Machine Learning Approaches To Determine Clinical Factors for Prediction of Immune Factors in Melanoma

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Purpose: Cutaneous melanoma causes over 8,000 deaths annually in the U.S. Survival differences may be linked to tumor-infiltrating lymphocytes (TILs), white blood cells that eliminates cancer cells. Effectiveness of TILs depends on their density and infiltration levels. However, TILs variations and interaction with other clinical factors are unclear. Available pathology is often incomplete and lacks quantifiable measures for TILs. Datasets are available for analysis of melanoma survival rates and to correlate with TILs levels. Procedure: I developed IF-PreDict (Immune Factor Predictor), a machine-learning model, using logistic regression in R. In a preliminary study, I applied IF-PreDict to the Genes, Environment, and Melanoma (GEM) study de-identified dataset. I assessed how different clinicopathological variables are related to TILs infiltration in tumors. Variables studied included age, sex, Breslow thickness, sex, median life UV Exposure, mitosis and tumor site ulceration. Specifically, extent of these variables affecting TILs distribution within tumors was studied. Results: IF-PreDict could show the significance of each variable in both TILs presence or absence, and Brisk, or Non-Brisk. The measure that consistently showed the best correlation was Breslow Thickness, which was significantly associated with immune infiltration in tumors, higher thickness was likely to have lower immune infiltration. Conclusions: Although in its initial stages, IF-PreDict has the potential to expand its application to other immune quantifications, aiding clinicians in unraveling the complex interplay of immune factors with clinicopathologic correlates. Future steps include finding better measures for predicting immune infiltration using more sophisticated variables and models.

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