

AbstractID: 5170 Title: Application of a Gaussian Mixture Model for the segmentation of lung tumors in Positron Emission Tomography

Purpose: FDG-PET is increasingly used in the gross tumor volume (GTV) definition of lung cancer patients undergoing radiotherapy. There is currently no reliable technique for segmenting GTV using PET, mainly due to varying background levels of the mediastinal blood pool and normal lung. We have developed a semi-automatic segmentation technique based on Gaussian Mixture Models (GMM).

Method and Materials: The PET image data (voxel intensities) are assumed to be realizations of random variables (RVs) whose density functions can be represented as a mixture of Gaussian density functions, each weighted by their mixing proportion. Each density function represents a level of activity concentration, called a "class". Four classes are defined to describe the data; Background-Low, Background-High, Target, "Mixing". We assume "Mixing" is a mixture of the other three classes, which are considered to represent Single Activity levels (SA). User interaction is limited to initial selection of an over-sized region around the tumor and initialization of model parameters. Expectation Maximization is used to calculate Maximum Likelihood estimates of the parameters (mean, variance, mixing proportions of each class) of the model. The results are then used to segment the image into the three SA classes. The algorithm was tested on the NEMA phantom with varying target/background ratios and ten patient studies.

Results: The GMM segmentation of the NEMA phantom spheres was comparable to thresholding at 40% of the maximum. For inhomogeneous tumors, segmentation with GMM was far superior to thresholding. For homogenous tumors GMM was as good or better than thresholding.

Conclusion: A segmentation technique based on Mixture Models was applied for the first time on PET images, with encouraging initial results. Segmentation obtained with the GMM model is based on statistical analysis of the images, making it more reliable than current thresholding methods. Additional studies will assess its accuracy.