



NISTIR 7750: Biological Cell Feature Identification by a Modified Watershed- Merging Algorithm

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Biological cells are composed of many subsystems and organelles. The subsystem called the cytoskeleton is composed of long rod-shaped filaments. They give the cell form and help attach the cell to the substrate and neighbors. One type of the filaments is made up of a protein called actin. In studying cells biologists use microscopes that can be focused at different levels and can be automated to take multiple images. Various stain treatments are used to bring out various cell characteristics. In this study a computational method is studied that automatically isolates the actin structures in cells. The algorithm begins by segmenting the cell with a scheme called a watershed. Due to noise and a large number of local minima the number of resulting segmented regions can be large and not informative. The object then is to merge regions, based on nearness and common properties, into regions called features. The merging approach used here involves a graph representation called an adjacency graph and a search algorithm that finds the connected components in the graph. These connected components become the merged features.

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