

Master « Sciences, Technologie, Sante » Mention « In Silico Drug Design »

Second Year

OFFER AN INTERNSHIP Academic Year 2013 – 2014

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Specialty training:	Research		Professional	
a few key words to describe the subject of training:				
Protein-protein docking, structural bioinformatics, homology modeling				
Title of internship:				

Expanding template-based protein-protein complex prediction by energy-based docking

this subject is a first step towards a thesis: Yes (depending on funding)

Short texte describing your project

The study of protein-protein interaction networks is essential to understand basic life processes at molecular level and to rationalize the increasing amount of genomic information for biomedicine purposes. However, available structures cover only a tiny fraction of the human interacome. Recent studies show that there could be templates to model a significant part of the interactome, but modelling accuracy and binding specificity are still unsolved problems. We will combine here template-based modeling approaches with protein-protein computational docking, in order to improve the prediction success rates and thus extend the structural coverage of protein interaction networks. Recent developments in docking scoring and treatment of flexibility, together with the high-performance computing facilities in the group, will help to make advances towards this challenging task.