K-MEANS CLUSTER BASED TRACKING ALGORITHM IMPLEMENTED FOR TWO AND THREE DIMENSIONAL MICROSCOPY DATA

David A. Hughes, Manli Chuai, Cornelis J. Weijer
Division of Cell and Developmental Biology
Welcome Trust Biocentre, University of Dundee
Dundee, Scotland UK
Email: d.a.hughes@dundee.ac.uk

KEYWORDS: Image analysis, image processing, live cell imaging, automated cell tracking

The ability to track objects has a wide range of applications in biology from single particles, cellular motility, up to fully formed organisms. There is much published work on various algorithms for achieving this [1], however, difficulties arise in practice due to low signal to noise ratios, objects colliding, and the changing density of populations from objects exiting or entering the field of view.

In this work we present a novel and simple method for analysing the motility of biological objects in dense and noisy video sequences. The method is based on a k-means neighbourhood clustering algorithm for segmentation and, secondly, a centre-of-mass tracking algorithm to join up the individual frames.

This method requires very little user parameters, and can also deal with objects entering and exiting the field of view. The algorithm has been implemented in C++ and also as an ImageJ plug-in using the Java programming language.

Time-lapse videos recorded from a fluorescent or bright-field microscope are filtered to improve contrast and then 'classified' for tracking. This classification procedure produces a one dimensional list of features inside the image which is passed to a clustering routine. The initial seeds for the clustering routine are provided from the previous frame's calculated cluster locations. The new cluster locations are then stored after each frame so that the path a cell takes through the video can be reproduced for quantitative analysis.

This will be demonstrated by using the algorithm to track the developmental processes of the social amoeba Dictyostelium discoideum in two and three dimensions. Furthermore, the discussion will be extended to show the migration of cells from the chicken embryo (Figure 1) during early stage development. Using the algorithm, it is possible to retrieve quantitative data such as velocities, directions and behaviours from the video sequences of these processes. This aids in the understanding of the processes that bring about development of multicellular organisms at the earliest stages of embryo-genesis.