GLOBAL ANALYSIS AND DESCRIPTION OF THE OBSERVABLE CHANGES OF A MOVING CELL

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ABSTRACT

Cell movement is a fundamental process of some importance to aspects of cell biology as diverse as migration of cells in embryological development, and to host defense mechanisms. It has become increasingly evident that the cell surface plays a pivotal role in the life, development, and regulation of cells. The surface function lies in the transmission of information from the environment to the cell. Not only are molecular signals involved, but also mechanical forces, stemming from adhesions and junctions that affect the cytoskeleton, which influence intra cellular events. For example, development of an embryo requires that cells know where they are and where they should be going. The mechanisms that regulate this social behaviour of cells are not understood. However, more than intuition informs us that the cell membrane is involved both as the donor and receptor of such social signals. Current studies related to cancer research (i.e. invasiveness and metastasis), are primarily concerned with the interaction between external factors and cell internal processes that occur at or within the cell membrane. However, there is no existing method to quantify the observable changes in membrane shape that occur in locomotion.

The main goal of this research is to develop an image interpretation system capable of analyzing a sequence of pictures in order to provide a description of the structural changes in the shape of a moving cell. To achieve this, the computer program would have to be able to: segment the moving cell, and detect the significant changes in its location, shape, and structure. A system which accomplishes these objectives involves three major areas of image processing: (1) automatic processing of microscopic images, (2) dynamic scene analysis, and (3) shape analysis and description.

A theoretical model for a general dynamic scene analysis system has been constructed. The model consists of three basic entities: (1) dynamic data, which change continuously during the analysis, (2) static data, which remain unchanged, and (3) a collection of analysis processors, each of which is assigned to a particular task. The different types of data which may be manipulated by the system have been classified as follows: (a) A sequence of images which forms the main input, (b) A group of objects (moving or stationary) and subobjects, each of which may be decomposed into its primitive subparts, to give a collection of subobjects, (c) A set of features which define the different properties of the shape, structure, or motion of the objects and subobjects to be analyzed, (d) A group of descriptors used to classify and describe symbolically the different numerical values of the different features, (e) A group of characteristics which describes the global behaviour of the moving object, (f) a set of rules, which may be classified into representational rules and control rules. Whereas the former are responsible for generating the descriptions and characteristics of the cells, the latter are needed for activating and scheduling the different processors of the system.

Based on this model, and by using a relational database structure, we have implemented a rule-based image interpretation system for moving cells. The system consists of different cooperating computational processors. Conceptually, two different memories are used, a Short Term Memory (STM) and a Long Term Memory (LTM). Both are implemented as a relational database. The STM is designed to work as a communication channel for all of the processes. It contains a dynamic record of the instantaneous cell motion, shape, and structural changes, as well as the current global description of the cell behaviour. The LTM data are static, and are implemented as rules. These describe the general model of the morphology of the cells under analysis, as well as control information pertinent to the computational processes. The latter are activated by the control rules throughout the three hierarchical analysis stages: static, incremental, and global. They interact through the STM using the information stored in the LTM, until a complete description of the dynamic cell motion and morphology is obtained.

The analysis is designed to execute through a hierarchial structure consisting of three levels: (a) Static Scene Analysis: to identify the desired moving object, segment it, and describe its morphology and location in each frame. (b) Incremental Change Detection: To detect and

describe the incremental changes in shape, structure, and motion of the moving object between two sequential frames. (c) Global Analysis: to analyze the static and incremental data, in order to detect and describe the global observable changes within a sequence of frames. In this way, a characterization of the consistent dynamic behaviour of the cell is obtained.

It is of interest to have the computer describe the dynamic activity of the cell using symbolic terminology which is meaningful to the concerned biologist. For example, with the aid of the global observable changes in the cell locomotion, one of the main behavioural characteristics is mathematically quantified and described; namely, the chemotaxis behaviour (the directional locomotion of the cell with respect to the directional effect of an external factor). Consequently, the effectiveness of an external factor on modifying the cell locomotion is quantified. Also, an expression for measuring the complexity of an arbitrary shape pattern has been developed and used to describe the membrane shape and its observable changes. The global changes in the cell structure are also analyzed; hence, a subpart of the cell is classified as being a "pseudopod or cell body", and a pseudopod is described as "growing, contracting, or stationary". Furthermore, some aspects of the global behaviour of the cell are summarized and described. For example, the "domination" of a pseudopod in leading the locomotion of the cell. Description (1) is an analysis of the global locomotion characteristics of a cell which was tracked for 450 frames.

This computer study might provide clues to the nature and distribution of "receptors" on or within the membrane, which is a vital link in the interaction between the external factors and cell internal processes. Also, it might lead to a better understanding of the role that the cell membrane plays in the mechanisms which regulate the social behaviour of cells.

KEY WORDS: DYNAMIC IMAGES, BLOOD CELLS, IMAGE UNDERSTANDING, RULE-BASED SYSTEMS.

DESCRIPTION <1>

GLOBAL LOCOMOTION ANALYSIS AND DESCRIPTION

INTRODUCTION

The following is a global discription of the locomotion analysis of a NEUTROPHILE cell. The cell motion was recorded in real time on 16mm cine film at rate of TWO frames per second. The cell was in the presence of BACTERIA which is located in the SOUTH-WESTERLY direction of the original location of the cell. The total observation time was 225 seconds (450 frames). The following is a description of the cell locomotion between frame number 200 and 450 (125.0 seconds)

CELL PATH and MOTION ANALYSIS :

The space domain of the cell motion is divided into EIGHT equal directions(states). First, the cell path was obtained by sampling the displacement between frames in increments of approximatly 2.0 microns. Then sequences with the same incremental direction were merged into one to produce the final cell path which consists of 34 steps. The description of the time, distance, speed, direction, and acceleration of the cell at each step is as follows :

TIME	DISTANCE	SPEED	DIRECTION	ACCELERATION
VERY SHORT	VERY SHORT	VERY SLOW	NORTH-EASTERLY	NONE
VERY SHORT	SHORT	VERY FAST	EASTERLY	VERY FAST POSITIVE
VERY LONG	VERY LONG	AVERAGE	WESTERLY	AVERAGE NEGATIVE
SHORT	VERY SHORT	VERY SLOW	NORTH-EASTERLY	VERY FAST NEGATIVE
SHORT	MEDIUM	VERY FAST	SOUTH-WESTERLY	VERY FAST POSITIVE
SHORT	VERY SHORT	VERY SLOW	NORTH-EASTERLY	VERY FAST NEGATIVE
MEDIUM	SHORT	AVERAGE	SOUTH-WESTERLY	VERY FAST POSITIVE
VERY LONG	MEDIUM	SLOW	SOUTH	NONE
LONG	MEDIUM	AVERAGE	SOUTH-WESTERLY	SLOW POSITIVE
SHORT	MEDIUM	VERY FAST	EASTERLY	VERY FAST POSITIVE
MEDIUM	LONG	FAST	SOUTH-WESTERLY	VERY FAST NEGATIVE
SHORT	MEDIUM	VERY FAST	EASTERLY	VERY FAST POSITIVE
SHORT	MEDIUM	VERY FAST	NORTH-WESTERLY	VERY FAST NEGATIVE
MEDIUM	VERY LONG	VERY FAST	SOUTH	AVERAGE NEGATIVE
MEDIUM	MEDIUM	AVERAGE	SOUTH-WESTERLY	AVERAGE NEGATIVE
LONG	MEDIUM	SLOW	SOUTH	AVERAGE NEGATIVE
MEDIUM	MEDIUM	AVERAGE	SOUTH-EASTERLY	AVERAGE POSITIVE
MEDIUM	MEDIUM	AVERAGE	SOUTH-WESTERLY	SLOW POSITIVE
SHORT	MEDIUM	VERY FAST	SOUTH-EASTERLY	VERY FAST POSITIVE

MEDIUM	MEDIUM	FAST	SOUTH-WESTERLY	VERY FAST	NEGATIVE
LONG	MEDIUM	SLOW	SOUTH	AVERAGE	NEGATIVE
MEDIUM	MEDIUM	AVERAGE	SOUTH-WESTERLY	AVERAGE	POSITIVE
MEDIUM	MEDIUM	AVERAGE	SOUTH	NONE	
SHORT	MEDIUM	FAST	SOUTH-WESTERLY	VERY FAST	POSITIVE
VERY LONG	VERY LONG	AVERAGE	SOUTH	AVERAGE	NEGATIVE
MEDIUM	LONG	VERY FAST	WESTERLY	VERY FAST	POSITIVE
MEDIUM	MEDIUM	AVERAGE	SOUTH-EASTERLY	FAST	NEGATIVE
VERY LONG	MEDIUM	SLOW	SOUTH	AVERAGE	NEGATIVE
LONG	MEDIUM	AVERAGE	SOUTH-EASTERLY	SLOW	POSITIVE
VERY SHORT	VERY SHORT	VERY SLOW	NORTH-EASTERLY	VERY FAST	NEGATIVE
SHORT	MEDIUM	FAST	EASTERLY	VERY FAST	POSITIVE
MEDIUM	VERY SHORT	VERY SLOW	NORTH-EASTERLY	VERY FAST	NEGATIVE
SHORT	SHORT	AVERAGE	EASTERLY	VERY FAST	POSITIVE
MEDIUM	MEDIUM	AVERAGE	SOUTH-EASTERLY	AVERAGE	NEGATIVE

CHEMOTAXIS ANALYSIS :

Chemotaxis is the response of a motile cell to the directional influence of a chemical substance or any external factor (BACTERIA in this film). The following is a summary of the directional movements of the cell under analysis when compared to typical random motion of a similar cell:

DIRECTION	TOTAL DISPLACEMENT
EASTERLY	AVERAGE
NORTH-EASTERLY	NONE
NORTH	NONE
NORTH-WESTERLY	SHORT
WESTERLY	AVERAGE
SOUTH-WESTERLY	VERY LONG
SOUTH	VERY LONG
SOUTH-EASTERLY	AVERAGE

CONCLUSION :

The resultant directional locomotion is in a SOUTH direction, which is ALMOST THE SAME direction in which the BACTERIA is located. This motion represents THREE-FIFTHS of the total displacement of the cell.

From the above analysis we may conclude that :

THE CELL HAS AN AVERAGE POSITIVE CHEMOTAXIS MOTION