

Purpose: There is a lack of software tools to analyze and quantify response assessment in large clinical trials studies using PET imaging. With PET imaging suffering from low spatial resolution and significant noise levels, standard voxel-comparison tools are not capable of capturing the small pattern changes characterizing a tumor's heterogeneous response. This study presents an algorithm that robustly identifies local changes in serial PET images through a clustering algorithm.

Materials and Methods: The developed clustering algorithm is an image analysis procedure aimed at grouping entities with similar characteristics together such that main trends or unusual patterns may be discovered. Our approach combines the concepts of voxel-based and distance-based techniques to classify the dataset into regions of both signal enhancement and reduction. The method combines serial PET imaging with treatment planning dose to associate enhancing regions as possible geographical miss due to setup errors or targeting inaccuracies. This software analysis tool was tested on a collection of 113 head and neck datasets from the National Biomedical Imaging Archive (NBIA) that was part of a randomized phase III trial of radiation therapy and chemotherapy for stage III and IV head and neck carcinomas.

Results: The technique was instrumental in detecting possible geographical and segmentation errors on the actual clinical cases by providing accurate analysis of metabolic changes. Results of the level-set based clustering algorithm are saved as a detailed report of enhancing /non-enhancing regions and their location, and can be further displayed as a colorwash overlaid over the original anatomy for in-depth analysis.

Conclusions: Level-set clustering applied to the NBIA imaging collection indicate that the method is reliable and ideally suited for large scale analysis providing a valuable tool to integrate accurate evaluation of treatment response into clinical trials.