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Heterogeneity of proliferating cell populations: Models and data

Recent years brought a deluge of technologies to observe biological processes at single-cell and sometimes at single-molecule levels. These include high-content microscopy as well as microfluidics and insertion of engineered fragments of genetic material into cells. Stochastic models introduced 20 or 30 years ago suffered from paucity or absence of such data. Some of these models can be now re-thought and re-applied in the new context. The talk, idiosyncratically, reviews some of these models conceived over past 20 years and confronts them with recent biological findings. This includes the pseudo-stochastic model of unequal division of cells, and the branching process model of gene amplification. Biological phenomena discussed include self-renewal and maturation of stem cells, variability of abundance of proteins in cells, and carcinogenesis.