AbstractID: 13371 Title: Reproducibility of DCE-CT kinetic analysis

Purpose: Reproducibility of dynamic contrast enhanced (DCE) CT kinetic analysis is sensitive to both the inherent uncertainties associated with data acquisition and the applied model. This study aims to ascertain the DCE-CT reproducibility of canine sinonasal tumors using three different kinetic models: a commercial deconvolution software and in-house deconvolution and distributed parameter models.

Methods and Materials: Anesthetized canine patients with sinonasal tumors were immobilized and underwent two DCE-CT scans approximately two days apart. Gross tumor volumes (GTV) were contoured by a veterinary oncologist and evaluated for each scan. Blood flow (BF), blood volume ratio (BVR), mean transit time (MTT), and permeability were generated using two in-house MATLAB deconvolution-based kinetic models and the commercially available GE Advantage Perfusion 4.0 software. Paired t-tests using the Bonferroni correction ($\alpha = 0.025$) were applied to assess the mean differences of the slices of a tumor GTV.

Results: Between the two reproducibility scans, BF had an average variation of 90% among the three models, which was significantly different ($p < 0.02$). MTT and BVR had an average variation of 30%, where the former was significantly different using commercial software ($p < 0.01$), while the latter was significantly different using in-house models ($p < 0.01$). Permeability had an average variation of 10%, which was not significantly different for any of the kinetic models.

Conclusions: None of the four perfusion parameters were found to be consistently reproducible among the applied kinetic models. The uncertainties may be linked to errors in patient setup and post-anesthetized scan time, which are associations of data acquisition rather than kinetic analysis. Further investigation is required to determine the extent to which these uncertainties may limit the reproducibility of DCE-CT kinetic analysis.