Automated tracking of label-free cells with enhanced recognition of whole tracks.

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Details

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Abstract

Migration and interactions of immune cells are routinely studied by time-lapse microscopy of *in vitro* migration and confrontation assays. To objectively quantify the dynamic behavior of cells, software tools for automated cell tracking can be applied. However, many existing tracking algorithms recognize only rather short fragments of a whole cell track and rely on cell staining to enhance cell segmentation. While our previously developed segmentation approach enables tracking of label-free cells, it still suffers from frequently recognizing only short track fragments. In

this study, we identify sources of track fragmentation and provide solutions to obtain longer cell tracks. This is achieved by improving the detection of low-contrast cells and by optimizing the value of the gap size parameter, which defines the number of missing cell positions between track fragments that is accepted for still connecting them into one track. We find that the enhanced track recognition increases the average length of cell tracks up to 2.2-fold. Recognizing cell tracks as a whole will enable studying and quantifying more complex patterns of cell behavior, *e.g.* switches in migration mode or dependence of the phagocytosis efficiency on the number and type of preceding interactions. Such quantitative analyses will improve our understanding of how immune cells interact and function in health and disease

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