JOBIM 2004 Mini-symposium

Towards accessible and reproducible computational systems biology model analyses.

Organised by
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As many experimental studies, a large number of published computational biological studies are barely reproducible, for various reasons: lack of a computer readable version of the published model in a standard format, inconsistencies in parameter settings, use of proprietary software, poor software / workflow versioning / documentation, cryptic system dependencies, etc.

Over the last decade, in the field of genomic data analysis, similar reproducibility challenges have been addressed through the development of software containers (e.g. Docker, Singularity) and electronic notebooks (e.g. R Makdown, Python Jupyter).

The speakers invited to this mini-symposium will review and discuss recent efforts for facilitating the reproducibility of dynamical modelling analyses of cellular networks. Indeed, the role of tools and their practical use in systems biology are currently quite different from bioinformatics.

The mini-symposium will cover the exploitation of background knowledge and good modelling practices, with reference to several popular tools such as the CoLoMoTo logical modelling toolbox, the BIOCHAM biochemical modelling software, as well as the MaBoSS Boolean stochastic simulation software and its recent extension PhysiBoSS.

Held in the context of JOBIM 2024, this mini-symposium should bring fruitful discussions with the bioinformatics community at broad.

Tentative program:

14h:00 Loïc Paulevé (CNRS, LaBRI, Bordeaux):
*The CoLoMoTo Notebook: a unified environment for combining tools
and writereproducible analyses of logical models of biological networks.*

14h20: Anna Niarakis (University of Toulouse):
*Community efforts in addressing barriers in comprehensiveness, accessibility, reusability,
interoperability, and reproducibility of computational models in systems biology.*

14h40: Mathieu Hemery (Inria, Saclay):
Biocham a rule based language for an easy use... and re-use !

15h00: Laurence Calzone (Institut Curie):
Modelling cancer invasion with PhysiBoSS.

15h20: Flash talks on selected poster abstracts.

15h30: Global discussion (round-table) with invited speakers + Jacques van Helden (IFB).