POLITECNICO DI TORINO

Dipartimento di Automatica e Informatica

PhD in Computer and Control Engineering

XXXI cycle

Supervisor

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Structure-function relationship in complex biological systems

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1. Context

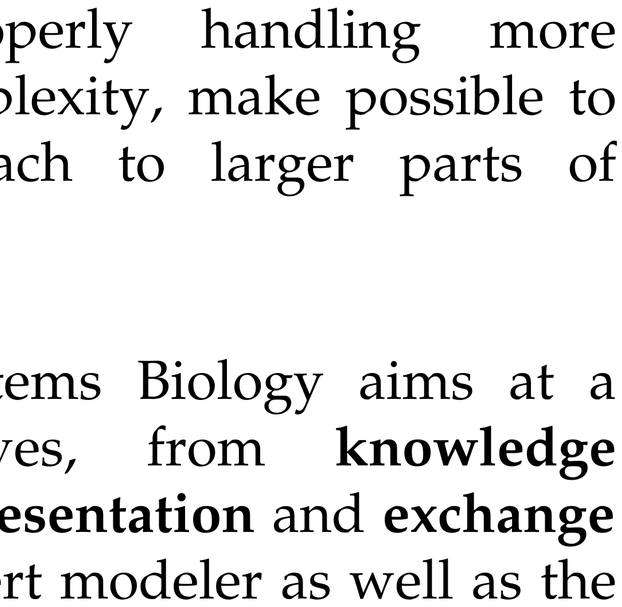
Computational Systems Biology aims to represent biological systems holistically, as more of the sum of their parts, with formal models that can be simulated. Rapid technological advancements in the last decades made the approach to life sciences more systematic, generating large amounts of quantitative data for enriching the more traditional functional, qualitative representations of biological mechanisms. Improvements on the computational side, allowing for properly handling more computational complexity, make possible to extend this approach to larger parts of biological systems.

2. Objectives

Computational Systems Biology aims at a range of objectives, from **knowledge inference** to its **representation** and **exchange** [1], serving the expert modeler as well as the experimentalist. The objective of this PhD work is to design a **predictive computational modeling approach for complex biological systems** focusing on the regulatory role of **spatiality**. **Accessibility** and **usability** are considered respect to the heterogeneity of this scientific domain.

3. Methods

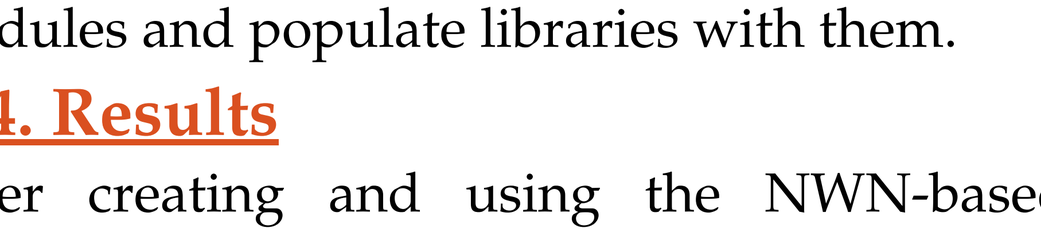
The high-level Petri Nets formalism **Nets-whithin-nets** supports simulable models expressing: **hierarchy**, **quantitative** information, **non-linearity**, **stochastic** behavior, **compartmentalization**. They suitably express **spatiality,** as well as supporting **hybridity** in model construction processes involving different subdomains of Systems Biology.



NWN models specify multiple regulation layers from the system and their dynamic hierarchical relations, including more of the complexity implied in phenomena of interest.
The **Biological Systems Description Language (BiSDL)** is a modular, domain-specific model description language. It makes NWN models accessible for non-expert users thanks to libraries of composable high-level functional modules. Expert users can build up custom modules and populate libraries with them.

4. Results

After creating and using the NWN-based modelling strategy for different targets, such as ontogenetic processes [2], antibiotic resistance spread dynamics [3, 4] and synthetic systems design [5], we intend to build a framework for the analysis, modeling and simulation of complex biological systems, firstly automating the flow from BiSDL descriptions to NWN models and their simulation.



Also, in the context of the VdAHeart project, we worked at the design of bioinformatic analysis pipelines for charachterizing the polyphenols and bioactive peptides profiles in local agrifood and dairy products respectively.

5. References

1. Bardini, R.; Politano, G.; Benso, A.; Di Carlo, S., *Multi-level and hybrid modelling approaches for systems biology*, CSBJ, 2017;
2. Bardini, R.; Politano, G.; Benso, A.; Di Carlo, S., Savino, A., *Using Nets-Within-Nets for Modeling Differentiating Cells in the Epigenetic Landscape*, LNCS (IWBBIO), 2016;
3. Bardini, R.; Politano, G.; Benso, A.; Di Carlo, S., *Using multi-level Petri nets models to simulate microbiota resistance to antibiotics*, BIBM 2017;
4. Bardini, R.; Politano, G.; Benso, A.; Di Carlo, S., *Modeling antibiotic resistance in the microbiota using Multi-level Petri Nets,* BMC Systems Biology, in print.
5. Bardini, R.; Politano, G.; Benso, A.; Di Carlo, S., *Computational tools for applying multi-level models to Synthetic Biology, Synthetic Biology:* Omics Tools and Their Applications, Springer Books, 2018;