Ecole Doctorale STIC

Sciences & Technologies de l'Information et de la Communication

MINES ParisTech

Université Nice SOPHIA ANTIPOLIS

ED STIC - Proposition de Sujets de Thèse

pour la campagne d'Allocation de thèses 2017

Axe Sophi@Stic :	BioSanté|
Titre du sujet :	Combinatorial optimization techniques leverage the reconstruction of atomic resolution models of large protein assemblies
Mention de thèse :	Informatique
HDR Directeur de thèse inscrit à l'ED STIC :	Frederic Cazals

Co-encadrant de thèse éventuel :

Nom :	Mazauric
Prénom :	Dorian
Email :	dorian.mazauric@inria.fr
Téléphone :	

Email de contact pour ce sujet :	dorian.mazauric@inria.fr
Laboratoire d'accueil :	INRIA

Description du sujet :

Voir descriptif en anglais.

URL : https://team.inria.fr/abs/files/2016/03/thesis16-large-assemblies2.pdf

English version:

CONTEXT

An antibody-antigen complex or an enzyme-inhibitor complex are example protein complexes involved in key biological functions, respectively the immune response and catalysis. The central problem in structural biology is to understand how the function of these molecular machines

emerge from their structure and dynamics. These studies are especially challenging since they require structural data, which are pretty scarce: as of today, the protein data bank contains circa 100,000 structures, while millions of coding sequences are known. Even worse, few of these structures concern protein complexes--the vast majority concern isolated molecules.

GOALS

The goal of this thesis is to develop novel methods to design atomic resolution models of molecular assemblies involving from 3 to 10 subunits. In such cases, two complementary sources of information are usually available: on the one hand, high resolution (i.e. atomic resolution) crystal structures of the isolated subunits; on the other hand, low resolution data for the whole assembly, typically coming from electron microscopy or mass spectrometry. A natural strategy therefore consists of combining these sources of information, to hopefully reach atomic resolution for the whole assembly. Doing so involves two mains steps, namely computing conformations of subunits compatible with low resolution data, and assembling these conformations to build the assembly. Both steps can be phrased as optimization and enumeration problems involving graphs, namely problems in the realm of graphical problems, and so graph algorithms techniques will be developed.

The goal of this thesis will be to contribute to such methods, and to validate them on systems involving from 3 to 10 subunits.

URL : https://team.inria.fr/abs/files/2016/03/thesis16-large-assemblies2.pdf