BioSynSys 2015

Program & abstracts

First conference of the GDR Synthetic & Systems Biology
September 7 - 10, 2015, Paris
University Paris Diderot, amphi Buffon
biosynsys2015.sciencesconf.org

Model and Simulation of Complex Biological Systems

Jérémy Rivière *† [1], Pascal Ballet [1], Gireg Desmeulles [1], Alexandra Fronville [1], Vincent Rodin [1], Abdoulaye Sarr [1], Anne Jeannin-Girardon [1]

[1] Laboratoire des Sciences et Techniques de l'Information, de la Communication et de la Connaissance (Lab-STICC) – Université de Bretagne Occidentale (UBO), Ecole Nationale d'Ingénieurs de Brest (ENIB), CNRS : UMR6285 – 20, avenue Le Gorgeu – 29238 Brest, France

The theory of complex systems has become more and more relevant over the last thirty years to understand concepts such as emergence and self-organization and their role in biological, physical, chemical and social systems. The use of an Individual-Based approach to model and simulate complex systems has proved to be an efficient way, both in research and teaching, of manipulating these complex systems. In our team, we use this approach to propose tools and methods for biologists to create realistic models and simulations of complex biological systems in order to (1) grasp the complexity of these systems, (2) test hypothesis and investigate dynamical systems that otherwise could not be systematically investigated. Among our previous works with biologists, we can mention works related to hematology [1], immunology and oncology. We have also proposed morphogenesis simulation tools which allow to simulate large scale tissue growth [2]. These tools are based on a flexible biomechanical cell model able to simulate cellular deformation and migration. Finally, we also designed an intuitive and open-source software called NetBioDyn [3] aimed at biologists for teaching and research, that does not require any skills in computer programming. In particular, a specific graphical user interface allows to create in a simple way bottom-up models where unexpected behaviours can emerge from simple interacting entities, and test hypothesis by creating various simulations. NetBioDyn has been successfully used in middle schools, high schools and universities since 2010.

G. Desmeulles, S. Bonneaud, P. Redou, V. Rodin and J. Tisseau. "In virtuo Experiments Based on the Multi-Interaction System Framework: the RéISCOP Meta-Model", Computer Modeling in Engineering & Sciences, 47(3):299-330, 2009.

A. Jeannin-Girardon, P. Ballet and V. Rodin. "Large scale tissue morphogenesis simulation on heterogenous systems based on a flexible biomechanical cell model", IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015.

http://virtulab.univ-brest.fr

---

*Speaker

†Corresponding author: Jeremy.Riviere@univ-brest.fr