Experimental and bioinformatic tools to study protein protein interactions

Aims:
To acquire knowledge on the basic interactions that contribute do molecular recognition; to learn the principles, practical uses and limitation of both classical and more recent experimental and computational techniques to study molecular recognition processes.

Program:
Fundamentals of light- matter interaction. Electromagnetic spectrum. Structure of matter. Absorption and luminescence phenomena. Absorption and fluorescence spectroscopy of biological samples. Polarization of light. Linear and circular dichroism. Fluorescence anisotropy. Infrared and Raman (SERS) spectroscopy.
Microscopy: Principles of optics and microscopy. Optical and confocal microscopy. Ultraresolution methods, Probe scanning microscopy (STM, AFM, SNOM).
Classic experimental methods: Chromatography, Coimmunoprecipitation, Cross linking, Two-hybrid assay, in yeast and bacteria. Fluorescent based methods, fragment complementation.
Advanced experimental methods: Surface plasmon resonance (SPR), Atomic force microscopy, Optical Tweezers, In vivo imaging (FRET, STED)
Overview of Computational Methods: overview of the principal sequence and structure databases, Secondary DB, Structural Modeling, Large language and Transformer Models applied to protein structure predictions, Molecular Dynamics, Docking.