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The viability theory to control complex food processes

Mariette Sicard, Nathalie Perrot, Cédric Baudrit, Romain Reuillon, Paul Bourguine

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Programme & Abstracts

pair, which is essential for a fair test of functional similarity. We find that many communities are functionally homogeneous, and moreover that there is substantial overlap between the communities that are functionally homogeneous between the two different proxies of gene function (GO annotations and growth rates following gene knockouts).

The viability theory to control complex food processes

Mariette Sicard, Nathalie Perrot, Cedric Baudrit, Romain Reuillon, Paul Bourguine, Isabelle Alvarez, Sophie Martin

Track E - From Molecules to Living Systems

The viability theory developed by Aubin (1991) has been adapted to calculate the optimal monitoring of cheese ripening process. This method was used efficiently in ecology or in finance but never in food process. The aim was to applied viability theory to find the controls allowing to reach a compromise between the quality of the ripened cheeses and the production costs. A viability kernel and the costs simulations of the viable trajectories were computed. Then, the optimal ripening trajectories were validated during pilot ripening trials. The results were finally compared to those obtained for cheeses ripened at 92% of relative humidity and 12°C of temperature, the conditions usually applied in dairy industries for Camembert ripening.

Tag-statistics in complex networks

Gergely Palla, Illés J. Farkas, Péter Pollner, Imre Derenyi, Tamas Tamás

Track E - From Molecules to Living Systems

We study the statistical property of tagged networks, where the further attributes (features, annotations, properties, etc.) provide essential information about the entities represented the nodes. Our main goal is to uncover the relations between the statistical properties of the node tags and those of the graph topology. We investigate the tag statistics in three large networks representing very different domains of complex systems. A number of the tag related quantities display analogous behaviour, while some other features show variability from network to network. We also find that for each network the topology and the tag distribution are scale invariant, and this self-similar property of the networks can be well characterised by a tag-assortativity exponent, which is specific to each system.

Multiclock discrete models of biological systems

Nolwenn Le Meur, Michel Le Borgne, Jérémy Gruel, Nathalie Thérét

Track E - From Molecules to Living Systems

Modeling biological systems requires precise temporal concepts. Biological observations are often issued from discrete event measurements, which make discrete modeling especially interesting. However time is absent of these models or defined a priori. In this paper, we propose a new formalism to specify time in discrete logical model and illustrate the power of our approach using a eukaryote cell cycle model.

Timing of molecular processes in a synchronous Boolean model of genetic regulatory network

Alex Graudenzi, Roberto Serra, Marco Villani, Chiara Damiani, Annamaria Colacci, Stuart Kauffman

Track E - From Molecules to Living Systems

A generalization of the model of random Boolean network (RBN) is presented, in which the concept of timing of regulatory processes is explicitly introduced, together with novel types of entity and interaction,