Machine Learning for Precision Therapy of Triple-Negative Breast Cancer: Exploring the predictive ability of blood cytokines for chemotherapy

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Abstract:

Triple-negative breast cancer (TNBC) is a highly aggressive type of breast cancer which does not express estrogen or progesterone receptors and does not overexpress the HER2 protein. Currently, treatment options for TNBC are limited. Recent research indicates that cytokines play roles in TNBC tumor growth and metastasis, and that chemotherapy can modulate the expression of cytokines. Thus, we hypothesized that cytokines may be useful for predicting the outcomes of chemotherapy of TNBC patients.

To test this hypothesis, we obtained cytokine measurements from blood samples of TNBC patients at multiple time points. We analyzed this data using Weighted Gene Co-expression Network Analysis (WGCNA) to find cytokines correlated with chemotherapy treatment outcomes, and calculated q-values to control the false discovery rate. We discovered five cytokines, IL-1α, TRAIL, SCF, RANTES, and IL-16, which were correlated with good chemotherapy outcomes. We performed protein-protein interaction analysis, which indicated that these cytokines are involved in immune response. We then performed logistic regression with L2 regularization, which indicated that IL-1α and TRAIL can reliably predict the outcomes of eribulin chemotherapy. These results indicate that cytokine expression levels in the blood may be effective tools in predicting the outcome of eribulin chemotherapy in TNBC patients.