Texture and Regression Tree Analysis in the Characterisation of Ovarian Lesions

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Target Audience Ovarian MR researchers – Physicians and Clinicians

Purpose The characterisation of complex ovarian lesions is an ongoing challenge. Because of its greater soft tissue contrast resolution MRI is the preferred technique for characterising complex adnexal masses1. However, the presence of solid components in benign lesions such as cystadenofibroma, a feature that overlaps with malignant lesions, causes diagnostic difficulty2. Correct diagnosis is very important since benign ovarian lesions may be treated by simple cystectomy or oophorectomy, whilst malignant lesions require hysterectomy, bilateral oophorectomy, omentectomy and possibly appendectomy. Textural analysis has previously been utilised in contrast enhanced MRI of the breast both as a diagnostic tool3 and as a predictor of chemotherapeutic response4. This study aims to explore the utility of texture analysis and subsequent regression tree analysis in the diagnosis of ovarian malignancy.

Methods Data from 96 women with histopathologically proven ovarian cancer (n=67), borderline ovarian tumour (n=28), cystadenoma (n=14) or cystadenofibroma (n=19) who underwent pre-operative pelvic MRI using a 32 channel phased array coil on a 3 Tesla scanner was retrospectively analysed. Texture analysis was performed on T2 weighted images acquired with the following parameters: TE 111 ms, TR 3431 ms, FOV 24×24 cm, matrix size 512×416, slice thickness/gap 4/1 mm, acquisition time 5 mins for ~40 slices. ROIs were manually drawn on a single slice by an expert radiologist, detailing the most complex portion of the lesion. ROI data was then reduced to 16 grey levels using histogram equalisation to ensure adequate counting statistics. Co-occurrence matrices, which represent the probability of finding 2 adjacent pixels of intensities i and j were then computed for four directions (0°, 45°, 90°, and 135°) to enable subsequent calculation of texture parameters \( f_1 \) to \( f_{16} \) as described by Haralick et al5 and Conners et al6. Since no intrinsic directionality is anticipated average texture parameters were utilised in statistical analysis. Due to the uneven group sizes, which can result in over emphasis on trying to correctly predict the largest group, repeated testing of equal sample sizes (n=14 for each group) via random sampling was employed. The Kruskal-Wallis test was utilised to determine significant differences between groups. Pearson’s correlation coefficient was then used to remove redundant parameters prior to regression tree analysis.

Results Significant differences between the four groups were consistently noted for 8 parameters \( f_2, f_4, f_6, f_7, f_{10}, f_{15}, f_{16} \) and \( f_{18} \) and are detailed in the accompanying table for one set of random data samples. Once correlation analysis was performed 5 parameters were retained and thus inputted into regression tree analysis using the CART algorithm. After tree pruning to prevent over fitting a final classification tree (see diagram) contained 3 parameters \( f_2 \) – contrast, \( f_{15} \) - cluster shade and \( f_{16} \) – cluster prominence). Using this model correctly categorises 11.4/14 (81%) of cystadenofibromas, 9.8/14 (70%) of cystadenomas, 8.7/14 (62%) of borderline ovarian tumours and 9.4/14 (67%) of ovarian cancers.

Conclusions Texture analysis has been successfully applied in the diagnosis of ovarian malignancy. After performing repeated testing, via random sampling, a robust diagnostic model has been developed, with an overall accuracy of 70%. By appropriate use of correlation analysis and tree pruning only 3 parameters were retained, thus avoiding over parameterisation in the final model. Future work may include incorporation of other MR quantitative features such as shape.