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Abstract

Image Processing to Detect Worms

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The nematode *C. elegans* is a widely used model organism. It has many cells with human equivalents, making it possible to study pathways conserved in humans and related conditions. Being small and transparent, it also lends itself well to a variety of high-throughput screening techniques. Worm identification should be as automated as possible since it is too labor-intensive and time-consuming to do it manually.

Here we present an image processing methodology to detect *C. elegans* in high-throughput microscope images. The provided semi-automatic solution makes it possible to effectively identify individual worms in worm clusters. In general terms, the process is as follows: A given image is segmented, thus separating groups of worms from the background. Individual worms are detected automatically, following a worm-shape matching process. For worm clusters, the matching process is based on finding feasible worm shapes by minimizing the distance between the cluster and generic worm shapes, which are deformed to fit it. Wrong and missing conformations can be quickly fixed manually.

The provided methodology is a novel approach to successfully detect individual *C. elegans* worms in high-throughput microscope images. Results show that this semi-automatic solution makes it possible to fit the shape of 100% of worms in the image, unlike previous automated methods that reach, at most, less than 90% in average, for similar test sets. The detection process is usually achieved in less than half a minute for difficult images. For easier images, the total match can often be calculated in a fully automatic way. Time cost and matching accuracy are considerably improved with respect to manual identification.

The solution was implemented in Java and adjusted to Endrov, which is an open source plug-in architecture for image analysis, and is to be used at the Department of Bioscience and Nutrition, Karolinska Institute, Sweden.

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