal form. Moreover, from Proposition A.0.1 $A^k = BJ^kB^{-1}$, where J^k consists of the diagonal blocks $J^k_{m_i}(\lambda_i)$ given by the formula

$$J^k_{m_i}(\lambda_i) = \begin{bmatrix} \lambda_i^k & \binom{k}{1}\lambda_i^{k-1} & \binom{k}{2}\lambda_i^{k-2} & \cdots & \binom{k}{m_i-1}\lambda_i^{k-m_i+1} \\ 0 & \lambda_i^k & \binom{k}{1}\lambda_i^{k-1} & \ddots & \binom{k}{m_i-2}\lambda_i^{k-m_i+2} \\ 0 & 0 & \lambda_i^k & \ddots & \vdots \\ \vdots & \vdots & \vdots & \ddots & \binom{k}{1}\lambda_i^{k-1} \\ 0 & 0 & 0 & \cdots & \lambda_i^k \end{bmatrix}$$

Hence, if $\rho(A) < 1$ implies $|\lambda_i| < 1$ for every $\lambda_i \in \sigma(A)$, and so for every i

$$\lim_{k\to\infty} J^k_{m_i}(\lambda_i) = 0 \;\Rightarrow\; \lim_{k\to\infty} J^k = 0.$$

Therefore, this gives

$$\lim_{k\to\infty} A^k = \lim_{k\to\infty}(BJ^kB^{-1}) = B(\lim_{k\to\infty} J^k)B^{-1} = B\cdot 0\cdot B^{-1} = 0.$$

On the other hand, if $\rho(A) > 1$, then at least one element of J^k is unbounded as $k \to \infty$, and so in this case $\lim_{k\to\infty} A^k \neq 0$. □

Definition A.0.4. Let $A = (a_{ij}) \in \mathcal{M}_{n\times n}(\mathbb{R})$. Then $|A|$ means the matrix with entries by $|a_{ij}|$, i.e. $|A| = (|a_{ij}|)$. Do not confuse this notation with determinants.

Remark A.0.1. Note that from the triangle inequality, if $\mathbf{x}\in \mathbb{R}^n$, we have

$$(|A\mathbf{x}|)_i = \left|\sum_{j=1}^n a_{ij}x_j\right| \leq \sum_{j=1}^n |a_{ij}|\cdot|x_j| = (|A|\cdot|\mathbf{x}|)_i \qquad (i = 1,\ldots,n)$$

Therefore, $|A\mathbf{x}| \leq |A| \cdot |\mathbf{x}|$. This fact is used to prove the next result.

Remark A.0.2. The first two properties of Lemma 2.1.1 say that if a matrix A is positive, we can assume without loss of generality, that $\rho(A) = 1$. Otherwise, we know that $\frac{A}{\rho(A)} > 0$, and therefore, property (b) tell us that we have

$$\rho\left(\frac{A}{\rho(A)}\right) = \frac{\rho(A)}{\rho(A)} = 1.$$

Theorem A.0.3. *Let $A_{n\times n}$ be positive. Then $\rho(A) \in \sigma(A)$, and if $(\lambda, \mathbf{x})$ is an eigenpair with $|\lambda| = \rho(A)$, then so is the pair $(\lambda, |\mathbf{x}|)$.*

Proof: Without loss of generality, assume that $\rho(A) = 1$. Then assume that $\lambda \in \sigma(A)$ is such that $|\lambda| = 1 = \rho(A)$. Then there is an $\mathbf{x} \in \mathbb{R}^n$ such that $A\mathbf{x} = \lambda\mathbf{x}$, and hence

$$|\mathbf{x}| = |\lambda| \cdot |\mathbf{x}| = |\lambda\mathbf{x}| = |A\mathbf{x}| \leq |A| \cdot |\mathbf{x}| = A|\mathbf{x}|.$$

Thus, $1 \cdot |\mathbf{x}| \leq A|\mathbf{x}|$, or $\rho(A) \cdot |\mathbf{x}| \leq A|\mathbf{x}|$. We must show that equality holds. Indeed, consider the nonnegative vector $\mathbf{y} = A|\mathbf{x}| - |\mathbf{x}| \geq \mathbf{0}$. Assume that $\mathbf{y} \geq \mathbf{0}$ but $\mathbf{y} \neq \mathbf{0}$. Then there exists an index i such that $y_i > 0$, and so by Lemma 2.1.1 we know that $A\mathbf{y} > \mathbf{0}$ and $A|\mathbf{x}| > 0$. Therefore, there is $\varepsilon > 0$ sufficiently small such that

$$A\mathbf{y} > \varepsilon A|\mathbf{x}| \;\Leftrightarrow\; A(A|\mathbf{x}| - |\mathbf{x}|) > \varepsilon A|\mathbf{x}|.$$

Now, letting $\mathbf{z} = A|\mathbf{x}|$, gives

$$A(\mathbf{z} - |\mathbf{x}|) > \varepsilon\mathbf{z} \;\Leftrightarrow\; A\mathbf{z} - A|\mathbf{x}| > \varepsilon\mathbf{z} \;\Leftrightarrow\; A\mathbf{z} > (1+\varepsilon)\mathbf{z} \;\Leftrightarrow\; \frac{A}{1+\varepsilon}\mathbf{z} > \mathbf{z}.$$

Thus, let $B = \frac{1}{1+\varepsilon}A$, and we have $B\mathbf{z} > \mathbf{z}$. Then by applying B to both sides of the inequality and using Lemma 2.1.1 part (f), we have $B^2\mathbf{z} > B\mathbf{z} > \mathbf{z}$, i.e., $B^2\mathbf{z} > \mathbf{z}$. Similarly, for any $k \geq 2$

$$B^k\mathbf{z} > B^{k-1}\mathbf{z} > \cdots > B^2\mathbf{z} > B\mathbf{z} > \mathbf{z} > \mathbf{0}.$$

However, since $\rho(B) = \rho(\frac{A}{1+\varepsilon}) = \frac{1}{1+\varepsilon}\rho(A) = \frac{1}{1+\varepsilon} < 1$, Theorem A.0.2 implies

$$\lim_{k\to\infty} B^k = 0.$$

This means that $\mathbf{0} = \lim_{k\to\infty} B^k\mathbf{z} > \lim_{k\to\infty} \mathbf{z} = \mathbf{z}$, i.e, $\mathbf{0} > \mathbf{z}$. This is a contradiction, and so $\mathbf{y} = \mathbf{0}$.

□

Therefore, we see that if A is a positive matrix, then its spectral radius $\rho(A)$ is an eigenvalue of A, and has $|\mathbf{x}|$ as an associated eigenvector, for some $\mathbf{x} \in \mathbb{R}^n$ with $(\rho(A), \mathbf{x})$ an eigenpair.

Definition A.0.5. Let $A \in \mathcal{M}_{n\times n}(\mathbb{C})$ and let λ be an eigenvalue of A. Then the *index* of λ is the smallest positive integer k, such that any one of the equivalent statements is true.

(a) $\text{rank}((\lambda I - A)^k) = \text{rank}((\lambda I - A)^{k+1})$

(b) $\text{row}((\lambda I - A)^k) = \text{row}((\lambda I - A)^{k+1})$

(c) $\text{Null}((\lambda I - A)^k) = \text{Null}((\lambda I - A)^{k+1})$

(d) $\text{row}((\lambda I - A)^k) \cap \text{Null}((\lambda I - A)^k) = \{\mathbf{0}\}$

(e) $\mathbb{C}^n = \text{row}((\lambda I - A)^k) \oplus \text{Null}((\lambda I - A)^k)$

and is denoted by $index(\lambda) := index_A(\lambda)$. We understand that if $\lambda \in \mathbb{C}$, then $index(\lambda) = 0 \Leftrightarrow$ is not an eigenvalue of A.

Theorem A.0.4. *Let $A \in \mathcal{M}_{n\times n}(\mathbb{R})$ be positive. Then*

(a) *$\rho(A)$ is the unique eigenvalue of A on the spectral circle,*

(b) $\text{index}(\rho(A)) = 1$, *i.e., $\rho(A)$ is a semisimple eigenvalue.*

Proof:

(a) Without loss of generality, $\rho(A) = 1$. Then assume $(\lambda, \mathbf{x})$ is an eigenpair of A such that $|\lambda| = \rho(A) = 1$. Then $(\lambda, |\mathbf{x}|)$ is also an eigenpair of A. Moreover, $\mathbf{0} < |\mathbf{x}| = A|\mathbf{x}|$, and so for all $i = 1, \ldots, n$

$$0 < |x_i| = (A|\mathbf{x}|)_i = \sum_{j=1}^{n} a_{ij}|x_j|.$$

On the other hand,

$$|x_i| = |\lambda| \cdot |x_i| = |(\lambda\mathbf{x})_i| = |(A\mathbf{x})_i| = \left|\sum_{j=1}^{n} a_{ij}x_j\right|.$$

Hence,

$$\left|\sum_{j=1}^{n} a_{ij}x_j\right| = \sum_{j=1}^{n} a_{ij}|x_j| = \sum_{j=1}^{n} |a_{ij}x_j|.$$

Therefore, having equality in the triangle inequality implies that for all $j = 2, \ldots, n$ there exists an α_j such that $a_{ij}x_j = \alpha_j(a_{i1}x_1)$. So, letting $\beta_j = \frac{\alpha_j a_{i1}}{a_{ij}}$, gives

$$x_j = \beta_j x_1, \quad \beta_j > 0 \qquad (j = 2, \ldots, n).$$

In other words, for an eigenvalue λ of A such that $|\lambda| = 1$, we have that

$\mathbf{x} = x_1\mathbf{v}$, where $\mathbf{v} = (1, \beta_1, \ldots, \beta_n)^T > \mathbf{0}$. Thus, we obtain

$$\lambda\mathbf{v} = A\mathbf{v} = |A\mathbf{v}| = |\lambda\mathbf{v}| = |\lambda|\mathbf{v} = \mathbf{v} \;\Rightarrow\; \lambda = 1,$$

i.e., $\lambda = 1 = \rho(A)$ is the only eigenvalue on the spectral circle of A.

(b) Assume that $\text{index}(\rho(A)) = \text{index}(1) = m > 1$. Then there is an $m \times m$ Jordan block J_m such that $\|J_m^k\|_\infty \to \infty$, and so $\|J^k\|_\infty \to \infty$ as $k \to \infty$. But then

$$\|J^k\|_\infty = \|P^{-1}A^kP\|_\infty \leq \|P^{-1}\|_\infty\|A^k\|_\infty\|P\|_\infty \;\Leftrightarrow\; \|A^k\|_\infty \geq \frac{\|J^k\|_\infty}{\|P^{-1}\|_\infty\|P\|_\infty} \to \infty.$$

Therefore, let $A^k = [a_{ij}^{(k)}]$, and let i_r be the row index such that

$$\|A^k\|_\infty = \sum_{j=1}^{n} a_{i_rj}^{(k)}.$$

Then there is a vector $\mathbf{v} > \mathbf{0}$ such that $\mathbf{v} = A\mathbf{v}$, which gives us

$$\|\mathbf{v}\|_\infty \geq v_{i_r} = \sum_{j=1}^{n} a_{i_rj}^{(k)} \cdot v_j \geq \sum_{j=1}^{n} a_{i_rj}^{(k)} \cdot \min_{1\leq j\leq n}\{v_j\} = \|A^k\|_\infty \cdot \min_{1\leq j\leq n}\{v_j\}.$$

However, this says that $\|\mathbf{v}\|_\infty \to \infty$ as $k \to \infty$. This contradicts the fact that $\mathbf{v}$ is a vector with scalar entries. Thus, $\text{index}(\rho(A)) = 1$.

□

Theorem A.0.5. *Let $A \in \mathcal{M}_{n\times n}(\mathbb{R})$ be positive. Then $\text{alg}_A(\rho(A)) = 1$, i.e., $\rho(A)$ is a simple eigenvalue of A, and*

$$\dim(\text{Null}(A - \rho(A)I)) = geo_A(\rho(A)) = \text{alg}_A(\rho(A)) = 1.$$

Proof: Without loss of generality, $\rho(A) = 1$. Assume that $\text{alg}(1) = m > 1$. Then 1 is semisimple, so that $\text{alg}(1) = geo(1) = m$. Thus, there are m linearly independent eigenvectors associated to $\lambda = 1$. Let $\mathbf{u}$ and $\mathbf{v}$ be any two such vectors. Then for all $\alpha \in \mathbb{C}$ we know that $\mathbf{u} \neq \alpha\mathbf{v}$. Now, since $\mathbf{v}$ is an eigenvector of A, $\mathbf{v} \neq \mathbf{0}$. Therefore, choose an index j such that $v_j > 0$, and define the following vector $\mathbf{w} = \mathbf{u} - \frac{u_i}{v_i}\mathbf{v}$. Then $\mathbf{w}$ is also an eigenvector of A associated to $\rho(A) = 1$, so that we have $A|\mathbf{w}| = |\mathbf{w}| > \mathbf{0}$. This is a contradiction, since $w_i = u_i - \frac{u_i}{v_i}v_i = 0$. Therefore, $m = 1$ and $\rho(A)$ is a simple eigenvalue of A. □

An eigenvector associated to the spectral radius of $A > 0$ is called a *Perron eigenvector* and the associated eigenvalue $\rho(A)$ the *Perron root* of A. Hence, a Perron vector $\mathbf{p}$ of $A > 0$ is strictly positive.

The next result tells us that eigenvalues of $A > 0$ may be positive or negative. However, regardless of the sign of $\mu \in \sigma(A)$, if $\mu \neq \rho(A)$ then no eigenvector associated to μ is nonnegative (and hence not positive). This says that any eigenvector $\mathbf{v}$ not a multiple of the Perron vector $\mathbf{p}$ has at least one negative entry $v_j < 0$.

Theorem A.0.6. *Let $0 < A \in \mathcal{M}_{n\times n}(\mathbb{R})$, and let $(\rho(A), \mathbf{p})$ be the Perron eigenpair of A. Then there are no nonnegative eigenvectors of A other than positive multiples of $\mathbf{p}$, i.e., if $\mathbf{v} \geq \mathbf{0}$ is an eigenvector of A, then $\mathbf{v} = \alpha\mathbf{p}$, where $0 < \alpha$.*

Proof: Assume $(\mu, \mathbf{v})$ is an eigenvector for A and that $\mathbf{v} \geq \mathbf{0}$, and let $\mathbf{q}$ be the left-hand Perron vector of A. Then $\mathbf{q} > \mathbf{0}$ and $\mathbf{v} \geq \mathbf{0}$ implies that

$\mathbf{q}^T\mathbf{v} \geq \mathbf{0}$. Hence, we obtain

$$\rho(A)\mathbf{q}^T = \mathbf{q}A \;\Rightarrow\; \rho(A)\mathbf{q}^T\mathbf{v} = \mathbf{q}A\mathbf{v} = \mu\mathbf{q}^t\mathbf{v} \;\Rightarrow\; (\rho(A) - \mu)\mathbf{q}^T\mathbf{v} = \mathbf{0}.$$

Therefore, $\rho(A) - \mu = 0$, i.e., $\rho(A) = \mu$. □

Theorem A.0.7. *Let $A \in \mathcal{M}_{n\times n}(\mathbb{R})$ be a nonnegative irreducible matrix. Then $(I + A)^{n-1} > 0$.*

Proof: Let $a_{ij}^{(k)}$ be the $(i, j)^{th}$ entry of A^k, and note that

$$a_{ij}^{(k)} = \sum_{h_1,\ldots h_{\text{k-1}}} a_{ih_1}a_{h_1h_2}\cdots a_{h_{\text{k-1}}j}.$$

Therefore, $a_{ij}^{(k)} > 0$ if and only if there are indices $h_1, \ldots h_{\text{k-1}}$ such that $a_{ih_1} > 0$, $a_{h_{\text{k-1}}j} > 0$, $a_{h_sh_{s+1}} > 0$ for all $1 \leq s \leq k-2$. However, this occurs if and only if there is a sequence of k paths from vertex v_i to v_j in the graph $\mathcal{G}(A)$, namely

$$v_i \to v_{h_1} \to v_{h_2} \to \cdots \to v_j.$$

In other words, we obtain the following equivalence:

$$a_{ij}^{(k)} > 0 \;\;\Leftrightarrow\;\; v_i \text{ connects to } v_j \text{ in the digraph } \mathcal{G}(A).$$

Now, A is irreducible so that for each position (i, j) there exists $0 \leq k \leq n-1$, such that $a_{ij}^{(k)} > 0$. Hence, from the binomial theorem, we get

$$[(I + A)^{n-1}]_{ij} = \left[\sum_{k=0}^{n-1}\binom{n-1}{k}A^k\right]_{ij} = \sum_{k=0}^{n-1}\binom{n-1}{k}a_{ij}^{(k)} > 0.$$

In other words all entries of $(I+A)^{n-1}$ are strictly positive, i.e., $(I+A)^{n-1} > 0$.

□

Theorem A.0.8. *Let $A \geq 0$ be irreducible, and let $r = \rho(A)$. Then A is primitive if and only if the limit*

$$\lim_{k\to\infty} \left(\frac{A}{r}\right)^k$$

exists; in such a case,

$$\lim_{k\to\infty} \left(\frac{A}{r}\right)^k = \frac{\mathbf{p}\cdot\mathbf{q}^T}{\mathbf{q}^T\cdot\mathbf{p}} > 0,$$

where $\mathbf{p}$ and $\mathbf{q}$ are the Perron eigenvectors of A and A^T, respectively.

Proof: Omitted. (See [74]) □