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Stochastic modelling of cell migration

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Abstract

Cell migration is a central process in normal human cellular development as well as in numerous disease states. Metastatic spread of cancer tumors occurs as a direct result of changes in cell migration, and further insight into the mechanisms behind cell migration is of great importance in cancer research. CMACs (cell-matrix adhesion complexes) are at the heart of the migratory system of the cell; elucidation of CMAC behaviour is essential in understanding cell migration. In this thesis, results from analysis of quantitative live cell microscopy data are used together with modern biological theory to develop a stochastic model describing the behaviour of the CMAC population of the wild-type cell with respect to CMAC areas and the number of CMACs. Analytical results are derived and simulations are performed to validate model performance. It is shown that the model is able to mimic CMAC behaviour with respect to most aspects of the properties described above, and also can predict the behaviour of new perturbed experimental conditions.

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