Semi-Automatic Normalized Entropy Characterization of Metastatic Renal Cell Cancer via Spatio-Textural Tumour Classification

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Abstract—Normalized entropy is a strong predictor of patient survival rate for lung and renal cell cancers in CT images. In this work, we present a semi-automatic algorithm to compute the normalized entropy of lung metastasis from renal cell cancer via spatio-textural tumour classification. The proposed algorithm only requires a single click from the user to calculate the normalized entropy for tumours, thus, minimizing the amount of user intervention required. We evaluated the performance of the proposed approach in computing normalized entropy with respect to the normalized entropy calculated via manual clinical segmentation, and a correlation of 0.87 was achieved.

I. INTRODUCTION

Annually, there are about 64,000 new cases of renal cell carcinoma (RCC) in the US where in 50%-60% of cases, RCC is metastasized to lung [1]. Recent studies have shown that texture features (e.g., entropy) of tumours in CT images for both primary lung cancer and lung metastasis from RCC can be indicator of tumour glucose metabolism and stage [2] and predict the response of metastatic RCC to treatment [3]. Most recently, it has been discovered that normalized entropy (NE) of the lung tumour is the strongest predictor of survival [4]. This is a promising result that can have a positive effect on cancer risk stratification and tumour recurrence monitoring.

Normalized entropy (NE) of a given ROI is calculated as:

\[
NE = \frac{\ln(\text{Ent})}{\ln(N)}
\]

where Ent is the ROI (i.e., tumour) entropy and N is the number of pixels in the ROI. To calculate normalized entropy, first, the ROIs in CT images must be delineated manually by a clinician. Nevertheless, manual delineation of tumours is a tedious task and it may take a long time per case (e.g., 30 min). This obviously limits the usability of the survival prediction in practice. In this work, we propose an algorithm to calculate normalized entropy of tumours with minimal user interaction (i.e., without the need for manual tumour segmentation) using a novel spatio-textural tumour classification approach.

II. SPATIO-TEXTURAL TUMOUR CLASSIFICATION

Based on the user’s single click roughly at the centre of the tumour as a seed point, our algorithm constructs a ROI around the seed point with a fixed size (e.g., 40 x 40 mm). A moving window of 3x3 pixels is used to calculate 6 texture features: mean, standard deviation, entropy, uniformity, kurtosis, and skewness. In addition, we incorporate the relative spatial location of the tumour pixels in the ROI as two extra features. This produces a total of 8 spatio-textural features. A Bayesian classifier trained by this spatio-textural feature model is then used to identify tumour tissue pixels from healthy tissue pixels in the ROI. The identified tumour tissue pixels are used to calculate the normalized entropy of the tumour.

III. TESTING METHODOLOGY AND RESULTS

A total of 19 CT cases (from 8 patients) of lung metastases from RCC, acquired at Sunnybrook Health Sciences Centre, were manually delineated by an experienced radiologist. A leave-one-out cross-validation was used to evaluate the performance of the algorithm for tumour classification; sensitivity, specificity, and accuracy of 90%, 79%, and 83% were achieved, respectively. For each ROI, the normalized entropy (Equation 1) was calculated using pixels labeled as tumour pixel by the proposed algorithm and compared to that of the manually delineated ROIs; a correlation of 0.87 was achieved (Figure 1). The fact that the normalized entropies of the ROIs calculated by the proposed algorithm with only a single click are highly correlated with the ones computed using manually segmented tumours indicates the potential for accurate survival prediction performed semi-automatically in a much shorter time compared to the manual approach.

Figure 1: NE - manual vs. semi-automatic delineation

REFERENCES
[1] National Cancer Institute, see cancer.gov/statfacts/html/kidtr.html