

MINISYMPOSIUM

HYBRID MODELLING IN BIOLOGY

Organizer

FRANCESCO GIANNINO

Dept. of Agricultural Sciences, University of
Naples Federico II, Napoli, Italy
giannino@unina.it

Co-organizer

CHRISTIAN E. VINCENOT

Dept. of Social Informatics, Kyoto University,
Kyoto, Japan
vincenot@bre.soc.i.kyoto-u.ac.jp

Minisymposium Keywords: ODE, PDE, IBM, Agent-based

Hybrid modelling is the integration of different modelling approaches [1]. This symposium will focus more particularly on the new paradigm emerging from the integration of differential equations (ODE and/or PDE) into individual-based models (IBM), two antithetical yet complementary views of systems.

In the last years, there have been an increasing number of examples of applications of this hybrid modelling approach in various scientific disciplines: ecology [2], engineering [3], but also humanities science [4]. This line of research has the big advantage of simulating complex systems as sets of different modules, which can be implemented in different mathematical approaches most appropriate to render the subsystem under consideration. On the other hand, agent-based hybrid modelling also comes with a reduction in analytical capabilities to understand model behavior, for it relies on distinct, apparently incompatible formalizations (algorithmic vs mathematical, discrete vs continuous time, etc).

In this context, we propose in this symposium to:

- Review and better define the agent-based hybrid model approach in theoretical biology
- Provide illustrations of some hybrid model in biology
- Investigate the possibility of analyzing hybrid model with an equation free approach

Minisymposium: Hybrid modelling in biology

VEGETATION PATTERN FORMATION: SYSTEM DYNAMICS, INDIVIDUAL-BASED HYBRID MODELLING EXERCISES

FRANCESCO GIANNINO

giannino@unina.it

Dept. of Agricultural Sciences, University of Naples Federico II, Napoli, Italy

Joint work with Fabrizio Cartenì (Department of Agricultural Sciences, University of Naples Federico II, Napoli, Italy) and Christian E. Vincenot (Department of Social Informatics, Kyoto University, Kyoto, Japan)

Keywords: Turing pattern, Partial Differential Equations, Plant dispersal, Plant-soil negative feedback, Agent-based.

Spatial patterns and self-organization of plants has been a subject of great interest because the underlying mechanisms have been diverse and hard to simulate, raising different explanatory hypotheses.

We present two hybrid models relying on the System Dynamics (SD) – Individual Based (IB) hybrid modelling approach [5] to simulate vegetation spatial dynamics. This line of research demonstrates the importance of integrating both the dynamics of individual plants and abiotic environmental factors to explain the spatial self-organization of vegetation.

In a first modelling exercise [2], plants with their individual characteristics (i.e. algorithmic life cycle based on metabolic processes with relevant state variables such as age or biomass) were naturally integrated inside of IB individuals. Likewise, the hydrology of soil parcels was simulated. SD-IB hybrid modelling made it possible to couple submodels computed in continuous time with other submodels taking decisions in discrete time. This technical capability increased the accuracy of the model by representing processes more naturally. Metabolism and local water dynamics are obviously biological and physical processes that happen continuously. On the other hand, the plant's life cycle and seed dispersal include temporally punctual phenomena and should be modeled in discrete time. We analyzed model behavior in relation to plant-specific parameters (seed dispersal distance and reproductive age) and climatic inputs (precipitation intensity and seasonality). The importance of the representation of individual biological dispersal was thereby also evaluated through a comparison with previous reaction-diffusion models.

In a second undertaking [6], a derived model, omitting hydrological components but integrating plant-soil negative feedback, was capable of reproducing many patterns visible in nature. Simulations also made it possible to deduce some characteristics of plant populations subject to self-organization and spatial patterning. Plant attributes, which could be studied with this hybrid approach, proved important drivers of patterning. Divergences between the hybrid and continuous diffusion model were noticeable in most of the simulation results, stressing the usefulness of fostering hybrid modelling approaches to overcome technical limitations and improve model accuracy [1].

Minisymposium: Hybrid modelling in biology

DYNAMIC COUPLING OF INDIVIDUAL-BASED WITH SYSTEM-DYNAMICS MODELS TO REPRESENT MULTI-SCALE SYSTEMS

GUDRUN WALLENTIN

Gudrun.Wallentin@sbg.ac.at

University of Salzburg

Keywords: Switching hybrid models, Fish-plankton lake ecosystem, Computational performance.

Ecological systems are organised across a range of nested hierarchical, spatial, and temporal scales. Consequently, ecological processes operate in, are bound by or are facilitated through several intertwined scales. In ecological modelling this scale-related complexity is often disregarded due to the principle of parsimony that suggests designing models as simple as possible. However, in cases where across-scale dependencies are strong, the simplification of the focus to one specific scale obscures the true behavior of the system. To offer a more holistic view on ecological systems, ecological models thus need to have the capacity of representing several interacting scales at the same time. Hybrid agent-based (AB) and system dynamics (SD) models have been suggested to capture the essence of these systems in a natural and computationally efficient way. However, the integration of the equation-based SD and individual-based AB models is not least challenged by considerable conceptual differences between these models. Examples of tightly integrated and dynamically switching hybrid models are rare.

In this contribution, I expand on theoretical frameworks of hybrid agent-based and system dynamics models in ecology to support the model design process of dynamically switching hybrid models. Taking a fish-plankton lake ecosystem as an example, a set of alternative model IB-SD designs are discussed in terms of their computational and predictive performance. Computational performance may become prohibitive in models that keep high levels of detail at lower scales, whereas too strong aggregation negatively impacts predictive performance. It thus turned out to be critical how a model retains and restores relevant spatial and attributive information when switching between scales. Important findings with respect to optimising computational versus predictive performance were (1) the most plausible results were produced by a spatially explicit design based on spatial plankton stocks and fish switching between individual agents and aggregate school-agents, (2) higher levels of aggregation did not necessarily result in higher computational performance, and (3) adaptive, emergence-based triggers for the paradigm switches minimised information loss and could connect hierarchical and spatial scales. In conclusion, I argue to reach beyond efficiency-oriented considerations and use emergent super-individuals as structural elements of dynamically switching hybrid models.

Minisymposium: Hybrid modelling in biology

BRIDGING SCALES: FROM THE ATOMISTIC SIMULATIONS TO THE SYSTEMATIC NUMERICAL ANALYSIS OF THE EMERGENT BEHAVIOUR

CONSTANTINOS SIETTOS

ksiet@mail.ntua.gr

School of Applied Mathematics and Physical Sciences
National Technical University of Athens

Keywords: Computer simulation, Emergent dynamical behavior, Large-scale models.

Agent-based models constitute the state-of-the-art in contemporary computer simulation of many complex systems ranging from ecology and epidemiology to economics and financial markets, and from traffic and supply-chain networks to biology and physiology. On the other hand, networks are identified as a key feature of the structure of many real-world systems and recent years' research on the subject is a part of a broader trend towards research on the dynamics of complex systems.

Up to date what is usually done with such detailed object-oriented large-scale models lacking explicit macroscopic descriptions is simple simulation: set up many initial conditions, for each initial condition create a large enough number of ensemble state and network realizations, probably change some of the rules and then run the detailed dynamics for a long time to investigate for example how things like vaccination policies, malignancy/ mutation of a virus - and resource availability may for example influence the spread of an outbreak. However, this simple simulation is most of the times inadequate for the systematic analysis, control policies design for emerging phenomena.

We will show how one can extract efficiently such "large-scale, system-level" information for the systematic analysis and the design of the emergent dynamical behavior of such large-scale simulators evolving on complex networks with important engineering, social and health implications. The key stones of the proposed framework lie on the "trijunction" between computational statistical mechanics, complex networks, bifurcation and dynamical systems identification and control theory.

For illustration purposes, I will present you problems from the fields of Social Dynamics, Computational Epidemiology and Computational Neuroscience.

Minisymposium: Hybrid modelling in biology

VALID REDUCED MICHAELIS-MENTEN MODELS

DIMITRIS GOUSSIS

dimitris.goussis@kustar.ac.ae

Khalifa University, UAE and National Technical University of Athens, Greece

Joint work with Dimitris Patsatzis, National Technical University of Athens, Greece.

Keywords: Michaelis-Menten, Asymptotics, Model reduction.

The intracellular Michaelis-Menten enzyme kinetics mechanism is one of the most simple and most popular ones in biology [12, 13]. It is also widely employed in enzymology, pharmacokinetics and ecology. The dynamics of the mechanism has been the subject of an extensive research effort [14, 15]. In this work the MM mechanism is analysed with the Computational Singular Perturbation (CSP) method, which is the algorithmic counterpart of geometric singular perturbation analysis. CSP is employed for the derivation of two new reduced models, which exhibit a large range of validity. The main purpose of this work is to establish the validity of the CSP-generated MM reduced models, by examining their stability and accuracy. This work aims to provide a methodology for the construction of robust reduced models, which are valid in the full domain of the parameter space where the full model is amenable to reduction.

References

- [1] Vincenot C.E., Mazzoleni S., Parrott L. *Hybrid Solutions for the Modeling of Complex Environmental Systems*. Frontiers Media SA. ISBN: 978-2-88945-055-8 (2017)
- [2] Vincenot C.E., Carteni F., Mazzoleni S., Rietkerk M., Giannino F. (2016). *Spatial Self-Organization of Vegetation Subject to Climatic Stress—Insights from a System Dynamics—Individual-Based Hybrid Model*. *Frontiers in Plant Science*, 7, fpls.2016.00636.
- [3] Tartakovsky A.M., Tartakovsky D.M., Scheibe T.D., Meakin P. (2008). *Hybrid simulations of reaction-diffusion systems in porous media*, *SIAM J. Sci. Comput.*, vol. 30, no. 6, pp. 2799-2816
- [4] Drogoul A., Huynh N.Q., Truong Q.C. (2016). *Coupling Environmental, Social and Economic Models to Understand Land-Use Change Dynamics in the Mekong Delta*. *Front. Environ. Sci.* 4:19. doi: 10.3389/fenvs.2016.00019
- [5] Vincenot C.E., Giannino F., Rietkerk M., Moriya K., Mazzoleni S. (2011). *Theoretical considerations on the combined use of System Dynamics and individual-based modeling in ecology*. *Ecological Modelling*, 222, 210-218
- [6] Vincenot C.E., Carteni F., Bonanomi G., Mazzoleni S., Giannino F. (2017). *Plant–soil negative feedback explains vegetation dynamics and patterns at multiple scales*. *Oikos*, 126, 1319-1328
- [7] Hay Mele B., Giannino F., Vincenot C. E., Mazzoleni S., Carteni F. (2015). *Cell-Based Models in Plant Developmental Biology: Insights into Hybrid Approaches*. *Frontiers in Environmental Science*, 3(November), 1–9.
- [8] Osborne J. M., Fletcher A. G., Pitt-Francis J. M., Maini P. K., Gavaghan D. J. (2017). *Comparing individual-based approaches to modelling the self-organization of multicellular tissues*. *PLoS Computational Biology* (Vol. 13).
- [9] Van Liedekerke P., Palm M. M., Jagiella N., Drasdo D. (2015). *Simulating tissue mechanics with agent-based models: concepts, perspectives and some novel results*. *Computational Particle Mechanics* (Vol. 2). Springer International Publishing.
- [10] Mirabet V., Das P., Boudaoud A., Hamant O. (2011). *The Role of Mechanical Forces in Plant Morphogenesis*. *Annual Review of Plant Biology*, 62(1), 365–385. <https://doi.org/10.1146/annurev-arplant-042110-103852>
- [11] Merks R. M. H., Guravage M., Inze D., Beemster G. T. S. (2011). *VirtualLeaf: An Open-Source Framework for Cell-Based Modeling of Plant Tissue Growth and Development*. *Plant Physiology*, 155(2), 656–666.
- t. *Chaos in Dynamical Systems*. Cambridge University Press, Cambridge, 2002.
- [12] Michaelis M. and Menten M.L. (1913) *Die kinetik der invertinwirkung*, *Biochem Z* 49:3337-369
- [13] Briggs, G.E., Haldane, J.B.S. (1925), *A note on the kinetics of enzyme action*, *Biochem. J.* 19:338–339.
- [14] Schnell S. (2014) *Validity of the Michaelis-Menten equation – Steady-state, or reactant stationary assumption: that is the question*, *FEBS J* 281:464–472
- [15] Cornish-Bowden A. (2015) *One hundred years of Michaelis-Menten kinetics*, *Perspectives in Science* 4:3-9