**Evaluation of machine learning methods that identify colorectal tumors with microbiota-associated biomarkers**

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As the microbiome field continues to grow, there is an ever-increasing demand for reproducible methods for identifying associations between members of the microbiome and phenotypes. Currently, the field’s use of machine learning lacks clarity and consistency. There is a need for guidance on how to implement good machine learning practices to generate reproducible and robust models.

One application of machine learning to microbiome data has been to classify patients as having colorectal tumors based on microbiota-associated biomarkers. Colorectal cancer is one of the leading cause of death among cancers in the United States. Colonoscopy as a screening tool is effective, however it is invasive and have a low rate of patient adherence. Previous studies have shown that bacterial abundances in the stool can predict colorectal tumors in the colon and can be used as a non-invasive screening tool. However, the prediction performance of these models vary greatly, with areas under the receiver operating characteristic curve (AUC) of 0.7-0.9 (1–4). The variation in prediction performance is based in part on differences in the study populations, and in part on the differences in modeling pipelines.

We used the fecal hemoglobin concentration and 16S rRNA gene sequences from stool samples to classify 490 patients as having advanced tumors or not. Modeling pipelines were established for L2-regularized Logistic Regression, L1 and L2 Linear Support Vector Machines (SVM), Radial Basis Function SVM, Decision Tree, Random Forest and XGBoost binary classification models. The mean AUCs of these models were 0.68 ± 0.04, 0.76 ± 0.05, 0.68 ± 0.05, 0.69 ± 0.05, 0.71 ± 0.04, 0.82 ± 0.04, and 0.76 ± 0.04, respectively. Random Forest and XGBoost methods were less susceptible to overfitting and in general had higher sensitivity and specificity for advanced tumors. Aside from evaluating generalization and classification performance of each model, this study established standards for modeling pipelines of microbiome-associated machine learning models.

**References**

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