Gut Microbiome-Cardiometabolic Disease Spectrum Association Analysis Using Machine Learning

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The human microbiome is a term for the community of microorganisms living in the human body. The composition of the microbiome has the ability to influence the expression of various diseases in humans, and this phenomenon is often studied by analyzing it. In this study we sought to examine whether machine learning is a reliable tool for predicting the state of various cardiometabolic diseases based only on the gut microbiome. The research compared between the predictive abilities of different models on a dataset containing sequenced & assembled microbiomial data, and analyzed the bacteria that influence these models the most. In the research, it was found that some models can be used as effective diagnosis tools for some diseases. In addition, specific correlations were found between the presence of specific bacteria and diseases, such as E. coli and Type 2 Diabetes, Streptococcus bacteria and Coronary Artery Disease and many more. These findings show that machine learning can be an accurate, efficient and cheap solution for diagnosing various diseases, and that the gut microbiome has substantial influence on these diseases. Future studies may use the approaches developed in this project for further analysis of microbiomial data. The code developed for this research has been published as open source software, and despite it having some research specific optimizations, it can be implemented on any dataset, not necessarily microbiome-related.

Awards Won:
Fondazione Bruno Kessler: Award to participate in summer school "Web Valley"