

## **SORS:Towards patient-specific multi-scale models and data integration for clinical stratification**

### **Objectives**

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**Abstract:** Due to the complexity and the heterogeneity of biological systems, mathematical models that take into account cell signalling, cell population behaviour and the extracellular environment are particularly helpful. A methodology to instantiate any generic logical model to a set of cancer patients has been developed to capture their diversity of functioning and response to perturbations. This framework allows for simulations tailored to a cell line or a patient's sample using a Boolean model of cancer. The method permits to compare these simulations to clinical data, such as drug response and survival time, but also to additional data analyses such as Independent Component Analysis.

Another open-source software that has also been developed in our group, PhysiBoSS, combines intracellular signalling using Boolean modelling (MaBoSS) and multicellular behaviour using agent-based modelling (PhysiCell). PhysiBoSS provides a flexible and computationally efficient framework to explore the effect of environmental and genetic alterations of individual cells at the population level, bridging the critical gap from genotype to phenotype.

The combination of those two tools pave the way to provide better insights into patient-specific response to treatments, mutation effects and different modes of invasion among other.



**Short Bio:** Arnau Montagud completed his BSc in Biology and

MSc in Cell Biology by the University of Valencia. After participating in Synthetic Biology's iGEM competition he discovered the use of models in Biology, which pushed him to pursue a PhD in the Department of Applied Mathematics in the Technical University of Valencia. His research on Metabolic Engineering of hydrogen in cyanobacteria led him to become a visiting researcher at Uppsala University, Denmark Technical University and EMBL Heidelberg. After graduating, he decided to apply modelling techniques to Cancer and moved to Institut Curie's Systems Biology department where he works as a postdoctoral fellow in data deconvolution and logical models.



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