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A new cancer drug regimen based on the interplay between tumor growth and angiogenesis – Predictions of a mathematical model

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Lack of tools for extrapolating intracellular drug effects on the patient's body as a whole is a significant impediment to successful drug treatment of oncological patients. We have mathematically modeled the dynamic interplay between key biological, pathological and pharmacological processes underlying drug-patient interactions, from the molecular level to that of the whole organism. These interactions create a complex network of positive and negative feedbacks, thresholds and time scales, whose balance determines treatment outcomes. We have implemented these interactive models in the computer and simulated a large number of treatment options for individual patients, whose baseline medical characteristics serve for estimating models' parameters. Our results show that the treatment schedule expected to be optimal for a large class of patients and for widely used anticancer drugs, such as docetaxel and doxorubicin, is one of relatively small doses, the dosing interval being one week. This general schedule is predicted to be significantly more efficacious than the recommended regimen, consisting of relatively large doses applied every three weeks.