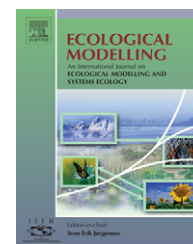


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# Dealing with uncertainty in qualitative models with a semi-quantitative approach based on simulations. Application to the Gironde estuarine food web (France)

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## ARTICLE INFO

### Article history:

Received 17 March 2008

Received in revised form

17 September 2008

Accepted 19 September 2008

Published on line 1 November 2008

### Keywords:

Semi-quantitative model

Interaction strength

Sensitivity analysis

Community matrix

Ecopath with Ecosim

Ecosystem model

ECEM 07

## ABSTRACT

In the context of ecosystem approach to fisheries, it is a critical issue to build management tools able to predict the possible trajectories of ecosystems under various human pressure or environmental variations, but also capable to point out influent and sensitive components.

A major drawback of quantitative models is that they require many data to be implemented, which are often not available. Qualitative modelling with loop analysis needs only few data and offers the possibility to predict effect of sustained perturbations on an ecosystem. It considers direct and indirect interactions by inverting its qualitative community matrix. However, depending on the complexity of the studied ecosystem, predictions can be very inaccurate.

Different approaches have been proposed to deal with uncertainty on the sign of the effects in loop analysis. However, as well as reducing uncertainty on their signs, we wanted to allow taking into account the strength of interactions. Thus, we developed a semi-quantitative method coupled with a simulation approach that also permits to use conjointly empirical data and expert opinion. The framework was applied to the Gironde estuarine ecosystem for which an Ecopath model has already been constructed.

A sensitivity analysis permitted to show up the uncertainty on the results and revealed the gain of precision on the results while using the semi-quantitative method. Moreover, it pointed out that the precision was much better on strong effects, which allows the identification of influent and sensitive components of the ecosystem. Finally, the correlation between the results of the inverse community matrix and those of the “mixed trophic impact” routine of Ecopath allowed to place our semi-quantitative method as an intermediate step between loop analysis and Ecopath but also as a complementary approach for network analysis.

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## 1. Introduction

Modelling trophic networks is a way to approach the functioning of ecosystems (Christensen and Pauly, 1993; Livingston,

2002; Ulanowicz, 2003). This allows the calculation of trophodynamic indicators (Cury et al., 2005) and the comparison of different systems (Baird et al., 1991; Baird and Ulanowicz, 1993). Another key issue is to make forecasts in order to anal-

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doi:10.1016/j.ecolmodel.2008.09.017

use changes in biological compartments or modifications in human pressures on the system. However, most of the time, such approaches require gathering detailed data, which can be very difficult when dealing with ecosystems where components are numerous and interactions are complex. In this way, qualitative approach offers attractive perspectives. In particular, “loop analysis” developed by [Levins \(1974\)](#) and derived from the construction of community matrices ([Levins, 1968](#)), is a powerful tool that allows taking into account direct and indirect interactions between components of an ecological network in order to make predictions regarding the food web response to perturbations ([Dambacher, 2001](#)). However, when trophic webs have a high number of components and numerous weak interactions as in the Gironde, the simulations of “loop analysis” can produce high sign indeterminacy for predictions ([Dambacher et al., 2002](#); [Yodzis, 1988](#)). [Puccia and Levins \(1985\)](#) suggest using knowledge of relative interaction strengths to improve predictions in loop analysis. But, applying this general method to a specific case implies to define values that are generally given with an uncertainty and it cannot be directly implemented in the loop analysis procedure. Moreover, if the sign of the predictions is considered in loop analysis, the magnitude of the response is not its objective despite its utility in our case. Thus, this study proposes an extension of the “loop analysis” method by allowing for interaction strength between food web components in a semi-quantitative way. A new matrix inversion permits to work with uncertainty on interactions and allows an update procedure for additional knowledge, when it progressively becomes available.

We used data available on the Gironde estuarine food web ([Lobry et al., 2008](#)) as a case study and we compared the results of our method with those of classical “loop analysis” thanks to a sensitivity analysis. Then, to place our method in the range of the existing ones on matrices inversion, we compared our results with those from the “mixed trophic impact” routine of Ecopath ([www.ecopath.org](http://www.ecopath.org); [Christensen and Pauly, 1992](#); [Christensen and Walters, 2004](#); [Christensen et al., 2005](#)).

## 2. Materials and methods

### 2.1. Two commonly used matrices inversion methods

#### 2.1.1. Community matrix and loop analysis

The community matrix developed by [Levins \(1968\)](#) is a way to describe interactions among species in an ecosystem at equilibrium and can be used as a predictive tool. However, as [Dambacher et al. \(2003a\)](#) indicated, “properly specifying a quantitative community matrix require many press experiments ([Bender et al., 1984](#)), which is at best a laborious and time consuming task and at worst impossible when important variables cannot be measured”. Therefore, to test interactions and responses of an ecosystem to a sustained perturbation, [Levins \(1974\)](#) developed a method derived from the community matrix approach but in a qualitative way, loop analysis.

This method involves the representation of interactions among species in an ecosystem in both a graphical form using

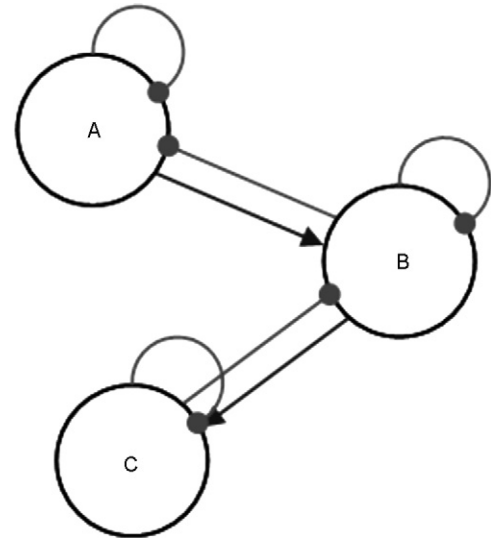


Fig. 1 – Representation of a signed digraph.

signed digraphs (Fig. 1), and in matrix form using squared matrices (Table 1). In fact, the interpretation of signed digraphs of community matrix models allows making qualitative predictions of system stability and perturbation response based on the balance of system feedback ([Dambacher et al., 2003a](#)). To do so, the community matrix **A** ([Levins, 1968](#)), which reports the direct relationships between components of the trophic network, is specified only by the symbol (–, +, 0) of the interaction.

The adjoint of the community matrix ( $\text{adj } -A$ ) is obtained thanks to a matrix inversion and Eq. (1) used by [Dambacher et al. \(2002\)](#). It is equivalent to the Levins’ table of prediction that reports the effects of a sustained perturbation on each component to the whole system, through the direct and indirect effects between components of a network near equilibrium:

$$-A^{-1} = \frac{\text{adj}(-A)}{\det(-A)} \tag{1}$$

The sign of each element  $\text{adj}(-A_{ij})$  in the adjoint matrix is the sign of the effect on the *i*th component (*i*th line of  $\text{adj } -A$ ) following a sustained positive perturbation of the *j*th component (*j*th column of  $\text{adj } -A$ ).

However, [Dambacher et al. \(2002\)](#) pointed out the high level of indeterminacy in the sign of the effects in the adjoint matrix thanks to the calculation of the “weighted prediction matrix”. To do so, the sum of cycles contributing to each element of the adjoint matrix,  $\text{adj } -A$ , is calculated in the “absolute feedback”

Table 1 – Community matrix corresponding to the previous signed digraph (Fig. 1).

	A	B	C
A	-	-	0
B	+	-	-
C	0	+	-

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