

# Feature Extraction, Shape Fitting and Image Segmentation

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These notes cover Part I of Session 3: Segmentation and Volume Measurement.

## ***Introduction***

This lecture covers the related topics of feature extraction, shape fitting and image segmentation. Just about all quantitative analysis of medical images requires some form of segmentation or feature extraction. Segmentation [3] [12] [13] distinguishes structures, regions or tissue classes of interest from other detail in the images. Feature extraction can be used to identify specific structures (e.g. points, blobs, curves, edges, surfaces etc) which often have biological importance e.g. organ or lesion boundaries, vessels etc. Some techniques begin with feature extraction to identify points of interest then build a generic shape model using those features as a reference and finally use the fitted shape model to perform image segmentation on new (i.e. previously unseen) images. Once structures are labelled, quantitative information about volume or shape can be extracted and comparisons can be made. The most common useful comparisons are in the same subject over time (e.g. to track growth) or between groups of subjects (e.g. to identify systematic structural brain differences between two groups of subjects who might score differently in psychological testing).

I will first briefly review some segmentation techniques that can be applied to distinguish tissue classes and then focus on methods of fitting shapes to medical images that include some knowledge of either the image properties or the population variation of the structure, or both. These methods are generically known as deformable models. A somewhat artificial division can be drawn between geometric deformable models and statistical shape models. The former are geometric models that evolve to match an instance of a structure. The evolution is driven by forces that are typically functions of the local image environment and constrained by prior knowledge often in the form of simple geometric constraints. Statistical shape models inherently require training data and produce compact representations of structural variation across a population. A wide range of plausible structure can be generated by varying a small number of parameters, resulting in an efficient optimisation task when fitting to new data.

There has been a vast amount of research in all the methods mentioned in these notes and to do justice to these topics would require a book. Therefore please use this material as pointers to further reading rather than a definitive account. Errors and omissions are my responsibility.

## ***I Tissue Segmentation Methods: A Brief Overview***

The properties of MR images have a strong influence on the usefulness of specific segmentation methods. Classical segmentation methods attempt to partition an image optimally into a number of regions that each satisfy some intensity uniformity constraint. In the ideal case, the resulting regions are meaningful and contain distinct sets of pixels. In MR images two important confounding factors complicate matters. First, intensity inhomogeneity [16] [17] can cause a variation in intensity of a particular tissue across the field of view, and second, the intensity of a single voxel

may be composed of signal from more than one distinct tissue type (i.e. the so-called partial volume effect where a voxel lies across a tissue boundary). Partial volume effects are inherent in MR and are particularly common when acquisitions have relatively high in-plane resolution and low thru-plane resolution (i.e. thick slices). One common example of partial volume effect is in classification of brain-tissue into grey-matter, white-matter and CSF in T1-weighted images. Partial volume effects between white-matter (bright) and ventricular CSF (dark) result in voxels with an inbetween intensity which are then misclassified as grey matter.

The most basic tissue-segmentation method is global intensity thresholding. This assumes a voxel intensity can be identified which assigns each voxel into a background class (voxels less intense than the threshold) or a foreground class (voxels more intense than the threshold). Selection of a global threshold may be done in several ways [22] and may not be appropriate in MR images due to intensity inhomogeneity. It may be possible to correct such intensity variation prior to segmentation. An alternative approach is to use local (adaptive) thresholding where the intensity threshold is variable and is computed over sub-images or over a region of interest around each voxel.

A slightly more sophisticated approach involves intensity-moderated region growing. Here a seed voxel is identified and an intensity uniformity constraint is set. Then all voxels around the seed are examined to see if their intensities are sufficiently similar to those already in the region. Those that satisfy the uniformity constraint are added to the region and then all their neighbours are examined and so on (e.g. [1]). Clearly the same caveats associated with intensity variation apply here too and if the initial constraint is too loose, it is common for the growing region to “escape” and label a much larger set of voxels than was intended. Different seed voxel positions may not result in the same generated regions. There are many ways for the constraints on region growth to be defined and the potential for human operators to intervene in the process e.g. by manually masking parts of the image to prevent region growth. It is also possible to start with a loose uniformity constraint and then to subdivide a single large region into multiple smaller ones by tightening the constraint.

Watershed methods [20] regard the grey-level intensities of an image as a set of topographic heights. An immersion model is one where the local intensity minima are considered to have holes in them and the image is “lowered” into liquid. As the liquid level rises, lakes form. Adjacent lakes separated by ridges may merge as the level rises further; at this point boundaries can be placed to prevent this merging and form a segmentation of separated regions. One common problem is over-segmentation where many small not very meaningful regions are generated. Therefore a region merge step is often required to create more meaningful larger regions. Sijbers et al [15] apply this approach to a voxel intensity gradient magnitude image and demonstrate its use in the segmentation of the cerebellum from 3D MR of the mouse brain. Rettman et al [14] use watershed methods to segment the sulcal region in humans. Grau et al [8] attempt to overcome some known problems of watershed algorithms (e.g. noise sensitivity and poor segmentation of very thin or low signal to noise structures) by introducing prior probabilistic knowledge. They demonstrate their approach on segmentation of knee cartilage and grey/white matter in MR images.

A general approach is to take advantage of multiple image acquisitions – the most common is T1, T2 and PD-weighted - and use multi-spectral methods. By considering the intensities from corresponding voxels as coordinates in an intensity space, clustering techniques can be applied to determine rules for segmentation of structures or tissues of interest. Many different approaches have been applied to this

clustering (e.g. artificial neural networks [9], k-nearest neighbours [6], k-means, fuzzy c-means [7] etc) but they all take advantage of multiple channels of data providing different information about the tissues.

A number of automated segmentation algorithms that account for the inhomogeneity as part of the segmentation process have been developed. Wells et al [21] introduced “adaptive segmentation” where an Expectation Maximisation scheme is applied iteratively and alternates between two steps: E: estimate tissue class probabilities when bias field is known and M: estimate bias field when tissue class probabilities are known. Such approaches have proved highly successful and spawned many variants and improvements (e.g. [11] [23] and many more). These approaches have been applied to both multi-channel and single-channel data. More recently, more integrated approaches have been proposed. For instance Ashburner et al [2] combine image registration, tissue classification and bias correction into a unified model based on a mixture of Gaussians, Fischl et al model the effect of image acquisition parameters on tissue contrast properties for segmentation [7] and Chen et al [5] have looked at simultaneous segmentation and registration of contrast-enhanced breast MRI.

Finally it must be remembered that changes in MR technology can affect quantitative analysis. For instance, much increased flow artefact has been observed in 3T brain acquisitions to the extent it dominates over noise in serial imaging [18]. More sophisticated segmentation techniques may be required to get the most out of these images.

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## II Geometric Deformable Models

The development of deformable models can be traced back to 1980's research in computer graphics and computer vision. One of the earliest and most well known deformable models is the active contour or "snake" [28] formed of connected spline segments. These models demonstrate most of the common principles of geometric deformable models and are usually posed as an energy minimization problem. The total energy of a snake can be written as follows:

$$E_{\text{snake}} = E_{\text{internal}} + E_{\text{external}} + E_{\text{constraints}}$$

$E_{\text{internal}}$  is an energy associated with bending or discontinuity in the snake and can be written as  $E_{\text{internal}} = \alpha E_{\text{tension}} + \beta E_{\text{curvature}}$ . The relative values of  $\alpha$  and  $\beta$  are crucial to the behaviour of the snake.  $E_{\text{external}}$  is derived from the action of forces that are functions of voxel intensity and typically attract the snake towards edges or lines.  $E_{\text{constraints}}$  are additional constraints. There is a contribution to each energy term from every point on the snake. Therefore the general form of the total energy is:

$$E_{\text{snake}} = \oint (E_{\text{internal}}(\mathbf{v}(s)) + E_{\text{external}}(\mathbf{v}(s)) + E_{\text{constraints}}(\mathbf{v}(s))) ds$$

where  $\mathbf{v}(s) = (x(s), y(s))$  specifies a point on the snake as a function of  $s$ , the arc length. The choice of energy minimisation strategy can have a large effect on snake performance. The original work used a variational approach implemented using gradient descent, but this proved sensitive to initialisation and image noise, and was susceptible to local minima because of the reliance on local information. Amini et al [24] suggested using dynamic programming resulting in a locally optimal contour at each iteration. Williams and Shah [35] proposed a fast greedy iterative algorithm that retained the advantages of the dynamic programming approach but was faster by an order of magnitude. Cohen and Cohen [27] took a different approach and suggested an additional energy term representing a "balloon" force that acted to steadily inflate (or deflate) the snake past weak edge features corresponding to local minima in the energy landscape. Staib and Duncan [33] build a parametric model from the elliptic Fourier decomposition of the object boundary, and bias the choice of shape during model fitting using probability distributions of the model parameters. An alternative formulation of the active contour is the discrete dynamic contour model [30] that defines the contour as a set of connected vertices that can be interacted with.

Xu et al [36] offered a solution to problems of boundary concavity associated with initialisation and poor convergence of conventional snakes. Their Gradient Vector Flow fields are non-conservative static external forces used to drive snakes. The GVF snake is insensitive to initialisation and can move into boundary concavities, unlike snakes driven by conservative external forces. The principal difference between GVF forces and traditional forces is that the latter can be written as the gradient of a static potential i.e. they are irrotational, but the GVF force has an additional solenoidal component and so is a general vector field in the Helmholtz sense. The GVF force reduces to the standard gradient of an edge map close to strong edges, but is interpolated from forces at the region boundaries away from strong edges "reflecting a kind of competition among the boundary vectors" [36].

Active contour methods are categorised by the use of parametric or implicit contour representations. Parametric representations specify the general class of contour in advance; examples include the original spline approaches, finite-element models [27] and analytical models such as super-quadratics [34]. Implicit representations lead to methods that can cope with topological changes. The most well

known implicit representations are snakes that use level-sets and, in particular, geodesic snakes. Implicit snakes define the evolving contour as the zero level set of a higher dimensional function (known as the embedding function). This approach allows topology changes of the snake while the embedding function remains well defined and extends naturally from contours to surfaces in higher dimensions. The original formulation of level-set snakes [25][31] could not be expressed as an energy minimization problem and therefore defining an appropriate stopping condition was difficult. Geodesic snakes introduce a modified distance measure that incorporates information about image gradient magnitude so that the level set evolves towards the appropriate minimum energy state [26] [29]. Geometric snakes [37] adopt an analogous approach. The appropriateness of the original formulations for complex medical images has been questioned [32].

Geometric deformable models in their pure form are still in use but there is a growing trend towards models that incorporate more specific prior knowledge about the expected variation of shape variation and image texture. These statistical shape models are described in the next section.

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### ***III Statistical Shape Models***

In contrast to the geometric deformable models described in the first section, statistical shape models use sets of well-characterised training data to learn about the shape of structures, their spatial relationships and (sometimes) their voxel intensity distribution. The goal is to build “generative” models where new realistic instances of shape data can be generated even when they are not explicitly represented in the training-set. Such models can be used to label previously unseen data and can make labelling algorithms robust to noisy or incomplete data. Two desirable properties of shape models are that they be both general and specific. Ideally, a general model is one that can generate all plausible instances of the structure it is modelling. A specific model is one that can only generate plausible instances of the structure. Statistical shape models aim to be both general and specific by capturing the variability of the training-set. In that regard, they can only be as general or specific as the training data so choice of training data is crucial to their success. Unlike the geometric deformable models considered above, considerable effort is often required to prepare annotated training data for use by statistical shape models. The other chief limitations are that the models cannot easily capture topology change and that the shape properties must be distinct enough to be described statistically. In practice this means that consistent features must be identified across the population.

Shape is usually defined as a property that is invariant to translation, rotation and scaling operations. The most common way to represent shape in statistical shape models is by a set of ordered landmarks defined in two or three dimensions [38]. Landmarks should always be defined at easily identifiable points in the images. In practice there are often too few well-defined points to fully capture the variability of a shape. Where there is a well-defined edge or surface connecting well-defined landmarks, additional landmarks can be placed at intervals between the original set. Obtaining ordered sets of corresponding landmarks can be difficult and tedious, especially for large studies and on 3D data. Two approaches for generating landmarks automatically have been proposed. The first [44] [47] uses an image (voxel) registration approach to find a dense set of correspondences between population images and a reference. Assuming the image registration is accurate (and this is by no means assured in general) then point correspondences are obtained automatically. The second approach [42] recasts the problem in terms of determining the set of shape parameterisations that result in the “best” model. Here “best” is defined as the Minimum Description Length model that is hypothesised to be the simplest (most compact, general and specific) model that accurately describes the data.

Once landmarks have been extracted for each subject in the training set a corresponding vector,  $\mathbf{x}$ , can be defined for each subject containing their landmark coordinates. For  $n$  landmarks the vector has  $2n$  entries in 2D ( $x$  and  $y$ ) and  $3n$  entries in 3D ( $x$ ,  $y$  and  $z$ ). The reason that statistical shape models work is that, in cases of interest, the coordinates of the  $n$  landmarks vary in a correlated way across the population. Building a statistical model of this variation allows the correlations inherent in the training data to be represented compactly. The first step is to remove differences between subjects that are due to translation and rotation (and sometimes, but not always, scaling). The second step is to compute the mean,  $\bar{\mathbf{x}}$ , and the covariance  $S$  of the training data. The third step is to use Principal Component Analysis (PCA) and compute the eigenvectors and eigenvalues of the covariance matrix. Each training example,  $\mathbf{x}$ , can then be approximated by a weighted linear

combination of the first  $m$  eigenvectors  $\mathbf{x} \approx \bar{\mathbf{x}} + \mathbf{b}\Phi$  where  $\mathbf{b}$  is an  $m$ -dimensional vector of weights and  $\Phi$  is a matrix containing the first  $m$  eigenvectors. This is an example of a Point Distribution Model (PDM). The more dependence there is between different coordinates in the training vector across the population, the smaller  $m$  needs to be to efficiently capture most of that variation. More explicitly, the eigenvalues associated with the eigenvectors in  $\Phi$  are the variance in the training-data in the direction of each eigenvector. Therefore  $m$  can be chosen to capture a given percentage (e.g. 95%) of the variance in the data. For a given  $\Phi$ ,  $\mathbf{b}$  can be varied to generate new instances of the shapes represented by the model that are not part of the training data.

The variation in shape is only one kind of variation that might be important in medical imaging; the variation in voxel-intensity within structures may also be of interest. The spatially correlated patterns of intensity variation constitute the “texture” associated with a structure. Statistical models of “appearance” are those that attempt to capture variation in both shape and texture. One approach is to first warp each training example to the mean shape (using knowledge of corresponding landmarks) so that the texture is not confounded by shape variation. Intensities are sampled from voxels in these normalised images and used to build a texture vector. This is analogous to the shape vector previously described, but instead of recording coordinates, we are now recording voxel intensities. Again however, we assume there will be consistent correlations in intensities from different voxels across the training set. It is important that the intensity distribution is consistent across the training set, so for medical images acquired on different scanners or with variable scanning conditions, some intensity normalisation may be required. PCA can be applied here too, to summarise the variation in texture in a compact manner. As before, a weighting vector fitting the model to each training example can be generated. As there may be correlations between shape and texture, it is possible to perform a further PCA on the set of combined weights resulting in a set of combined eigenvectors and eigenvalues that capture the correlation and relative contribution of shape and texture.

To be useful in a labelling or segmentation context we need a strategy for fitting shape and texture models to new (or “unseen”) data. The new data is not assumed to have any annotation – the usefulness of the statistical model is that new data can be labelled at low cost. The most intuitive approach is to define a function that measures the “goodness-of-fit” of the model to the new data. Then we can imagine varying the weighting parameters,  $\mathbf{b}$ , to generate new instances of the model in some systematic way to maximise the goodness-of-fit (or minimise the error). For the pure shape models, there are two main approaches. A simple geometric strategy is to apply an edge or boundary detector to the new data and obtain a set of candidate points on edges in the image. The mean distance between the model points and nearest edge points in the image can be used as an estimate of fitting error. An alternative approach is to look along normals to each model point at its currently estimated position in the new data. The strongest edge along each normal is chosen to be the next candidate model point. This latter approach is prone to failure but suggests a better strategy that has become known as the Active Shape Model (ASM) [39][40]. In the ASM, an intensity-normalised spatial derivative of voxel intensity is sampled along normals associated with each model point in each member of the training set. For each model-point, these are assumed distributed as a multi-variate Gaussian that can be summarised by its mean and variance. Then the quality of the fit of a candidate point to the model can be measured using the Mahalanobis distance, which is linearly related to the log probability that the new point is drawn from the

model distribution. Standard techniques such as multi-resolution searches are used for speed and robustness. To fit combined shape and texture models to unseen data requires a slightly different approach such as the so-called Active Appearance Model (AAM) [41]. In this case new instances of images can be generated using the Appearance Model and a measure of image similarity computed between the new data and the current instance. To solve this problem efficiently a pre-processing step is applied to learn the likely variation in model parameters that lead to good model fitting.

Statistical shape models can be constructed using different representations of the underlying shape. For instance, in [48] a coarse-scale medial [46] description derived from a fine-scale spherical harmonic boundary description is used and in [45] the vibration modes of a spherical deformable mesh are used. Principal Component Analysis is not always the most appropriate decomposition of variance due to linearity assumptions. Other approaches include Independent Component Analysis (e.g. [49]) and many different approaches collectively called non-linear PCA (e.g. [43]).

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## ***IV Applications Developments in Deformable Models***

A huge number of papers describe applications of deformable models or a range of improvements and variations on the standard approaches. We mention only a few in this section and point to some recent reviews [57] [58] [60] [62] [63] [65] [70] for the interested reader.

Many researchers have applied deformable surface models to extract representations of the cerebral cortex e.g. [54] [72] [73]. Ghanei et al [56] describe a deformable surface model for automatic prostate segmentation in ultrasound images. Shen and Davatzikos [68] extend the simple snake models to consider the local geometry around each contour point, the statistical confidence of the match and the energy along contour segments, rather than points, to improve robustness. Shen [69] extends this approach to measure the size and shape of hippocampi. Joshi et al [59] described a multi-scale Bayesian approach based on a medial representation where the parameter distributions naturally capture population variation and can describe localised growth and bending. Chan et al [53] combine elements of curve evolution, a Mumford-Shah segmentation functional and level sets to cope with noisy images or objects with very diffuse boundaries. Brock et al [51] describe a finite element based registration scheme that models multiple organs and can be used for image-guidance procedures and treatment planning. Deformable surfaces have also been used to segment time-series of 3D cardiac images [50] [64] [66] [67]. Active appearance models have also been applied to this problem [55]. A proposed two-stage segmentation of echocardiographic data uses registration of a voxel template to initialise a wire-frame mesh [74]. Deformable models have also been used to segment vascular structures in MR angiography [61] [71]. Active shape models have been extended for tubular structures by independently modelling axis deformation and cross-sectional deformation and by incorporating additional cylindrical deformation modes [52]

In summary, both geometric deformable models and statistical shape models are well-developed techniques that have been applied in a variety of situations and can be used in new segmentation applications. Work continues to improve these techniques and combine them to produce more robust and generic algorithms.

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