OPTIMIZATION OF COMBINED ANTITUMOR TREATMENT BY MEANS OF MATHEMATICAL MODELING

Kolobov A.V.[1,2], Kuznetsov M.B. [1,2]

[1] Lebedev Physical Institute of RAS, Leninskiy prospect, 53, Moscow, 119991
[2] Peoples' Friendship University of Russia, Miklouho-Maclay street, 6, Moscow, 117198

In the 21st century, in oncology along with “classical” cytotoxic and cytostatic drugs, molecular-targeted drugs have been actively used. One of these drugs is bevacizumab - a monoclonal antibody to angiogenesis activator - vascular endothelial growth factor (VEGF). Antitumor antiangiogenic therapy, proposed by J. Folkman as early as 1971, is not aimed at killing actively dividing cells, both malignant and normal, but at slowing down or, ideally, stopping tumor growth by reducing the influx of nutrients. However, experimental and clinical studies have demonstrated insufficient antitumor efficacy of antiangiogenic monotherapy, so bevacizumab is currently used in combination with “classical” chemotherapy or radiotherapy. In this case, the acute question of adequate prediction of the characteristics of their joint use arises. In this talk, with the help of a multicomponent spatially distributed dynamic model of tumor growth and therapy, the capabilities of mathematical modeling to evaluate the antitumor efficacy of the existing and search for new combined treatment regimens using bevacizumab will be demonstrated. In particular, the combination of cisplatin - bevacizumab will be considered and the model and existing clinical protocols will be compared. The proposed approach can be easily developed for the study of various types of combination antitumor therapy, including both “classical” and a wide range of targeted therapeutic effects.