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Modeling the evolution of drug resistance in cancer

Despite the effectiveness of many therapies in reducing tumor burden during the initial phase of treatment, the emergence of drug resistance remains a primary obstacle in cancer treatment. Tumors are comprised of highly heterogeneous, rapidly evolving cell populations whose dynamics can be modeled using evolutionary theory. In this talk I will describe some mathematical models of the evolutionary processes driving drug resistance in cancer, and demonstrate how these models can be used to provide clinical insights. In particular I will describe several branching process models of tumor evolution and analyze the timing of tumor recurrence. These models will be applied to study the impact of dosing schedules and the tumor microenvironment on the emergence of drug resistance in lung cancer.