Impact of serum metabolome isolation process on models' prediction of critically ill patients' mortality

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Metabolomics has emerged as a powerful tool in the discovery of new biomarkers for medical diagnosis and prognosis. Metabolomics of biofluids, such as serum, can therefore potentially deliver biomarkers that may be applicable in patients' monitoring [1]. This is especially relevant in the management of critically ill patients. However, there are numerous challenges, including the metabolome isolation process and the subsequent platform applied to analyze it. FTIR-spectroscopy presents diverse advantages for metabolome analysis, since it may be applied in rapid, economic, and high-throughput mode, while enabling to acquire the system's metabolic status with a high sensitivity and specificity [2,3]. In the current project, two extraction protocols of the serum metabolome were evaluated. Both protocols included macromolecules precipitation induced by mixtures of methanol, acetonitrile, and water. Replicas of 5μL extracted serum metabolome, from critically ill patients, were plated in 384 wells-microplates, and after a rapid dehydration step, spectra were acquired between 400 to 4000 cm^{-1}. The impact of the two extraction procedures to isolate the serum metabolome, on reproducibility, based on FTIR-spectra principal component analysis (PCA) was studied. The impact of the two extraction procedures on the performance of predictive models, based on spectra PCA-discriminant analysis of patients' mortality, was also conducted. Serum samples from critically ill patients were obtained according to legal and ethics requirements, including project ethics approval by the Hospital Ethics Committee (Centro Hospitalar Universitário Lisboa Central), and patients' informed consent.

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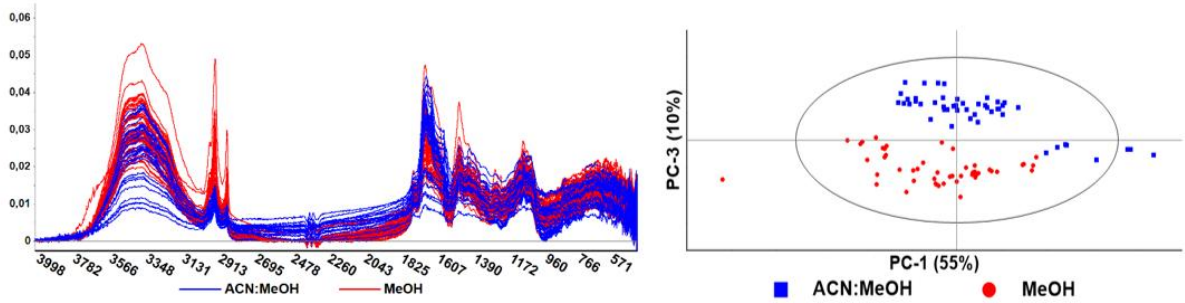

FTIR-spectra of serum metabolome from critically ill patients and its PCA. Serum metabolome was isolated by macromolecules precipitations by methanol or a mixture of methanol, acetonitrile and water.