

Identifying Relationships Between the Gut Microbiome and Melanoma Patients' Responses to Immunotherapy Using Machine Learning Techniques

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Melanoma is a rapidly metastasizing deadly cancer making it crucial to find the most effective treatment immediately. This year in the US, it is expected to be diagnosed in 97,610 patients and kill 7,990. The human microbiome (the community of microorganisms in a human) is a reflection of the health of the human body and has also been shown to affect the body's reaction to immunotherapy. In our project, we were able to uncover relationships between the microbiome and how the patients would respond to two different immunotherapies for melanoma; PD1 and PD1/CLA4. Our data consisted of 16S rRNA sequencing of stool samples from 90 patients, the type of immunotherapy received, and the patient response. First, we trained a Naive Bayes Classifier to predict what species of bacteria each rRNA sequence belonged to. We applied the classifier to each patient's 16s rRNA sequences to construct a table of species of Bacteria and their abundance in each patient. Then, a Random Forest Classifier (RFC) was trained to predict whether or not a patient responded based on the immunotherapy received and their gut microbiome. The RFC attained an AUC of 0.714. Finally, multivariate analysis was conducted using the CodaCore algorithm which identified 17 genera of bacteria associated with response to PD1 and 19 genera of bacteria associated with response to PD1/CTLA4. Our findings suggest that machine learning can be used to uncover the interactions between the microbiome and immunotherapy to improve the outcomes of cancer patients.

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