若手研究者インターナショナル・トレーニング・プログラム(ITP)
バイオインフォマティクスとシステムズバイオロジーの国際連携教育研究プログラム　応募書類

Name: Yang Zhao
Title: Modelling the Robustness of Metabolic Pathways
Institute: Bioinformatics Center, Institute for Chemical Research, Kyoto University
Partner institute of your choice: Centre for Computational Biology, Mines ParisTech
Duration of your choice: September 9, 2011 – November 27, 2011

Plan

Background

My current research focuses on analysis of tree-like compounds, which deals with synthesis analysis, tree-structured data compression and enumeration of tree-like compounds.

For synthesis analysis, a dynamic programming algorithm was proposed to predict synthesis processes of tree-structured compounds with graph grammar. This research was presented in the Tenth Annual International Workshop on Bioinformatics and Systems Biology (IBSB2010) held in Kyoto, Japan.

The second study firstly proposed integer programming-based methods for finding the minimum grammars to generate given strings, ordered trees and unordered trees. We applied these methods to glycan tree structure data to confirm the accuracy, and extract interesting patterns. This research was presented in SIG-FPAI 78 held in Kobe, Japan and in The 21st International Conference on Genome Informatics (GIW2010) held in Hangzhou, China. And this research was also published in BMC Bioinformatics, BioMed Central, 11(Suppl 11): S4, 2010.

The ongoing research is enumeration of chemical molecules. In this work, an efficient algorithm to enumerate tree-like molecules without duplications has been proposed by similarly treating tree-like molecules as rooted trees. As computational experiments indicated, this method reduces the search space and has high speed. For chemical molecules which have cycles, an extension of this proposed method is being done.

Research objective

The partner laboratory is Centre for Computational Biology belonging to Mines ParisTech. The group leader is Prof. Jean-Philippe Vert. One of the researches of this lab is bioinformatics analysis of cancer genomic data. As we know that metabolic pathways are complex systems of chemical reactions taking place in every living cell to degrade substrates and synthesize molecules needed for life. Reactions can be perturbed by, e.g., drugs or mutations in DNA. When one or a few reactions are perturbed, the impact of this perturbation on the cell can vary widely, depending on how many other reactions are impacted in cascade. The group is recently interested in the project of modeling the robustness of metabolic pathways in cancer research. And the motivation is to propose and implement new computational models to quantify the impact of inhibiting one or a few reactions on the global metabolic network, and to evaluate the robustness of metabolic networks based on this model.

Plan

The specific work is as follows:

- ✧ Learn related knowledge about kernel methods, Bayesian network, branching process and network biology from Prof. Jean-Philippe Vert, who is an expert in these fields.
- ✧ Study a similar model which better takes into account the structural properties of the metabolic network than the recent one (<Analysis of the impact degree distribution in metabolic networks using branching process approximation>, *Physica A*, to appear) did.
- ✧ Learn how to implement this model to quantify the impact of inhibiting one or a few reactions on the global metabolic network, and also learn how to evaluate the robustness of metabolic networks based on this model.
- ✧ Develop advanced computational and mathematical methods for modelling the robustness of metabolic pathways in cancer research, such as computational tools to predict the effects of combinatorial inhibitions, which could help in the design of new cocktails of drugs targeting several proteins.
- ✧ Improve English skill by communicating with native speakers, giving presentations and writing academic papers.
- ✧ Learn the way of international collaboration through collaboration on this project.