A Novel Level Set Active Contour Algorithm Using the Jensen-Renyi Divergence for Tumor Segmentation in PET

Innovation/Impact: This work presents a novel segmentation algorithm using the Jensen-Renyi (JR) Divergence metric to evolve the geometric level set contour. This information-theoretic metric offers improved noise robustness characteristics and is thus more promising for use in segmentation of targets using positron emission tomography (PET) imaging compared to traditional methods. This can have a direct impact on the quality of radiation therapy treatment planning in terms of delineation guidance and improved target definition.

Introduction: PET images present a valuable resource for delineating the biological treatment volume (BTV) for image-guided radiotherapy. Therefore, a large number of methods have been proposed for segmentation of target volumes as seen on PET images. Thus far this has proven to be a challenging task due to poor spatial resolution, noise and lack of a consistent unit. Despite their popularity, thresholding methods have been shown to be inconsistent performers and highly dependent on data acquisition and processing parameters. Improved results have been observed for adaptive algorithms that use observed distributions on a case-by-case basis. However, many algorithms such as fuzzy clustering and active contours based on intensity means are particularly susceptible to image noise. The JR Divergence metric has shown improved robustness to noise when applied for segmentation due to the fact that the curvature of its energy space can be controlled with the parameter α and distribution weights as shown in Figure 1. In this study, a new level set segmentation algorithm based on the JR divergence is developed and applied to quantification of PET.

Methods: The JR Divergence criterion is defined by the following conditional expectation:

\[
E(\phi) = \frac{1}{1-\alpha} \left[ \log \int_{\mathbb{R}} (w_1 P_1 + w_2 P_2)^\alpha d\tilde{x} - w_1 \log \int_{\mathbb{R}} (P_1)^\alpha d\tilde{x} - w_2 \log \int_{\mathbb{R}} (P_2)^\alpha d\tilde{x} \right]
\]

where \([w_1, w_2]\) are the weighting parameters for the probability distribution functions \(P_1\) and \(P_2\). \(P_1\) and \(P_2\) in this context are defined by the intensity distributions inside and outside the active contour, respectively. The JR Divergence is in fact a family of divergence measures defined by the choice of parameter α. The value \(k\) defines the number of bins used for discretizing the intensity range, for instance a value of \(\alpha=1\), will correspond to the known Shannon entropy metric used in mutual information.

Figure 1. The JR divergence function for a Bernoulli distribution with parameters \(\alpha = 0.5\), \(w_1 = w_2 = 0.5\) (left), \(\alpha = 5, w_1 = w_2 = 0.5\) (middle) and \(\alpha = 5, w_1 = 0.75, w_2 = 0.25\) (right).

PET images of 7 patients with T3-T4 pharyngolaryngeal squamous cell carcinoma taken from the Louvain database were used for performance evaluation. Segmentation results were compared to BTV defined histologically from resected tissue. This dataset was recently used to
evaluate a large number of alternative PET segmentation methods and thus our results allow a
direct comparison with these methods [1]. Two performance metrics were used to this end,
classification error (CE) and concordance index (CI).

\[
CE = \frac{(PCE + NCE)}{(Vol)} \times 100% \\
CI = \frac{(A \cap B)}{(A \cup B)}
\]

Here positive CEs (PCE) is the volume identified as background that is actually part of the
tumour and negative CES (NCE) is the volume identified as tumour that is actually background.
Vol is the volume of the histologically derived contours. With respect to CI, A and B are defined
as the segmented volume and histologically derived volume, respectively.

**Results and Discussion**: The images were segmented following a denoising procedure which
consisted of smoothing using a bilateral 3D filter followed by deconvolution using the Landweber
algorithm. Figure 2 shows a visual comparison of a segmented volume defined by the proposed
method (in red) compared to the contour defined by histology (green).

![Figure 2](image1)

**Figure 2** – Two slices taken from a PET image volume of one of the 7 test cases.
The results (in red) are visually similar to the registered BTV defined from histology (in green).

![Figure 3](image2)

**Figure 3** – Bar graphs comparing results from Zaidi et. al., 2012 to the performance of
the proposed JR Divergence method using classification error and concordance index.

Figure 3 shows the performance results of the JR algorithm alongside the results for a number
of alternative segmentation methods tested from the same data as reported in [1]. The results
show that the JR method performed with the second lowest mean classification error (63.5%)
and highest mean concordance index (5.44).

**References**

squamous cell carcinoma," European Journal of Nuclear Medicine and Molecular Imaging; published online January 2012.
2. A. B. Hamza, H. Krim "Image registration and segmentation by maximizing the Jensen-Rényi divergence EMMCVPR 2003, LNCS