Imaging Genomics: Associations and Biological Correlates of Radiomics

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With the growth of quantitative imaging and quantitative image analysis, image-based biomarkers (i.e. image-based phenotypes) are becoming potential descriptors in personalized medicine as well as in cancer discovery research. Genomic study measures molecular cancer status and provides abundant information about cancer development mechanism. There is a need to understand the relationship between the image-based cancer phenotypes (from radiomics) and the underlying molecular and genomic system. Imaging scientists and genomic scientists need to be able to speak the same language in this common era of Big Data. The objective of this session is to learn the basics and mathematics of phenotype-genomics correlation and association studies, in particular radiomic phenotype-genomic studies. We will take genomic data from The Cancer Genome Atlas (TCGA) and imaging data from The Cancer Imaging Archive (TCIA) as an example to show how to organize multi-platform genomic data and integrate with quantitative tumor image phenotypes to perform association studies. We will show the software and procedure of discovering statistically significant associations between various imaging phenotypes (such as those characterizing tumor size, shape, margin, enhancement texture, and blood flow kinetics) and genomic features involved in multiple molecular regulation layers (including pathway gene expressions, pathway copy number variations, gene somatic mutations, miRNA expressions, and protein expressions). These findings form a basis for future studies using non-invasive imaging techniques for accurate cancer diagnosis and prognosis and for discovering the genetic mechanisms leading to specific tumor phenotypes for the development of personalized cancer treatment.