TISSUE-LIKE P SYSTEM FOR REGION-BASED AND EDGE-BASED IMAGE SEGMENTATIONS

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This thesis is dedicated to:

- ✓ The living memories of my father, my mother
- ✓ My Husband and two beautiful daughters (Nadeen and Zahraa)
 - $\checkmark \qquad \text{My brothers and sisters}$

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ABSTRACT

Membrane Computing (MC), a relatively recent branch of natural computing is an emerging field in molecular computing. MC aims at abstracting models, called membrane systems or P systems, which mimic the function and structure of a biological cell. Many studies have utilized MC in various applications such as image segmentation. Due to the high computational cost of conventional segmentation techniques, bio-inspired models including MC may be applicable to tackle this limitation. In this study, tissue-like P systems, a variant of MC, with sophisticated communication rules were developed to improve regionbased and edge-based segmentation algorithms for manual and automatic segmenting of 2D artificial and real images. Manual segmentation was applied for artificial images, whereas, the automatic segmentation was applied for artificial and real medical images. The manual segmentation of 2D artificial images was achieved using four, six and eight adjacency pixel connectivity relationships, whereas, the automatic segmentation of 2D artificial and real medical images were achieved using four and eight adjacency pixel connectivity relationships. Two methods were used to realize the automatic edge-based and region-based segmentations. The first method is for 2D artificial images using P-lingua linked to Java Netbeans using the P-linguaCore4 Java Library. The second method is for the 2D real and real medical images using C# linked to P-linguaCore4 Java library. The results of the second method demonstrated the ability of the system to automatically segment 2D real and real medical images with arbitrary sizes and different image formats. The experimental results statistically proved that the methods markedly outpaced the state-of-the-art methods of 2D real image segmentation using the same data set. Furthermore, the methods showed better segmentation accuracy and ability to deal with images of different sizes and types. Extra efficient results such as reducing the number of rules and computational steps were achieved for 2D hexagonal artificial images based on Tissue-like P systems. The main contributions of this study are automatic loading and codifying of the input image as well as automatic visualization of output images after segmentation. Furthermore, six and eight adjacency pixel connectivity relationships should be considered for reducing computational steps, number of rules used and processing time in molecular computing.

ABSTRAK

Pengkomputeran Membran (MC), secara relatifnya adalah cabang terkini pengkomputeran asli dalam bidang baharu pengkomputeran molekul. MC bertujuan untuk model pengabstrakan, dipanggil sebagai sistem membran atau sistem P, yang meniru fungsi dan struktur sel biologi. Banyak kajian telah menggunakan MC dalam pelbagai aplikasi seperti pengsegmenan imej. Oleh kerana kos pengkomputeran yang tinggi bagi teknik pengsegmenan konvensional, model bio-inspirasi termasuk MC mungkin boleh diterima pakai untuk menangani kekangan ini. Dalam kajian ini, sistem P seperti tisu, satu varian MC, dengan kaedah-kaedah komunikasi canggih telah dibangunkan untuk meningkatkan algoritma pengsegmenan berasaskan kawasan dan pinggir untuk pengsegmenan manual dan automatik imej tiruan 2D dan imej sebenar. Pengsegmenan manual telah digunakan untuk imej tiruan, manakala, pengsegmenan automatik telah digunakan untuk imej perubatan tiruan dan sebenar. Pensegmenan manual imej tiruan 2D dicapai menggunakan empat, enam dan lapan hubungan sambungan pixel bersebelahan, manakala pengsegmenan automatik imej perubatan 2D tiruan dan sebenar dicapai dengan menggunakan empat dan lapan hubungan sambungan piksel bersebelahan. Dua kaedah telah digunakan untuk merealisasikan pengsegmenan automatik berasaskan pinggir dan berasaskan kawasan. Kaedah pertama adalah bagi imej tiruan 2D menggunakan P-lingua dipautkan kepada Java Netbeans menggunakan Perpustakaan P-linguaCore4 Java. Kaedah kedua adalah bagi imej sebenar 2D dan imej perubatan sebenar mengunakan C# yang dipautkan kepada perpustakaan PlinguaCore4. Keputusan kaedah kedua menunjukkan keupayaan sistem untuk secara automatik mengsegmen imej perubatan 2D sebenar dan imej sebenar dengan saiz arbitrari dan format imej yang berbeza. Keputusan eksperimen secara statistik membuktikan bahawa kaedah yang ketara mengatasi kaedah canggih pengsegmenan imej 2D sebenar menggunakan set data yang sama. Tambahan pula, kaedah menunjukkan ketepatan dan keupayaan pengsegmenan yang lebih baik untuk berurusan dengan imej pelbagai saiz dan jenis. Hasil kecekapan tambahan seperti mengurangkan bilangan peraturan dan langkahlangkah pengkomputeran telah dicapai untuk imej heksagon 2D tiruan berdasarkan sistem P seperti tisu. Sumbangan utama kajian ini adalah pemuatan dan pengekodan automatik imej input serta visualisasi automatik imej output selepas pengsegmenan. Tambahan pula, enam dan lapan hubungan sambungan bersebelahan pixel patut dipertimbangkan bagi mengurangkan langkah-langkah pengkomputeran, bilangan peraturan yang digunakan dan masa pemprosesan dalam pengkomputeran molekul.

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LIST OF ABBREVIATIONS

2D	-	Two dimensional						
2D	-	Two dimensional						
2D-ES	-	Edge-based segmentation of 2D						
3D	-	Three dimensional						
3D	-	Three dimensional						
ACO	-	Ant Colony Optimization						
AGP	-	A Graphical P segmentator						
API	-	Application Program Interface						
BBC	-	Black Connected Component						
BMP	-	Bitmap Picture						
BSDS	-	Berkeley Segmentation Dataset						
СТ	-	Computed Tomography						
СТ	-	Computed Tomography						
CUDA TM	-	Compute Unified Device Architecture						
CUDA TM	-	Compute Unified Device Architecture						
FPGA	-	Field-Programmable Gate Array unit						
FPGA	-	Field-Programmable Gate Array unit						
FPGAs		Field Programmable Gate Arrays						
FPGAs		Field Programmable Gate Arrays						
GA	-	Genetic Algorithm						
GPU	-	Graphics Processing Unit						
GPU	-	Graphics Processing Unit						
HSV	-	Hue-Saturation-Value						
JPEG	-	Joint Photographic Experts Group						
MAQIS	-	Membrane Algorithm With Quantum-Inspired						

		Subalgorithms							
MAQIS	-	Membrane	Algorithm	with	Quantum-Inspired				
		Subalgorithm	S						
MATLAB	-	Matrix Laboratory							
MC	-	Membrane Computing							
MC	-	Membrane Co	omputing						
NMS	-	Nested Membrane Structure							
PC		Personal Com	puter						
PNG	-	Portable netw	ork graphics						
PSNR	-	Peak Signal to	o Noise Ratio						
PSO	-	Particle Swarm Optimization							
RGB	-	Red, Green and Blue							
RGB	-	Red, Green and Blue							
TIFF	-	Tagged Image File Format							
TSP	-	Travelling Salesman Problem							
VHDL	-	Very High-Level Design Language							
WBCs	-	White Blood Cells							
WBCs	-	White Blood Cells							
XML	-	Extensible Markup Language							

LIST OF SYMBOLS

Π	-	Whole system
Γ	-	A finite alphabet whose symbols
Σ	-	Input alphabet
ε	-	Objects in the environment
$W_1, \dots Wq$	-	Multisets of objects
R	-	Rules
iπ	-	Input of the system
<i>о</i> _П	-	Output of the system
μ	-	Initial mmbrane
<i>z</i> ₁	-	Represent counter
B_{ij}	-	Blue object
G _{ij}	-	Green object
R _{ij}	-	Red objects
X	-	Marked pixel
RX	-	Marked Red pixel
GX	-	Marked Green pixel
BX	-	Marked Blue Pixel
S	-	Segmented results
G	-	Ground truth

LIST OF ALGORITHMS

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CHAPTER 1

INTRODUCTION

1.1 Introduction

In recent years, computing systems inspired by biological systems, or bioinspired computing, has been considered as a promising area of theoretical computer science for the next generation computing devices (Ishdorj, 2007).

Natural computing extracts concepts from nature to abstract and improve computational models and to develop new computational devices as well as make use of materials from the environment (e.g., molecules) for computation (De Castro, 2006). Natural computing can be viewed in Figure 1.1 from three different perspectives. First, new computing technology inspired by biological processes, known as bio-inspired computing is composed of the fields of evolutionary computing, swarm intelligence, artificial immune system and artificial neural networks. Second, the use of computer science to explore biology or natural processes taking place in nature and the fields that compose this branch are quantum computing and molecular computing, which branch to DNA computing and membrane computing. Third, the use of novel natural materials for computation, known as simulation of natural phenomena in computers, and as such, natural computing represents a paradigm for the substitution or supplementation of current silicon-based computers, the fields of which are composed of fractal geometry and artificial life (De castro and Von zuben, 2005).



Figure 1.1 Taxonomy of natural computing branches (Alsalibi *et al.*, 2014)

Logically, inspiration deriving from various processes in nature has led to studies under the umbrella of natural computing. Figure 1.2 illustrates some branches of natural computing which include Neural Computing (based on brain processes); Evolutionary Computing (based on processes of evolution); and DNA Computing (based on DNA processes). Moreover, membrane computing (MC) is a new branch that appears in the umbrella of natural computing that is based on the several functions of membranes in cellular organisms (Woodworth, 2007).



Figure 1.2 Natural Computing inspiration in various studies (Woodworth, 2007)

The above-mentioned natural computing areas do not take into account the internal structure of the cell. This is the start point of membrane computing. In 1998, Păun studied the behaviour of living cells and introduced membrane computing, or P systems, in honor of their initiator G. Păun, with the latest version related to his initial research studies published in 2000 (Păun, 2000). The primary models for MC began with a single cell and its hierarchical structure of organized compartments, or membranes, where localized 'biochemistry' took place. The resulting computing device comprised a distributed parallel model with multisets of objects or "chemicals" placed in regions (tree-like nodes) processed as "reactions" similar to those of natural biochemistry. The model was extended according to different biological suggestions to include the processing of objects by means of operations patterned after bio-symport/antiport functions, or as computational motivations extended from single cells to cell populations, or from tree-like membrane arrangements to arbitrary graph techniques, as well as other biological processes such as neuro-pathways (Păun, 2002).

Several features of MC are of great interest. These include (i) distribution with significant system-part interactions as well as emergent behaviours and nonlinearity resulting from local behavioural composites; (ii) algorithmicity and easy programmability; (iii) scalability and extendibility (major challenges when using differential equations in biological applications); (iv) transparency (multi-set rewriting rules are little more than equations that mimic chemical reactions); (v) parallelism (a computer science dream, but commonly observed in biology); (vi) non-determinism; and (vii) communication with the marvellous and yet not perfectly understood life phenomenon that coordinates numerous processes within a cell. These approaches all stand in stark contrast to the costly, parallel, coordinating, and synchronizing computations of electronic computing architectures (Păun, 2005).

MC is an emerging field of research due to its inherent parallelism and it has attracted widespread attention from all over the world since its introduction. Its purview includes computer science, biology, biomedicine, bioinformatics, and multiple disciplines such as mathematics, artificial intelligence, automation, and economics. Extensive models of computation involving mathematics, computer science, and biology are derived from cell-type membrane systems, group weave-type membrane systems and neuronal membrane systems. They have applications in computer graphics, approximate optimization, cryptography, parallel computing, and many other areas (Ciobanu and Păun, 2006).

Researchers of MC have applied useful techniques from cell biology in computer science, such as using cell organization in tissues as populations of cells (bacteria) as well as using organizational schemes similar to the pattern of neurons in the brain. P systems can be broadly classified into three fundamental models (Gelenbe, 2009). The first is modelled after a membrane structure or tree-like group and is called cell-like P systems (Păun, 2000). The main component of cell-like P systems is that membranes are structured in a hierarchical arrangement of three dimensional vesicles. The second model is tissue-like P systems (Martın-Vide *et al.*, 2003), which consist of several cells which can evolve in the same environment and object multisets. Certain cells are directly related by supply channels and these cells can communicate with the environment. The third model is spiking neural-like P systems (Ionescu *et al.*, 2006), which use only a single set of objects called a 'spike' where the basic data is the distance between successive spikes.

The motivation of using tissue-like P systems is that tissue-like P systems have two biological inspirations: intercellular communication and neuron cooperation. These two mechanisms have a common mathematical model that utilizes a network of processors that work with symbols through specific channels. The basic feature of the tissue-like P system is that the cell is not polarized and the structure of the graph is general (Christinal *et al.*, 2009).

1.2 Problem Background

P systems have a number of interesting features that open new lines of research that were recently launched to solve several problems related to digital imagery such as the encapsulation of data, the simple representation of information and parallelism, all of which are appropriate for digital images (Díaz-Pernil *et al.*, 2010). According to these features, MC is used in image segmentation by an extensive number of researches as shown in the related works.

The fundamental objective of digital image processing is to extract meaningful information from images without human assistance. The goal of digital imagery is quality enhancement or artistic effect (Pham, *et al.*, 2000). Segmentation is an important task in image processing for satellite and medical images (Somasundaram and Alli, 2012). Technically speaking, in computer vision (Shapiro and Stockman, 2001), segmentation is the process of partitioning a digital image into multiple segments (sets of pixels) to simplify or modify the representation of an image to be more expressive and easier to analyze and understand. Image segmentation is typically used to locate objects and boundaries (lines, curves) in images. More precisely, image segmentation is the process of assigning a label to every pixel in an image, so that pixels with the same label share certain visual characteristics.

Segmentation in Digital images has features that are parallel and/or local and can be solved regardless of image size. Parallel implementation becomes more practical at different local areas. Another feature is that the basic information can be easily encoded according to bio-inspired representations. These features make digital imaging flexible and amenable for nature-inspired techniques (Díaz-Pernil *et al.*, 2013).

Limited work on segmentation methods based on P systems has been published and two types of MC methods have been used in segmentation, which are MC rules and MC algorithm.

In 2009, Christinal *et al.* (Christinal *et al.*, 2009) proposed a new and promising line of research for a family of tissue-like P systems using communication rules to perform edge-based segmentation for 2D images by employing 4-adjacency and 26-adjacency relationships as has been used for 3D digital images. Their results show a constant number of steps (9 steps) of computation to segment a image.

Later (Christinal *et al.*, 2010a) calculated some algebraic-topological information for two-dimensional (2D) and three-dimensional (3D) images in a general and parallel manner with P systems by presenting two areas implemented by tissue-like P systems using communication rules. First, the edge-based segmentation segmentation of 2D images by employing 4-adjacency and 26-adjacency has been used for 3D digital images. Their results show a constant number of steps (9 steps) of computation to segment an image. Second, Homology, this work paved the way for another areas of study in which efficiency and power are used in topological processes for the first time by presenting new rules to achieve the homologous groups of 2D digital images in logarithmic time with respect to input data.

For threshold segmentation, Christinal *et al.*, proposed two works for two types of P system. In the first work (Christinal *et al.*, 2010b), Christinal *et al.*

designed an MC approach to solve the threshold problem by using cell-like P system rules where in the massive parallelism of MC allowed the solution to be reached in linear time. In the second (Christinal *et al.*, 2012), tissue-like P systems have been proposed for the parallel colour segmentation of simple artificial images. The images were segmented such that a threshold was employed to search for edge pixels.

For region-based segmentation (Christinal *et al.*, 2011) proposed new tissuelike P system rules for region-based segmentation, in which a 4-adjacency relationship between pixels was adapted to segment 2D digital images, and a 6adjacency relationship was used for 3D digital images.

Many limitations can be found in the works of Christinal *et al.*, like the need to manually codify the input image and the need to manually visualize output images. They did not consider that the time of segmentation is not feasible when dealing with big real images, that only one type of segmentation was obtained, that only 4-adjacent relations were used, and that no evaluation procedure has been considered to validate the quality of segmentation.

Two studies have been designed by (Díaz-Pernil *et al.*, 2010) and (Díaz-Pernil *et al.*, 2012) based on a new software tool for segmenting based on edge-based segmentation of 2D digital images using a tissue-like P system based on Christinal's work (Christinal *et al.*, 2009) with object oriented C++ language with one differnce (Díaz-Pernil *et al.*, 2012b), which was the addition of only one extra image for experimental purposes. The drawbacks were that only 4-adjacency was used, the technicalities that surround it were not clarified, no standard medical dataset has been used for the experiments, only edge-based segmentation was obtained, and that the accuracy of segmentation to evaluate and validate their proposed approach was not computed. Later, a novel device architecture called Compute Unified Device Architecture (CUDATM) was proposed by (Díaz-Pernil *et al.*, 2013) to implement

tissue-like P systems with new rules for segmenting images by the use of gradientbased edge-detection to enhance the classical methods of segmentation.

In (Isawasan *et al.*, 2014), tissue-like P system rules were used to perform the region-based segmentation of 2D hexagonal images using a minimum number of steps (7 steps). Whether or not P-Lingua was used to perform the segmentation is unclear and the details that backup the usage were not illustrated, nor did they not consider the time of segmentation. In addition, only region-based segmentation has been considered and no evaluation procedure has been performed to validate the segmentation results.

In the work of (Sheeba *et al.*, 2011), the authors constructed a family of tissue-like P systems based on Christinal's work (Christinal *et al.*, 2009) using edgebased segmentation to segment medical images (nuclei of the white blood cells, or WBCs). This technique was implemented through Matlab, only edge-based segmentation was obtained, 4 and 8-adjacency are used, the differences of both types of adjacency has not been illustrated, and the evaluation procedure and the method to compute the success rates have not been mentioned.

(Carnero *et al.*, 2011) proposed two studies using MC rules based on tissuelike P systems to segment images by designed new hard ware tools, namely a Field-Programmable Gate Array unit (FPGA), to perform various types of segmentation. First is (Carnero *et al.*, 2010) to segment digital images and to address edge-based segmentation. Second is (Carnero *et al.*, 2011) to remove noise and threshold segmentation. Later Carnero *et al.* (Carnero *et al.*, 2014) proposed new MC rules by adding multiple membranes to solve segmentation issues using cleaning, thresholding and edge-segmentation in Python. They did not consider the time, obtained only one type of segmentation, and no evaluation procedure was used. Reina-Molina *et al.* (Reina-Molina *et al.*, 2011) proposed new tissue-like P system rules by replacing single cells with multiple auxiliary cells to deal with segmentation problems and to exploit potential parallelization. No evaluation procedure has been performed to validate the segmentation results.

(Zhang and Peng, 2012) proposed MC algorithms using cell-like P systems for a novel infrared object segmentation technique based on the thresholding method to quickly get the best set of parameters.

(Peña-Cantillana *et al.*, 2011) presented two types of MC methods to solve the threshold problem. First, MC rules suggested by the authors in (Peña-Cantillana *et al.*, 2011) using tissue-like P systems with an innovative device architecture called CUDATM. Second, MC algorithm in which the authors in (Peng *et al.*, 2012) and (Peng *et al.*, 2015) proposed MC algorithms based on cell like-P systems to improve the performance of threshold segmentation. However, (Peng *et al.*, 2015) proposed a multi-level thresholding with enhanced computation efficiency.

In region-growing, another work of (Peng *et al.*, 2014) proposed new tissuelike P system rules based on region-growing based colour image segmentation. The proposed image segmentation has the advantage of fast segmentation. The experimental results also show improved segmentation performance. They have not explained the programming language that has been used in their work.

(Yang *et al.*, 2013) have proposed an image segmentation technique using new tissue-like P systems rules to perform traditional region-growing based segmentation. In a special work only for gray-scale image, they used 4 and 8 adjacency but the differences of both types of adjacency have not been illustrated, and the programming language that has been used was not mentioned. From the literature review, there is a lack of region-based segmentation for real images. In other words, researchers have not obtained two types of segmentation using the same rules at the same time. Despite extensively cited efforts and achievements, there remains room for numerous improvements for MC in image segmentation. Difficulties for newcomers to understand the concept means that its complex methodology has yet been clarified.

1.3 Problem Statement

Traditional segmentation methods have several drawbacks including the high computational time. Hence, a recent research trend has been shifted towards using MC for image segmentation (Christinal *et al.*, 2009). Based on observations of previous studies that are mentioned in the previous section, MC has reduced iteration time and computational cost for region-based segmentation and edge-based segmentation.

The majority of the literature lacks a comprehensive explanation of the methodological entities of the proposed approaches, which makes understanding the literature a tedious task. Thus, a more comprehensive illustration of MC models pertaining to image segmentation is of great importance.

The main limitation of the previous studies pertaining to MC based image segmentation is the manual processing of images which makes its practical applications not straightforward.

These studies depend on the manual codification of the input image pixel by pixel and the manual visualization of the output images after segmentation.

Furthermore, the majority of the works use only the tissue simulator tool to perform segmentation. However, P-lingua programming language has only been used in few studies and without much explanation. Another limitation of the literature is that there is no standard evaluation procedure to validate the efficiency of segmentation.

This thesis proposes a bio-inspired MC technique for the automatic segmentation of artificial and real images. This will be accomplished through the development of a new technique based on MC rules. This study will address the following issues:

- a. Large number of rules is required to segment large images (Christinal *et al.*, 2011).
- b. Lack of region-based segmentation for real images (Christinal *et al.*, 2011).
- c. The lack of edge-based segmentation for hexagonal images (Isawasan, *et al.*, 2014).
- d. Difficulties in manually codifying input images (Christinal *et al.*, 2011).
- e. Difficulties in manually visualizing output images (Christinal *et al.*, 2011).
- f. The lack of attention paid to real images because of tissue simulator limitations and drawbacks (Christinal *et al.*, 2011).

This proposed study will answer the following research questions:

- 1. How can tissue-like P systems be effectively adapted for hexagonalartificial image segmentation using edge-based segmentation and regionbased segmentation?
- 2. How can tissue-like P systems be used to perform the automatic segmentation of artificial images using 4-adjacency and 8-adjacency edge-based segmentation and region-based segmentation?

- 3. How can the proposed tissue-like P system be improved to automatically segment real images using edge-based segmentation and region-based segmentation?
- 4. How can the intrinsic parallelism inherent in the structure of MC models be fully exploited to enhance segmentation results (improve the segmentation accuracy) and reduce computation time?
- 5. How can the proposed tissue-like P system be evaluated using image segmentation datasets and benchmarks?

1.4 The Aim of the Study

The goal of this thesis is to propose a parallel tissue-like P system framework for image segmentation that draws inspiration from cell biology and membranes. The proposed approach will enhance segmentation quality and obtain better results than previous methods.

1.5 Research Objectives

The goal of this study is to use tissue-like P system concepts and models to improve image segmentation performance using less effort, time and computational steps. The main objectives of this thesis are:

1. To propose a new scheme of the effect of color correlations on the performance of artificial image segmentation.

- 2. To propose a novel tissue-like P system for the segmentation of square and hexagonal images using three types of adjacency relationships between pixels, 4-adjacency, 6-adjacency, and 8-adjacency.
- To design automatic region-based and edge-based image segmentation using both 4-adjacency and 8-adjacency relationships using tissue-like P systems.
- 4. To improve the proposed tissue-like P system to handle real medical images using region-based and edge-based segmentation. A fair comparison between different adjacency relationships will be conducted to assess the efficiency of the tissue-like P system.

1.6 Scope of the Study

This thesis centers on the basic structure or framework of a tissue-like P system. All of the communication rules used in this thesis are based on the work of Christinal *et al.* (2011). The image datasets that have been used in this thesis are as follows:

- a. The first dataset is associated with skin cancer images. The Dataset was used with permission from the Central Laboratories of the Ministry of Health in Iraq.
- A bone image available at CTisus was used (Computed Tomography, 2013). [avilable online; http://www.ctisus.com]
- c. A tree image available at the Friedrich-Alexander-Universität was used (Technische Facultat, 2016). [avilable online; https://www5.cs.fau.de/research/data/msseg]
- d. A lung image (CT scans) available at CTisus was used (Computed Tomography, 2013). [avilable online; http://www.ctisus.com]
- e. An apple image available at Nexusmods (2016) was used. [available online; http://www.nexusmods.com/skyrim/mods/74627/?]

Note that the artificial images used in this thesis and their characteristics are as follows: RGB apple image with size 13×13 , face with size 14×14 and house with size 30×30). These simple apple images have three colors (Red, Blue, and Green) which have been drawn manually.

The Jaccard index method was used for the evaluation of the proposed segmentation approach. Furthermore, two different machine platforms (i7 and i5) have been used to implement the system. In the first part of the study, the tissue simulator tool has been used to implement and execute the proposed P system. Then, P-lingua, the official programming language of MC has been used instead. P-Lingua programming language has been linked to Java (PLinguaCore4 Java library) and C# environments.

1.7 Organization of the Thesis

The thesis is organized as follows. Chapter one presents the introduction, problem background, research questions, objectives, and scope. Chapter two provides a review of the general concepts pertaining to membrane computing, and tissue-like P systems as well as a literature review for image segmentation. Chapter three presents the research methodology with the methods used in each phase of this study. Chapter four provides an explanation of previous work done by (Christinal *et al.*, 2011) to illustrate how the membrane system works. Chapter five introduces a tissue-like P system framework to manually segment artificial images using P-Lingua and three types of adjacency relationships. Chapter six presents an automatic simulation of the region-based segmentation and edge-based segmentation of 2D real images using 4-adjacency and 8-adjacency relationships and a comparison of two different hardware platforms.

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