

Minkowski Functionals in MRI: A new texture analysis tool in breast MRI

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TARGET AUDIENCE: Breast MR researchers: physicists and clinicians.

PURPOSE: Minkowski Functionals (MF) have been used as a method of texture analysis in CT for many years [1]. They can potentially provide a new way of observing and describing tumours in MRI, and may be useful as a diagnostic tool or as an input parameter of a predictive model of response [2].

METHODS: The patient cohort consisted of 100 cases (98 patients with two presenting bi-laterally), median age 48 years (31-77 years), all with biopsy confirmed breast cancers. MR scans were taken before neoadjuvant chemotherapy (NAC) began, using a dedicated 8-channel breast coil with a fat nulled Volume Imaging Breast Assessment (VIBRANT) sequence to produce sagittal images on a 3T HDx (GE Healthcare, Milwaukee, WI) scanner. Software was developed in house using MatLab (MathWorks, Natick, MA) to take images from the scans, segment the tumour using previously created ROIs, and threshold the resulting cropped images to 101 different threshold levels. Threshold levels ranged from 0.0 to 1.0 with the 0.0 and 1.0 set to the maximum and minimum pixel intensities, defined as the median of the top and bottom 1% of image pixel intensities respectively. All analysis was carried out on images taken at 1-min post contrast to give the largest tumour enhancement compared to background enhancement. Three MF values were calculated for each thresholded image representing area ($A = n_s$), perimeter ($U = -4n_p + 2n_e$), and Euler value ($\chi = n_p - n_e + n_v$), where n_s = number of white pixels, n_p = number of edges, and n_v = number of vertices. The area and perimeter values were standardised to represent a fraction of the largest values to remove bias created by size of tumour, whereas Euler value is unchanged as it is size independent. Analysis was conducted with a combination of MatLab and SPSS v.20 (Chicago, IL). Three 5th order polynomials were calculated for each patient describing the change in MF values as the threshold was raised. These 6 coefficients were then used to perform Mann-Whitney U-Tests looking for differences between patient sub-groups. Patients were split into sub groups based on biopsy grade (3 vs. all others), triple negative (TNEG) status (ER, PR, and HER2 negative vs. all others), lymphovascular invasion (positive vs. negative), and chemotherapy response (partial responder vs. non-responder) where response is determined as >50% reduction in longest diameter, and non-response as <50% reduction.

RESULTS: For analysis carried out with 101 levels of thresholding statistically significant differences ($p < 0.05$) were found between all patient sub-groups except partial-responders vs. non-responders. The highest number of differences were found between TNEG vs. Other patients (12/18), with all polynomial coefficients for area and Euler values resulting in statistical differences. Further, 11 of the 12 significant parameters for TNEG sub-groups resulted in p -values < 0.02 .

DISCUSSION: Minkowski Functionals have already proved themselves to be able to distinguish between image homogeneity and heterogeneity (an established marker of malignancy) [3, 4], and the results presented here suggest that they can also be used to identify between different cancer groups. Two-thirds of the parameters tested were found to be able to distinguish between TNEG patient groups, suggesting that MFs may be used as a poorer prognosis indicator.

CONCLUSION: This work demonstrates that Minkowski Functionals, as a form of texture analysis, can be used to distinguish between +/-ve Triple Negative breast cancer patients, and between grade 3 and grade 1/2 cancer grades. Both of these findings are useful in the borderline cases where biopsy samples or reports can be mis-read or mis-interpreted.

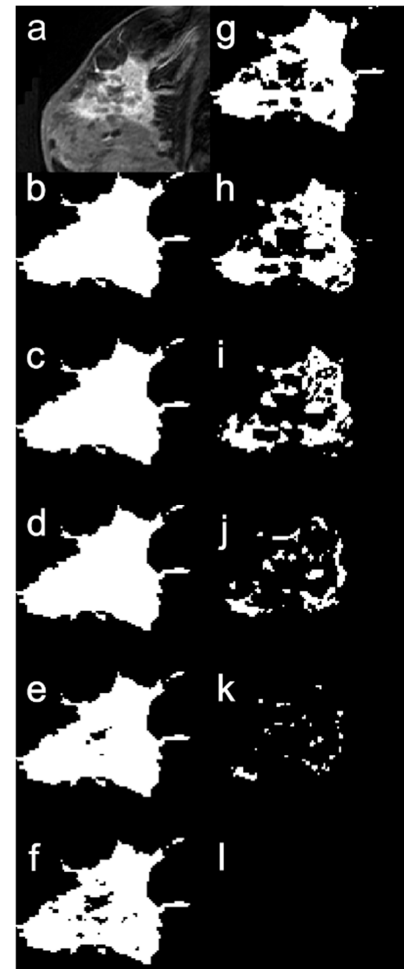


Figure 1: Image generation for analysis using Minkowski Functionals with 11 thresholds. The lesion is segmented from the original T1W MR scan (a), and the binarised at different threshold levels from 0.0 – 1.0 (b-l), (b) represents the full lesion area (0.0) and (l) is set as containing no white pixels

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