



Pre-processing Algorithm for Confocal Raman Spectra of in-vivo Human Skin

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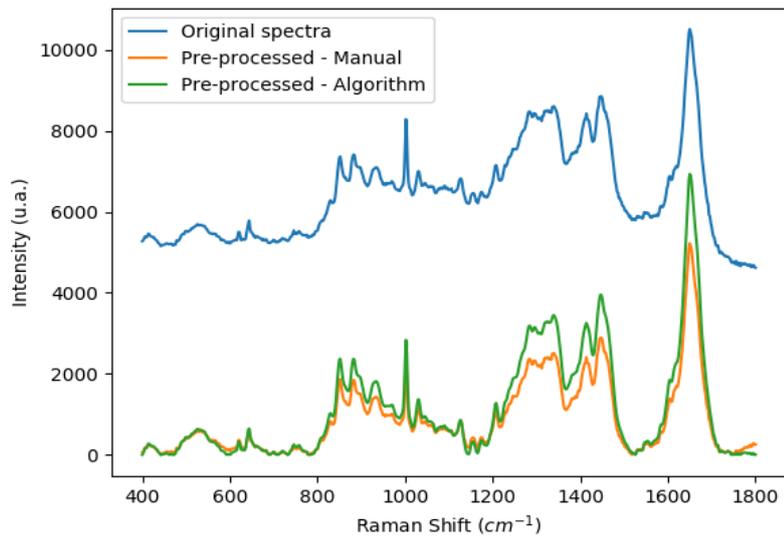
Background. The Raman spectroscopy is a non invasive technique that can provide substancial information about the composition of materials like minerals and biological tissues. It has been used in the biomedical field as an important diagnostic tool because it can show biochemical alterations on the tissue. The skin analysis can be performed by Raman Confocal Spectroscopy that can provide information in the diferent layers of the skin due its confocal len that can obtain spectra from stratum corneum until to dermis by changing the laser focus. **Motivation.** Before extract information from the spectra, it is necessary to apply the pre-processing on the data in order to obtain an spectrum without noise that represents real information, the basic pre-processing steps are the baseline removal, smooth and normalization. In a study the number of spectra to be analised can be huge, and the manual pre-processing can insert human mistakes in the data. **Objective.** The present work aims to develop an algorithm to perform the whole spectra pre-processing with a standard and reliable process.

Methods. The Raman spectra used to develop and test the algorithm were obtained by using a confocal Raman Spectrometer (River Diagnostics® - Model 3510) that was made specifically to analyse skin. The algorithm was developed using the Python programing language, the main features of it is to perform the baseline removal besides a smooth in the same process.

Results. It can be verified that the resultant spectrum after the pre-processing algorithm presented significant improvement in comparison to the manual pre-processing, as shown in the Figure 1.

Discussion and Conclusions. According to the first results, the algorithm showed to be reliable and the most important point is that it presents a pattern, mainly in the baseline removal when applied in Raman spectra in diferent skin depths, with no need to apply additional manual processing to correct the baseline.

Figure 1 - Comparison between spectra.



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