

Derek Miles

u1123571

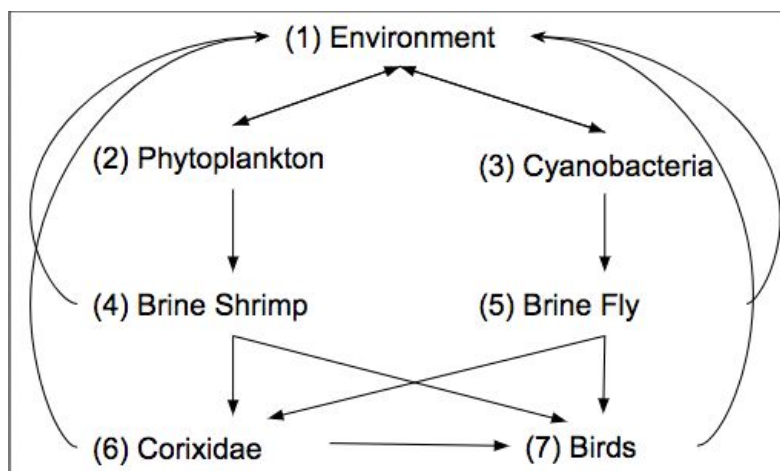
## Simple Ecosystem Analysis Using Linear Algebra

### Introduction

One of the many possible applications of linear algebra is the potential for analysis of an ecosystem. This can be done by creating or obtaining a food web from an ecosystem and then constructing an adjacency matrix from the food web. From this adjacency matrix, characteristics about an ecosystem can be mathematically determined. One such characteristic is which species are relatively critical to an ecosystem and which species have a degree of safety if one of their feeding options goes extinct. Structural diversity can also be calculated when looking to compare ecosystems.

### A Basic Analysis of a Simple Ecosystem

For this paper, a simple adjacency matrix will be calculated from a simplified food web of the Great Salt Lake to be used as an example. In this simplified ecosystem, phytoplankton feeds brine shrimp, cyanobacteria feeds brine flies; brine flies and brine shrimp are both eaten by corixidae, and birds consume brine shrimp, brine flies, and corixidae. The environment is also involved which includes dead matter, nutrients in the water, sunlight, etc. The environment “feeds” phytoplankton and cyanobacteria and the environment is “fed” by the death of every species. The food web of such can be represented as below, where the numbers next to each species will be used to represent the species’ row/column in the adjacency matrix.



Several matrices can be created based on the food web above. Matrix M0 represents a symmetric matrix that simply shows the connections between species. A 1 in the  $i,j$  spot in M indicates that the two species are connected - one eats another. However, due to the one-way nature of many of the connections in this food web, matrix M1 is the adjacency matrix for the ecosystem with one-way predation taking into account. A 1 in the  $i,j$  spot in M1 now indicates that species  $j$  eats species  $i$ . However, M0 and M1 both have 1's in every place, so M is created with some variance in number to indicate potential differences in relative quantities of consumed species. In this paper, both M and M1 will be used for various purposes.

$$M0 := \begin{bmatrix} 0 & 1 & 1 & 1 & 1 & 1 & 1 \\ 1 & 0 & 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 1 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 1 & 1 \\ 1 & 0 & 1 & 0 & 0 & 1 & 1 \\ 1 & 0 & 0 & 1 & 1 & 0 & 1 \\ 1 & 0 & 0 & 1 & 1 & 1 & 0 \end{bmatrix} \quad M1 := \begin{bmatrix} 0 & 1 & 1 & 1 & 1 & 1 & 1 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 & 1 & 0 \end{bmatrix} \quad M := \begin{bmatrix} 0 & 1 & 1 & 1 & 1 & 1 & 1 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 5 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 5 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 10 & 10 & 1 & 0 \end{bmatrix}$$

Some extremely basic facts about the ecosystem can be extracted from matrix M1. The sum of each row gives the number of species that species  $i$  eats in the food web. The sum of each column gives the number of species that use species  $j$  as a food source. However, this information is pretty rudimentary and can also be easily read from the food web itself. More detailed information is found by more complex operations.

The amount of potential food chains that can be created from the ecosystem can be calculated by simple matrix multiplication. The amount of food chains in this ecosystem is calculated by multiplying M1 by itself by the amount of trophic levels, 5 in this case. Then the last  $n$  entries of the first column are added, where  $n$  is given by the amount of species in the last trophic level, 1 in this case.  $M1^5$  is given by:

$$\begin{bmatrix} 10 & 14 & 14 & 14 & 14 & 10 & 8 \\ 8 & 5 & 5 & 6 & 6 & 4 & 2 \\ 8 & 5 & 5 & 6 & 6 & 4 & 2 \\ 2 & 4 & 4 & 3 & 3 & 2 & 2 \\ 2 & 4 & 4 & 3 & 3 & 2 & 2 \\ 4 & 2 & 2 & 4 & 4 & 2 & 0 \\ 4 & 4 & 4 & 6 & 6 & 4 & 2 \end{bmatrix}$$

The last entry in the first column is 4, which means there are 4 food chains through the food web from environment to birds.

Another statistical measure that can be obtained from the adjacency matrix of an ecosystem is its structural diversity. A larger number indicates a more sound ecosystem, in that a species could lessen in number and the ecosystem would still go on. This structural diversity is calculated by the dominant eigenvalue from the Perron-Frobenius theorem - the largest absolute value of the eigenvalues of a matrix. In the Perron-Frobenius theorem, it's stated that as the values in a matrix increase, its dominant eigenvalue also increases. This is true in the sense of an ecosystem as well, as species have increased feeding opportunities, an ecosystem will be more structurally sound.

Consider matrix M1 from above. Its dominant eigenvalue calculated by Maple is 2.043. If hypothetically, birds could only now consume brine shrimp, and the last row of M1 was replaced with <0,0,0,1,0,0,0> to form a new matrix M2, the structural diversity, and hence the dominant eigenvalue should decrease. This is true, and the dominant eigenvalue decreases to 1.952, as calculated in Maple. The eigenvalues of M1, M2, and M2's eigenvalues are displayed below.

$$\begin{bmatrix} 0. \\ 0. \\ 2.042657287 \\ -0.03912763614 + 1.098665873 I \\ -0.5890184631 \\ -1.375383552 \\ -0.03912763614 - 1.098665873 I \end{bmatrix} \quad M2 := \quad \begin{bmatrix} 0 & 1 & 1 & 1 & 1 & 1 & 1 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 \end{bmatrix} \quad \begin{bmatrix} 0. \\ 0. \\ 0. \\ 1.952310360 \\ -1.435994088 \\ -0.2581581364 + 1.001720020 I \\ -0.2581581364 - 1.001720020 I \end{bmatrix}$$

As M1 is changed into M by the increase of selected values, the dominant eigenvalue of M should reflect that increase. As mentioned earlier, the dominant eigenvalue of M1 is 2.043. The increased values lead matrix M's dominant eigenvalue to become 3.641, a greater structural diversity. M's eigenvalues are displayed below.

$$\begin{bmatrix} 0. \\ 0. \\ 3.640558980 \\ -0.2131584831 + 3.090588080 I \\ -0.09165890824 \\ -3.122583105 \\ -0.2131584831 - 3.090588080 I \end{bmatrix}$$

Associated with dominant eigenvalues are dominant eigenvectors. Given an  $n \times n$  matrix  $A$ , and a  $n \times 1$  vector  $\mathbf{x}$  with every element being 1,  $A^m \mathbf{x}$  is a vector whose components are in the same ratio as the dominant eigenvector as  $m$  approaches infinity. In the dominant eigenvector of an ecosystem such as the ones analyzed in this paper, the values relative to each other show the relative feeding opportunities of the species. The dominant eigenvector for  $M$  is displayed below; with the 7th component set as 1, the other components show the relative feeding opportunities for the other species. This vector shows that birds have about 10 times the feeding opportunities as corixidae, and about twice as many feeding opportunities as the environment.

$$\begin{bmatrix} 0.4696082743 \\ 0.1289934710 \\ 0.1289934710 \\ 0.1771616247 \\ 0.1771616247 \\ 0.09732660318 \\ 1. \end{bmatrix}$$

### **Limitations and Potential for Further Analysis**

Due to data constraints, the analysis of the Great Salt Lake ecosystem was extraordinarily simplified in this paper. For example, relative quantities such as 5 and 10 were used in matrix  $M$ , when in reality the actual quantities of how much of each species is consumed by another likely differs greatly. The top trophic level was also just defined as being Birds, when in reality, there are many different species of birds that live in the Great Salt Lake, and many that just visit as well. By separating birds into the different species, a more complex and accurate analysis could be performed.

This analysis was also simplified by simply using adjacency matrices representing quantities for consumption and food chains, and there is a lot more potential than what was shown here. For example, rather than quantity consumed, the matrices could hold data such as energy or concentrations of chemicals such as pesticides like DDT, and examine the upwards flow of those.

The Perron-Frobenius theorem also has numerous other applications including its use in web search algorithms and ranking of football teams.



## Works Cited

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Maple commands:

```
M1:=<0,1,1,0,0,0,0|1,0,0,1,0,0,0|1,0,0,0,1,0,0|1,0,0,0,0,1,1|1,0,0,0,0,1,1|1,0,0,0,0,0,1|1,0,0,0,0,0,0,0>;
```

```
M:=<0,1,1,0,0,0,0|1,0,0,5,0,0,0|1,0,0,0,5,0,0|1,0,0,0,0,1,10|1,0,0,0,0,1,10|1,0,0,0,0,0,1|1,0,0,0,0,0,0,0>;
```

```
M0:=<0,1,1,1,1,1,1|1,0,0,1,0,0,0|1,0,0,0,1,0,0|1,1,0,0,0,1,1|1,0,1,0,0,1,1|1,0,0,1,1,0,1|1,0,0,1,1,1,0,0>;
```