Lecturer: Renzo vanna

Preprocessing and analysis of hyperspectral maps: playing with RamApp (it includes a practical session)

Hyperspectral mapping techniques—particularly Raman imaging—provide rich biochemical information, but the raw data are often affected by instrumental and sample-related artefacts that can obscure meaningful trends and compromise quantitative analysis. This lecture introduces the practical foundations of preprocessing hyperspectral datasets, with a focus on Raman maps from biological samples. We will first review the main sources of noise and artefacts commonly encountered in spectral measurements (e.g., cosmic spikes, fluorescence/background contributions, baseline drifts, shot noise and detector artefacts), and discuss why preprocessing is not a “one-size-fits-all” procedure but should be tailored to the experimental goal and data characteristics. The session will then cover the core principles behind typical preprocessing steps, including calibration, interpolation, denoising, baseline correction, background subtraction, normalization, and related operations, highlighting their impact on downstream analysis and interpretation. Standard preprocessing algorithms will be presented alongside more advanced approaches, including semi-automated pipelines and AI-assisted strategies. The final part of the lecture will be a hands-on tutorial using **RamApp**, a free web-based platform developed by the speaker and collaborators (CNR, Politecnico di Milano, and Datrix S.p.A.), where participants will interactively preprocess and explore Raman hyperspectral maps from biological specimens. Participants are encouraged to bring a laptop with internet access to follow the practical session.