

Time and Space Splitting Methods for Systems of Partial Functional Differential Equations Modeling Tumor Growth

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Abstract

This talk is devoted to computer simulations and mathematical modeling of the development of cancer cells in the mammalian cell division cycle under therapy [1],[2]. The mathematical model is written in terms of partial functional differential equations and used to predict the reaction of cells to mitotic arrest. The goal is to carefully estimate the parameters of the model equations for each melanoma cell line exposed to anticancer drugs. However, determining the parameters in light of experimental data is a computationally heavy task that can easily become lengthy to run when doing so by means of sequential computations. We introduce new splitting methods and a fast algorithm constructed to compute approximate solutions to the model equations in a parallel computing environment. As opposed to traditional approaches [3], our new algorithm does not impose restrictions on the choice of the number of processors to be used and is based on a decomposition of the time domain and on a reassignment of the spatial grid-points that depends on the given number of available processors. Theoretical results validating the robustness of the algorithm will be presented together with a series of numerical simulations for different numbers of independently working processors.

References

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