Biological network reconstruction from a combination of perturbative and non-perturbative data

Résumé du projet de recherche (Langue 1)

The objective of this PhD project is to develop and implement a novel information-theoretic method to reconstruct biological networks from a combination of perturbative and non-perturbative data. Perturbative data are obtained by intervening on a biological system for instance through gene silencing or drug treatment. Our group has recently developed an efficient algorithmic approach, MIIC, to recontruct a broad range of causal and non-causal networks from non-perturbative data alone (Sella et al. Bioinformatics 2017, Verny et al. PLoS Comput Biol 2017). However, when available, controlled perturbation experiments may also provide useful information in many biological and medical contexts, such as silencing of gene expression or clinical assays for drug treatments.

This PhD project aims at extending MIIC network reconstruction method to integrate both perturbative and non-perturbative data, and apply it to large scale gene expression and knockdown data from the literature and public databases as well as breast cancer genetic and clinical data from our collaborators at Institut Curie.

Informations complémentaires (Langue 1)

Applicants should have a strong background in computer science or machine learning and a keen interest to analyze complex heterogeneous data of biological and medical interests. Applicants should be proficient in programming and willing to interact with scientists from different disciplines, from data scientists to medical doctors.

For more information on the group: http://kinefold.curie.fr/isambertlab