STOCHASTIC PROTEIN PATTERN FORMATION IN ELASTIC EPITHELIAL TISSUE IN APPLICATION TO CARCINOMA MODELING

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It is known that the noise during gene expression comes about in two ways. The inherent stochasticity of biochemical processes such as transcription/translation generates "intrinsic" noise. "Extrinsic" noise refers to variation in identically-regulated quantities between cells. The small number of reactant molecules involved in gene regulation leads to significant fluctuations in intracellular protein concentrations, and there have been numerous recent studies devoted to the consequences of such noise at the regulatory level.

To study the spatial effects of intrinsic and extrinsic noises on gene regulation determining the emergence and development of carcinoma we have applied a multiscale chemo-mechanical model of tumor development in epithelial tissue proposed recently in [1,2]. The epithelium is represented by an elastic 2D array of polygonal cells with its own gene regulation dynamics. The model allows for the simulation of evolution of multiple cells interacting via the chemical signaling or mechanically induced strain. The algorithm includes also the division and intercalation of cells, as well as the transformation of normal cells into a cancerous state triggered by a local failure of spatial synchronization of the cellular rhythms driven by transcription/translation processes. To model the delay-induced stochastic chemical signaling we have used a generalization of the Gillespie algorithm that accounts for delay suggested in [3]. The possibility of the stochastic pattern formation produced by the joint action of time delay and noise was demonstrated in [4].

In this work, we study the effect of the stochastic spatial oscillations induced by cell-to-cell communications on the emergence of tumor. Both the intrinsic and extrinsic contributions to stochastic pattern formation and its impact on tumor have been explored numerically.

References

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