Texture Analysis of DCE Breast Imaging: Single slice vs. multi slice

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Introduction Textural analysis has recently shown positive results when utilised in MRI, particularly in the brain [1-3], but also in other organs such as the breast [4] wherein lesion morphology is known to be an important diagnostic and prognostic indicator [5]. The spatial grey-level dependence matrix method, as proposed by Haralick [6], appears to be the commonest form of analysis. We previously conducted a study to systematically assess the efficacy of DCE-MRI based textural analysis in predicting response to chemotherapy in a cohort of breast cancer patients and found significant differences for texture with respect to nodal status and partial responders vs. non responders [7]. This study aims to compare texture analysis on the same data cohort but using a single slice and single ROI to verify if texture analysis works best on multi or single slice MR images. If proven that single slice works just as well this would save processing time by 4 fold (17 minutes per patient down to 4 minutes) as well as a significant reduction in time taken to define the ROI.

Methods 100 patients were scanned on a 3.0T HDx scanner immediately prior to neo-adjuvant chemotherapy treatment. For all patients a 3D dynamic dataset was acquired using VIBRANT (FOV 20×20 cm, acquisition matrix 220×160, slice thickness 2 mm, 12 phases with average tdel=33.7 s, range 25.5-44.7 s) Malignant tissue ROIs were generated semi-automatically on all slices utilising early arterial phase data. Texture analysis was then performed on 2 minute post-contrast data. To prevent sparseness within subsequently calculated co-occurrence matrices the ROI data underwent grey level decimation via histogram equalisation. ROI data was reduced to 16 grey levels (reducing the number of grey levels improves SNR at the expense of discriminatory power). The same tests were repeated on single slice, single slices were selected on the basis of largest ROI from each selection of slices in an attempt to try and cover the largest possible cross sectional area of the lesion.

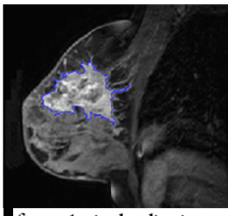
figure 1: single slice image

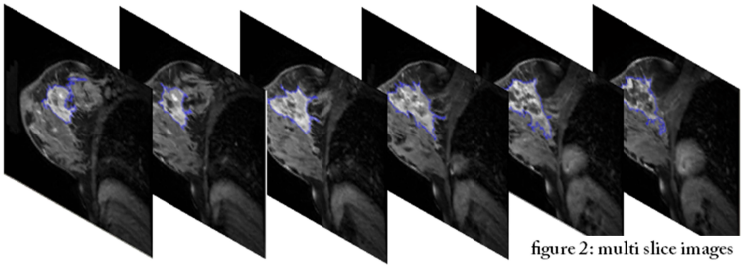
figure 2: multi slice images

Results Nodal status was determined in 91 patients (45 node –ve vs. 46 node +ve) and response data was available in 89 patients (40 partial responders vs. 49 non-responders). Regarding nodal status significant differences in f_6 (sum average) and f_{15} (cluster shade) were noted at 2 minutes post-contrast administration for 16 grey levels. Differences were noted between partial responders and non-responders for f_2 (contrast) and f_{10} (difference variance). The same tests were repeated for single slice ROIs and no significant differences in texture were seen for nodal status or partial responders vs. non responders data.

Multi slice: partial responders vs. non responders				**Single slice**: partial responders vs. non responders		
	PR (mean± sd)	NR (mean± sd)	*P value*	PR	NR	*P value*
f2 (contrast)	8.02±1.86	8.89±2.05	0.042	Median = 9.53 Range = 4.57 – 21.61	median = 9.56 Range = 2.19 – 23.12	0.908
f10 (difference (variance)	3.83±0.82	4.20±0.85	0.043	Median = 4.38 Range = 2.23 – 10.17	Median = 4.37 Range = 1.05 – 9.17	0.908

Table 1: PR vs. NR for multi slice (left) and single slice (right)

Multi slice: Nodal status				**Single slice**: Nodal status		
	Nodel+ve (mean± sd)	Node -ve (mean± sd)	*P value*	Node +ve	Node –ve	*P value*
f6 (sum average)	17.73 ± 0.32	17.58 ± 0.37	0.043	Median =17.66 Range= 16.62 – 18.22	Median= 17.57 Range= 16.46-18.89	0.468
f15 (cluster shade)	(-)63.23 ± 19.37	(-)51.05 ±32.13	0.031	Median= (-)49.37 Range= (-)102.79 – 31.70	Median= (-)41.42 Range= (-)122.82-69.11	0.704

Table 2: Nodal status (node +ve vs. node -ve) for multi slice (left) and single slice (right)

Discussion This work has highlighted that textural differences between groups (based on response or nodal status) are apparent at 2 minutes post-contrast administration. Significant differences in f_6 and f_{15} for nodal status, and f_2 and f_{10} for response, are observed when run on multi slice MR images, but when tested with single slice data no significant differences were observed. The study shows taking the largest cross sectional area does not necessarily mean it is biologically the most important region. Despite the reduction in processing time clearly with single slice texture mapping we lose counting statistics and important tumour information is missed. This justifies the use of multi slice data in textural analysis.

[1] PA Freeborough and NC Fox (1998) *IEEE Transactions in. Medical Imaging* 17:475-479. [2] V Kovalev *et al* (2001) *IEEE Transactions in Medical Imaging* 20:424-433. [3] D Mahmoud-Ghoniem *et al* (2003) *Magnetic Resonance Imaging* 21:983-987. [4] P Gibbs and LW Turnbull (2003) *Magnetic Resonance in Medicine* 50:92-98. [5] L Esserman *et al* (2001) *Annals of Surgical Oncology* 8:549-559. [6] RM Haralick (1979) *Proceedings of the IEEE* 67:786-804. [7] P Gibbs *et al* (2011) Proceedings of the 19th ISMRM Annual Meeting 1576.