

一种基于区域生长的 CT 序列图像分割算法^{*}

彭丰平 鲍苏苏

(华南师范大学计算机学院 广州 510631)

摘 要 提出一种基于区域生长的 CT 序列图像的分割算法。在第一张待分割目标区域中选取一个种子点,利用四邻域的生长规则对种子点进行区域生长,得到一组点集,将这个点集投影到下一张 CT 图像中,得到一组新的点集,再提取该点集的轮廓,最后对该轮廓上的点进行四邻域的区域生长,分割出最终的目标区域。实验结果表明,该分割算法不仅适用于简单的图像分割问题,而且对于背景复杂、光照不均匀的图像也能取得较好的分割效果。

关键词 CT 序列 区域生长 种子点 轮廓 生长规则

中图分类号 TP391.41

1 引言

图像分割是图像处理领域中极为重要的内容之一,它以图像的某些特征为标准,把图像划分一些具有“某种意义”的区域。根据分割算法适用性的不同,图像分割方法主要分为两大类:一类是基于区域的方法,通常利用同一区域内的均匀性识别图像中的不同区域;另一类是边缘分割方法,通常利用区域间不同的性质划分出各个区域之间的分界线。本课题的研究对象是实际的 CT 腹部图像序列,它以两两间距很小的序列二维切片传递三维信息。我们的任务是:首先在序列中每一幅二维图像上将肝脏及其血管分离出来,然后利用分割的结果序列实现单独器官的三维重建。其重点就是在保证单个图像分割结果正确的同时,提高序列意义上分割的自动化程序。

2 区域生长算法原理

2.1 域生长的基本思想是将具有某种相似性质的像素集合起来构成区域

具体先对每一个需要分割的区域找一个种子像素作为生长的起点,然后将种子像素周围邻域中与种子像素有相同或相似性质的像素合并到种子像素所在的区域中。将这些新像素当做新的种子像素继续进行上面的过程,直到再没有满足条件的像素可被包括进来。

2.2 灰度相似性判决

设分割区域 R 的灰度均值为 \bar{x} ,待测像素点灰度为 y ,则待测像素点与已分割区域相似性 s 表示为

$$s = w(y - \bar{x})^2 \quad (1)$$

式中, w 为非负权值。对于足够小的 s ,可认为待测像素与已分割区域相似,并入已分割的目标中,否则,不进行合并。同时用 y 更新均值。

$$x_{new} = (x + y) / (n + 1) \quad (2)$$

式中, n 是已生长区域的像素个数。

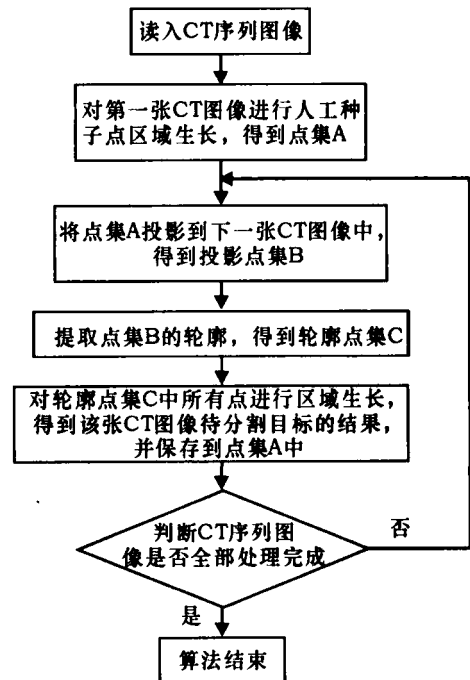


图 1 算法流程

^{*} 收到本文时间: 2006 年 8 月 7 日

基金项目: 广东省教育厅自然科学基金 (编号: ZL03090014) 资助。

作者简介: 彭丰平, 男, 硕士研究生, 主要研究医学图像的分割和三维重建技术。鲍苏苏, 博士, 博士后, 教授, 硕士生导师, 主要从事信号处理和数字图像处理、模式识别的研究。

3 序列图像分割考虑

实现序列化分割,要充分利用基于模型分割方法的优点,有两种方案可以参考:(1)将前面图像的分割结果作为后面图像的先验知识,即轮廓初值。(2)将序列图像分成若干组,每组共用一个人工的初始化轮廓。由于 CT造影的特点,相邻切片的二维形状非常类似,再加上第二种方案需加入更多的人工干预,为此,本文选择了第一种方案。

4 本文的算法思想

4.1 算法流程图(如图 1)

4.2 算法具体实现步骤

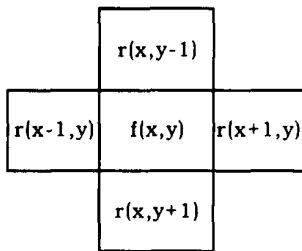


图 2 具体实现图

(1)在第一张 CT 图像的待分割区域中人工选取一个种子点,并把该种子点保存到种子队列 Q 中,然后利用四邻域的生长规则,如图 2 所示,按逆时针方向进行种子点生长。

具体实现是:先计算该种子点及其相邻四个点的灰度值,分别用 Gray, Gray1, Gray2, Gray3 和 Gray4 表示,然后根据灰度相似性判决,确定这四个相邻的点是否可以做为新的种子点,如果可以则把它保存到种子队列 Q 中,再在队列中取下一个种子点,继续上面的步骤,直到队列为空,这样得到第一张 CT 图像的要分割区域的结果,用点集 A 表示,同时用两个数组分别保存点集 A 中每个点的 X 坐标(用 Seed_x 保存)和 Y 坐标(用 Seed_y 保存),并计算出该目标区域的平均灰度值(用 AveGray 表示)和方差(用 Squire 表示)。

(2)将上张分割结果点集 A 中所有的点投影到下一张 CT 图像上,这样得到一个投影点集,用

B 来表示。这里考虑到,在 CT 序列图像中,下一张图像待分割的目标区域可能比上一张分割出来的目标区域要小,所以点集 B 中的点不一定都能作为种子生长点,必须对其进行一些优化。具体解决方法是这样的:计算点集 B 中所有点的灰度值并将它们与 AveGray 比较判断(阈值设定为方差 Squire 的值),确定哪些点可以作为种子点,这样可以得到种子点集,用 C 来表示,同时用数组 Seedx 和 Seedy 保存这些种子点的 X 坐标和 Y 坐标。

(3)算法考虑到,在 CT 序列图像中,下一张图像待分割的目标区域可能比上一张分割出来的目标区域要大,所以用四邻域方法对种子点集 C 进行轮廓提取,得到一组轮廓点集,用 D 来表示,接着用四邻域的生长规则,根据灰度相似性判决,对轮廓点集 D 中所有点进行区域生长,这里的阈值设定为 AveGray,把满足生长规则的点保存到点集 A 中,最终得到该张 CT 图像待分割目标的结果。

(4)判断 CT 序列图像是否全部分割完成,否则转(2)继续,直到所有图像分割完成。

5 实验结果与分析

本算法是在 Window XP 操作系统平台上,使用 Delphi7.0 编程工具来实现的。实验中所用到的 CT 序列图像是由该项目的合作单位提供的。下面分别是实验 1 和实验 2 的结果,图 a 和图 b 分别是序列图像中的第 28 张和第 29 张(CT 造影图像),在实验 1 中,选取的种子点坐标是(116, 148),图 c 和图 d 分别是图 a 和图 b 的分割结果;在实验 2 中,选取的种子点坐标为(151, 170),图 e 和图 f 分别是图 a 和图 b 的分割结果。从实验的结果分析可以得出:本文提出的区域生长算法对 CT 序列图像的分割有一定的效果,特别适用于肝脏中血管的分割。

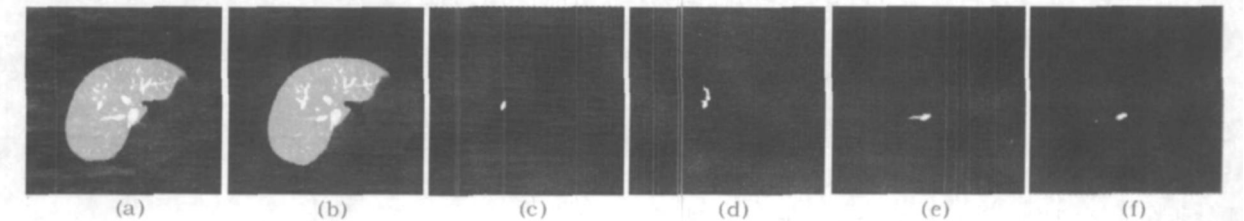


图 1 实验 1(a, b, c, d)结果

参考文献

- [1] 杨加,吴祈耀,田捷,杨骅.几种图像分割算法在 CT 图像分割上的实现和比较[J].北京理工大学学报,2000,12(6)
- [2] 陆仁枝,宋志坚,唐厚君. CT 序列图像分割的实现及分割结果的重建[J].计算机工程,2003,8(13)
- [3] 张玲,郭磊民,何伟,陈丽敏.一种基于最大类间方差和区

图 2 实验 2(e, f)结果

- 域生长的图像分割法[J].信息与电子工程,2005,6(2)
- [4] 章毓晋.图像分割[M].北京:科学出版社,2001
- [5] 田捷,包尚联,周明全.医学影像处理与分析[M].北京:电子工业出版社,2003
- [6] 阮秋琦,阮宇智译.数字图像处理(第二版)[M].北京:电子工业出版社,2003

A Algorithm for Segmenting CT Sequence Image Based on Region Growing

by Peng Fengping

Abstract This paper puts forward a algorithm for segmenting CT sequence image based on region growing. Firstly, selectes a seed from the aim region to be segmented in the first CT image, makes the seed grow based on four neighbors method and get a aggregate of points. Then let the aggregate project to the next CT image and gain a new aggregate of points. Finally distill the contour from the new aggregate and make the points of the contour grow based on the same method as far as get the final aim region. With this method, the target can be extracted without any pixel of the background.

Key words CT sequence, region growing, seed point, contour, grow ing strategy (Page: 1)

Array-based Association Rule Mining Algorithm

by Guo Fuliang

Abstract The article shows the foundation of classic algorithm of association rule Apriori, then make it more suitable in some special cases. The changes doesn't cose too much but can accelerate the algorithm.

Key words data mining, association rule, frequent item - set (Page: 3)

Research on Fingerprint Enhancement Algorithm by Time - Frequency Analysis

by Peng Zhangping

Abstract Fingerprint enhancement is a critical step in automatic fingerprint identification system, a good enhancement algorithm can improve the accuracy of minutiae extraction, which consequently improve the robustness of recognition system. The local fingerprint image frequency spectrum property is investigated, a time - frequency method and a new probabilistic approximation method for ridge orientation and frequency acquirement are adopted. A robust method of modifying ridge orientation and frequency estimation is proposed, an adaptive frequency filter is designed. Experimental results show that the method has prominent effect on fingerprint images, which is helpful to minutiae extraction.

Key words fingerprint, fingerprint enhancement, time - frequency analysis (Page: 5)

A Overview on Decomposition Method of Support Vector Machines

by Li Xiangdong

Abstract Decomposition method is currently major training algorithm for large - scale Support Vector Machines. Various decomposition method mainly according to the size of working set, selection rule and different solution on sub - problem optimization. This paper first reviews the history and development of decomposition method, and also introduce specific working set selection. Mainly introduce the some new strategy for the solution of sub - problem and working set selection rule.

Key words support vector machines, decomposition method, working set selection (Page: 9)

Research on Static Disassembly Algorithm

by Xu Min

Abstract Malicious codes are always distributed in binary codes, which is very difficult to analyze the basic function of the program, but if we convert binary codes into easier understood assembly codes by disassemblers, it will become more convenient to analyze malicious codes. Thus it becomes extremely important to explore the methods for disassembling binary codes. At first, this paper presents two traditional static disassembly algorithms: linear sweep and recursive traversal algorithm, analyzes their advantages and existing problems. Finally, some of the new research progresses of modern static disassembly algorithms are introduced.

Key words static disassembly, linear sweep, recursive traversal, speculative disassembly, hybrid disassembly

(Page: 13)

Research on View - Dependent Dynamic ROAM Algorithm

by Ren Yuanhong

Abstract Three - dimensions terrain rendering is always a hot topic in the field of computer graphics. In this paper, we conclude the advantages and disadvantages of every main algorithms by systematically research on the popular terrain rendering algorithms. Then we select the ROAM algorithm whose applicability is comparatively wider and analyze the idea of the algorithm, in the end we make some improvement to it and finally apply it to the actual model rendering of three - dimensions terrain.

Key words terrain rendering, LOD technology, ROAM algorithm (Page: 17)

A New Algorithm of Link Layer Topology Discovery Based on SNMP

by Huang Hui

Abstract This paper propose and prove the theorem for the determining the connection between two Ethernet devices. A new algorithm for determining the topology of subnet is given based on the theorem. Compared with other algorithms, it doesn't need the switch's every port has a completed forwarding table information and doesn't need to analyze every port of the switch. And it can discovery the network topology more quickly and accurately. A program based on the algorithm has been tested in the actual network, the result validate the algorithm.

Key words network management, network topology, SNMP (Page: 20)

Slicing of Quasi - Physical Algorithm for Protein Folding Problem

by Yi Guohong

Abstract The protein structure estimate problem has the important theoretical meaning and realistic meanings in the biology realm, this text puts forward a kind of draw up the thing slice calculate way, depended on the grid point model to solve fastest effect the calculate way PERM that the protein folds the problem to carry on the contrast analysis with currently in the cultural heritage.