Unraveling the Complex Interplay Between Immune Cells and Cancer Progression Utilizing a Novel Application of an Artificial Neural Network

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1 in 5 people develop cancer in their lifetime. Due to treatment inefficiency, cancer is the leading cause of death worldwide. Deciphering immune cell-cancer cell interactions within the tumor microenvironment (TME) is paramount for developing effective cancer treatments. This research developed a novel artificial neural network (ANN) to successfully uncover the interplay between immune cells and cancer gene sets. It addressed hidden crosstalk among immune cells, tumor heterogeneity, and TME interconnection through its multi-layer model architecture, enabling simultaneous analysis of all components. Using data from 70 patients across six solid cancers, gene expression and bulk RNA-seq data were normalized in R programming. This selected 54,675 probes and 51,140 TPM values per sample for subsequent analysis. Gene Set Enrichment Analysis (GSEA) was then conducted to gather normalized enrichment scores (NES) for five major gene sets. CIBERSORT was used for immune cell fractions, with feature selection choosing seven significant immune cell types. Synthetic Minority Oversampling Technique (SMOTE) augmented and generated 1,050 predictors and 750 responses for the ANN. The model was trained using TensorFlow's Sequential class, involving meticulous hyperparameter tuning and backpropagation. The model achieved 92% accuracy and an R-squared value of 0.93, effectively predicting the correlation between immune cells and cancer gene sets. Sensitivity analysis was conducted to reveal the impact of individual immune cell types. This model allows tailored treatments based on unique TME profiles, reducing treatment inefficiency, and revealing novel therapeutic targets. This model conducts years of lab research in mere hours with optimal accuracy.

Awards Won:

Second Award of $2,000