The Estimation of Fetal Organ Volume Using Statistical Shape Analysis.

C F Ruff[1], A Bhalerao[2], S W Hughes[2], T J D'Arcy[3], D J Hawkes[1]

Division of Radiological Sciences[1], United Medical and Dental Schools of Guy's and St Thomas' Hospitals.
Departments of Medical Physics[2], Obstetrics & Gynaecology[3], Guy's and St Thomas' Hospital Trust, London, SE1 7EH, UK.

1. SUMMARY

For many years fetal weight has been determined from regression analysis using biometric measurements. From these measurements pregnancies have been assessed and clinically evaluated to improve perinatal outcome. Examination of growth retarded babies have shown significant changes in the weight of organs such as the thymus, spleen, liver and kidneys. Ultrasound examination is the usual modality of choice for fetal imaging, but conventional ultrasound is a 2D imaging modality, lacking the positional information necessary for the reconstruction of 3D shapes.

Different organs have different 3D shapes and the similarity in individual shapes helps identify that particular organ. In most instances, normal growth results in an increase in size with general preservation of shape. In this work we describe a method of capturing the normal range of variation in shape exhibited in fetal livers, using a form of statistical shape analysis known as the Point Distribution Model (PDM). We then show how it can then be used to estimate the volumes of fetal livers from a limited number of measurements, with a view to using the model to interpolate between ultrasound images to provide a measure of volume.

2. INTRODUCTION

The shape of an anatomical organ such as the heart, kidney or liver, and in particular its change in size and shape over time is an important indicator of function. Volume reflects change in 3D shape and summarises multidimensional variation as a single number, and is the most commonly used clinical measure of shape. For many years fetal weight has been derived from biometric measurements, and used to assess and clinically evaluate pregnancies to improve

perinatal outcome. The hypothesis for such studies is that change in volume over time will follow some normal growth curve. Abnormal growth, i.e. an organ volume outside the range considered normal for a given stage in pregnancy, may suggest developmental problems requiring a different management strategy. However, there are problems with such an approach due to the simplicity of the shape models used and the coarseness of the volume estimation measure.

Global parameters such as fetal weight and volume are determined using models based on the combined measurements of head circumference, abdominal circumference and femur length [1-3]. In turn fetal growth retardation is defined as a measured weight less than the 10th, 5th or 3rd centile for gestation. This current definition of growth retardation is now regarded as unsatisfactory by its failure to identify those fetuses that are nutritionally deprived and truly growth retarded. The organ volume of malnourished infants are less than those of normal healthy infants, in particular the liver spleen thymus and kidneys. Volumetric measurements of intra-abdominal organs such as spleen and kidney are estimated using formulae based on ellipsoids and spheres [4,5]. To improve these measurements would require either multiple images that fully sample the organ being measured, or a more complex shape model that can be fitted to a smaller set of images in order to more accurately estimate volume.

3. THE POINT DISTRIBUTION MODEL (PDM)

The PDM is a form of statistical shape modelling that has been shown to be a robust method for capturing the variation in shape exhibited by a set of example shapes [6], often referred to as the *training set*. To build the model we must first identify a number of labelled points, that can be reproducibly located on each example shape. Although each point needs to be labelled - that is, it has to be defined at the same location on each image - not all the points need to be significant geometric or anatomical features. First, a number of key anatomical or topological points are identified, and then the rest of the shape is labelled by interpolating between these points along the surface or boundary of the example shape. The shapes are then registered and transformed to a common coordinate system, and a mean shape is calculated as the mean position of each of the labelled points. This mean shape is then subtracted from the example shapes, and a covariance matrix is constructed [7].

Eigenvector analysis is then performed on the covariance matrix giving N eigenvectors and their associated eigenvalues, where N is equal to the number of points marked multiplied by the number of dimensions the shape occupies. The eigenvectors are principle components of the given shape distribution, and are of the form of a list of the deviations in the point locations from their mean positions for each independent mode of variation. The eigenvalues are the variances associated with each mode of variation, as exhibited in the training set. In geometric terms the eigenvectors form the principle axes of the hyper-ellipse that encloses the set of shape vectors.

3.1. Construction of the Shape Space

The resultant modes of variation, represented by the eigenvectors, form an orthogonal set. We can, therefore, construct a shape space with each eigenvector representing an axis. Initially there are N eigenvectors giving an N-dimensional space, with each dimension having the range of ±∞. This shape space encompasses all the possible shapes that can be defined with the number of points used. However, not all eigenvectors have significant eigenvalues, so we can limit the dimensionality of the shape space by rejecting axes corresponding to low significance eigenvalues, and keeping only the most significant eigenvectors, the sum of whose eigenvalues encompass a set percentage of the total variance described by the model, usually 95%, 99% or 99.9%. Furthermore, we can limit the extent of the remaining axes based on their associated eigenvalues. The resultant shape space is now restricted to an n-dimensional hyper-ellipse that describes only those shapes that conform to the "rules" exhibited in the training set, where n is the number of significant modes of variation produced in the model.

3.2. Shape Reconstruction

Any of the example shapes, and indeed any allowable shape contained within the shape space described by the model can now be reconstructed by adding weighted amounts of each eigenvector to the mean shape;

$$S = \bar{S} + \sum_{i=1}^{N} w_i E_i$$

Where $\bar{S}$ is the mean shape, and w_i is the weight applied to the ith eigenvector E_i.

The model can therefore be used to fully reconstruct a 3D shape from a limited number of measurements, by calculating the values of the weighting factors associated with each mode of variation, that provide the best fit of the model to the given data.

4. METHOD

10 cadaveric fetal livers, chosen from fetuses with normal organ structure and development, were scanned in a Magnetic Resonance (MR) scanner with a voxel resolution of 0.7 x 0.7 x 1.5 mm. The livers were segmented by thresholding the images, and then registered to a common coordinate system by identifying three distinct points in 3D. These points were chosen as the end points of the two lateral lobes, marked A and B in figure 1, and the upper apex of the "dome" of each liver, marked as point C.

Next, the data was re-sliced parallel to the axis AB to give 25 slices. The surface of the liver on each slice was then delineated and marked with ten points equally distributed around the slice contour, giving 250 (x,y,z) triplets for each liver.
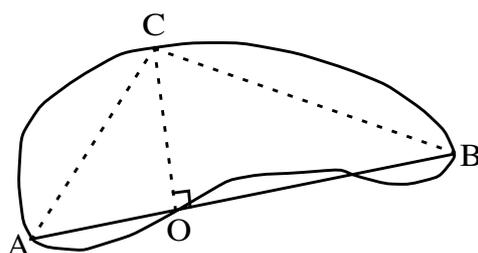
Figure 1. Section through a liver showing the 3D points used to register the individual livers.

Liver volumes were calculated using the 250 points by determining the slice area bounded by the slice contour, and multiplying by the slice thickness, given by the length AB divided by 25. The slice area was approximated by calculating the sum of the set of triangles formed by joining each of the points on a slice.

A PDM was then constructed using all 10 of the test shapes, and a further 10 models were constructed from subsets of 9 of the example shapes, with each shape being excluded from the model in turn. The utility of the models produced was tested by simulating poorly sampled data by excluding all but 3 of the original slices on each shape, and then finding the best fit of both the full PDM and the model built without using the relevant shape. The slices used for the reconstruction test were the 3rd, 13th an 22nd slices from the set of 25.

5. RESULTS

Table 1 shows the relative importance of each of the modes of variation for the full model. Figure 2 shows the effects of applying an amount equivalent to one standard deviation of mode 0 to the mean shape. Mode 0 can be seen to be

Table 1: Relative importance of the modes of variation of the full PDM, total variance (4338.78).

Mode	Variance	Percentage
0	1160.98	26.76
1	1126.55	25.96
2	719.42	16.58
3	506.11	11.66
4	272.10	6.27
5	230.58	5.31
6	131.78	3.04
7	122.37	2.82

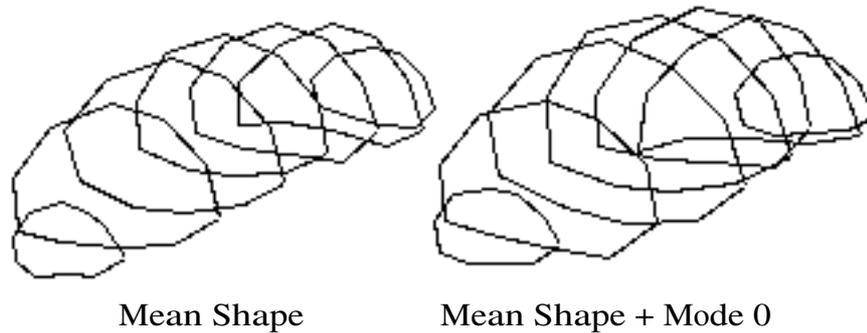Mean Shape   Mean Shape + Mode 0

Figure 2. Diagram showing the effect of adding 1 standard deviation of mode 0 to the mean shape.

primarily concerned with describing global scaling of the livers, giving a 29.63% increase in volume over the mean shape for the addition of one standard deviation of the mode to the mean. Subsequent modes are associated with more subtle shape changes, such as bending and twisting along the AB axis.

Table 2. shows the volumes calculated for each liver using the original shape description, and the reconstructions of the partial shapes using both the full PDM and the exclusive models.

Table 2: Volume calculations using PDM to reconstruct poorly sampled shapes, (all volumes are in cc).

Liver	Original Volume	Full PDM reconstruction	Partial PDM reconstruction
1	14.61	14.61	16.52
2	20.84	20.83	21.62
3	29.95	29.95	26.56
4	27.25	27.25	22.46
5	32.49	32.48	28.55
6	14.01	14.01	14.46
7	19.87	19.87	21.25
8	19.11	19.11	18.88
9	12.17	12.17	13.51
10	20.87	20.87	20.99

6. DISCUSSION

This paper has looked at the practicalities of performing multi-variate statistical analysis, in the form of PDMs, on 3D images of fetal livers. The main aim of this work was to assess whether PDMs can capture the normal range of shape associated with fetal livers, and then to assess their use in predicting volume from a limited number of sections through the liver.

This work has shown that PDMs are powerful tools for capturing the multi-dimensional shape associated with fetal livers. Specifically, the livers which were modelled required only 8 significant modes of variation to describe 99.9% of the total variation in the training set, and thus enabled shapes to be accurately reconstructed from as few as 3 slices. The aim is to extend this work to use data collected from an ultrasound scanner, connected to a locating device, to provide the necessary positional information between slices.

7. REFERENCES

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