Cancer invasion and progression: insights from agent-based models

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Cancer invasion may be viewed as collective phenomenon emerging in populations of normal and malignant cells. As such it can be studied with agent-based models, e.g. cellular automata. I will provide examples of such models to analyze breast and glioma invasion as well as the emergence of phenotypic heterogeneity due to cellular interactions in growing tumors. Furthermore, I will present models which shed light on cancer progression.

References

[1] A. Deutsch, J. M. Nava-Sedeño, S. Syga, H. Hatzikirou. BIO-LGCA: a cellular automaton modelling class for analysing collective cell migration. PLoS Comput Biol 17(6), e1009066 (2021).
[2] O. Ilina, P.G. Gritsenko, S. Syga, J. Lippoldt, C.A.M. La Porta, O. Chepizhko, S. Grosser, M. Vullings, G. Bakker, J. Starruß, P. Bult, S. Zapperi, J.A. Käs, A. Deutsch, P- Friedl. Cell–cell adhesion and 3D matrix confinement determine jamming transitions in breast cancer invasion. Nature Cell Biology 22, 1103–1115 (2020).
[3] A. Deutsch, S. Dormann. Cellular automaton modeling of biological pattern formation: characterization, examples, and analysis. Birkhauser, Basel (2018).