Biomarker Analysis by Mass Spectrometry and Artificial Intelligence Techniques of Obese Human Plasma

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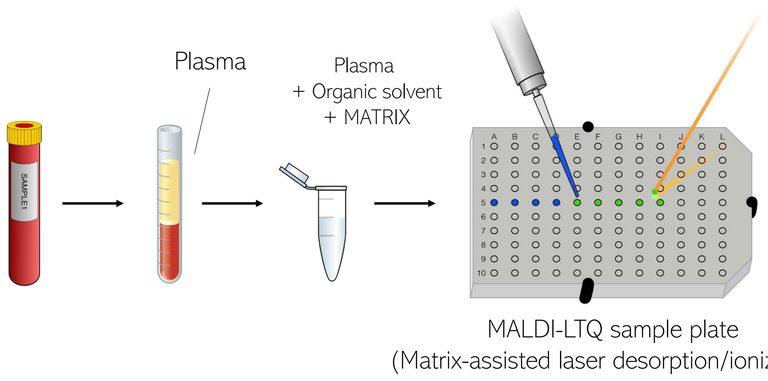
INTRODUCTION

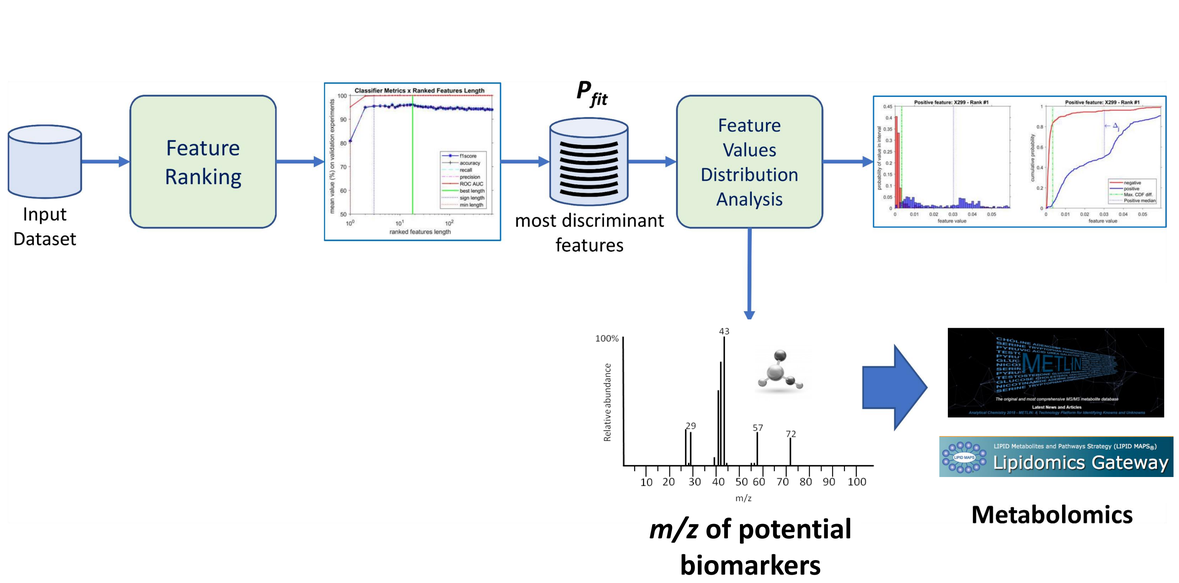
Obesity is characterized as a worldwide epidemic, accounting for more than 1.9 billion overweight adults and 600 million diagnosed with obesity. It occurs due to an energy imbalance resulting in the accumulation of fat in the cells of adipose tissue. Clinical recognition of obesity already has pre-established parameters, but the involvement of metabolic variations and tissue dysfunctions makes functional diagnosis and prognosis difficult. Although it's possible to classify individuals from new diagnostic methods, these methods do not contemplate all stages of the metabolic process related to adipogenesis. Following the advances of genomics and proteomics, new fields of "omics" are emerging. The metabolomics complement the studies in the area of genomics and proteomics, analyzing the final products of the cellular metabolic pathways. Therefore, the aim of this study is the determination of biomarkers present in the plasma of obese patients by mass spectrometry.

METHODOLOGY

To carry out the project, 90 volunteers of both sexes with diagnosis of overweight and obesity were selected. The participants were selected according to the Body Mass Index (BMI) with BMI individuals above 26 kg / m². For the control group, 90 volunteers of both sexes, eutrophic and free of obesity-associated comorbidities, were selected. From each individual of the groups, a 10mL blood tube with heparin was collected. From this material, 100µL of plasma was used for metabolomic analysis.



Plasma samples were immersed in organic solvent (CH3OH) and subjected to chemical protonation or deprotonation. They were then analyzed in Mass Spectrometers MALDI-LTQ-MS (Thermo Scientific) and LTQ-Orbitrap Discovery (Thermo Scientific).



Chemical markers will be determined from a machine learning algorithm (Random Forest). Random Forest is a robust and reliable classification method with high predictive performance and low generalization error that fits multiple decision trees and chooses a class that best aggregates the results of those trees.

RESULTS

The mean BMIs for the non-obese and obese groups were 22.3 kg/m2 (SD: ± 2.8; range: 17.4-32.0 kg/m2) and 33.3 kg/m2 (SD: ± 6.5; range: 25.1-66.1 kg/m2), respectively ($p<0.0001$). The body fat percentage (BF%) average in non-obese and obese groups was 21.7% (SD: ± 3.5; range: 13.7-29.9 %) and 40.3% (SD: ± 9.2; range: 24.9-62.0 %), respectively. The waist circumference average in obese group was 107.1cm (SD: ± 14.6; range: 75-149 cm). The non-obese group had no comorbidities (high blood pressure or diabetes), whereas 15 (37.5%) had hypertension and 7 (17.5%) had diabetes in the obese group.

Table 1. Anthropometric data of subjects

	Mean Control Group	Men	Women	Mean Case Group	Men	Women
No. Patients	90	31	59	90	19	71
Age (y)	35.1	35.02	35.39	38.9	44.26	37.4
Weigh (kg)	63.96	64.19	57.82	88.65	102.32	85.0
BMI (kg/m²)	22.26	22.28	20.96	33.33	34.15	33.1
Body fat percentage (%)	21.68	21.57	23.19	-	-	-
Waist circumference (cm)	-	-	-	107.1	108.9	105.3

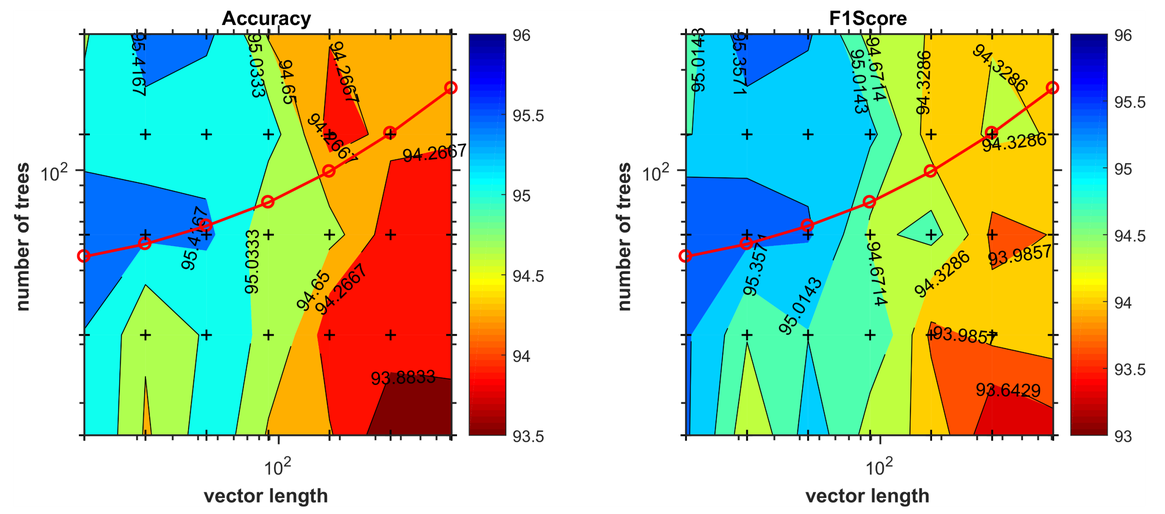


Figure 2 - Number of trees given by the grid-search procedure as a function of vector length. Cross marks inside the chart denote values evaluated during the grid search. The red line corresponds to the function used later in the method to compute the number of trees during the training stage for the determination of most discriminant features.

CONCLUSIONS

From the algorithm, 8 specific markers were identified for the obese group. We are now in the stage of elucidation of the molecules and their metabolic pathways.

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