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Stochastic modelling of cell migration

Cell migration is a central process in normal human tissue development as well as in numerous disease states. Metastatic spread of cancer tumours 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 [1] [2]. In this work, quantitative time-series live cell microscopy data are used together with existing knowledge 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. New CMACs are born according to a Poisson process and then the subsequent multiplicative growth and decline of CMAC area and final death is described by means of a random walk with a Markov process regime. 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 is able to predict the behaviour of new perturbed experimental conditions.

References

[1] John G. Lock, Bernhard Wehrle-Haller and Staffan Strömblad, *Cell–matrix adhesion complexes: Master control machinery of cell migration* Seminars in Cancer Biology, Volume **18**, Issue 1, February 2008, Pages 65-76.

[2] John G. Lock and Staffan Strömblad, *Systems microscopy: An emerging strategy for the life sciences* Experimental Cell Research, Volume **316**, Issue 8, 1 May 2010, Pages 1438-1444.