



Jewish General Hospital
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"Radiogenomics: Predicting and understanding normal tissue complication with genomics and machine learning"

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Abstract

The risk of normal tissue complications is one of the most important considerations in radiotherapy treatment planning. It has been observed that normal tissue response to the same dose level is heterogeneous among cancer patients. Radiogenomics is a study that searches for heritable genomic variations - coded by single nucleotide polymorphism (SNP) - that correlate with the heterogeneity in normal tissue response. Machine learning helps unveil the true correlates from high-dimensional genomic data. This talk will summarize the current status of Radiogenomics, and the works conducted by my research group at Memorial Sloan Kettering Cancer Center.