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Type	Poster
Session	Bioimaging
Title	Cell migration analysis by multi-component model
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Motivation

Cultured eukaryotic cells are fundamental model systems both in basic and in clinical studies. Within a culture dish, cells interact with plate surface via focal adhesions and other structures to produce movement patterns which may vary in response to different stimuli and reproduces, at different extents, in vivo migration. According to environmental conditions, cell movement ranges between completely diffusive and superdiffusive behaviour, usually due to different degrees of directional persistence or bias. This work describes a method which overcomes some difficulties of other commonly used models and effectively describes the path followed by cells grown on culture plates under different experimental conditions.

Methods

Experimental data were generated by growing murine fibroblast cell lines (NIH3T3 and NIHRas), human prostate cancer cells (PC3) and human immortalised cells derived from cervical cancer (HeLa) and by observing them by time-lapse microscopy. A directional stimulus was introduced by inflicting a wound in cell layer. To study the role of specific molecules in the migration process, some of them have been targeted by using specific inhibitors. Phase contrast images of the different samples were acquired and cell displacements were tracked and stored in a text file by using MotoCell, an application previously developed in the laboratory and revised and expanded during this work. Mathematical, statistical and graphical analyses were carried out in R. All procedures and tools were implemented in MotoCell by using the PHP scripting language and by taking advantage of the object oriented programming paradigm.

Results

The main focus of our work was to develop an integrated model, able to correctly describe movement of cultured cells in different experimental conditions. The described method characterises cell movement by modelling cell displacement as the vectorial sum of three components: random, persistence and directional bias. The mathematical model was elaborated and implemented in a tool able to identify and quantify movement features and to calculate the contribution of each movement component to overall migration. The tool was used to characterise cell migration followed in time-lapse microscopy to obtain profiles able to describe motion under standard culture conditions, as well as in presence of directional stimuli and/or perturbation of signalling pathways. The analysis procedure developed on the basis of the described model is able to fully distinguish the three movement components and to describe the migration behaviour of different cell lines, highlighting specific modifications of cell movement patterns in different experimental contexts.

Info

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Figure

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Availability	-

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