Multi-Modality Medical Image Segmentation

Segmentation is a common task in medical image analysis, and one which forms a basic component of many other algorithms, for example measurements of tissue volumes for tracking tumour growth or brain atrophy in dementing diseases. Many medical imaging modalities, including MR and CT. produce images in which the voxels representing each tissue can be described by a well-defined mean intensity, with some distribution due to noise and biological variability. Therefore, a model containing distributions (typically Gaussian) for each tissue present can be constructed and fitted to the intensity histogram of the image, thus identifying the tissue to which each voxel belongs and performing segmentation. Segmentation algorithms of this type have the added advantage that the intensity histogram can easily be extended to contain data from multiple images of the same region by adding each image as a separate dimension. This allows the segmentation of multi-modality image data. However, the model must also take account of the partial volume effect i.e. the presence of voxels containing more than one type of tissue. This effect produces uniform distributions between the pure tissue distributions for each pair of pure tissues that share a common boundary. Therefore, situations may arise where a pure tissue has a mean grey level that lies between two other pure tissues that produce partial volume voxels, leading to ambiguity between partial volume and pure tissue intensities.

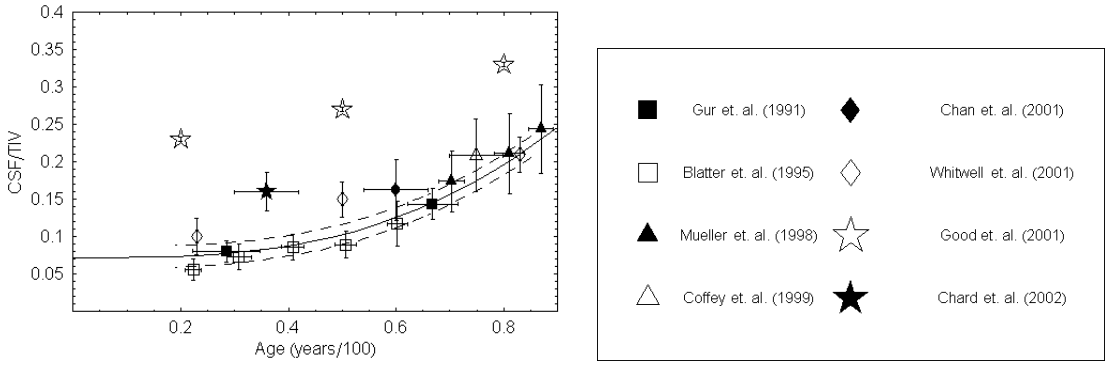
The medical image segmentation algorithm implemented in TINA allows the segmentation of data of arbitrary dimensionality, and allows the user to specify which tissues are present within an image, and which are allowed to produce partial volume distributions. Pure tissues are modelled using Gaussian distributions, and partial volume contributions are modelled as uniform distributions convolved with Gaussians. However, the histogram is built from image gradients as well as image intensities. This disambiguates partial volume and pure tissue contributions, as partial volume voxels occur at boundaries between pairs of tissues i.e. positions of high image gradient. An outlier class is also included to account for pathological tissues. The model is fitted to the image using the expectation-maximisation algorithm, identifying the most likely tissue volume contribution to each voxel.

In order to compare the TINA medical image segmentation algorithm to other techniques, a meta-study on cerebro-spinal fluid (CSF) volume measurements was performed. This application was chosen due to its clinical relevance (measurement of cerebral atrophy due to dementing diseases) and the availability of previous measurements produced using a variety of techniques. Inversion-recovery turbo-spin echo (IRTSE) images were acquired from 70 healthy controls (32 male and 38 female) ranging in age from 19 to 85 years with a mean age of 57 ± 20 years. The TINA medical image segmentation algorithm was applied to measure the CSF volume, which was normalised to the total intracranial volume (measured using the same technique) to account for differences in head size. Eight papers published between 1991 and 2002, which quoted CSF and total intracranial volume measurements from MR images in normal subjects, were then collected. These previous studies used a variety of MR pulse sequences, definitions of the measurement space, and segmentation routines, summarised in Table 1. Therefore, exact agreement between the various data should not be expected: instead, the results are expected to lie on a set of approximately parallel curves, indicating the variation in the volume measurement introduced by the various experimental procedures.

Reference	No. subjects	Definition of measurement space	Segmentation
Gur et. al. 1991 [6]	69 T	Excludes cerebellum	T2/PD 2D histogram fitting
Blatter et. al. 1995 [1]	89 M 105 F	TIV	ANALYZE
Mueller et. al. 1998 [7]	46 T	Excludes brainstem	REGION
Coffey et. al. 1999 [4]	122 M 198 F	Excludes slices below midbrain	MedVision
Chan et. al. 2001 [2]	10 T	TIV	MIDAS
Whitwell et. al. 2001 [8]	55 T	Excludes slices below cerebellum	MIDAS
Good. et. al. 2001 [5]	265 M 200 F	TIV	SPM99
Chard et. al. 2002 [3]	13 M 14 F	Excludes slices containing cerebellum	SPM99

Table 4: Details of the experimental method adopted by studies used in the meta-study, showing the number of subjects included (M=male; F=female; T=total, where the number of each sex was not given), the definition of the measurement space (where TIV is indicated, the whole CSF pool inside the cranium was used), and the software used to perform the segmentation.

Fig. 1 shows the meta-study results. Most of the data show a remarkable level of consistency with each other and with the functional fits to our own data, considering the variations in the experimental procedures. Indirectly, this implies that across these studies as a whole, the variations in volume measurements introduced by the different



(a)

Figure 1: Previous published TIV normalised CSF volume measurements. The solid curves show functional fits to our own data: the dashed curves are the upper and lower 1σ error bounds. The points show data from the literature. Points with error bars in both the x and y directions represent data published numerically, whilst points with error bars only in the y direction represent data read from graphs.

experimental procedures are comparable to or smaller than the inherent biological variability in total intracranial and CSF volumes. Some outliers are present, representing the results published in [5] and [3], both of which used SPM'99 to perform the segmentation. Significantly higher CSF volumes were quoted by these authors than are supported by the rest of the literature. However, the magnitude of the disagreement with the rest of the literature, particularly in the case of [5], is too great to explain as genuine measurements of unexpectedly high CSF volumes. It seems more plausible that these results represent methodological flaws in the studies concerned. Therefore, we conclude that the TINA medical image segmentation algorithm produces results that are at least as accurate as, and in some cases more accurate than, the algorithms presented in the literature.

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