Bifurcations in slow-fast models for the budding yeast cell cycle.

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Abstract
Basic knowledge of the cell cycle of various types of cells consists of the substances involved in the process (cyclins etc.) and the regulatory network. At present much is still unknown, what makes it a hot topic for research. Dynamical systems models based on this regulatory network are fairly recent. A survey of the already impressive literature was recently published by A. Csikasz-Nagy (see [1]).
The group of John. J. Tyson and Bela Novak built the most detailed model so far of cell-cycle regulation by describing the control network of budding yeast *Saccharomyces cerevisiae* (see [2]). We discuss a computational and bifurcation study of two related models and highlight a few phenomena that were so far not discussed in this context. This includes a rather unexpected relation between the growth rate of the cell and the mass increase after DNA-replication. We show that the transition of G1 phase to S-G2-M phase can either correspond to a Type I or a Type II excitation, depending on the parameters of the system, and we compute the non-central homoclinics that mark the transition between Type I and Type II excitation. We further discuss the implications of the funneling effect for the cell cycle as a boundary value problem, and the robustness of the model under parameter variation.

References
