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Hidden cancer immunology insights from tumor RNA-seq

I will introduce our work in mining and integrating large-scale tumor molecular profiles to inform cancer immunology and immunotherapy. Tumor RNA sequencing has become cost effective over the years, and I will discuss three algorithms that we developed to extract useful insights from treatment naïve RNA-seq samples in The Cancer Genome Atlas. First, TIMER can estimate immune cell components in tumors, and a webserver has been created for users to explore immune infiltration across TCGA tumors and make inference on user-provided samples. Second, TRUST can assemble T cell receptor (TCR) and B cell receptor (BCR) complementarity-determining regions (CDR3s) from unselected bulk tumor RNA-seq data. Third, TIDE derived tumor immune dysfunction and tumor immune exclusion gene expression signatures from pretreatment tumors to predict patient response to anti-PD1 and anti-CTLA4 treatment. Our work indicates that tumor RNA-seq, even on treatment naïve tumors, is cost effective to inform tumor microenvironment and tumor immunity.