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OncoPeptTUME – An *in silico* platform to study tumor micro-environment

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Abstract

Cancer immunotherapy is now established as a major therapeutic modality, and 70% of all cancer patients are estimated to receive some form of an immunotherapy treatment as a part of their disease control by 2025. Several different tumor cell-intrinsic and extrinsic features including the tumor microenvironment, driver gene mutations, host genetics, microbiome and environmental factors modulate response to immune checkpoint inhibitors. The tumor microenvironment plays the most significant role harbouring various components that influence the malignancy of a disease. Clinical investigations on tumor infiltrating immune cells have established the roles of cytotoxic T cells (CTLs) and tumor-associated macrophages (TAMs) in several cancers. It is now strongly evident that cancer outcome and response to therapy is guided by diverse immune cell activity in tumors.

We have developed an *in silico* platform to profile immune cell type for tumor samples from gene expression data. Using an integrated knowledge based method on pure cell type gene expression samples, we have created gene signatures for 8 different immune cell types (Bcell, CD4, CD8, Monocyte, Treg, Macrophage, Neutrophil, NK) summing up to a total of 42 genes. The identified signature was validated on pure cell samples from RNA-seq, microarray and IHC. Comparison of our immune signatures with some of the published signatures showed better performance of our signatures.

We applied our *in silico* platform on the TCGA cancer samples. Our analysis showed that patients with higher CD8 score have better survival in bladder carcinoma, endocervical adenocarcinoma, head & neck, sarcoma, melanoma, thyroid, whereas, patients with higher monocyte score have poor survival in endocervical adenocarcinoma, kidney renal clear cell carcinoma, kidney renal papillary cell carcinoma, lower grade glioma and liver hepatocellular carcinoma.

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