1. Record Nr. UNINA9910300369103321

Autore	Radmaneshfar Elahe
Titolo	Mathematical Modelling of the Cell Cycle Stress Response / / by Elahe Radmaneshfar
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2014
ISBN	3-319-00744-0
Edizione	[1st ed. 2014.]
Descrizione fisica	1 online resource (122 p.)
Collana	Springer Theses, Recognizing Outstanding Ph.D. Research, , 2190-5053
Disciplina	570.285
Soggetti	Biophysics Biological physics Cell cycle Biomathematics Bioinformatics Physics Biological and Medical Physics, Biophysics Cell Cycle Analysis Physiological, Cellular and Medical Topics Computational Biology/Bioinformatics Applications of Graph Theory and Complex Networks
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references.
Nota di contenuto	A biological overview of the cell cycle and its response to osmotic stress and the -factor -- ODE model of the cell cycle response to osmotic stress -- Boolean model of the cell cycle response to stress -- Conclusion -- List of equations, parameters and initial conditions -- Effect of methods of update on existence of fixed points.
Sommario/riassunto	The cell cycle is a sequence of biochemical events that are controlled by complex but robust molecular machinery. This enables cells to achieve accurate self-reproduction under a broad range of conditions. Environmental changes are transmitted by molecular signaling networks, which coordinate their actions with the cell cycle. This work presents the first description of two complementary computational

models describing the influence of osmotic stress on the entire cell cycle of S. cerevisiae. Our models condense a vast amount of experimental evidence on the interaction of the cell cycle network components with the osmotic stress pathway. Importantly, it is only by considering the entire cell cycle that we are able to make a series of novel predictions which emerge from the coupling between the molecular components of different cell cycle phases. The model-based predictions are supported by experiments in S. cerevisiae and, moreover, have recently been observed in other eukaryotes. Furthermore our models reveal the mechanisms that emerge as a result of the interaction between the cell cycle and stress response networks.