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Enhancing Microbiome Based Disease Prediction with SuperTML and Data Augmentation

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Abstract: *Accurate disease prediction using microbiome data remains a major challenge due to high dimensionality, compositional complexity, and limited sample sizes. Traditional machine learning models frequently struggle to capture the subtle interactions and patterns within such data, leading to reduced predictive performance and poor generalization to unseen cases. To address these limitations, this project introduces an advanced framework that integrates Super Tabular Machine Learning with data augmentation techniques. SuperTML enables deep feature representation to capture subtle microbial patterns. By transforming raw microbiome data into a structured, learnable representation, SuperTML allows the model to uncover hidden correlations and discriminate between healthy and diseased conditions with higher accuracy. Data augmentation techniques expand the effective size and diversity of the training dataset, mitigating the risk of overfitting and improving the model's ability to generalize to new, unseen samples. This ensures the model remains robust even when faced with sparse or noisy data. By integrating SuperTML with data augmentation, this project not only improves the predictive accuracy of microbiome based disease classification but also enhances interpretability, allowing researchers and clinicians to better understand the microbial signatures associated with different diseases.*

Keywords*:* ML, SuperTML, Data Augmentation, Microbiome

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