

## Signal Intensity Analysis of Ecological Defined Habitat in Soft Tissue Sarcomas to Predict Metastasis Development

Magnetic Resonance Imaging (MRI) is the standard of care in the clinic for diagnosis and follow up of Soft Tissue Sarcomas (STS) which presents an opportunity to explore the heterogeneity inherent in these rare tumors. Tumor heterogeneity is a challenging problem to quantify and has been shown to exist at many scales, from genomic to radiomic, existing both within an individual tumor, between tumors from the same primary in the same patient and across different patients. In this paper, we propose a method which focuses on spatially distinct sub-regions or habitats in the diagnostic MRI of patients with STS by using pixel signal intensity. Habitat characteristics likely represent areas of differing underlying biology within the tumor, and delineation of these differences could provide clinically relevant information to aid in selecting a therapeutic regimen (chemotherapy or radiation). To quantify tumor heterogeneity, first we assay intra-tumoral segmentations based on signal intensity and then build a spatial mapping scheme from various MRI modalities. Finally, we predict clinical outcomes, using in this paper the appearance of distant metastasis - the most clinically meaningful endpoint. After tumor segmentation into high and low signal intensities, a set of quantitative imaging features based on signal intensity is proposed to represent variation in habitat characteristics. This set of features is utilized to predict metastasis in a cohort of STS patients. We show that this framework, using only pre-therapy MRI, predicts the development of metastasis in STS patients with 72.41% accuracy, providing a starting point for a number of clinical hypotheses.

## Classification of Progression Free Survival with Nasopharyngeal Carcinoma Tumors

Nasopharyngeal carcinoma (NPC) is an abnormal growth of tissue which arises from the back of the nose. At the time of diagnosis, detection of tumor features with prognostic significance, including patient demographics, imaging characteristics and molecular characteristics, can enable the treating clinician to select a treatment that is optimized for the individual patient. At present, the analysis of tumor imaging features is limited to size criteria and macroscopic textural semantic descriptors, but computerized quantification of intratumoral heterogeneity and their temporal evolution may provide another metric for predicting prognosis. We propose medical imaging feature analysis methods and radiomics machine learning methods to predict failure of treatment. NPC tumors on contrast-enhanced T1 (T1Gd) sequences of 25 NPC patients' diagnostic magnetic resonance images (MRI) were manually contoured. Otsu segmentation was applied to segment the tumor into highly enhancing vs. weakly enhancing signal intensity subregions. Within these subregions, texture features were extracted to numerically quantify the intraregional heterogeneity. Patients were divided into two prognostic groups; a progression-free-survival group (those without locoregional recurrence or distant metastases), and the disease progression group (those with locoregional recurrence or distant metastases). We used Support Vector Machines (SVM) to perform classification (prediction of prognosis). The features from the highly enhancing subregion classify prognosis with 80% predictive accuracy with  $AUC=0.60$ , while the captured features from the weakly enhancing subregion classify prognosis with 76% accuracy with  $AUC= 0.76$ .