A Knowledge-Based Approach for Failure Detection and Correction of Partially Failed Segmentations of Radiological Images

Aldo v.Wangenheim[1]; Harley Wagner[1]; Peter Conrad[2]; Michael M. Richter[2]; Eros Comunello[1];Dirk Krechel[2]

[1]The Cyclops Project
Department of Computer Sciences
Universidade Federal de Santa Catarina
88049 Florianópolis, Brazil
{harley,awangenh}@inf.ufsc.br

[2]The Cyclops Project
Knowledge-Based Systems Group/AG Richter
Universität Kaiserslautern, Postfach 3049
67553 Kaiserslautern, Germany
{krechel,richter}@informatik.uni-kl.de

Abstract. The segmentation of images with inadequate contrast characteristics is an important challenge in Computer Vision: images are either oversegmented, with "objects" divided into parts, or images are incorrectly segmented, with two or more objects segmented as one object. This is a problem that occurs in all types of segmentation approaches, but is of particular importance in the field of region-growing algorithms, which are used in many medical applications. We present a new knowledge-based method, based on the inexact consistent labeling method, that enables the automated consistency checking of the results of region-growing segmentations and that is capable to automatically "fitting" erroneous segmentations, when they are oversegmented, given there exists a reliable domain model.

Keywords: Knowledge-based image segmentation, consistent labeling

1 Introduction

A challenge in image analysis and computer vision is the segmentation of images with inadequate contrast characteristics: images are either oversegmented, with "objects" divided into parts, or images are incorrectly segmented, with two or more objects segmented as one object or even parts of different image objects considered to be a new object by the segmentation algorithm. This is a problem that occurs in all types of segmentation approaches, but is of particular importance in the field of region-growing algorithms, such as Watershed [1] or Mumford & Shah [2], which are used in many medical applications. The fact that such important step in image analysis is not stable has been a major fallback in former attempts to develop "fully automated" medical image analysis applications.

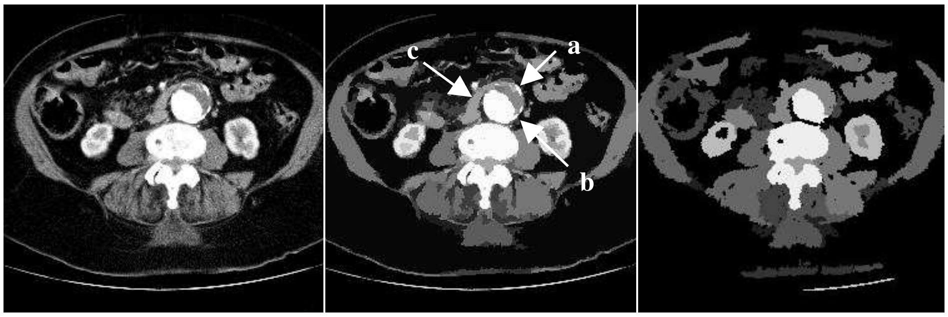

Fig.1. CT image of a human's abdomen and 2 different segmentations performed intending to detect the aneurismatic tissue and aortic light. The first is oversegmented and aneurismatic tissue and peripheral vascularizations (a) are represented by several segments. Aortic light was correctly segmented (b) and adjacent tissue (c) was also separated. The second segmentation shows a common leaking of aneurismatic tissue segments into adjacent tissues.

The method described here was specially developed to be used in the medical domain, more specifically, in the radiological domains of CT and MR images, where segmentation problems occur, but can be corrected by a posterior knowledge-based approach, since there is a well defined domain knowledge available. Fig.1 shows two different segmentations performed on a CT slice of a human abdomen intending to separate aneurismatic tissue from the aorta and aortic light from other structures represented in the image. Cases like this, where a segmentation either produces segments that "leak" into other structures or produces oversegmentated images, are one of the most important challenges in image understanding. For an oversegmentation to be useful, it is necessary to identify which segments pertain to the targeted structure and to "glue" them together, automatically generating a new segment as a result of the merging of the correct segments. This work is part of the Cyclops Project [3], which is a German-Brazilian joint project aimed at the development of a framework for intelligent radiological image analysis and decision support.

2 Objectives

Given a) a medical CT or MR image segmented by any region growing technique and b) a model of expected "consistent" results for this image segmentation, this approach should match the model with the segmentation results and to classify these as correct or not, trying to fix them if possible. The model should be a description of anatomic structures expected to be found in the image, along with a list of parameters describing the appearance of these structures, so that an automated identification and matching between model and resulting segments is possible. This model should also allow the analysis of medical images where pathologies are searched for, but that are not necessarily present in the image, enabling the description of "obligatory" and "optional" structures. Obligatory are all anatomies that have to be well segmented in this particular image, optional are all pathological structures, that can be in the image, but should not necessarily be there.

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3 Methods

Our approach was developed as an extension of the inexact consistent labeling method developed by Haralick and Shapiro [4]. This method was extended to enable the use of a) complex models of expected results where each unit has an *a priori* label and also to b) enable the use of "optional" labels representing pathologies. The representation of units is done as a pattern of segment parameters extracted by different algorithms, where some of them are general and other diagnosis-task specific. The *a priori* labeling is done by backpropagation neural networks based on prior training. Changing an *a priori* label will increase the error. Otherwise, if two segments are merged and the result is more similar to a prototype in the model, the global error decreases. The model can be generated from a static representation in a database or through a structured bayesian network using an approach based on Shastri´s model and parameters about the position of CT or MR slices.

3.1 Procedure

Based on the type of examination that is performed and on the position of the slice being examined, a graph structure representing the expected results of image processing is generated and passed to the Failure Detection Module. Each node of this graph contains an object describing on anatomical or pathological structure by means of a set of parameters retrieved from the domain database. The parameters are described in Table 1. For each segment generated during segmentation, a list of parameters is calculated, which is used as a segment description in the consistent labeling that will be performed afterwards. For each segment during the labeling process, there are generated description parameters that differ partially from the domain database parameters: Bounding Box, Area, Grayvalue and Neighbors are computed the same way; Anatomy and Type are substituted by other parameters.

Table 1. Parameters used to represent views of anatomies in radiological images as stored in the domain knowledge database. The values are generated based on mean values obtained from a base of CT and MR images of different patients.

Parameter	Description	Type
Bounding Box	Rectangle parallel to the *xy* axes, describing the simplest possible convex hull for the image.	Pair of xy coordinates
Area	Area of the pixels representing the anatomy. Can be stated either in pixels or in tomograph coordinates.	Real
Grayvalue	Mean grayvalue of the anatomy. Can be either in HU values or in absolute pixel values.	Real
Neighbors	List of all other anatomies adjacent to this one.	List of anatomies.
Anatomy	Anatomy of the application domain represented by the image.	Domain specific symbol.
Type	A structure can be optional or obligatory. Optional structures always refer to pathologies.	Symbol

Table 2 shows the extra parameters generated for each segment and used during the labeling. For the neural network preclassification, some extra grayvalue distribution parameters such as the grayvalue variance are calculated. The task of the consistent labeling is to match the segmentation results with the domain model provided for this specific image. This matching allows an error that is bound to a threshold and is based on the differences between "ideal" parameters from the database and the calculated ones. If the error rises above the threshold, the segmentation is considered to be failed.

Table 2. Parameters generated for each image segment resulting from an oversensitive segmentation that differ from those of the database prototypes.

Parameter	Description	Type
Gravity Center	Center of mass of the segment. Used by the Unit-Label-Constraint-Relation: if the center lies outside of the bounding box of a label, this label cannot be given to it.	xy-point
Preclassification	Anatomy of the application domain most likely to be represented by this segment, as classified by a domain specific neural network.	Domain specific symbol.
Reliability	Value stating how reliable is the preclassification symbol. Based on the neural network error.	Real

The consistent labeling problem in our approach is defined as follows: A *set of Units U*, given by the set of resulting segments and their parameters. A *set of Labels L*, given by the list of anatomies and pathologies expected to be found in the image and their parameters. A *Unit-Constraint-Relation T*, given by all pairs of adjacent image segments, represented as a neighborhood function. A *Unit-Label-Constraint-Relation R*, given by a set of functions that match parameter sets between segments and anatomies. An *Error Function w*, also given by a set of functions, that can handle future error calculations with possible segment merging. The *Error Threshold e* is a real value that gives the maximum allowed error in one search branch.

3.2 Main Extensions to Haralick and Shapiro´s Model

Error Estimation: Since not all labels are optional, the future error estimation cannot be performed over the unlabeled units. In our approach, it is based on the *not already given* obligatory labels and coded into a Future Error Table (FTAB).

A priori labeling: Each Unit has an a priori label with an associated error, both generated by a neural network preclassification. An a priori label can only be changed if it reduces the global error by a significant amount.

A same label can be given to more than one Unit: If the merging of two adjacent segments results in a parameter set for a new unit that reduces the global error, than they will be merged and a new unit will be generated. The merging is performed by a special Merging Function, that also calculates the new future error and that can be passed as a parameter to the labeling function.

4 Results

The approach was implemented and successfully tested on different segmentations of brain MR images. Now it is being used in an application for the 3D reconstruction and measurement of aortic aneurysms for the production of personalized endoluminal protheses. In this application domain, the aneurismatic tissue, which has to be detected, measured and rendered, has radiological densities very similar to other anatomies around the abdominal aorta and images have to be oversegmented.

The parameters used for the description of the anatomies and segments are very simple, but had shown very good results. The positional constraints based on bounding box, gravity center and neighborhood lists play the most important role, being complemented by the other data. Since these position parameters can be well defined in a database in medical domains and also made general through a parameterization based on body position registration in CT and MR volumes, they do not represent a restriction to the generalized use of this method.

5 Literature

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