

Marcelo Teran¹

J.J. Ruiz², N. Carbo^{3,4}, P. Fernandez-Nogueira^{5,6}, G. Fuster^{3,4,6,7}, P. Loza-Alvarez², D. Masip¹, and D. Merino¹.

¹UOC, 08018, Barcelona, Spain, ²ICFO, Castelldefels, 08860, Spain, ³Dept. of Biochem. and Molecular Biomed., UB, 08028, Barcelona, Spain, ⁴IBUB, 08028, Barcelona, Spain, ⁵Unit of Biophys. and Bioeng., UB, 08014, Barcelona, Spain, ⁶FUBalmes, UVIC-UCC, Vic, Spain, ⁷MBM, IRIS-CC, UVIC-UCC, Vic, Spain.

mteranm@uoc.edu

Explainable, automated molecular abundance estimation in biological Raman spectra via Transformers and SHAP

The clinical adoption of Raman spectroscopy (RS) is often limited by expert-dependent preprocessing and a lack of model interpretability. Deep learning models, such as our Transformer-based RamanTF, automatically estimate the abundances of key biomolecules in biological samples from raw spectra. However, they are limited by their absence of prediction explainability. To overcome this, we developed a Biologically Informed Masked KernelSHAP explainability framework. Our method partitions the spectral domain into the known peak regions assigned to the predicted biomolecule and gap regions. It then calculates predictive importance (SHAP values) for each region by masking combinations of these regions to zero and measuring the impact on the model's output. We evaluated region attributions using the Peaks Importance Ratio (PIR) and Peaks Positive Contribution Ratio (PPCR) metrics, benchmarking RamanTF against a CNN across two cellular datasets (an in-house breast cancer and a public immune/stem cell dataset). SHAP analysis showed that RamanTF consistently based its predictions on biologically meaningful spectral bands. Consequently, the proposed biologically informed SHAP framework, combined with RamanTF, offers an automated, explainable pipeline for molecular abundance estimation contributing to the clinical translation of RS.

References

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Figures

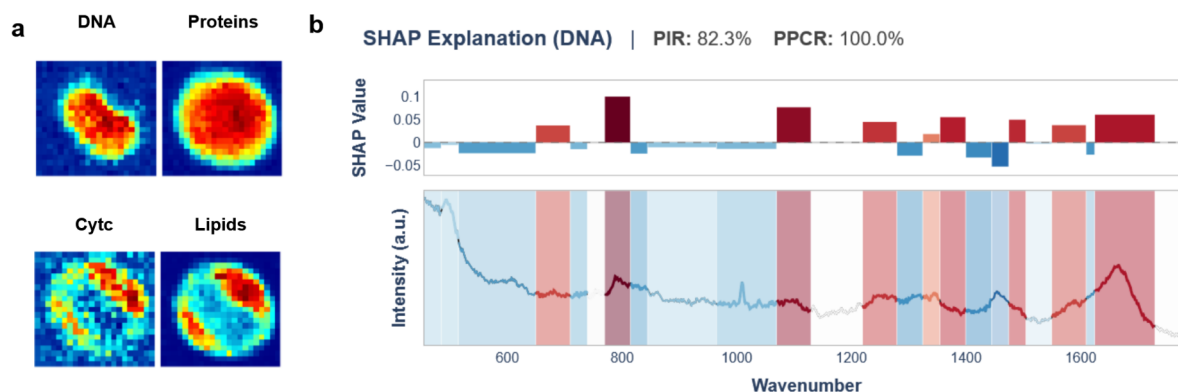


Figure 1: Results for a breast cancer cell. a) RamanTF abundance predictions of DNA, proteins, cytochrome c (cytc), and lipids. b) Biologically Informed Masked KernelSHAP output of the DNA prediction for a cell spectrum.