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Qualitative analysis of lamella and cell body shape during cell migration

The aim of our work is to investigate migration of single cells on two-dimensional substrata. To this end, we label adhesion sites and the interior keratinocyte cell body by staining vinculin and tubulin with fluorescence dyes. This enables us to reliably distinguish between cell body and the surrounding lamella.

For time-lapse image processing we quantitatively determine the lamella edge as well as the cell body outline by an adaptive *stochastic chain* algorithm [1], also known as *active contour* model [2, 3]. The stochastic chain adapts to the cell outline by interpreting the information given by phase contrast micrographs or corresponding fluorescence images. Chain adaption follows from different "image forces", which involve (i) chain stiffness, (ii) retrograde centripetal pulling and (iii) gradients in picture brightness. The evolution of the chain stops when the stochastic fluctuations have become stationary.

Our statistical analysis investigates cell body and lamella shape, which are independently quantified by the positions of the interior body chain and the exterior edge chain, respectively. Spatio-temperal auto- and cross-correlations reveal the time-lag relation between mean protrusion vector and cell migration velocity. Moreover, we find that the cell body has an elliptic shape during forward migration, whereas upon turning it becomes almost circular. The overall lamella dynamics is mainly influenced by the underlying cell body shape. Significant deviations from this protrusion pattern appear, particularly when the cell changes its migration direction.

References

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