

AbstractID: 11274 Title: Sensitivity of biological correlations to different registration parameters

**Purpose:** Determining spatial correlation between biological phenotypes is important for understanding tumor biology necessary for biologically-based radiotherapy or treatment assessment. Inaccurate image registration is one of the major uncertainties in determining such correlation. This study aims to investigate the sensitivity of correlation between different biological phenotypes to different registration techniques and parameters.

**Method and Materials:** Seven HNSCC patients underwent PET/CT imaging with [ $^{18}\text{F}$ ]FDG, [ $^{18}\text{F}$ ]FLT, and [ $^{61}\text{Cu}$ ]CuATSM imaging to assess multiple biological phenotypes-- metabolism, proliferation, and hypoxia respectively. Rigid and deformable registrations with various set of parameters (included similarity measures, optimizers, and resampling schemes) were performed on both CT and PET images sets for tumor co-registration. Correlation was measured by the correlation coefficient (CC), which was calculated based on registered tumor regions. Differences among CCs and joint histograms with respect to different registration techniques and parameters were used to quantify the sensitivity of image correlations.

**Results:** Correlations were rather sensitive to similarity measures. Normalized Mutual Information exceeded Euclidean and Correlation measures with CCs of 0.25 and 0.19 respectively. Varying resampling schemes had no significant effect on the correlation as changes in CC were  $<0.03$ . More moderate changes were observed when different optimizers were varied (differences in CC were  $<0.15$ ). In addition to the optimization parameters, the choice of the manually segmented registration region had a significant effect on the overall level of correlation. Deformable registration of CT occasionally introduced unnecessary tumor size variation thus leading to lower CC than rigid registration by as much as 0.16.

**Conclusion:** Correlations between different phenotypes of tumors are most sensitive to similarity measures and registration techniques (includes rigid and deformable registration). Uncertainty in the correlations is mainly due to misregistration of different biological representations of tumor. Uncertainty can be reduced with more precise segmentation of the registration region, which contains only tumor.