Combined x-ray interaction data for biological tissue classification
A preliminary analysis of data.

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Introduction and Aim

The aim of this piece of work was to carry out a feasibility study on liver tissue classification using our proposed x-ray interaction techniques. The experiment consisted of carrying out the collection of diffraction data, then collecting Compton scatter and XRF data together. Due to the very large flux of x-rays we were able to get very good counting statistics for each sample in less than one hour.

Objectives

- To collect diffraction spectra, XRF spectra and Compton Scatter spectra for 60 liver samples.
- To collect Compton spectra from 5 electron density calibration solutions.
- To measure the linear attenuation coefficients of all 60 samples.

All but the attenuation measurements were successfully carried out in the time available.

Methodology

The samples were 30 matched pairs of liver each pair consisting of a sample of secondary colorectal liver cancer and a piece of tissue taken at a distance from the cancer in the same liver. This piece of tissue was classified as normal. Once back in the UK histopathology analysis undertaken.

Results *Diffraction data.*

Figure 1 below shows the average diffraction data for the normal samples and tumour samples. It can clearly be seen that between scatter angles 5 degrees to approximately 20 degrees there is a difference in the intensity of the signal. After this the response is the same. The increase seems to be centred around a scatter angle of 12-13 degrees. This is the value for the response from adipose (fat) tissue. This would indicate that tumour tissue has a decreased level of fat tissue compared to that of the normal tissue in the same liver. In order to estimate the ability of this data alone to predict tissue types, principal component analysis was carried out. The results on all the samples is shown in figure 2. There is a clear grouping of tissue types distinguished easily by 2 principal components.

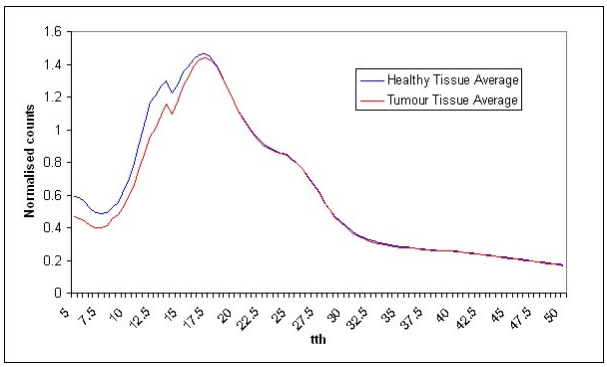


Figure 1 : Averaged normal and averaged tumour response.

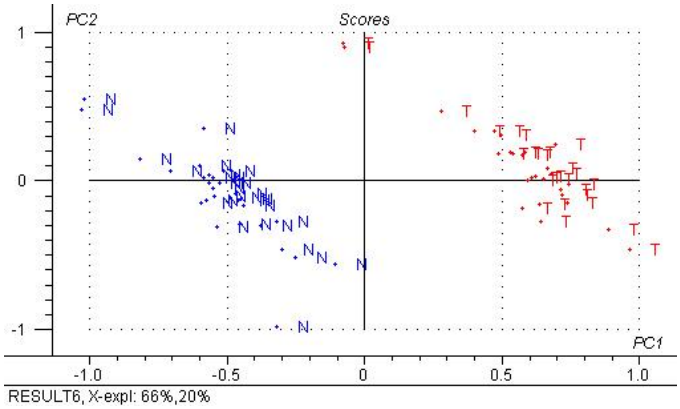
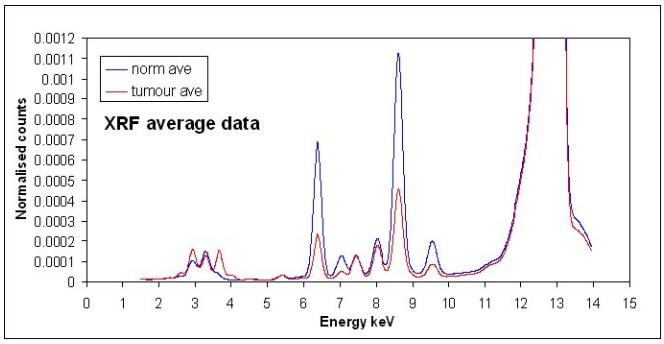


Figure 2 : PCA analysis (with outlier excluded.)

Results *XRF (Elemental analysis) data.*

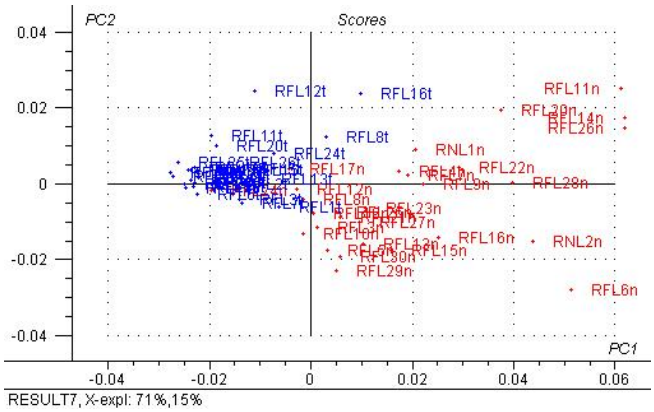
Figure 3 shows the average XRF spectra for the normal and the tumour samples.

The peaks from left to right represent the presence of ;
Chlorine (CL) energy approximately 2.6 keV : Argon (Ar) energy approximately 2.9 keV (argon comes from ionisation of the air) : Potassium (K) energy approximately 3.2 keV : Calcium (Ca) energy approximately 3.6 keV : Iron (Fe) energy approximately 6.4 and 6.9 keV : Nickel (Ni) energy approximately 7.5 keV : Copper (Cu) energy approximately 8 keV : Zinc (Zn) energy approximately 8.6 and 9.5 keV



From previous work on breast tissue and the advice of our clinical collaborators, the elements of interest in this study are potassium, iron, copper and zinc.

Figure 3 : Averaged spectra for normal and tumour samples.



In order to see how this parameter in isolation could be used as a tissue predictor, PCA was carried out. Figure 4 shows the results.

Figure 4 : PCA grouping of classifications can be seen in PC1

Results *Compton Scatter (electron density) data.*

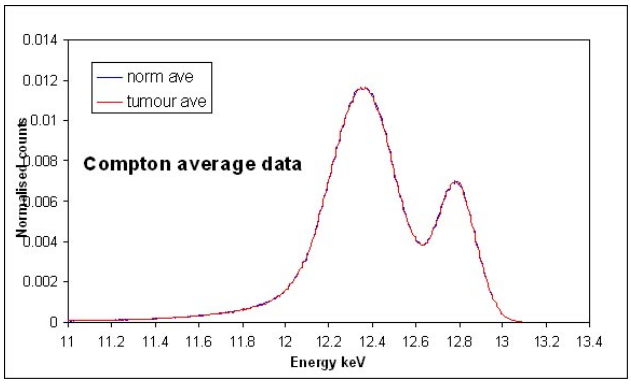


Figure 5 shows the average response for half of matched pairs. It can be seen that there appears to be no difference in this measurement at all between the normal and tumour samples.

Figure 5 : Averaged Compton scatter response for half the normal and tumour samples

Multi-parameter modelling.
The diffraction data and the xrf data were combined in two simple ways in order to see how they performed as a tissue predictor. It must be noted that in the time available these models are on data that has has little or no post processing. (A subset of 5 normals and 5 tumours were used at test objects.)

The model in figure 6 used fitted peak data from the XRF measurements and a simple summation of a region of the diffraction data as well as the physical density of the sample as an additional variable. In this particular representation all samples should ideally have a value of 1.

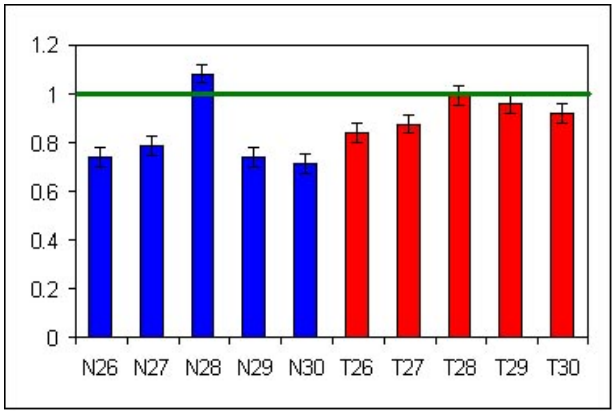


Figure 6 : Predictions for 5 normal and 5 tumour samples. All samples should ideally have a value of 1

Comments.
This report shows the ***preliminary*** analysis of the data obtained at the ESRF on liver samples. It can be clearly seen that the measurement parameters appear to offer tissue classification abilities. The data needs much closer inspection before the full potential of these results is seen. One important consideration is the presence of certain outliers within the sample population. The PCA analysis did pick these out and they have been removed in the above figures.. However histopathology reports have shown that 1 sample matched pair was classified the wrong way round and a further 3 samples were necrotic tissue which could not be used.