Texture Analysis Parameters and the Point Spread Function

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Introduction: Texture analysis is becoming increasing used in MRI to distinguish types of tissue and aid diagnosis (1, 2). The benefits of texture analysis are that it is easy to implement, can be applied to any image or parameter map and does not depend on complicated pulse programming. However the texture parameter values (TP) obtained will be dependent on the type of image acquired, and, as it is basically a series of parameters describing various details of the distribution of grey levels within the image, any change in the acquisition may alter the values seen. The point spread function (PSF) describes the spread of signal from a voxel, which should theoretically be an impulse function. This will affect the TP as it often spreads into neighbouring pixels causing a modulation of the signal seen; hence altering the relationship between these pixels. The PSF differs between the phase and frequency encoding directions, so in certain - admittedly rare - circumstances such as thin lesions being perpendicular to each other and aligned with the x- and y- axes of the image differences might be seen in TP which should be identical. The purpose of this work is to investigate this effect and assess the magnitude of any changes to the TP.

Methods: The 14 texture parameters described by Haralick (3) were used to investigate the problem; these are derived from the grey level co-occurrence matrix which is effectively a 2D histogram of the pair of grey levels of two pixels at various distances and directions and includes quantities such as entropy and variance. For this work only the 8 in-plane nearest neighbours were used to calculate the TP values, as is generally used in MRI studies (1) with thick slices. The number of grey levels in the images was reduced and standardised to 128. Images were acquired using a uniform spherical spectroscopy phantom filled with metabolites in solution (SP), a commercial geometric distortion phantom containing structured elements (GP) and 2 healthy human subjects (HS). Imaging was performed on a Signa Excite 1.5 T scanner (GEMS, Milwaukee, WI, USA). The sequences used were axial a) Spin-echo (TE/TR = 20/540 ms, FOV = 24x24 cm, 1 NEX, matrix = 256x256, slice thickness = 5 mm), b) EPI (4 shot, TE/TR = 35/1000 ms, FOV = 30x30 cm, 4 NEX, matrix = 128x128, slice thickness = 5 mm). Each of these sequences was performed four times on each subject with the phase encoding direction varied in an interleaved manner. For the human images the brain was extracted from the skull using bet, part of the FSL package (4). A number of values were then calculated for each image a) TP values from the whole image, b) TP values for the rows and columns of each image separately c) the difference between the row and column TP values. From these a number of other values were computed, a) the mean and SD for all 4 image sets of the same sequence and object, b) the mean, difference and SD for the two pairs of images with the same phase encoding direction, c) the difference in mean between the two pairs, d) the ratio of this difference to i) the average difference of the two pairs, ii) the means of the two pairs and iii) the mean and SD of all 4 images of the same type. These figures allow assessment of whether the phase encoding direction has an effect on the TP values obtained, whether any difference is significant in terms of the magnitude of the TP values and whether the object studied has an effect on the results obtained.

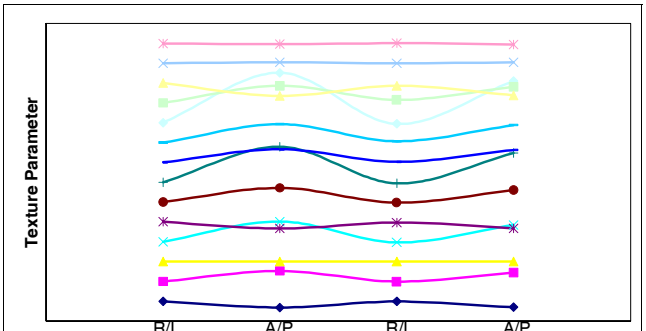

Figure 1

Results: Figure 1 shows the TP values for the SP for the four runs of the SE sequence normalised so that they appear on a similar scale and are all visible. As can be seen the TP values appear to vary as the phase encoding direction is changed. A similar pattern can be seen in the difference between the TP values obtained for the rows and columns and for the GP and to a lesser extent in the brain. In the brain some of the parameters followed this pattern while others did not and there was greater variability in the TP values produced from the sequences with the same phase encoding direction. Table 1 shows the ratio of the difference between the averages of the two pairs of observations to the average of the difference within each pair for each sequence and object, although a difference from 2 observations is not totally unreliable the fact that this ratio is >1 in the majority of cases indicates that the effect of the PSF is of a scale similar to if not greater than the reproducibility of the TP.

Discussion: The results show that the phase encoding direction, and by implication, the PSF affects the TP obtained from an object. This appears to apply to all objects, although it is more acute for objects which are not subject to effects such as motion and contain little native texture. It also appears that the EPI sequence is more susceptible to changes in the phase encoding direction than the SE sequence, this is not surprising, but implies that more care must be taken to preserve the encoding directions when using these sequences. Although this problem is unlikely to cause any serious effects it appears to cause differences in texture parameters of a scale similar to or greater than random noise. In practise it is unlikely that the phase encoding direction will differ between subjects in a study, however under certain circumstances it may be important. For example, when imaging, the phase encoding direction may be switched to avoid artefact or to avoid peripheral nerve stimulation. Also the TP values obtained from long thin objects which lie perpendicular to each other and parallel with one of the major imaging axes may have artefactual differences in texture.

	TP1	TP2	TP3	TP4	TP5	TP6	TP7	TP8	TP9	TP10	TP11	TP12	TP13	TP14
SP-SE	22.0	10.83	3.40	8.73	13.34	9.77	8.73	21.83	16.15	9.79	7.33	6.81	6.55	6.53
SP-EPI	133.7	15.83	34.42	11.35	27.27	22.86	11.32	70.68	51.21	16.16	21.66	11.83	175.3	74.31
GP-SE	7.27	1.94	9.98	12.91	6.225	2.41	13.21	6.42	6.13	2.38	5.12	5.48	5.11	10.80
GP-EPI	33.49	26.65	19.65	16.81	31.44	42.11	16.62	35.19	33.43	26.36	12.89	11.54	51.07	0.071
HS1-SE	1.36	0.97	2.05	1.07	1.44	1.70	1.08	1.33	1.34	0.81	1.29	1.33	1.26	8.72
HS1-EPI	3.18	0.10	16.91	2.87	1.72	0.97	3.06	4.51	3.25	0.16	1.027	14.59	14.51	16.54
HS2-SE	0.33	0.71	1.47	1.02	0.31	0.34	1.04	0.45	0.43	0.87	0.38	0.22	0.62	1.91
HS2-EPI	13.49	7.68	15.54	9.28	14.76	10.38	9.38	10.72	11.55	7.27	10.40	6.32	8.21	13.40

Table 1.

References and Acknowledgements: This work was funded by the Multiple Sclerosis society of Great Britain and Northern Ireland.

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