

Impact of COVID-19 on critically ill patients' - mortality prediction models based on serum FTIR-spectra

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Abstract

Due to the relevance of mortality prediction of critically ill patients, it is common practice at intensive care units (ICU) to use physiological scores, e.g., APACHE II. However, these type of scorings don't enable to predict individual patients' outcome, mostly used for comparing groups of patients and ICUs [1]. It is therefore relevant to discover robust biomarkers of mortality prediction at ICU. Since FTIR spectroscopy can capture the whole molecular fingerprint of a system in a very specific and sensitive mode [2,3], in the present work, diverse mortality predictive models of support vector machines (SVM), based on FTIR-spectra of serum of critically ill patients, were developed. Serum samples from 200 patients at an ICU, with half presenting COVID-19 and the other half not presenting this infection, were considered. SVM models were optimized by combining spectral regions with diverse spectra pre-processing methods. A model cross-validation strategy, based on 10 random iterations, with 80% of samples for training and 20% for validation, was implemented. It was possible to develop very good SVM models to predict mortality based only on patients without COVID-19 (AUC=0.90), and a slightly better model was achieved for patients with COVID-19 (AUC=0.93). This difference can result from COVID-19 patients presenting a different metabolic status in relation to non-COVID-19 patients. Indeed, a very good SVM model enabled to discriminate these two populations (AUC=0.83). When considering the mixed population (i.e., with and without COVID-19), a slightly worse predictive SVM model was obtained (AUC=0.88).

Keywords

FTIR, COVID19, Mortality, ICU, Biomarkers

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References

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Figure captions

Fig.1. t-SNE of COVID-19 (red) and non-COVID19 (blue) patients.

Fig.2. t-SNE of deceased (red) and discharged, i.e., survived (blue) patients.