AbstractID: 14047 Title: Monitoring and validating metastatic tumor growth in lung CT

Purpose: The advent of body SRT has lead to dramatically improved survival of patients with metastatic spread to the lung. In turn, there is a renewed interest in CT surveillance of at-risk cancer survivors and for radiologist-assist diagnosis tools for early-stage metastatic disease. Accurate measurement of nodule growth is critical for diagnosis of active disease and quantification of treatment response, but validation of methods for measuring growth is impeded by the large variability in radiologists' estimates of nodule volume.
Method and Materials: A simulated nodule growth CT database is being created based on real nodule morphology and image features. The database's utility is demonstrated on an automated growth assessment approach and the same tool is then applied to a patient with multiple metastases to the lung followed over a two-year duration.
Results: An initial simulated nodule dataset was created incorporating juxta-vascular, juxta-pleural, and parenchymal nodules. The automated assessment tool identified correctly growth as small as 16%, with the largest errors in the juxta-pleural dataset. In a patient with multiple (>15) bladder cancer metastases, nodule growth rates were found to vary among nodules, suggesting that regional heterogeneity in lung perfusion and/or oxygenation may affect growth rates of metastases.
Conclusion: A realistic simulated 3-D CT lung nodule dataset has been initiated with the capacity to accurately mimic small changes in volume. Simulated nodules reconstructed from real patient lung metastases were employed to evaluate the efficacy of a novel 3-D growth assessment algorithm. The validation of volume change accuracy in this manner reduces a great deal of the ambiguity and subjectivity that is encountered when radiologist measurements are utilized as the gold standard for nodule size. Assessment of variable growth rates of multiple metastases in an example patient shows promise for improved selection of active disease and characterization of treatment response.