Internship, Master Thesis and PhD Thesis subjects proposed by
3BIO-BioInfo
Computational Biology and Bioinformatics

Our lab

Computational biology and bioinformatics is a field that permeates through all levels of science, from fundamental research to technology development and application. Our lab focuses on the development of bioinformatic tools and computational approaches that can be used both for investigating fundamental questions in biology and designing practical solutions particularly in biotechnology and medicine.

The methods used to build these tools are varied but mainly revolve around artificial intelligence, machine learning, data analysis, statistical physics, stochastic modelling and quantum chemistry. Experimental data is of paramount importance for most of these methods and we have therefore established strong connections with experimental labs from both academia and the industry. Moreover, our lab is part of a network of collaborators within the ULB-VUB (IB)[2] Interuniversity Institute of Bioinformatics in Brussels.

The bulk of our work consists in developing a suite of tools that enables the prediction of the changes caused by mutations on the biophysics of proteins (stability, solubility, binding affinity, …) and DNA (ionisation potential). These tools can be applied to study fundamental questions such as the identification and modelling of the mechanisms of natural selection, as well as bringing solutions to the design and optimisation of enzymes used in biotechnological processes or the identification of deleterious variants in diseases like cancer and autism.

Furthermore, we are developing tools for the prediction of epitopes in antigens, which can be applied to vaccine and antibody design, and the understanding of the mechanisms behind certain cancers, auto-immune diseases and allergies.

Finally, we are also working on the stochastic modelling of complex biological systems in order to gain insight on the properties that arise from the noisy interactions in complex systems like genetic circuits or cooperatively binding oligomers. This approach seeks to extend our fundamental understanding of biology as well as establishing design principles for application in synthetic biology.

Hereafter you can find the topics on which we can establish projects (internship, master thesis, PhD thesis) tailored to the student's interests, and the associated contact information.
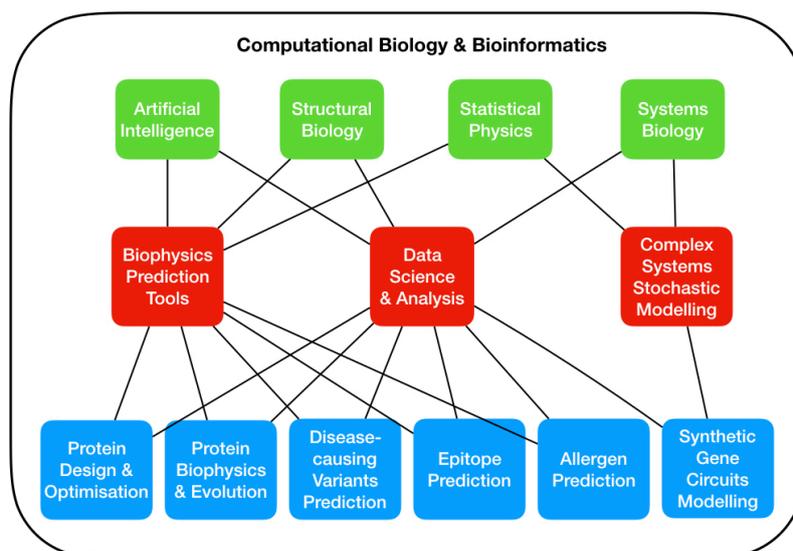
Schematic representation of our lab's topics of research (blue) according to the methods used (red) and their relevant fields of study (green).

Topics

1. Rational design of modified proteins [Marianne Rooman & Fabrizio Pucci]

Proteins carry out a large variety of biological functions in living organisms. Some proteins, for example, act as particularly specific and efficient catalysts. The possibility to exploit the functional properties of proteins in industrial applications (food industry, chemical processes, pharmaceutical developments, etc.) is extremely interesting; however, one of its major limitations is that proteins generally lose their stability and activity under non-physiological conditions. The ability to design modified proteins that remain structured and active at higher (or lower) temperatures is therefore an important objective of research. Moreover, the understanding of how changes in the coding sequence of proteins affect their biophysical properties is essential in fundamental research such as molecular evolution and phylogeny. This project consists in developing efficient and fast computational tools to predict changes in stability, solubility or interactions of proteins upon mutations, which are applicable on a genome-wide scale. This software will be applied to rationally modify proteins of industrial interest and increasing their efficiency within a given application, or to study fundamental questions of interest in biophysics and molecular evolution. This project is part of a spin-off company creation and allows for collaborations with experimental laboratories in academia or the industry.

2. Prediction of disease-causing variants in the human genome [Marianne Rooman & Fabrizio Pucci]

Next Generation Sequencing produces massive amounts of genome data that are revolutionizing biological and medical research, and paves the way towards personalized medicine. Among the exome variants that lead to amino acid mutations, most are neutral in the sense that they only modify the individual's phenotype, but some are the cause of diseases. The identification of deleterious mutations and their characterization are of prime importance for setting up personalized therapies. This them consists in developing and applying bioinformatics tools to predict disease-causing protein variants and trying to understand why they are so, in terms of protein characteristics such as stability, solubility, flexibility and function, or in terms of DNA characteristics such as ionisation potential. Moreover, this approach can be applied at a genome scale to specific case studies such as cancer or neurodevelopment disorders.

3. Prediction of B-cell epitopes for the rational design of vaccines [Marianne Rooman & Fabrizio Pucci]

Maintaining global health requires the development of generic and versatile technologies that allow fast and effective responses to the large variety of disorders, in particular cancer and emerging infectious diseases. Among these, peptide and protein vaccines play an important role. The *in silico* identification of immunogenic B-cell epitopes on potential antigens, which could be included in vaccines, is thus a challenging goal, and requires the development of reliable B-cell epitope prediction tools. To design such predictors, we will rely on experimentally characterized antibody-antigen complexes, detect informative sequence- and structure-based features, and combine them into a predictor using state-of-the-art machine learning techniques. This project can be applied to specific case studies such as chronic lymphocytic leukemia and allows for collaborations with cancer immunologists.

4. Synthetic gene circuits and noise control [Marianne Rooman & Fabrizio Pucci]

Synthetic biology is a relatively new field whose focus is on improving already existing and engineering new gene circuits. In order to implement a new gene circuit one must understand its behavior in terms of the system parameters. This requires that we understand not only the system's averaged deterministic behavior, but also how random variations, *i.e.* internal and external noise, affect its performance. This project consists in modeling systems of increasing complexity, using stochastic differential equations, and analyzing their noise levels defined as the variance of the number of molecules. We will investigate models of various biological systems, such as prokaryotic and eukaryotic gene regulation and protein oligomerization, and attempt to understand the general relationship between noise, complexity, and some key characteristics of the systems.

5. Food and house dust mite allergens [Dimitri Gilis]

Allergy represents an important public health problem. On the one hand, we are developing bioinformatics tools to predict whether a protein corresponds to a food allergen. Such tools are very important for the development of new food products. On the other hand, we are studying certain structural and dynamic properties of house dust mite allergens.

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