[BIOINFO 2023]

Estimation of immune cell type composition from microRNA expression data

Seo-Young Park[1], and Je-Keun Rhee[1*]

[1] *Department of Bioinformatics & Life Science, Soongsil University, Seoul, Republic of Korea*
[*] *Corresponding author: jkrhee@ssu.ac.kr*

The biological characteristics of tumor tissues can be better understood by identifying the immune cell composition at the tumor microenvironments, and eventually, it can help to predict tumor progression and the response to the immunotherapy. Previously many studies have been developed to infer the immune cell composition using gene expression profiles or DNA methylation of bulk tumor tissues. However, microRNAs (miRNAs) can be also utilized to predict the immune cell composition. Here, we propose a model to predict immune cell composition with miRNA expression profiles from bulk tumor tissues. We built a model using XGBoost, which is an ensemble algorithm in boosting method and has interpretability, and we confirmed that our model showed a high correlation between the predicted cell composition and target values. Moreover, the variables significant in predicting the immune cell composition were selected based on the feature importance of the model, and we confirmed that pathways related to the significant miRNAs were related to tumor and immunity.