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Use of eco-exergy in ecological networks

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ABSTRACT

Eco-exergy (EE) has previously been used in ecological network calculations. It is the work energy including the work energy of the embodied information. Eco-exergy is calculated for living organisms as $\beta \times B \times f$ kJ, where β is covering the information contained in the genome, B is the biomass (for instance in g) and f is the work energy per unit of biomass, which on average is 18.7 kJ/g. The β -value is a weighting factor that expresses the ratio between the work energy of an organism including the work energy of the embodied information and the work energy of the biomass. The work energy of information transfer is, however, different for the donor and the receptor. This is in part because the receptor uses the work energy to grow, which means it gains the work energy including the information on the level of the receptor while the donor is losing the work energy including the information of the donor. This difference between the donor and recipient has to be considered when we illustrate the ecological networks, their respective transfer processes, and their total system throughflows (TST). It is also critical when we determine the eco-exergy (EE), which is equal to the work energy including the information stored in the network. Two examples are used to illustrate the differences between ecological networks, based on either donor determined work energy including information or on work energy, where the donor and receptor determined work energy of information are different due to differences in the β -values. The results of the latter are presumed to give the correct calculations of the transfer processes in ecological networks.

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1. Introduction

Ecological networks are living ecosystem components that are linked by processes transferring matter, energy and information. Living organisms carry an enormous amount of information contained in the genome, which is inevitably participating in the transfer process. We define eco-exergy (EE) of organisms or ecosystems as the chemical work energy (WE) including the work energy that is embodied in the information. Thus, EE is the work energy of a system using the same system at thermodynamic equilibrium as reference (the system is in balance with its environment and has no physico-chemical gradients and no active information any longer). EE is calculated for living organisms as $\beta \times B \times f$ and has the unit of the energy kJ, where β is a weighting factor covering the information, *B* is the biomass (for instance in g) and *f* is the chemical work energy (WE) per unit of biomass, which in average is 18.7 kJ/g, but may be higher in the case of animals with a high fat content. If B is replaced by the concentration, c, i.e. B per unit of area or volume,

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http://dx.doi.org/10.1016/j.ecolmodel.2014.05.007 0304-3800/© 2014 Elsevier B.V. All rights reserved. we get $\beta \times c \times f$ in the unit kJ per unit of volume or area, which is the EE-density. The weighting factor β measures the content of information embodied in the genome and determines the life processes of the biomass. The value β can be shown to be equal to RTK, where R is the gas constant, T is the absolute temperature and K is Kullback's measure of information (see Jørgensen et al., 1995; Jørgensen, 2002, 2012) in the non-dimensional case. This measure of information is nowadays better known as the Kullback-Leibler divergence which in brief represents the difference between expected (theoretical) and observed (actual) distributions of data. The β -value is a weighting factor that expresses the ratio between the work energy of an organisms including the work energy of the embodied information and the work energy of the biomass. It implies that $(\beta - 1) \times B \times f$ will cover the work energy of the information and $B \times f$ the chemical work energy of the biomass. This allocation of the work energy of information and of chemical work energy of the biomass is of course valid for both storage of work energy in the organisms (compartments) and for the transfer processes and may therefore potentially be applied to analyze ecosystem networks. The β -value is found from the information embodied in the genome, and it is this information that in turn determines how many amino acids that are in the right sequence to make up all the enzymes controlling the life processes of the respective organism (see Jørgensen et al., 2005). In







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addition, it has been shown that β is a measure of the free energy of the enzymes with their amino acid sequence determined by the genome (Jørgensen et al., 2010).

Normally, analyses of energy flows in ecosystems follows an approach taking its entrance point based on the first law of thermodynamics. As energy is conserved it is possible to construct conceptual models that are perfectly balanced, no energy is created or destroyed.

It would of course be possible to evaluate an ecosystem based on the chemical exergy (equivalent to WE) of its compositional elements meaning that all components – dead or alive, primitive as well as highly complex organisms – would be ascribed the same work energy content, e.g. evaluated as Gibbs free energy of organic matter (the approx. 18.7 kJ per gram used in the previous).

In the case of simple work energy-based merely on chemically bound energies (WE equal to G) – it is feasible to establish a similar accounting. Only, it is necessary to assure that all exported or dissipated work energies, are included in the conceptualization of the system. Such studies may comprehend both energy and matter fluxes and can be formulated in terms of energy.

Nevertheless, as indicated above this way of calculation has been considered too simplistic as it does not consider the complexity and organizational state of the organisms but simply considers biomass of bacteria and other primitive organisms and highly developed vertebrates to be alike and count equally in the ecosystem and in determining the structure of the ecosystem network. It is directly counterintuitive and probably also erratic. For an ecosystem to exist we need the organisms to be alive and exerting their respective activities whatever they may be, in other word they need to be functional playing out their roles in the ecosystem network. It is these concerted actions that are responsible for the resulting network.

In order to perform and do this the organisms need information – but not only passive information – they also need the information to be processed. So if there is no life, there is only dead material, no processes, no useable information, no flows nor network and thus no ecosystem. Information therefore plays just as important an element to the ecosystem as the biomass of the individual components, species or organisms. The importance of this information in shaping the state of the ecosystem tends to be an issue that has been overlooked and neglected in ecosystem theory so far.

The elements necessary to carry out this function are believed to be included among the genes, i.e. in the overall genome of the organisms. This information is used to raise the system level to a functional state beyond and above that of a collection of a similar amount of dead, decaying matter.

This realization leads to the construction of a new form of exergy (WE) usually referred to as eco-exergy (EE), which includes not only biomass but also the information that lies behind the performance and activities of the living organisms and thus the network. It is hypothesized that this way of calculation the work energy of ecosystems including the work energy of information will be better in expressing the overall function of the ecosystem network encompassing storages and flows of both biomass and information. It has therefore been used here to illustrate some principles of network properties as advocated by Patten (e.g. Finn, 1976; Patten, 1998).

Now, when a system description is converted to also include information, i.e. the work energies of the information embodied in the collection of organisms composing the system, the conservation principle does not hold as information is not conserved during transfers and processes. This means that the amount of EE leaving (exported, EEE_j) a compartment (the donor) is not the same as the work energy (incl. information) which is entering (imported, EEI_i) the accepting compartment (the receptor), because the β -value generally will be different for the donor and the receptor, resulting in two possible ways of calculating the total system throughflow,

namely either as donor based
$$(TST_j)$$
 or receptor based (TST_i) . As a result:

$$\Gamma ST_j \neq TST_i$$

where

$$\text{TST}_j = \sum_i f_j$$

 $TST_i = \sum_i f_i$

 f_j and f_i are the flows leaving and entering a compartment, respectively, and the f_j 's are calculated as WE times β -value of the donor (and a 1. order transfer rate) and the f_i 's in a similar manner are calculated as WE-value of the receptor times the respective β -value (and the transfer rate). As a result, the two latter equations not equal due to the fact that EE is not conserved.

Therefore, the introduction of work energy including the work energy of the information requires an extension of the network analysis exactly because of the just described property of nonconservation of information.

The scope of the present paper is to demonstrate how such an analysis may be carried out, as well as to illustrate the consequences and results of such an implementation. Two hypothetical, historical networks are used to elucidate this. Thus, this paper examines how the ecological network calculations are changed, if these more correct calculations of eco-exergy, i.e. work energy including work energy of the information, are applied. How will these calculations change the sum of all the through-flows of all the compartments (TST, total system throughflow), and the aggradation index = TST/sum of all input flows? Notice that the aggradation index is the total flows of the network relative to the inflows that feed the network (see also Finn, 1976; Jørgensen et al., 2000) or expressed differently the number of times the feeding (input) flows are magnified due to the network. The calculations are based on the same equations as applied for all other network calculation (see for instance EcoNet, Kazancı, 2007), but- Eco-exergy is substituted for the typical energy or mass. Given this change, are the obtained results understandable and can they be explained by network theory and thermodynamics? TST used to designate total system through-flow has been an established term for the analysis of ecosystems at least since the seminal paper of Finn (1976). Now the question is:

What additional knowledge can we obtain by examination of networks properties where the analyses are based on storage and flows that include the EE in the analyses of flows?

2. A simple network

Eco-exergy has previously been used in ecological network calculations; see for instance Jørgensen et al. (2007), Jørgensen and Ulanowicz (2009) and Jørgensen (2012). Meanwhile, the above mentioned inclusion of information is likely to have some consequences, but it is not easily predictable what such consequences might be. Since β -values vary between trophic components and thus throughout the ecological network calculations, the EE of flows in the system will vary with calculation when for instance calculated on either donor or receptor based cases. This may at best be illustrated by introduction of two minor sample cases.

Fig. 1 shows a hypothetical ecosystem network 1500 million years ago at steady state. The same system may be represented by a directed flow matrix as shown in Table 1 to facilitate calculations. The processes represent work energy transfers controlled by the

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