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Quantifying COPD Disease Severity with CT-Derived Perfusion Imaging

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MEDICAL PHYSICS

TH-B-207-04, Quantifying COPD Disease Severity with CT-Derived Perfusion Imaging: A Nowacki[1]*, G Nair[2], Y Liu[1], C J Galban[3], C Stevens[4], E Castillo[1],(1) University of Texas at Austin, Austin, TX, (2) Beaumont Heath System, (3) University of Michigan, Ann Arbor, MI, (4) William Beaumont Hospital, Royal Oak, MI

Purpose: CT-derived perfusion (CTP) is a novel image processing modality that quantifies pulmonary perfusion from non-contrast inhale/exhale CT image pairs. While existing imaging markers for COPD primarily depend on morphological features or HU thresholding, CTP provides a quantitative marker of blood flow and has been shown to identify disease progression prior to the appearance structural abnormalities. In this study, we assess the potential utility of CTP as a disease severity marker for COPD. **Methods:** CTP was computed from high-resolution inhale-exhale CT scans for 785 patients with a Global Initiative for Obstructive Lung Disease (GOLD) score ranging from 0 to 4 participating in the COPDGene® multi-center trial. Mean CTP (mCTP) was computed for each patient and the Spearman correlations with GOLD score and Forced Expiratory Volume after 1 second (FEV1) were computed. **Results:** The Spearman correlations, across all patients, between mCTP and GOLD score and mCTP and FEV1 were -0.61 and 0.59, respectively. Both correlations achieved statistical significance (p-value < 0.05). **Conclusion:** mCTP correlation with FEV1 is higher but comparable to correlations generated by competing state-of-the art imaging markers. Moreover, higher mCTP is associated with higher lung function, which implies that its negative correlation with GOLD score is indicative of CTP's potential as a tool for characterizing disease severity. When combined with CT-derived ventilation methods, CTP has the potential to provide VQ mismatch scoring, in addition to perfusion quantification, that could be used to identify and diagnose COPD with higher fidelity. Future work includes incorporating the spatial distribution of function, therefore using CTP for each voxel rather than whole-lung mCTP, to characterize disease progression in different regions of the lung and monitor more minute changes in perfusion and, therefore, lung function.

TH-B-207-05, Reproducibility of a Dynamic CT Pulmonary Perfusion Technique Using Only Two Volume Scans: Y ZHAO*, N Luu, S Molloi, University of California, Irvine, CA

Purpose: Existing dynamic CT perfusion (CTP) techniques are limited by their high radiation dose and lack of reproducibility. The purpose of this study is to investigate the reproducibility of a low-dose CTP technique using only two volume scans**. Methods:** Seven Yorkshire swine (52.0±6.8kg) were used in the study with 40 independent CTP acquisitions using a 320-slice CT scanner. Dynamic CTP scans were performed twice with the same scan parameters. For each dynamic CTP acquisition, two volume scans were prospectively acquired. The first volume scan (50mA) was acquired before contrast injection. The second volume scan (full-dose) was acquired after intravenous contrast administration (370 mg/ml iodine, 0.5ml/kg, 5ml/s) with bolus-tracking within the main pulmonary artery and a time-to-peak delay. Two scan modes were used for the CTP acquisition: the volume scan mode (16 cm z-coverage, 0.35 s rotation time, 300mA) and a fast helical scan mode (23.6 cm z-coverage, ~2.5 s scan time, 200mA). Each pair of the prospective CTP measurements were quantitatively compared to each other by linear regression, Bland-Altman analysis and t-test. The CT dose index (CTDI) of the two-volume CTP using volume and helical scan modes were calculated to be 9.3mGy and 4.8mGy, respectively. **Results:** The repeated CTP measurements using the volume scan mode were correlated by PVOL1=1.03PVOL2 - 0.82 mL/min/g (r=0.97, RMSE = 1.04, p =0.21). The repeated CTP measurements using the helical scan mode were correlated by PHEL1=0.93PHEL2 +1.07 (r = 0.98, RMSE = 1.00, p = 0.04). **Conclusion:** The results show excellent reproducibility of the two CTP measurements using both volume and helical scan modes. The two-volume CTP using the helical scan mode enables the whole-lung dynamic CTP measurement.

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TH-B-207-06, Segmentation of High-Resolution Blood Vasculature Trees in CT: D Yang[1]*, Y Hao[2], Y Duan[3],(1) Duke University, Chapel Hill, NC, (2) Washington University School of Medicine, St. Louis, MO, (3) University Of Missouri,

Purpose: Because vasculature is involved in many diseases, vasculature segmentation is an important middle-level image processing task for supporting higher-level tasks such as lung ventilation function measurement, motion estimation, treatment response evaluation and disease diagnosis. In this study, we developed a comprehensive procedure to segment high-resolution vasculature tree in CTs, and to detect vessel bifurcations, i.e., the anatomically stable landmarks. The success of the proposed work will support future studies to automatically detect stable landmark pairs between pair of CTs and to provide high-quality high-density benchmark datasets to verify deformable image registration algorithms**. Methods:** A novel workflow was developed to segment high-resolution vasculature trees in CTs. Important steps are 1) segmenting target organ, 2) denoising image to enhance the contrast between the vessel and the background, 3) computing vesselness, 4) hysteresis thresholding the computed vesselness map to

