

# HEAVY-TAILED DISTRIBUTIONS IN BRANCHING PROCESS MODELS OF SECONDARY CANCEROUS TUMORS

MAREK KIMMEL

Recent progress in microdissection and in DNA sequencing has facilitated the subsampling of multi-focal cancers in organs such as the liver in several hundred spots, helping to determine the pattern of mutations in each of these spots. This has led to the construction of genealogies of the primary, secondary, tertiary, and so forth, foci of the tumor. These studies have led to diverse conclusions concerning the Darwinian (selective) or neutral evolution in cancer. Mathematical models of the development of multi-focal tumors have been devised to support these claims.

We offer a model for the development of a multifocal tumor: it is a mathematically rigorous refinement of a model of Ling et al. (2015). Guided by numerical studies and simulations, we show that the rigorous model, in the form of an infinite-type branching process, displays distributions of tumor size which have heavy tails and moments that become infinite in finite time. To demonstrate these points, we obtain bounds on the tails of the distributions of the process and an infinite series expansion for the first moments. In addition to its inherent mathematical interest, the model is corroborated by recent literature on apparent super-exponential growth in cancer metastases.

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