

## A computational model of triple-negative breast cancer heterogeneity

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Tumors are heterogeneous populations of cells with different genetics, epigenetics, receptor numbers, to name a few. We have developed a computational model that takes into account the heterogeneous nature of breast cancer cells. We specifically simulate triple-negative breast cancer using the MDA-MB-231 cell line as the basis of our model. The model consists of stem cells that give rise to other stem cells and progenitor cells. Stem cells have unlimited replicative potential, are resistant to death signals, and can produce progenitor cells. Progenitor cells have limited replicative potential, senesce and die, and can only produce other progenitor cells. Each cell also has a CCR5 status, either high or low, which governs its migrate rate. We study the effects of tumor cell heterogeneity in the primary and metastatic environment. We find that having a high CCR5 status results in a transition from Gompertzian growth to exponential growth.