

Purpose: Simple comparison tools and measures such as the maximum standardized uptake value (SUV) are currently used to gauge treatment response with PET imaging. In reality, the tumor and its response are heterogeneous and metabolic changes should be characterized by local measures. This study presents a tumor response algorithm that corrects for anatomical changes and robustly identifies local changes in serial PET images through a clustering algorithm.

Materials and Methods: A two-step analysis was performed for this study. First, pre and post-treatment images are rigorously aligned using a deformable registration to correct for posture and soft tissue changes. The detailed mapping is modeled by free form deformations B-spline optimized using the limited memory *BFGS* algorithm. A clustering algorithm further detects voxel changes in proximity to the user-delineated structures. The level set clustering is an advanced approach that combines the advantages of pixel-based and distance-based techniques to classify the dataset into regions of both signal enhancement and reduction. The enhancing regions, where the treatment failed, are correlated with the RT Dose and Structure Set objects from the treatment plan. While enhancing regions inside the tumor receiving a high dose are associated with poor biological response, enhancing regions near tumor margins are associated with geometrical misses due to setup errors or targeting inaccuracies.

Results: Results of the level-set based clustering algorithm are presented to the user as colorwash displays overlaid over the original anatomy. The technique was instrumental in detecting geometrical and segmentation misses on actual clinical cases and provided an indispensable tool for accurate, outcome-based quality assurance of the radiation treatment process.

Conclusions: Patient studies have indicated that the method is reliable and provides a valuable tool to integrate imaging information into treatment assessment for image guided radiation therapy.