



Process algebra-based computational tools in ecological modelling

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ABSTRACT

Ecological systems and processes are inherently variable. The multiplicity of interacting processes and the variety of components call for multi-level, integrative models that keep track of stochasticity and quantify its consequences. Mathematics and physics already helped biologists a lot, but the composability feature of process algebra-based computational tools may provide additional help in modelling interacting stochastic processes. Compositional models can be built in a modular way, and can be easily standardized and evaluated rigorously. Following initial applications in systems biology, the concepts of parallelism and concurrency can also be of key importance to future systems ecology. We provide an overview of process algebra-based approaches in ecology, discuss the perspectives of this research line and provide a toy and a real example for illustration.

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1. Introduction

Since the influential works of Clements (1916) and Gleason (1926), ecologists typically approach most problems from two major directions: searching for global laws (implying top-down rules and well-determined patterns) or local rules (providing bottom-up determination and contingent, stochastic processes). We argue that computer science may help in integrating these research strategies.

Public databases and computational power are both growing continuously in biology. Still, what we call systems biology today is nearly exclusively based on collecting huge amounts of information without a hierarchical perspective or coherent integration (see Klipp et al., 2009). In order to improve the predictive power of biological models, novel computational tools will be important (DeAngelis and Gross, 1992; Green et al., 2005). Apart from managing huge databases and visualising complex systems, new kinds of algorithms could link community and systems ecology by providing tools for process-based approaches. The solution to these problems will become computable by increasing computer power and introducing novel conceptual and computational tools (Levin et al., 1997).

Although many works have already suggested focusing more on ecological processes and less on structures (Thompson, 1988), new tools are required to represent functional issues (Clark, 2009). A

number of studies are still focused on static patterns, while dynamic behaviour is only inferred from certain static properties (such as scale-free distribution used as a proxy for vulnerability against attacks and robustness against errors, Solé and Montoya, 2001; Dunne et al., 2002). Considering environmental noise may also be important for modelling ecodynamics (Björnstad et al., 1999). The sensitivity of genotypes (*i.e.*, reaction norm, Angilletta et al., 2003) and interspecific interactions (*i.e.*, interaction norm, Thompson, 1988) to environmental variation is well known. Environmental stochasticity and contingency provides the freedom of choice for individual organisms within various constraints (Belovsky, 1981). All of these reasons point to the pressing need for improved techniques for stochastic modelling (Ebenman and Jonsson, 2005). For future conservation management (and likely also in humanities), noise and variability will be studied for the sake of providing a pool of solutions for adaptive management, rather than looking for strategies to minimize their impacts (Holling, 2001).

In the present paper, we provide an overview of the need for and the first applications of process algebra-based models in biology and ecology. We discuss their composable property and relevance in ecological modelling. Finally, we present two illustrative examples: a toy model and a real case study.

2. Individual-based models

Individual-level variability (DeAngelis and Mooij, 2005), stochasticity and local interactions (Levin, 1998; Brose et al., 2005) call for individual-based models (IBMs, Grimm et al., 2006; McKane and Drossel, 2006; Grimm and Railsback, 2005) in the case

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of several ecological problems. Although standardization (Grimm et al., 2006) and evaluation of these models are difficult (e.g., because of the extensive lack of published computer codes, Judson, 1994), and their generality is poor, they provide powerful solutions for particular case studies. The key challenge here is to identify relevant local mechanisms that can trigger macroscopic patterns, as this is the way to link population biology to communities and ecosystems (Huston et al., 1988; Johnson and Stinchcombe, 2007; Loreau, 2010). In particular, novel conceptual tools and algorithms are needed to model concurrent, multiple effects. IBMs provide a bottom-up (Grimm et al., 2005) approach based on sophisticated local mechanisms (Seth, 2007). Another advantage of IBMs is their ability to supply detailed predictions on real systems (e.g., modelling the effects of five killer whale individuals on sea otters, Williams et al., 2008), although this goal is fulfilled at the price of generality. This approach makes it possible to consider intra-individual level information (e.g., trait-based, McGill et al., 2006; Peacor et al., 2006) or aggregating individuals to larger groups (e.g., superindividuals, Scheffer et al., 1995). If a given amount of biomass is consumed, deterministic models clearly cannot show the difference between a single tuna individual, hundreds of small pelagic animals or millions of meso-zooplankton organisms. Heterogeneous, hierarchical, flow-based, nonlinear ecological systems are coined complex adaptive systems (Levin, 1998; Grimm et al., 2005). Here, bottom-level variability (Björnstad et al., 1999) leads to adaptability and evolvability. The bottom-up, local rules-based view seems to be also more intuitive in biology (Judson, 1994), as opposed to top-down descriptions.

3. Algorithmic challenges

The multiplicity of system components and interactions, as well as the large number of parameters in ecosystems, pose huge computational problems (McKane and Drossel, 2006; Pascual, 2005). To deal with these difficulties, modellers have been taking advantage of the increased processing power of modern computers as well as developing novel tools and algorithms. Beyond the recently introduced algorithmic toolkit (e.g., cellular automata: Oborny et al., 2000, genetic algorithms: Ruiz-Moreno et al., 2006, formal logic: Robertson et al., 1991, particle tracking: Kazanci et al., 2009, Petri nets: Gronewold and Sonnenschein, 1998, and swarm intelligence: Dorigo and Stutzle, 2004), a new stream of computational techniques – based on quantitative extensions of process algebra (Priami et al., 2001) – has already been used in molecular computational and systems biology (Priami and Quaglia, 2004).

4. Process algebra-based modelling in biology

Several process algebra-based programming languages have been developed to explicitly model interactions of biological entities (e.g., Weighted Synchronous Calculus of Communicating Systems – WSCCS, Tofts, 1993, or BlenX, Dematté et al., 2008a; Priami, 2009). Their important feature is composability: a model is nothing more than the ‘sum’ of its parts, which can be individually modelled then put together. Building models by composition has several advantages: model development can be modular, standardization is relatively easy and the evaluation can be rigorous. Furthermore, composability enables the modeller to begin with a simple well-characterized toy model and increase it in complexity gradually by adding additional elementary elements, instead of rewriting major parts of the code and risk introducing new bugs. An initial model can be easily fine-tuned according to pilot studies or sensitivity analyses, or can be simply extended and modified. These features are advantageous for recurrent application and

standardization (in contrast to *ad hoc* model building, Scheller et al., 2010).

BlenX (Dematté et al., 2008b), a process algebra-based language, has been developed within the framework of algorithmic systems biology (Priami, 2009). It enhances current modelling capabilities (i.e., ease of use, composability and reusability of models) and is explicitly designed to describe interactions of (biological) entities (i.e., quantitative information about speed and probability of actions is provided with systems specification). Individuals are represented by boxes, composed by interfaces (sets of binders) and internal programs that are executed simultaneously. The interaction sites on boxes are called binders. The internal structure of the process influences the interactions of each box with other boxes, modifies the interface of the process, and can also change the internal structure of other processes through interactions mediated by binders. For example, when a box is used to model an individual organism, binders are characterized by different levels of affinity to interact with other species (e.g., predator–prey or plant–pollinator relationships). In the case of food webs, interaction strength (i.e., prey preference extracted from weighted food webs) is considered as the “kinetic rate”. The internal structure codes the mechanism that transforms an input signal into demographic (e.g., reproduction, death) or behavioural (e.g., changed prey preference) change of individuals. Signals are represented as messages exchanged over communication channels. Once internal processes within boxes and interactions involving several boxes are defined, the system behaviour emerges out of lower-level dynamics. Since the hierarchical view is implicit, it is suitable for modelling the links between different organizational levels and among interconnected, multiple, parallel processes. The stochastic approach can be of key importance for studying ecological interactions, particularly in models with small population size. In fact, stochastic simulations allow the modeller to complement deterministic dynamic models. These latter are feasible when the population size is sufficiently large to minimize noise in the overall system. In models with small population size, stochasticity can be modelled explicitly. To this end, BlenX can capture the inherent variability of biological systems, as opposed to ordinary differential equation-based simulations which rely on a homogeneous set of components. While the latter represents a view based on equations to provide general laws with some (mostly external) noise, the former describes a situation where variability is inherent and influential. Important features of BlenX are composability, propensity to describe parallel events and the opportunity of including multiple interactions. Composability refers to model construction and development. It allows to extend models by adding simple and modular elements instead of complete rewriting program codes. In ecology, predation and facilitation shape animal communities, but their concurrent interactions are difficult to integrate. BlenX offers the language for modelling these parallel (i.e., concurrent) events. Simulating concurrent interactions also corresponds to investigating predator–prey, plant–pollinator and host–parasite relationships under this unique approach.

Various process algebras have already been used in biology (Table 1). At the molecular level, the Chemical Model Definition Language was successful in predicting rRNA synthesis (Ciocchetta et al., 2008), Bio-PEPA models fitted well to measured intracellular Ca^{2+} oscillations (Ciocchetta and Guerriero, 2009) and the *in silico* evolution of MAPK pathways modelled in BlenX language produced remarkable patterns (Dematté et al., 2008a,b).

The first ecological applications addressed social insect colonies. The WSCCS language-based theoretical investigations of Tofts (1993) were supported by experiments (Sendova-Franks and Franks, 1993, 1994). These studies suggested that not only the age of ant individuals but also their precise spatial location determines

Table 1
Some biological applications of various process algebra-based languages.

Field	Key finding (PA used)	Reference
Division of labour (ants)	'Foraging for work' algorithm optimizes task allocation (WSCCS)	Tofts (1993)
Colony dynamics (ants)	Cues, not signals help colony synchronization (WSCCS)	Sumpter et al. (2001)
Thermoregulation (bees)	Real spatial patterns (e.g. disk) emerge from local rules (WSCCS)	Sumpter and Broomhead (2000)
Parasite dynamics (bees)	Aphid dynamics influenced by summer migration (WSCCS)	Sumpter and Broomhead (2001)
Epidemiology (bees)	Crossing epidemic threshold breaks mite/virus/bee balance (WSCCS)	Sumpter and Martin (2004)
Epidemiology (human)	SIR model of HIV fits well to data (WSCCS)	McCaig et al. (2009)
RNA synthesis	Simulated data fit well to measurements (CMDL)	Ciocchetta et al. (2008)
Membranes	Intracellular Ca^{2+} oscillation predicted (BioPEPA)	Ciocchetta and Guerriero (2009)
Signalling	<i>In silico</i> MAPK cascade evolution is punctuated (BlenX)	Dematté et al. (2008a)
Food web dynamics	Community importance quantified (BlenX)	Livi et al. (2011)

division of labour. The role of learning and the dominance of older individuals were also theoretically predicted and experimentally demonstrated.

Sumpter and colleagues applied the same language with great success in better understanding thermoregulation (Sumpter and Broomhead, 2000), parasite dynamics (Sumpter and Broomhead, 2001) and epidemics (Sumpter and Martin, 2004) in honey bees. Process algebra-based models helped also understanding colony-level synchronization processes in insect colonies (Tofts, 1993; Sumpter et al., 2001). Extensions towards population biology and

epidemiology are being quickly developed (Norman and Shankland, 2004; McCaig et al., 2009).

5. Process algebra applications in ecology

Several stochastic approaches to ecological modelling and simulation (Kazanci et al., 2009; Powell and Boland, 2009; Matamba et al., 2009) use the Markov process-based Gillespie algorithm (Gillespie, 1977). Here, kinetics adopted in computational cell biology has been typically imported to ecology, but

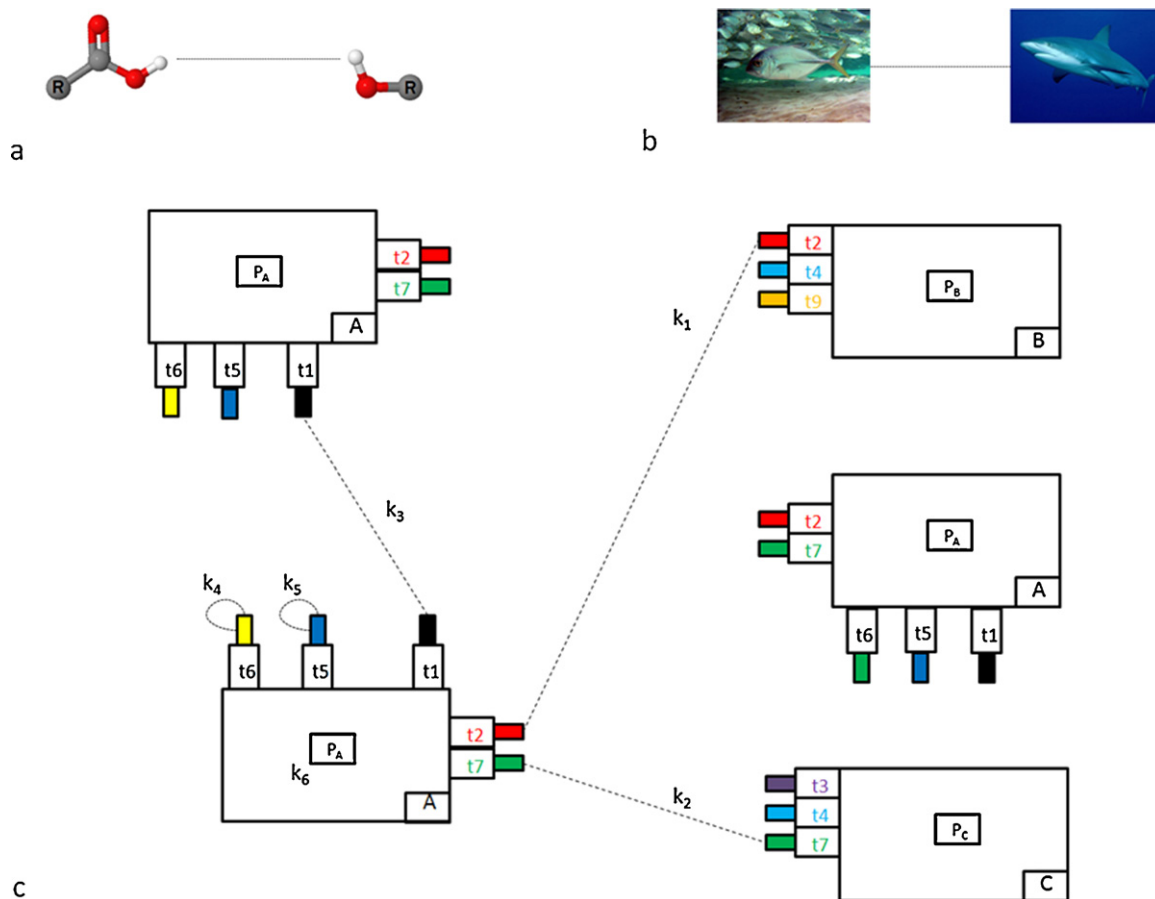


Fig. 1. (a) Two molecules can interact if they have compatible functional groups: organic acids (R-COOH) and alcohols (R-OH) form esters (picture made by <http://www.jmol.org>). (b) Prey–predator interactions are also based on behavioural, anatomical and spatiotemporal compatibility (pictures from <http://www.fishbase.org>). In both cases, interactions are characterized by certain rates that are measurable and frequently known. In (c), we see a box-representation of a process algebra-based ecosystem model. Individual A can be involved in six kinds of processes: with rate k_1 , it can eat B (compatibility coded by the same t2 type of binder); with rate k_2 , it can pollinate the plant C (t7 is their shared communication channel); with rate k_3 , it can form a social tie to another conspecific individual (disposing identical binder types); with rate k_4 , it can switch spatial location between habitat patches (t6 is yellow between the social partners but no social tie can be established with the conspecific A individual in a different habitat marked by a green t6); with rate k_5 , it can change developmental status (i.e. mature, resulting in altered rates) and finally, with rate k_6 , it can reproduce. The first three processes require two individuals, while the latter three ones are performed by a single individual. All these processes can be very simply combined in process algebra-based languages offering modular model construction, rigorous standardization and easy evaluation.

there is a compelling need for implementing other theories with specific relevance in ecology (e.g., functional responses, Abrams and Ginzburg, 2000; Okuyama, 2009). Nonetheless, simple kinetic rules seem to apply quite well in several cases. For example, the number of shark-bitten pinnipeds is proportional to shark and pinniped abundance (Stevens et al., 2000) and community shift in a study of exploitative competition is proportional to prey availability, relative competitive abilities and the relative densities of consumers (Stevens et al., 2000). These parameters correspond to kinetic rates and concentrations in simple chemical reactions. If two molecules A and B have compatible functional groups, they may react (Fig. 1a). The probability of reaction depends on the concentration of both molecules and the reaction rate (as well as on the concentration of products if the reaction is reversible). The simplest kinetics for an interspecific interaction may follow the same logic: prey density, predator density and the prey preference of the predator comprise the three parameters describing the probability of feeding (Fig. 1b). Process algebras provide tools for studying the interactions among several types of processes described by suitable kinetics (Fig. 1c).

The major advantage of process algebra-based approaches is that, given only a few initial parameters, they can model relatively complex systems, whose behaviour can then be simulated taking into account the influence of relevant environmental effects (as opposed to modelling overly complicated behaviour in an oversimplified environment, Ginzburg and Jensen, 2004; McNamara and Houston, 2009). As adding complexity to a model always needs to be justified (see Clark, 2009), these tools are useful in calibrating both environmental and internal complexity and optimizing the number of parameters used.

6. Composability and modelling different interaction types

A major challenge in community ecology is how to integrate our increasing databases on various interaction types (Bertness and Callaway, 1994; Olff et al., 2009). Food webs, mutualistic networks and competitive interactions are very rarely modelled in parallel. One problem is that different studies do not overlap (e.g., they describe the food web of community A and the plant-pollinator network of community B). The larger problem consists of using different currencies to characterize different interaction networks, under a unique framework (e.g. carbon flow for food webs and visitation frequency for plant-pollinator webs). These biological issues cannot be fully addressed by process algebraic models, but efficient and simple solutions can help and contribute to model development.

Fig. 2 shows an illustrative case study, where the problem was modelled with the BlenX process algebra. We show a simple toy food web (Fig. 2a), with mutualism (Fig. 2b), direct competition (Fig. 2c) and facilitation (Fig. 2d) added separately. Fig. 2e shows the network with all of the three non-trophic interactions added simultaneously. Variation in population size of species B, under the above scenarios, is illustrated by Fig. 2f. Very simple modifications of the initial model can flexibly cope with these situations. Composability ensures that increasing model complexity does not require linearly increasing programme size. Instead, the relationship is saturating: after some point, several new parameters, functions and variables can be added by only slightly increasing the size of the computer programme. These features also offer new ways of explicitly studying additivity and non-linearity. The stochastic simulation outcome shown in Fig. 2f is intuitively understandable. Different interaction intensities (currencies) are

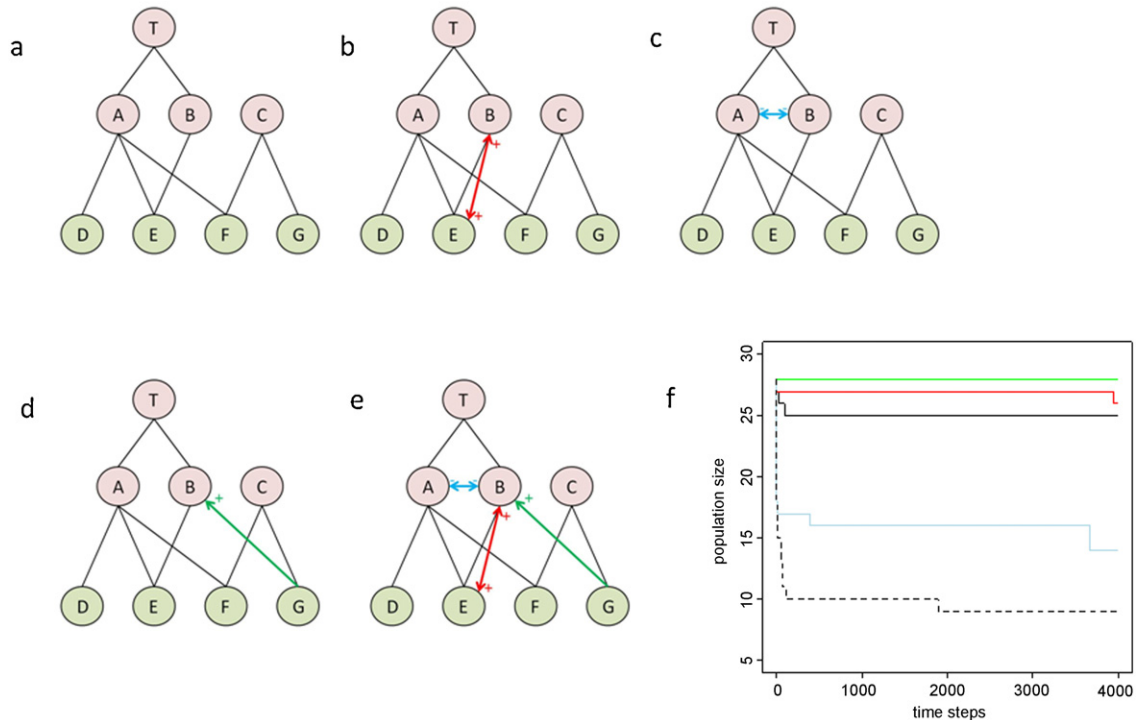


Fig. 2. Toy food web composed of eight species. It illustrates how to integrate different interaction types in the BlenX process algebra. The food web shows only prey–predator interactions (a), but it can be improved by adding a mutualistic (+/+) interaction between species B and E (b), a competition (–/–) between species A and B (c) or a facilitation effect (+/0) from species G to species B (d). In (e), all of these three non-trophic effects are added simultaneously. In (f), the simulated time-series of species B are shown for the above cases (black for the food web, red is for adding mutualism, blue is for adding competition, green is for adding facilitation, and dashed line shows the case where all non-trophic effects are added). The initial population size of B slightly decreases in the food web. This effect is counterbalanced by positive effects (mutualism and facilitation). The decrease is even larger with competition. The overall effect is more or less the sum of the others according to the simulation of this simple toy model. Despite biological complexity, combining all these effects is easy in process algebras, because of composability.

all expressed in terms of reproduction rate, allowing to consider several concurrent relations under a single, integrative framework.

7. Process algebra and conservation biology

Stochastic simulations focusing on individuals and local, parallel processes are especially promising in conservation practice. Here, what we are seeking to model and understand is the behaviour and extinction risk of rare species. The weakest aspect of traditional models (e.g., deterministic simulations) is that they describe these species by means of average population features, whereas the more important feature under extreme circumstances is the peculiar behaviour of each individual. As population size becomes smaller, genetics and demography, environmental variability and also unique interactions can be of major importance (Lande, 1988). Also, below some critical population size, interaction patterns and rates may change, and the modeller has to be able to redefine or

update parameters, and even model structure. This can easily be tackled in a modelling framework if the rules are local and model specification is bottom-up.

For any practical application, simulation and sensitivity analysis are of highest importance, regardless of the modelling tool used (Ginzburg and Jensen, 2004). Stochastic, individual-based or event-based simulations make it possible to study the variability of system behaviour. Apart from average responses, variance responses can also be measured after disturbance. Another parallel in evolutionary biology is quantitative genetics, where the ultimate question is how genetic variance can contribute to phenotypic variance (Roff, 1997).

Based on a simple food web model, where ecosystem dynamics are implemented in BlenX, we can illustrate how sensitivity analysis can be used for quantifying community importance of species, offering quantitative tools for conservation practice. Fig. 3 summarizes an ecosystem simulation, where biomass and trophic flow

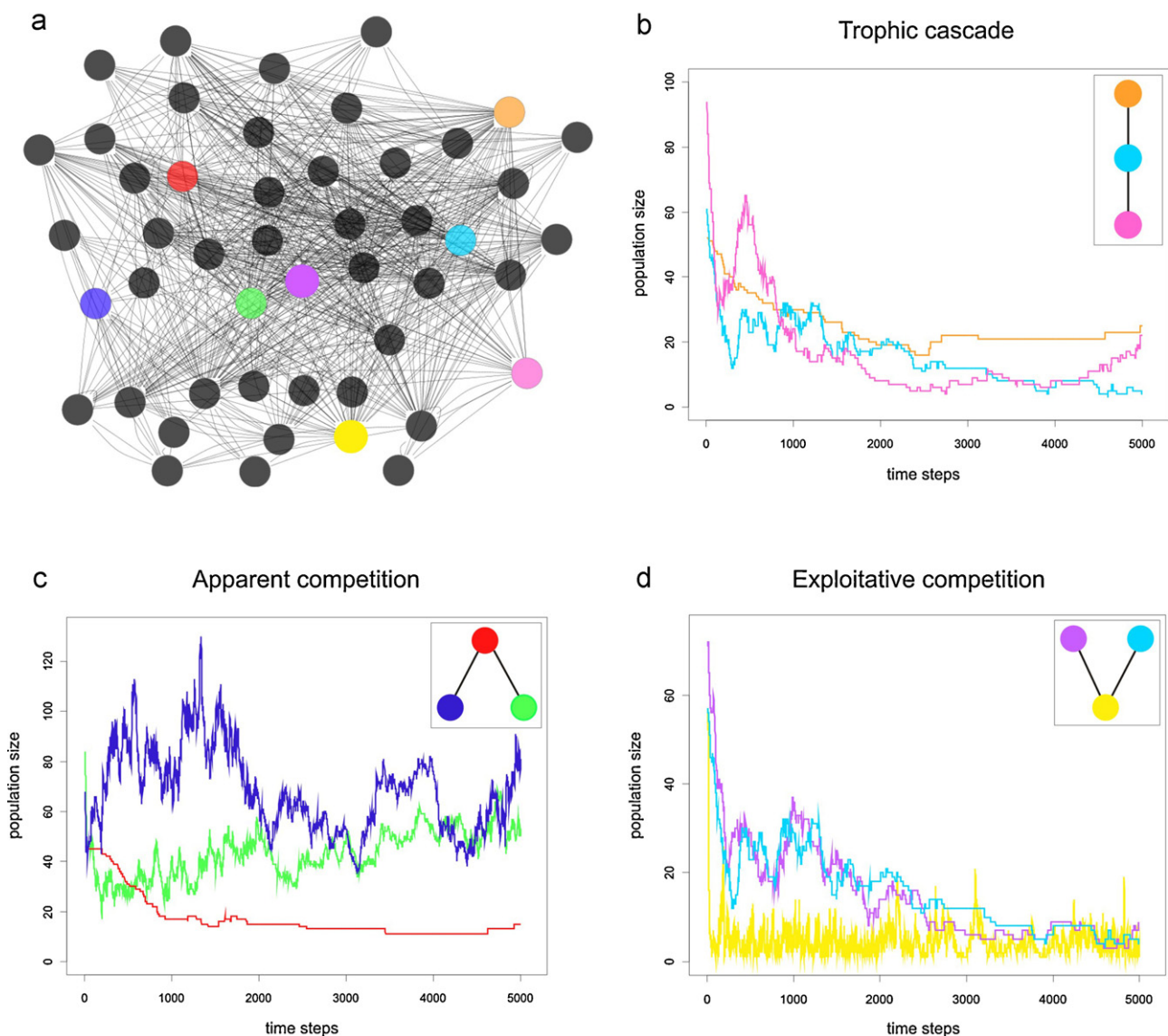


Fig. 3. (a) Prince William Sound food web simulated by the BlenX process algebra-based language. Colour codes correspond to species in (b), (c) and (d). (b) The simulated time series of three species in a trophic cascade constellation: pacific cod (orange) eating nearshore demersal fish (light blue) eating shallow large epibenthos (pink). (c) An apparent competition: sablefish (red) consuming jellies (dark blue) and juvenile herring (green). (d) An exploitative competition: adult pollock (violet) competes with nearshore demersals (light blue) for herbivorous zooplankton (yellow). In the plots, curves show the population size of selected species in time. Time series are not as clear as in textbooks: one reason is stochasticity and the other is the larger context: the triplets of species are not isolated but have other interactive partners in the food web. Yet, some patterns are intuitively understandable. In (b), the final part of the simulation shows a synchronous increase of the first and third trophic level, while a decrease of the middle level. In (c) and (d), competitors often change in reverse direction.

data have been translated to number of individual and interaction rates, respectively. The original database describes the food web of Prince William Sound (Okey and Pauly, 1999; Okey, 2004; Okey and Wright, 2004). With all the parameters used (number of individuals, reaction rates, birth and death rates), conventional modelling tools would be extremely computationally expensive. Process algebra substantially reduces computational costs and opens possibilities for using a number of other parameters (e.g., age structure and genetic variance; not presented here for simplicity). The present model, thus, illustrates a closed ecosystem with no evolution. The simulation plot shows the temporal behaviour of eight fish from the food web, while the dynamics of all species are simulated. In the reference simulation, based on many runs with the same initial conditions and parameters, we can measure the variability of system behaviour. Then, parameters can be changed one by one, or in combinations, in several ways. In a simplistic, illustrative case, we only change the initial number of individuals of each species, one by one. For each disturbance regime we run the model several times and measure the response of each other species (in terms of either mean or variance of population size). Based on these response values, a matrix can be created, informing us how large is the variation of species in column j after disturbing species in row i . Row and column sums provide measures of community importance and community sensitivity, respectively. The first expresses the magnitude of community-wide effect of disturbing a focal species, while the latter expresses the sensitivity of a focal species to variations in others. Community importance indicators, like these quantitative, stochastic simulation-based importance measures are strongly needed in conservation biology (Mills et al., 1993). The final outcome can be a species importance rank based on a dynamical model parameterized with realistic values (Livi et al., 2011).

As the structural (positional) importance of species can be measured simply by network analysis, this simulation framework can be used for approaching the classical “structure to dynamics” problem of ecology (Patten, 1991; Pimm, 1991; Polis and Winemiller, 1996; de Ruiter et al., 2005; Dunne, 2006). Moreover, the food web model can be extended towards the analysis of individual populations (explicit consideration of the social network) and metacommunities studied in space. Building such a hierarchical model in process algebras is extremely simple and intuitive.

8. Perspectives and conclusions

Novel conceptual and computational tools (e.g., stochastic programming languages) can help in investigating the link between local and global processes, simulating density dependence (Björnstad et al., 1999), and explicitly modelling hierarchical organization (Levin, 1998; Kolasa, 2005; Lafferty and Dunne, 2010). This kind of bottom-up modelling may build bridges between genetics (variability), behaviour (local interactions), ecology (interaction system dynamics) and evolution (evo-mecho, McNamara and Houston, 2009). In practice, these tools may serve to plan systems-based conservation strategies (Berkes, 2004), for example in managing multispecies fisheries (Yodzis, 2001). Key directions for future research include broadening the available set of implemented kinetics (e.g., various functional responses), developing standards of common currencies for different processes (e.g., comparing competition and dispersal) and creating tools to allow ecologist users to apply process algebra-based languages without the hassle of writing low-level code (even if the later phase of model development is easier). In spite of these open problems and difficulties, we believe that computer science will provide a vital contribution to future systems ecology.

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