

Séminaire HélioBio du 18 avril 2017

Bioinformatics: Structure-Function-Evolution.

From molecular chaperones and protein folding to SAXS and membrane proteins.

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SWING beamline

What can bioinformatics do for You? As a protein biochemist - turned bioinformatician I travelled a strange road from in-vitro experiments on molecular chaperones, through evolutionary analysis, molecular modelling and dynamics to protein folding problem. I would like to start by briefly presenting the different perspectives and techniques which I learned along this road and show the synergy between them. This synergy is, however, incomplete without the experimental structural data, preferably from solution. This leads directly to my work in Soleil: modelling of membrane proteins using SAXS (and if possible other) data. I will mainly focus on our work on Memprot and ABCComplex - two programs developed at SWING beamline. Memprot can model the detergent corona based on SAXS curve and I would like to present our first attempts at using it with user-provided experimental data. ABCComplex is still in development program for ab-initio modelling of complexes of proteins and nucleic acids.