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Phenotypic inheritance transforms heterogeneity in tumor growth

Cell-to-cell variation is seen in almost all aspects of cancer from initiation to invasion and subsequent metastasis. Our current understanding at the genetic scale gives little information on translating to actual changes in cell behavior, which will ultimately dictate tumor aggressiveness and treatability. Cell behavior can be described in terms of phenotypic traits, e.g., proliferation, migration, and apoptosis rates. Because these traits vary across a tumor population a useful way to represent them is in terms of distributions. How traits are passed on as cells divide and compete for space and resources affects how the trait distributions evolve.

An off-lattice cellular automata model is built where cells are either initiated as a tight cluster, to simulate a growing tumor mass, or as a dispersed population, to represent a cell culture experiment. These initial spatial distributions give different outcomes and lead us to question how heterogeneity *in vitro* can be translated *in vivo*. We combine the model's trait distributions, repopulation times, and morphological features with biological data to analyze how treatment resistance emerges and how it might be regulated.