

Machine Learning-based analysis of metagenomic profiles for the stratification of patients affected by type I Diabetes

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Although diabetes is known to be a disease that is closely linked to genetics and epigenetics, the mechanisms underlying the onset and/or progression of the disease have sometimes not been fully addressed in order to help patients. In recent years and due to a large number of recent studies, it is known that changes in the balance of the microbiota can cause a battery of diseases. Nowadays, massive sequencing techniques allow us to obtain the metagenomic profile of an individual, whether from a part of the body, organ or tissue, thus being able to identify the composition of a given microbiota. The use of Machine Learning (ML) techniques, which do not have any biological assumptions, are capable of identifying expression patterns and relationships between characteristics. We present a model based on ML techniques and a metagenomic signature capable of stratifying patients with Type I Diabetes (T1D), to serve as a support tool for clinical decision making.