Ecological Modelling 364 (2017) 25–41

Contents lists available at ScienceDirect

Ecological Modelling

journal homepage: www.elsevier.com/locate/ecolmodel

Research Paper

Generation of extensible ecosystem models from a network structure and from locally executable programs

M. Varga*, B. Csukas

Kaposvar University, Institute of Methodology, Research Group on Process Network Engineering, 40 Guba S, 7400, Kaposvar, Hungary

ARTICLE INFO

Article history:
Received 11 March 2017
Received in revised form
12 September 2017
Accepted 15 September 2017
Available online 16 October 2017

Keywords:
Model generation
Network structure
Dynamic mass balance
Extensible model
Ecosystem modelling

ABSTRACT

Analysis and planning of the Water/Food/Energy Nexus must be extended with the Ecosystem related interactions. Considering this, present work studies the further development and implementation of a methodology that has already been tried for the modelling and simulation of other processes within the Nexus. This methodology aims to support the unified and integrated dynamic modelling of multidisciplinary process networks, instead of interfacing amongst various field-specific tools. An additional challenge, inspired also by different approaches of food web modelling, is to build bridge between the topological network analysis and the mass/energy conservation based dynamic simulation of the underlying (often non-linear) processes. In the proposed framework the generated model appears in form of a modifiable and extensible GraphML structure that, having edited, may be interpreted into a model database for a general purpose simulation program. A very simple, food web example helps to illustrate the general method.

1. Introduction

Analysis and planning of the Water/Food/Energy Nexus (Smajgl et al., 2016) must be extended with the ecosystem related interactions to support sustainable development (Bidoglio and Brander, 2016). In this field, modelling and simulation are intended to support the more effective analysis and planning. However, interfacing between the various modelling tools of the multidisciplinary nexus elements is difficult. Considering this challenge, present work studies the further development and implementation of our Direct Computer Mapping based methodology that has already been applied for the modelling and simulation of various processes within the nexus. Considering ecological modelling, it is to be mentioned, that having acquainted with different approaches of food web modelling, it has inspired building bridge between the topological network analysis and the mass/energy conservation based dynamic simulation of the underlying (often non-linear) processes. That's why we use a very simple, food web example to explain the general modelling framework. Of course, there are more plausible examples for the nexus/food web interaction e.g. in cage aquaculture or in agroforestry, as well as other important fields that need linking ecosystems to the Water/Food/Energy Nexus.

This paper proposes a methodology for the algorithmic generation of extensible simulation models of ecological processes from the network structure and from the field-specific, local program declaring elements, called prototypes. For the comparison, first the available modelling approaches of (basically aquatic) ecological systems will be overviewed, in comparison with our approach regarding to connectivity with other, e.g. Water/Food/Energy Nexus (Smajgl et al., 2016) related process models.

In ecological network analysis, an early endeavour was the collection of the usable analytical tools at the end of 1980's. As a collective name, this set was called "ecosystem network analysis" (ENA) tools (Wulff et al., 1989). By now, ENA became a comprehensive modelling approach that comprises analytical methods and tools for the study of structure and dynamics of material and energy flows between the individual compartments of ecology, assuming that the investigated system can be described as nodes and connections between them. Several analytical tools were developed to support the modelling of ecosystem networks. Without a complete list, we can mention e.g. NETWRK (Ulanowicz and Kay, 1991), EcoNetwrk (Ulanowicz, 2004), WAND (Allesina and Bondavalli, 2004), NEA by Patten and Fath (Patten, 1978; Fath and Patten, 1999), the MATLAB implementation of NEA by Fath and Borrett (2006), enaR (Borrett and Lau, 2014) or DEA tool by Shevtsov et al. (2009), Shevtsov and Rael (2015).

In fisheries science Ecopath with Ecosim (EwE) is a continuously evolving modelling framework for the mass balance analysis

---

* Corresponding author.
E-mail address: varga.monika@ke.hu (M. Varga).

http://dx.doi.org/10.1016/j.ecolmodel.2017.09.014

and dynamic modelling of aquatic ecosystems (Christensen and Pauly, 1992; Walters and Juanes, 1993; Walters and Martell, 2004; Christensen and Walters, 2004; Christensen et al., 2005, 2009), coupled with GIS tool in some cases (e.g. Steenbeek et al., 2013). In line with the arising demand for the complex ecological-environmental assessment, application field has been widened further toward terrestrial ecosystems.

The balance equations are usually described by sets of algebraic and/or differential equations. However, to combine these sophisticated mathematical apparatuses or their numerical solutions with various other (e.g. agri-food, hydrological, environmental, etc.) process models might be difficult, especially in the case of multiple coupling between the underlying models.

Agent based (ABM) and individual based (IBM) models have got an increasing importance for the past decades (Grimm, 1999; Recknagel, 2003; Bousquet and Le Page, 2004; Grimm et al., 2005; DeAngelis, 2005; Smajgl and Gehrke, 2007; Smajgl et al., 2009). The straightforward IBM application of (Ma and Kazanci, 2012) is fully compatible with the ODE representation of the ecosystem model. Agent based modelling and programming has a quite plausible principle at first look, however it is quite diversified and even case specific in details. This can be seen in the limelight of the standardization efforts of ABM/IBM, also within ecological modelling. For example, ODD (Overview, Design concepts, Detail) protocol (Grimm et al., 2006) is designed as a general protocol for communicating individual based and agent based models. It is an excellent and general set of model development heuristics, however it does not guarantee the connectivity of the agent based models and programs, developed in various disciplines.

A user-friendly web-based simulation tool is afforded by EcoNet (Kazanci, 2007), supporting both network analysis and dynamic simulation. The model starts from an input, declaring the initial stock of the species (represented by nodes) and individual consumption flows (represented by edges), and generates the set of differential equations automatically. EcoNet model apparently uses the assumption that the individual predator-prey related flows do not depend on availability of the alternative resources. On the contrary, if we calculate the consumption of the individual preys from the ratio of its (optionally weighted) “concentration” and the (optionally weighted) sum of all possible prey “concentrations”, then we shall need less input data, while the resulting non-linear formulation of the model describes some adaptability to the changing scenario. Accordingly, the well defined individual consumption flows are not constant, but depend on the temporal behaviour of the model.

Other approaches, such as process algebra-based programming languages (e.g. BlenX from Dematté et al., 2008; Livi et al., 2011), Ecological DYnamic Simulation Model (Mclendon et al., 2009; Coldren et al., 2011), neural network (Zhang et al., 2007; Zhang and Zhang, 2008) or System Dynamics based applications (Matinzadeh et al., 2017) were also utilized for the analysis of various ecosystems.

System Dynamics based ecosystem models seem to be connectable with other models of complex Water/Food/Energy systems. However, System Dynamics builds its models without distinguishing clearly between the problem specific conservation laws based additive balance measures and the over-writeable qualitative information. Shortly speaking the feasible result and the fulfilment of conservation laws might not be guaranteed.

Network analysis methods have significantly contributed to the deeper understanding of ecosystem processes and dynamics. However, in line with the increasing complexity of ecosystems models, the demand for the integrated modelling platforms to combine ecosystems with dynamic processes of hydrology, biogeochemistry, plant biology, etc. is also appeared (Larocque et al., 2014).

The limitations of many available tools originate mainly from the steady state assumptions, while the necessary balancing of the data may also affect the results. There have been several attempts on extending steady-state tools to dynamic networks, dating back to a couple of decades (Hippe, 1983; Hallam and Antonios, 1985). Recent ones have been successful, even though computationally time consuming (Shevtsov et al., 2009; Kazanci and Ma, 2012).

Considering the dynamic (non steady state) models, neither the conventional differential equation based, nor the agent based model representation support the combined, integrated use of ecosystem models with models of other disciplines in complex problem solving.

2. Objective

The objective of this work is the further development and implementation of our Direct Computer Mapping based methodology for the generation of extensible and connectable ecological simulation models. The specific aims are the followings:

- Automatic transformation of the underlying network to a programmable net, composed of the pairs of prototyped state and transition elements;
- Local and modifiable programming of functionality prototypes;
- Automatic generation and execution of the dynamic food web simulation models;
- Evaluation of experiences, obtained from the illustrative example for the robustness, flexibility, extensibility and connectivity.

3. Applied method and illustrative example

3.1. Direct Computer Mapping of process models

The complex models claim for clear and sophisticated coupling of structure with functionalities. Both natural and human-built process networks may contain more complex structures and elements, than any single, well-defined mathematical apparatus. Considering the topological approach, the essential structure of processes may be more complex, than the simple networks. Moreover the nonlinear dynamics cannot be taken into consideration by the linear state space model, associated with these networks. Considering the functional approach, the dynamic mass/energy balances, described by differential and algebraic equations, hardly manage the event- or time-driven discrete changes. Additional difficulties might appear if the sub-models of various disciplines are to be integrated into a complex model. Nevertheless it is obvious that the extensive/intensive properties of mass and energy balances may be characterized by state elements, while the elementary transformations and transportations may be described by transition elements in every sub-model. Also the functionalities for the large number of elements may be determined by stereotypic set of expressions (i.e. by locally executable programs) that may be defined in the limited number of so-called prototype elements.

In our approach, called Direct Computer Mapping (DCM) of process models (Csukas, 1998; Csukas et al., 2011; Varga et al., 2016) the natural building blocks of the elementary states, actions and connections are mapped onto a unified set of building elements determining an executable computer code, directly, without any specified mathematical apparatus. Actually, the elements of the cognitive model are mapped onto state and transition elements, executing the local programs, described by the respective “prototype elements”. This principle was successfully applied for a broad range of processes from the low-scale cellular biosystems (Varga et al., 2017) through technological process systems (e.g. Csukas et al., 2013) up to the large-scale agri-food (Varga