# Exploring ligand-receptor pairs associated to cancer immunotherapy responses using machine learning

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## Abstract

Cancer is still major worldwide health issue, needing the development of new improved therapeutic strategies. Recently, cancer immunotherapies which harness the patient's own immune system to target tumor cells, have emerged as innovative approaches. The efficacy of such therapies hinges crucially on intricate ligand-receptor interactions between the tumor cells and immune cells. Here, we employed machine learning models to discover ligand-receptor pairs essential for the success of these treatments.

For the experiments, we downloaded RNA-seq gene expression data with non-small cell lung cancer (NSCLC) from The Cancer Genome Atlas (TCGA). Then the immunotherapy responses in these samples was estimated using the Tumor Immune Dysfunction and Exclusion (TIDE) score.

Using Ligand-Receptor (LR) pairs from CellTalkDB, we produced an LR pairs expression dataset, then built the machine learning models to predict the immunotherapy responses based on the LR pairs. As a result, LR pairs that significantly influence the immunotherapy responses to were investigated.