Whole Yeast Model: What and Why

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Abstract

One of the most challenging fields in Life Science research is to deeply understand how complex cellular functions arise from the interactions of molecules in living cells. Mathematical and computational methods in Systems Biology are fundamental to study the complex molecular interactions within biological systems and to accelerate discoveries. Within this framework, a need exists to integrate different mathematical tools in order to develop quantitative models of entire organisms, i.e. whole-cell models. This note presents a first attempt to show the feasibility of such a task for the budding yeast *Saccharomyces cerevisiae*, a model organism for eukaryotic cells: the proposed model refers to the main cellular activities like metabolism, growth and cycle in a modular fashion, therefore allowing to treat them separately as single input/output modules, as well as to interconnect them in order to build the backbone of a coarse-grain whole cell model. The model modularity allows to substitute a low granularity module with one with a finer grain, whenever molecular details are required to correctly reproduce specific experiments. Furthermore, by properly setting the cellular division, simulations of cell populations are achieved, able to deal with protein distributions. Whole cell modeling will help understanding logic of cell resilience.

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