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REVIEW ARTICLE

A new perspective of ecosystem health

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Abstract: Ecosystem health has attracted considerable attention from different disciplines in recent years. However, it still remains a disputed issue whether to focus on its general concept or on operational practice. As a result, these disputations have caused confusion and limited further research in the field of ecosystem health. In this paper, we attempt to introduce a new perspective to the concept of ecosystem health. With the aid of modern statistical methodology, such as factor analysis and normal distribution theory, we provide a conceptual approach to the quantitative assessment of ecosystem health and our method could be applied to various categories of ecosystems.

Keywords: ecosystem health; majority; factor analysis; normal distribution theory

Introduction

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With the population explosion and the increasing human impact on nature, most ecosystems throughout the world are under excessive stress, causing a series of environmental problems at the local, regional, and global scales, such as biodiversity loss, land degradation, air and water pollution, and global climate change. Hence, ecosystem health (abbreviated as EH) has emerged as a

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major organizing paradigm for protecting and sustaining environmental quality and human well-being. How EH is defined is therefore critical. Ecosystem health lies at the interface of ecological and health sciences, related to the health concept in medical sciences (Rapport 1998). Ecosystem health is also a fundamental conceptual tool for developing new ways to evaluate and manage environmental resources and risks (Rapport et al 1998). However, owing to the complexity of an ecosystem and the different perspectives of researchers, a variety of definitions with various indicators of ecosystem health have been proposed (Costanza et al, 1992; Mageau et al, 1998). In this paper, we shall present a new type of perspective on the concept and assessment of EH, based on the theory of statistics.

The implications of ecosystem health

"Ecosystem health" was first proposed as a theoretical term and an emerging practice in the writings of a Scottish geologist, James Hutton, who presented the notion of the earth as an integrated system (Hutton 1788). It can also trace its origin back to the literature of the naturalist Aldo Leopold of the 1940s (Leopold 1949). Publications in the late 1970s and early 1980s (Rapport et al, 1985) provided fresh views in similar veins and showed great similarities between diagnostic challenges at the level of the individual and of the whole system. The term "ecosystem medicine" was created to depict this new arena of investigation (Rapport et al, 1979). This idea was eventually developed into the principles and concepts of EH (Rapport 1989).

Until now, a large body of research has been constructed around the concept of EH (Christensen and Van Thi, 2008; Venkiteswaran et al, 2008; Stephens et al, 2007). However, some fundamental perceptions are still controversial: for instance, how to define a suitable condition for the health state of an ecosystem, and what constitutes a set of universally accepted indicators to measure EH (Rapport et al, 2003). Similar questions limit further research in the orientation of EH. In short, the definition and assessment of EH remain vague and slippery, and have different meanings for different people (Gatto 1995).

Despite controversies, generally, defining EH is a process involving the identification of important indicators of health, the

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identification of proper space-time scales of health, and finally, the identification of a healthy state incorporating human values.

Before health can be measured, we need to identify the relevant indicators (with acceptable ranges) that we are going to use in assessing the health of a particular ecosystem. Over the past decades, many such variables and parameters have emerged in ecological books and magazines, and later, new indices have been developed that reflect the complexity of the ecosystem and are being used for management purposes. For example, the Index of Biotic Integrity (IBI), the original multi-metric index, was first developed to evaluate stream water quality by Dr. James Karr for use in small warm water streams in central Illinois and Indiana, US. (Karr 1981). The Index of Network Ascendency, which incorporates four important characteristics of ecosystems: species richness, niche specialization, developed cycling and feedback, and overall activity, was first developed by Robert Ulanowicz (Ulanowicz 1980).

But in the real world, the large number of components, nonlinear interactions, time delays and feedbacks, and spatial heterogeneity together often make ecological systems overwhelmingly complex. This complexity must be effectively dealt with in order to further human understanding (Wu 1999). In a word, the ecosystem is so complex that its measurements cannot be expressed through a single indicator, but rather require a set of indicators at different spatial, temporal, and hierarchical levels of ecosystem organization. Thus, the indices which are potentially useful tools to interpret EH must be integrated.

Suppose the same type of ecosystems, E_1, E_2, \ldots, E_m , at the same hierarchical level, need to be assessed for EH. A series of indices $X_1 = \{x_{11}, x_{12}, ..., x_{1n}\}\)$ are used to interpret the ecosystem E_1 after careful consideration, where *n* indicates the number of indicators. Then, a matrix of indices to interpret the ecosystems E_1, E_2, \ldots, E_m could be obtained, where *m* is the number of ecosystems,

$$
X = \begin{cases} x_{11}, x_{12}, \dots, x_{1n} \\ x_{21}, x_{22}, \dots, x_{2n} \\ \dots \\ x_{m1}, x_{m2}, \dots, x_{mn} \end{cases}
$$
 (1)

where *n* indicates the number of indicators, and *m* is the number of ecosystems. In the index matrix (1), the *i*th row $e_i = \{x_{i1}, x_{i2}, ..., x_{in}\}\$ depicts a set of indices which are used to interpret a particular ecosystem, and the *j*th column $X_j = \left\{ x_{1j}, x_{2j}, ..., x_{mj} \right\}^T$ represents a particular index which is used to interpret one aspect of the investigated ecosystems.

Suppose each index X_i is a vector which reflects a faceted aspect of EH. At each dimension, according to the central limit theorem (Appendix 1), the distribution of X is approximately normal if *m* is big enough. Thus, the normal distribution theory could be used to test the quality of EH at each dimension.

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According to the Lindberg-Levy central limit theorem (Appendix 2), if $X_j = \left\{ x_{1j}, x_{2j}, ..., x_{mj} \right\}^T$ are a sequence of i.i.d. random variables, with a population mean μ_i and a population variance σ_i , i.e. $X_i \sim N(\mu_i, \sigma_i)$. Then, if *m* is big enough, we have,

$$
Z_j = (X_j - \mu_j) / \sigma_j, Z_j \text{-N}(0,1), j=1,2,...,N.
$$
 (2)

The density function of Z_i is,

$$
\phi(x) = \frac{1}{\sqrt{2\pi}} e^{-\frac{x^2}{2}}.
$$
\n(3)

which has the same form as the standard normal distribution (Appendix 3). The curve of the possibility function of Z_i is shown as the Fig. 1,

Fig. 1 The curve of the possibility function of Zj

Therefore, the matrix of indices $X(1)$ can be converted to $Z(4)$ as follows,

$$
Z = \begin{cases} z_{11}, z_{12}, \dots, z_{1n} \\ z_{21}, z_{22}, \dots, z_{2n} \\ \dots \\ z_{m1}, z_{m2}, \dots, z_{mn} \end{cases}
$$
 (4)

This theory provides us some insights to distinguish the abnormal part from the normal part of a population, and helps us to find a statistical way to assess EH.

According to the normal distribution theory (Appendix 3), we know that, $\mu \pm \sigma$ (the mean \pm 1 standard deviation) covers 66.7% of the area under the normal curve; $\mu \pm 2\sigma$ (the mean \pm 2 standard deviation) covers 95% of the area under the normal curve; $\mu \pm 3\sigma$ (the mean \pm 3 standard deviation) covers 99.7% of the area under the normal curve.

Thus, we can say that we are confident that 95% of the area under the normal curve (which corresponds to the majority of

investigated ecosystems) lies between $\mu - 2\sigma$ and $\mu + 2\sigma$. According to the normal distribution theory, given $\int_{-t}^{t} \phi(x) dx = 0.95$, the interval (-*t*, *t*) is thus determined, where *t* is a critical value constrained by the formula, $\int_{-t}^{t} \phi(x) dx = 0.95$. In this case, *t* is 1.96, which is obtained by means of the table of standard normal distribution. Hence, for a specific ecosystem E_i , according to the above analysis, the item Z_i could be calculated by the formula (2). If Z_i value falls between -1.96 and 1.96 , E_i is attributed to the healthy ecosystems. Otherwise, if Z_i value of E_i falls outside the interval of -1.96 to 1.96, then *Ei* is attributed to the abnormal, and thus unhealthy ecosystems.

Applications of factor analysis and multiple normal distribution theory

Since the ecosystem is complex, and the indices used to interpret the ecosystem are inevitably complex, and further more the indices may be associated with each other, we need to develop some methods to deal with these indices. In this section, we introduce factor analysis.

Factor analysis is used to study the patterns of relationships among many dependent variables, with the goal of discovering something about the nature of the independent variables that affect them, even though those independent variables were not measured directly. Since the important indicators of EH need to be integrated for assessing, factor analysis is a good way to solve the problem.

> 0.16 0.14 0.12

$$
Z = Af + e \tag{5}
$$

where *A* is the matrix of factor loadings, *f* is the common factors, and *e* is the specific factor.

Through factor analysis, supposing the common factors f_2 and *f2* contributed most of the sample variance, for which the criterion is usually 85%, either f_1 or f_2 is the combination of several Z_i values. As $Z_i \sim N(0, 1)$, either f_1 or f_2 also follows the normal distribution.

Let η_1 , η_2 be the integrated indices,

$$
\eta_1 = \frac{f_1}{p_1}, \eta_2 = \frac{f_2}{p_2}, \tag{6}
$$

where p_l is the number of Z_i embodied in f_l and p_2 is the number of *Z_j* embodied in f_2 . Thus, $\eta_1 \sim N(0, 1)$, $\eta_2 \sim N(0, 1)$. Therefore, the joint distribution of η_1 , η_2 obeys the standard normal distribution for two-dimension, (η_1, η_2) ~ N(0, 0,0,1,1).

The density function of the standard normal distribution for two-dimension is,

$$
\phi(x, y) = \frac{1}{2\pi} \exp[-\frac{1}{2}(x^2 + y^2)]
$$
\n(7)

The curve surface of the density function of the standard normal distribution for two-dimension is shown as the Fig. 2,

 0.1 0.08 0.06 0.04 0.02 $\begin{array}{c}\n1_{0.5}\n\end{array}\n\qquad\n\begin{array}{c}\n1_{0.5}\n\end{array}\n\qquad\n\begin{array}{c}\n-0.5 \\
\end{array}\n\qquad\n\begin{array}{c}\n-1.5 \\
\end{array}\n\qquad\n\begin{array}{c}\n-2\n\end{array}\n\end{array}$ 1.5 $\overline{1}$. 5 0.5 $\overline{0}$ -0.5 \mathbb{Z}_1 -1.5

Fig. 2 The curve surface of the density function of the joint distribution of η1 and η² X-axis is the value of η 1 and η 2, and Y-axis is the value of $\phi(x, y)$ of the vector $\Gamma = (\eta 1, \eta 2)^T$ on two dimensions.

Given that the contract of the

 $P(-a \le x \le a, -a \le y \le a) = \int_{-a}^{a} \int_{-a}^{a} \phi(x, y) dx dy = 95\%$, the independent variable domain $(-a \le x \le a, -a \le y \le a)$ is thus determined by this equation, where a is the critical value constrained by 95% of the criterion. Then, for a certain ecosystem E_i , if its corresponding point of (x, y) lies in the domain $(-a \le x \le a$, $-a \le y \le a$), E_i , can be attributed to the majority, i.e., the healthy ecosystems. Accordingly, the rest ones, of which corresponding points of (x, y) lie outside the domain $(-a \le x \le a$, $-a \le y \le a$), are attributed to the unhealthy ecosystems.

Furthermore, the indices applied to assess EH are multiple, and through factor analysis, the indices may be integrated into more than two common factors contributing most of the variance. Since these common factors are independent, and each common factor is a linear combination of several Z_i values. Thus, the integrated index η_i obeys the standard normal distribution at each dimension. Therefore, the joint distribution of the integrated indices obeys the multiple standard normal distribution.

Supposing $\Gamma = {\{\eta_1, \eta_2, ..., \eta_r\}}^T$, *r* is the number of the integrated indices η_i , thus, $\Gamma \sim N(0, E_{r \times r})$, the density function of Γ is,

$$
\phi(x_1, x_2, ..., x_r) = (2\pi)^{-\frac{r}{2}} \exp[x_1^2 + x_2^2 + ... + x_r^2]
$$
 (8)

Thus, we could use multiple normal distribution theory to assess EH, similar to the analysis above-mentioned. According to the multiple normal distribution theory, given $P(-a \le x_1 \le a, -a \le x_2 \le a, ..., -a \le x_n \le a)$ $=\int_{-a}^{a}\int_{-a}^{a}...\int_{-a}^{a}\phi(x_1, x_2,...,x_r)dx_1dx_2...dx_r=95%$, the independent variable domain $(-a \le x_1 \le a, -a \le x_2 \le a, ..., -a \le x_r \le a)$ is thus determined by this, where a is a critical value constrained by 95% of probability. If the point of (x_1, x_2, \ldots, x_r) for a specific ecosystem E_i does belongs to the domain $(-a \le x_1 \le a, -a \le x_2 \le a, ..., -a \le x_r \le a)$ *E_i* is attributed to the healthy ecosystems. On the contrary, if the point of $(x_1, x_2, ..., x_r)$ does not belong to the domain $(-a \le x_1 \le a, -a \le x_2 \le a, ..., -a \le x_n \le a)$, are attributed to the unhealthy ones, which usually occupy 5 percent of all the investigated ecosystems.

As a result, we can distinguish some samples which are far away from the majority at several dimensions in a dataset according to the analysis mentioned above. These samples are attributed to be in the abnormal state, as they are always characterized by obviously deteriorative features, and located far away from the regular trajectory of ecosystem development, succession and evolution. Therefore, EH could be explained by the conceptual tool of 'healthy state' based on statistics, which stands for the majority state in the investigated ecosystems on the same hierarchical level according to the similar spatial and tem-2 Springer

poral scale.

Discussion

Reviewing the published literature developed around the notions of EH, we found that the conclusions are highly subjective to vagaries of indicators, and understandings of EH criteria (Rapport 1998; Rapport et al 1998; Costanza et al 1992; Rapport et al 1985; Rapport 1979; Rapport 1989; Christensen and Van Thi 2008;Stephens et al 2007; Rapport et al 2003; Gatto 1995; Ulanowicz 1980). A method sound in theoretical basis and operational standards is necessary. Our central idea in EH assessment is that the majority of ecosystems are healthy at equilibrium; that means the exchange of energy and mass between the investigated ecosystem and the outside environment is in a steady state. This excludes the ecosystems which are undergoing catastrophic climate conditions since they have to acclimate themselves by changes of state variables in rather short time intervals. From the point of evolution, the concept of equilibrium here also means that ecosystems keep a sound adaptability to their surroundings, not in a transitional or drift state caused by environmental catastrophes between two genetically stable periods.

Based on the above hypotheses, we introduced the factor analysis into EH assessment. In defining the healthy state of an ecosystem, there were many controversies concentrated on what state variables are suited to choose as indicators. To confuse matters more, those variables might be mutually connected in a variety of ways and, thus, might exhibit a complex pattern of different functions. Because different ecosystems might exhibit completely different spatial and temporal patterns of species abundance and of functional activity (Levin 1995), the attempt to refine the notion of health for any particular system by selecting a specific set of indicators could undermine any long lasting and unifying idea of EH. The factor analytic technique we used in this paper is applied as a data reduction method to reduce the number of variables and to classify variables, and could be used to examine a wide range of data sets. Factor analysis assumes that all the data on different dimensions can be reduced to a few important dimensions, and there is no specification of either dependent variables, independent variables, or causality. This reduction is possible because the indicators involved in measuring an ecosystem are mostly related. More EH indices inputted into the analysis would guarantee the generality and objectivity of EH assessments. Thus, comparing with other methods, this method is more tolerant of vagaries of the indicator selections coming from different EH standards that various researchers hold, and facilitates the forming of an unifying notion of EH and a widely accepted framework in which the EH assessment process would be objective and applicable.

It is undeniable that natural disturbance, internal ecological mechanisms and genetic drift often drive most of the natural ecosystems change from equilibrium points (Ehrenfeld 1993; Kimura 1968). In our EH conceptual framework, these changes will be reflected by the leftward transfer or the right transfer of the mean value for a certain state factor of ecosystems as shown

in Fig. 1 and Fig. 2. The changes would probably distort the form of standard normal distribution temporarily during a transitional time interval and reach the normal distribution again at a new equilibrium point. The distortion of normal distribution for the ecosystems corresponds to the "excited state" in physics, as does the standard normal distribution to the "ground state". How to deal with EH evaluation for the ecosystems at the "excited state" would be the topic of our further research. It is well known that in quantum mechanics the determination of "ground state" is prerequisite for "excited state". Analogously, at present, although our method for EH assessment is mainly workable for ecosystems at equilibrium, it sets necessary reference lines for evaluating EH of those ecosystems at non-equilibrium and facilitates the future studies along this line.

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Appendix 1

Central Limit Theorem

According to the central limit theorem, it basically states that as the sample size m becomes large, the following occurs:

1. The sampling distribution of the mean becomes approximately normal regardless of the distribution of the original variable.

2. The sampling distribution of the mean is centered at the population mean μ , of the original variable. In addition, the standard deviation σ of the sampling distribution of the mean approaches σ / \sqrt{m} .

Appendix 2

Asymptotic Normality: Lindberg-Levy Central Limit Theorem

Suppose X_1, X_2, \ldots, X_n are a sequence of i.i.i. random variables with population mean μ and population variance σ^2 , n indicates the number of the variables. Consider the sample mean,

$$
\vec{X}_n = \frac{1}{n} \sum_{i=1}^n X_i
$$
\n⁽⁹⁾

The expectation will be,

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$$
E\left(\vec{X}_n\right) = \mu \tag{10}
$$

And the variance is,

$$
Var\left(\vec{X}_n\right) = \frac{\sigma^2}{n} \tag{11}
$$

Note that the distribution of \vec{X}_n is collapsing to 0, so we want to blow it up so it does not degenerate. Look at,

$$
Z_n = \frac{\sqrt{n}(\vec{X}_n - \mu)}{\sigma} \tag{12}
$$

Here, Z_n has mean zero and variance 1. Equivalently, you can write,

$$
Z_n = \frac{\vec{X}_n - \mu}{\sqrt{\frac{\sigma^2}{n}}}
$$
\n(13)

Which makes it clear that the Z statistic is dividing by the square root of the variance.

By the Lindberg-Levy Central Limit Theorem,

$$
Z_n \to N(0,1) \tag{14}
$$

Appendix 3

The normal distribution theory for one-dimension

The normal distribution, also called the Gaussian distribution, is an important family of continuous probability distributions, applicable in many fields. Each member of the family may be defined by two parameters, location and scale: the mean *μ*and variance σ^2 respectively. The standard normal distribution is the normal distribution with a mean of 0 and a variance of 1. Carl Friedrich Gauss became associated with this set of distributions when he analyzed astronomical data using them, and defined the equation of its probability density function in the following form, on the domain $x \in (-\infty, \infty)$,

$$
\varphi(x) = \frac{1}{\sqrt{2\pi}} e^{-\frac{x^2}{2}}.
$$
\n(15)

Then, the probability function $\varphi(x)$ gives the probability that a standard normal variate assumes a value in the interval $(-\infty, \infty)$. It is often called the bell curve because the graph of its probability density resembles a bell, shown as the following,

Fig. 3 The curve of the possibility function of the standard normal distribution

The cumulative distribution function $\Phi(x)$, which gives the probability that a variate will assume a value $\leq x$, is then the integral of the normal distribution,

$$
\Phi(x) = \int_{-\infty}^{x} \varphi(t) dt
$$
\n(16)

The area under the standard normal distribution curve from negative infinity to infinity is equal to 1. It means that,

$$
\int_{-\infty}^{\infty} \varphi(t) dt = 1 \tag{17}
$$

In order to find the relative frequency of being in an interval (which we shall later call the probability of being in an interval), the area under the normal curve to right side of a cutoff has been tabulated ($x \in [0, \infty)$). For the left side ($x \in (-\infty, 0]$), because of the curve is symmetric around the mean (two halves of the curve are the same), we have,

$$
\Phi(x) = 1 - \Phi(-x) \tag{18}
$$