Model-based segmentation of radiological images

G. Székely*and G. Gerig†
*Computer Vision Laboratory, Swiss Federal Institute of Technology,
ETH Zentrum, CH-8092 Zürich, Switzerland
†Department of Computer Sciences, University of North Carolina
at Chapel Hill, NC 27599-3175, USA

December 8, 1999

Abstract

Segmentation is in many cases the bottleneck when trying to use radiological image data in many clinically important applications as radiological diagnosis, monitoring, radiotherapy and surgical planning. Especially in case of large 3D medical data sets is the availability of efficient segmentation methods is a critical issue. While manual image segmentation is regarded up to now as a gold standard, its usage is not acceptable in some clinical situations due to unjustifiable amount of user interaction or the poor reproducibility of the results, making automatic segmentation is a very important issue in medical image analysis. This paper gives a short overview of efforts to automatize anatomical object identification in radiological images with special emphasis on model-based methods. The underlying principles are illustrated using selected examples of segmentation systems.

1 Introduction

Segmentation is in many cases the bottleneck when trying to use radiological image data in many clinically important applications as radiological diagnosis, monitoring, radiotherapy and surgical planning. Especially in case of large 3D medical data sets as obtained today by the routine use of 3D imaging methods like magnetic resonance imaging (MRI), computer tomography (CT) and ultrasound (US) the availability of efficient segmentation methods is a critical issue.

While manual image segmentation is regarded up to now as a gold standard, its usage is not acceptable in some clinical situations. In some applications such as computer assisted neurosurgery or radiotherapy planning e.g., a large number of organs have to be identified in the radiological data sets. While a careful and time-consuming analysis may be acceptable for outlining complex pathological objects, no real justification for such a procedure can be found for the delineation of normal, healthy organs at risk. Delineation of organ boundaries is also necessary in various types of clinical studies, where the correlation between morphological changes and therapeutical actions or clinical diagnosis has to be analyzed. In order to get statistically significant results, a large number of data sets has to be segmented. For such applications manual segmentation becomes questionable not only because of the amount of work, but also with regard to the poor reproducibility of the results.

Due to the above reasons, automatic segmentation is a very important problem to be solved in medical image analysis. This paper gives a short overview of efforts to automatize anatomical object identification in radiological images. Due to the importance of the topic, a huge collection of methods have been developed during the past decades approaching this problem and a detailed overview of the proposed methods would by far blow the limits of a short overview. Instead, this paper just tries to analyze the underlying principles and provide a few selected examples from the previous experience of the authors as illustrations.

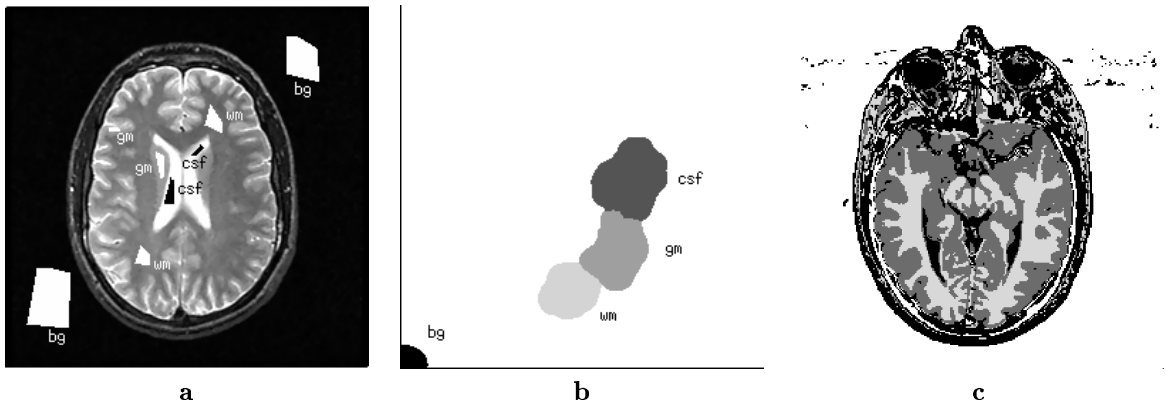
2 Early approaches

Early approaches for automatic segmentation fundamentally use the assumption, that radiological images are basically "self-contained", i.e. they contain most of the information which is necessary for the identification of anatomical objects. In some limited applications such techniques can be very successful, as the automatic segmentation of dual-echo MR images [12], e.g. This example will be used here as an illustration as it addresses most aspects of intensity-based medical image segmentation. The method uses

a **b** **c**

Figure 1: Spin-echo MR image pair (an early echo is shown on the left, a late echo on the right). In the middle the two dimensional intensity distribution is given

two perfectly registered echos of a spin-echo MR acquisition as illustrated by Figure 1(a,c). The applied procedure can be regarded as a generalized thresholding, aiming at the identification of areas in a feature space, i.e. in the two-dimensional intensity distribution (Figure 1b), which uniquely characterize the different tissue classes (as gray or white matter of the brain). These areas are usually determined during a training phase, where the user identifies examples for each tissue class (e.g. in the form of regions of interest as illustrated on Figure 2a). Standard pattern recognition procedures [9] can be used to derive a corresponding tessellation of the feature space (Figure 2b) leading to the classification of the entire image (Figure 2c).



a **b** **c**

Figure 2: Segmentation of the dual-echo MR image using training. The left image shows user-defined training regions for the different tissue classes. The corresponding tessellation of the feature space is show in the middle, resulting in the segmentation on the right

An important limitation of this procedure is, that it handles pixels in the image completely independently. Spatial correlation between the single pixels can be introduced using more or less complex interaction models as Markov random fields, e.g. [24, 2], or by post-processing techniques as mathematical morphology [14], The latter is illustrated on Figure 3.

The success of the segmentation basically depends on the assumption, that tissue classes can perfectly be separated in the feature space provided by the measurements. Beside physiologically induced overlaps between features of different tissue classes, limitations of the acquisition process as the presence of noise and global intensity inhomogeneity can seriously compromise the efficiency of the method. Several preprocessing techniques have been developed for efficient, structure-preserving noise reduction [11] and

bias field correction [26, 13], which lead in many cases to impressive results based on this very simple segmentation paradigm.

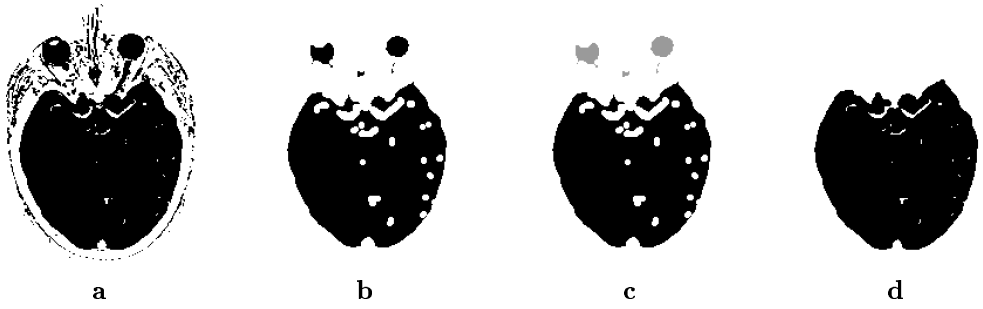


Figure 3: Brain segmentation based on morphological post-processing. Image (a) shows the result of thresholding, which has been eroded (b) in order to break up unwanted connections between different organs. Brain tissue has been identified by connected component labeling (c) and has been dilated back to its original extent (d).

3 Model-based segmentation

Even the most sophisticated pre- and post-processing techniques cannot, however, overcome the inherent limitation of the basically intensity-based methods, namely the assumption that segmentation can be carried out solely based on information provided by the actual image. This assumption is fundamentally wrong, and the radiologist uses a broad range of related knowledge on the field of anatomy, pathology, physiology and radiology in order to arrive at a reasonable image interpretation. The incorporation of such knowledge into the algorithms used is therefore indispensable for automatic image segmentation.

Different procedures have been proposed in the literature to approach the problem of representation and usage of prior knowledge for image analysis. Due to the enormous complexity of the necessary prior information, classical methods of artificial intelligence as the use of expert systems [18, 21] can offer only limited support to solve this problem.

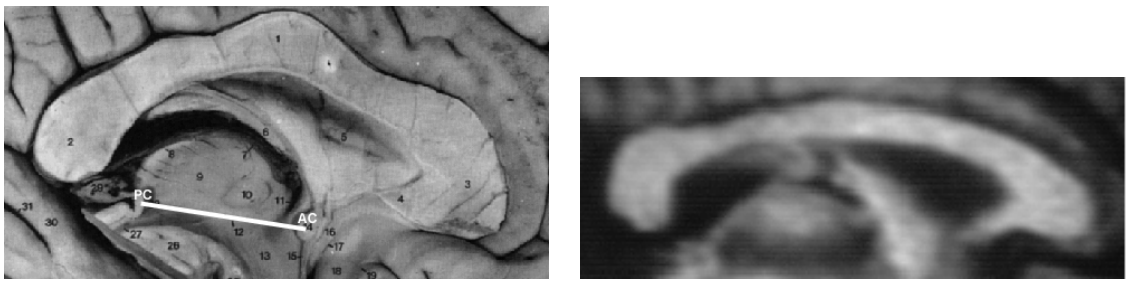
During the past few years, the usage of deformable anatomical atlases has been extensively investigated as an appealing tool for the coding of prior anatomical information for image interpretation. The method is based on a representative deterministic [1] or probabilistic [10] image volume as an anatomical model, which is then registered with the actual patient data. The applied registration procedure ranges from simple parametric methods [1] to complex physically-inspired algorithms as elastic deformation or viscous fluid motion [5]. In the latter he transformations are constrained to be consistent with the physical properties of deformable elastic solids or those of viscous fluids. Viscous fluid models are less constraining than elastic models and allow long-distance, nonlinear deformations of small subregions. In these formulations, the deformed configuration of the atlas is usually determined by driving the deformation using only pixel-by-pixel intensity similarity between the images in case of fully automatic procedures.

The usage of deformable atlases seems to be a very elegant way to use prior anatomical information in segmentation, as it allows to gain support from the success of current image registration research. Once the spatial mapping between the atlas and the individual data has been established, it can be used to transfer all spatially related information pre-defined on the atlas (as organ labels, functional information, etc.) to the actual patient image.

This approach is, however, fundamentally dependent on the anatomical and physiological validity of the generated mapping. It has to be understood, that a successful *morphing* of one dataset into the other, does not guarantee, that it also makes sense as an anatomical mapping. In other words, the fact, that the registration result *looks* perfect (in the sense of computer graphics) offers no guarantee, that it *makes sense* from the image analysis point of view. To morph a leg into a nose is perfectly possible, but will not allow any reasonable physiological interpretation.

To make the results of the registration sensible, i.e. useful for image segmentation, one has to solve

the correspondence problem. This means, that we have to ensure, that the mapping establishes a correspondence between the atlas and the patient which is physiologically and anatomically meaningful. For the time being, purely intensity driven registration cannot be expected to do so in general. Therefore, in the praxis such correspondence usually has to be strongly supported using anatomical landmarks [3, 10]. Landmark identification needs, however, in most cases tedious manual work, compromising the quest for automatic procedures.



a **b**

Figure 4: The corpus callosum from an anatomical atlas (**a**) and the corresponding region of interest in a midsaggital MR image (**b**). On the left image the connecting line between the anterior commissure (AC) and the posterior commissure (PC) which is used for normalization is also shown.

4 Statistical models

Statistical shape models offer a way to incorporate the (large, but still strongly limited) variability of organ shape into the basically static view of the anatomy provided by the atlases described above. The idea is to code the variations of selected shape parameters in an observed population (the training set), and characterize this in a possible compact way.

Such methods fundamentally depend on the availability of parametric models suitable to describe biological shapes. Several methods have been proposed for such parametric shape descriptions, as deformable superquadrics augmented with local deformation modeling [23, 25], series expansions [19, 4] or simply using the coordinates of selected organ surface points (point distribution models [7]).

Once the parametrization is selected, the anatomical objects of interest are fully described (at least from the point of view of the envisioned segmentation procedure) by the resulting parameter vector $\mathbf{c} = \{c_1, c_2, \ldots, c_n\}$, where n can of course be fairly large for complex shapes. Possible variations of the anatomy can be precisely characterized by the joint probability function of the shape parameters c_i, which information can be integrated into a stochastic Bayesian segmentation framework as a prior utilizing the knowledge gained from the training data for constraining the image analysis process [25, 20]. It has to be, however, realized that the usually very limited number of examples in the training set forces us to very strongly limit the number of parameters involved in a fitting procedure. A very substantial reduction of the number of parameters can be achieved based on the fact, that the single components of the vector $\mathbf{c}$ are usually highly correlated. A simplified characterization of the probability density is possible based on the first and second order moments of the distribution (for a multivariate Gaussian distribution this description is exact). The resulting descriptors are

- the mean shape:

$$\bar{\mathbf{c}} = \frac{1}{N}\sum_{j=1}^{N}\mathbf{c}_j \quad ,$$

  where the training set consists of the N examples described by the parameter vectors $\mathbf{c}_j$;

- the covariance matrix of the components of the parameter vectors:

$$\mathbf{\Sigma} = \frac{1}{N-1}\sum_{j=1}^{N}(\mathbf{c}_j - \bar{\mathbf{c}}) \cdot (\mathbf{c}_j - \bar{\mathbf{c}})^T$$

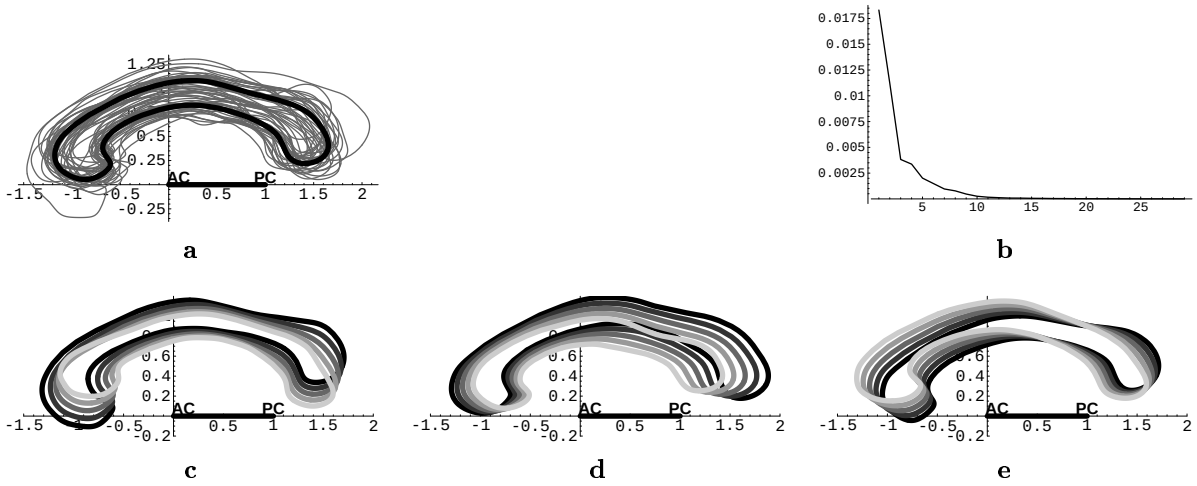


Figure 5: Building the active shape model for the corpus callosum. **a** shows the 71 outlines of the training set normalized in the anatomical coordinate system defined by the anterior and posterior commissures (AC/PC). The eigenvalues resulting from the principal component analysis are plotted on **b**, while the eigenvectors corresponding to the three largest eigenvalues are illustrated on **c**, **d** and **e**. The deformations which correspond the eigenmodes cover the range $-\sqrt{2}\lambda_k$ (light gray) to $-\sqrt{2}\lambda_k$ (dark gray)

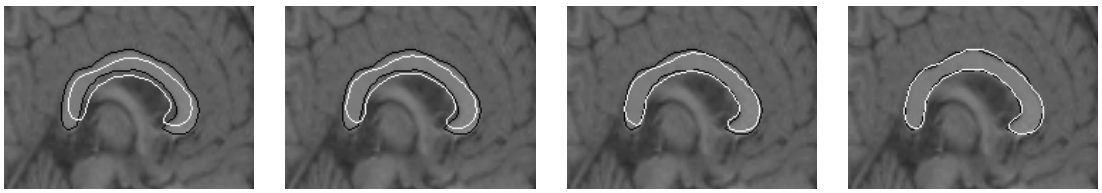
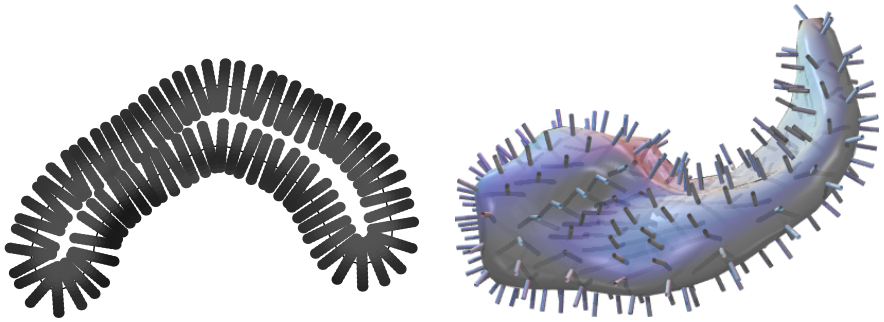


Figure 6: Segmentation of the corpus callosum. The first image shows the initialization, resulting from the average model and a subsequent match in the subspace of the largest four deformation modes. The other images illustrate the deformation of this model during optimization using all selected deformation modes, allowing fine adjustments. The black contour is the result of a manual expert segmentation

The existing correlations between the components of the vectors $\mathbf{c}$ can be removed by principal component analysis, providing the matrix $\mathbf{P}_c$ constructed from the eigenvectors $\mathbf{c}_j$, where $\mathbf{\Sigma P}_c = \mathbf{\Lambda P}_c$ and $\mathbf{\Lambda}$ is the diagonal matrix of the eigenvalues of $\mathbf{\Sigma}$. Experience shows, that even highly complex organs can well be characterized by the first few eigenvectors with the largest eigenvalues. This results in a description called active shape model [6], which allow to reasonably approximate the full variability of the anatomy by the deviation from the mean shape as a linear combination of a few eigenmodes of variation. The linear coefficients provide a very compact characterization of the possible organ shapes.

The automatic extraction of the outline of the corpus callosum on midsaggital MR images [22] nicely illustrates the basic ideas of using active shape models for segmentation. Figure 4 shows the region of interest covering the corpus callosum on a brain section (**a**) and on an MR image slice (**b**). Several examples have been hand-segmented, providing a training set of 71 outlines, which have been parametrized by Fourier coefficients up to degree 100. In order to incorporate not only shape-related but also positional variations into the statistical model, the contours have been normalized relative to a generally accepted neuroanatomical coordinate system, defined by the anterior and posterior commissures (Figure 4). The training data used and the shape model resulting from the principle component analysis is illustrated by Figure 5. As image **b** nicely illustrates, the largest 12 eigenvalues (defined by the 400 original parameters) already reasonably represent the variability (covering about 95% of the full variance).

This statistical description can easily be used as a parametric deformable model allowing the fully automatic segmentation of previously unseen images. Based on the concept of deformable contour models or snakes [17], the corpus callosum outline can be searched in the subspace spanned by the selected



a **b**

Figure 7: Intensity profiles along the boundary of a 2D (**a**) and a 3D (**b**) object

number of largest eigenmodes using the usual energy minimization scheme as illustrated on Figure 6 . The efficiency of the fit can be vastly increased by incorporating information about the actual appearance of the organ on the radiological image, for example in the form of intensity profiles along its boundary, as illustrated on Figure 7**a**, leading ultimately to the usage of integrated active appearance models [8] incorporating the shape and gray-level appearance of the anatomy in a coherent manner.

The illustrated ideas generalize conceptually very well to three dimensions, as illustrated on the anatomical model of the basal ganglia of the human brain shown on Figure 8. The corresponding active shape model has been successfully applied for the segmentation of neuroradiological MR volumes [15]. Remaining interactions needed for the establishment of the anatomical coordinate system can be eliminated using automatized adaptation of the stereotactical coordinate system [16].

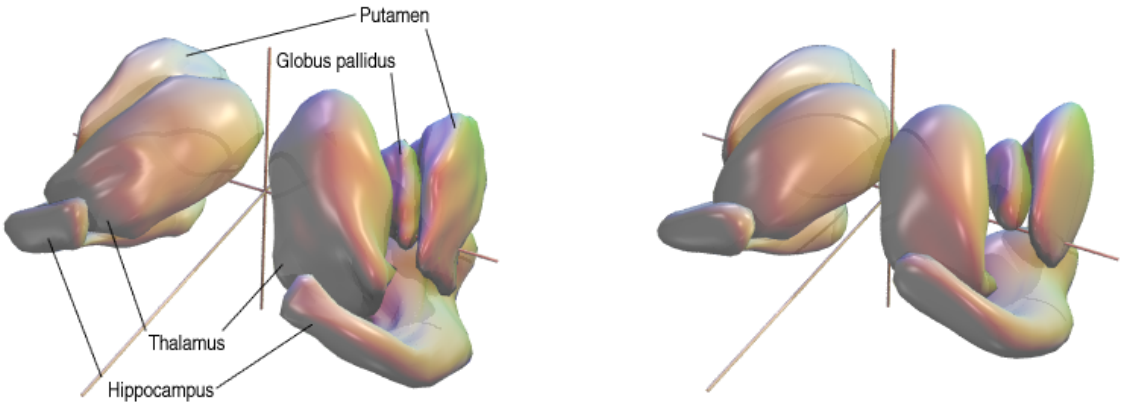


Figure 8: 3D model of the basal ganglia of the human brain. On the left an individual anatomy from the training set is shown, while the the average model is presented on the right image

It should be noted, that the establishment of correspondence is still a major matter of concern while the training set is created, which further complicates the generation of suitable data collections for training. The intensive manual work needed is, however, *limited to the training phase*, while the actual segmentation of the unseen data is fully automatic. The correspondences including the behavior of the anatomical landmarks are integrated into the statistical model and will be transfered to the new images during the fitting process.

5 Conclusions

While first results demonstrate the power of the above discussed model-based techniques, generic segmentation systems capable to analyze a broad range of radiological data cannot be expected in the near future. The discussed methods allow to work within a very narrow, specialized problem domain and fundamental difficulties have to be expected if trying to establish more generic platforms. The practically justifiable number of examples in the training sets can only cover very limited variations of the anatomy and usually only applied today to analyzing images without large pathological changes (which is still very relevant in many clinical applications such as radiotherapy planning or psychiatric studies). It still needs a long way to go, before the computer representation and usage of the prior knowledge involved in the interpretation of radiological images can be represented and used in a computer in complexity which is sufficient to reasonably imitate the everyday work of an experienced clinical radiologist.

References

[1] R. Bajcsy and S. Kovacic. Multiresolution elastic matching. *Computer Vision, Graphics and Image Processing*, 46:1–21, 1989.

[2] A. Blake and A. Zisserman. *Visual Reconstruction.* MIT Press, 1987.

[3] F.L. Bookstein. Shape and the Information in Medical Images: A Decade of the Morphometric Synthesis. *Computer Vision and Image Understanding*, 66(2):97–118, May 1997.

[4] C. Brechbühler, G. Gerig, and O. Kübler. Parametrization of closed surfaces for 3-D shape description. *CVGIP: Image Understanding*, 61:154–170, 1995.

[5] G.E. Christensen, M.I. Miller, and M.W. Vannier. Individualizing neuroanatomical alases using a massively parallel computer. *Computer*, pages 32–38, January 1996.

[6] T. F. Cootes, C. J. Taylor, D. H. Cooper, and J. Graham. Active Shape Models - Their Training and Application. *Computer Vision and Image Understanding*, 61(1):38–59, 1995.

[7] T.F. Cootes, D.H. Cooper, C.J. Taylor, and J.. Graham. Training Models of Shape from Sets of Examples. In *British Mach. Vision Conf.*, pages 9–18. Springer-Verlag, 1992.

[8] T.F. Cootes, G.J. Edwards, and C.J. Taylor. Active appearance models. In *Proc. of the European Conference on Computer Vision*, volume 2, pages 484–498. Springer-Verlag, 1998.

[9] R.O. Duda and P.E. Hart. *Pattern Classification and Scene Analysis.* John Wiley & Sons, 1973.

[10] A.C. Evans, M. Kamber, D.L. Collins, and D. MacDonald. An MRI-based Probabilistic Atlas of Neuroanatomy. In S.D. Shorvon, editor, *Magnetic Resonance Scanning and Epilepsy*, pages 263–274. Plenum Press, New York, 1994.

[11] G. Gerig, O. Kübler, R. Kikinis, and F.A. Jolesz. Nonlinear anisotropic filtering of mri data. *IEEE Trans. Med. Imaging*, 11(2):221–232, June 1992.

[12] G. Gerig, J. Martin, R. Kikinis, O. Kübler, M. Shenton, and F. Jolesz. Automatic Segmentation of Dual-Echo MR Head Data. In *IPMI'91*, pages 175–187. Wye, GB, 1991.

[13] R. Guillemaud and M. Brady. Estimating the bias field of mr images. *IEEE Trans. Med. Imaging*, 16(3):238–251, June 1997.

[14] Serra J. *Image Analysis and Mathematical Morphology.* Academic Press, 1982.

[15] A. Kelemen, G. Székely, and G. Gerig. Elastic model-based segmentation of 3-d neuroradiological data sets. *IEEE Trans. Medical Imaging*, in press.

[16] F. Kruggel and G. Lohmann. Automatical Adaption of the Stereotactical Coordinate System in Brain MRI Datasets. In *Information Processing in Medical Imaging*, pages 471–476. Sringer, June 1997.

[17] T. McInerney and D. Terzopoulos. Deformable models in medical image analysis: a survey. *Medical Image Analysis*, 1(2):91–108, 1996.

[18] S.P. Raya. Low-Level Segmentation of 3-D Magnetic Resonance Brain Images – A Rule-Based System. *IEEE Trans. on Medical Imaging*, 9(3):327–337, September 1990.

[19] L.H. Staib and J.S. Duncan. Boundary Finding with Parametrically Deformable Models. *IEEE Transactions on Pattern Analysis and Machine Intelligece*, 14(11):1061–1075, November 1992.

[20] L.H. Staib and J.S. Duncan. Model-based Deformable Surface Finding for Medical Images. *IEEE Transactions on Medical Imaging*, 15(5):1–12, October 1996.

[21] S.A. Stansfield. ANGY: A Rule-Based System for Automatic Segmentation of Coronary Vessels From Digital Subtracted Angiograms. *IEEE Trans. on Pattern Analysis and Machine Intelligence*, 8(2):188–199, 1986. March.

[22] G. Székely, A. Kelemen, Ch. Brechbühler, and G. Gerig. Segmentation of 2-D and 3-D objects from MRI volume data using constrained elastic deformations of flexible Fourier contour and surface models. *Medical Image Analysis*, 1(1):19 – 34, 1996.

[23] D. Terzopoulos and D. Metaxas. Dynamic 3D Models with Local and Global Deformations: Deformable Superquadrics. *IEEE PAMI*, 13(7):703–714, 1991.

[24] K. Van Leemput, F. Maes, F. Bello, D. Vandermeulen, A. Colchester, and P. Suetens. Automated segmentation of ms lesions from multi-channel mr images. In Ch. Taylor and A. Colchester, editors, *Proc. Second Int. Conf. on Medical Image Computing and Computer-Assisted Interventions, MICCAI'99*, volume 1679 of *Lecture Notes in Comp. Sci.*, pages 11–21. Springer-Verlag, 1999.

[25] B.C. Vemuri and A. Radisavljevic. Multiresolution Stochastic Hybrid Shape Models with Fractal Priors. *ACM Trans. Graphics*, 13(2):177–200, 1994.

[26] W.M. Wells, W.E.L. Grimson, R. Kikinis, and F.A. Jolesz. Adaptive segmentation of mri data. *IEEE Trans. Med. Imaging*, 15(4):429–443, August 1996.