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: Unyanee Poolsap

Title: Computational methods for predicting single and interacting RNA secondary structures

Institute: Bioinformatics Center, Institute for Chemical Research, Kyoto University

Partner institute of your choice : Department of Biology and Computer Science Program in Bioinformatics Boston University

Duration of your choice: February 19 - May 18, 2010

Plan :

**Background**:

The research that I have been doing is RNA secondary structure analysis using the mathematical methods and computational algorithms to model and predict RNA secondary structures and RNA-RNA interaction structures.

In particular, the first project was RNA secondary structure prediction using integer programming. The structure prediction problem is modeled as an optimization problem under some constraints. Since the arbitrary structure is NP-hard for prediction, we constructed some constraints to limit the scope of structures that our algorithm can predict. We proposed integer programming model for prediction of RNA secondary structure with a subclass of pseudoknot. This research was presented in The Seventh Asia Pacific Bioinformatics Conference (APBC2009) held in Beijing, China. It was also published in BMC Bioinformatics, vol. 10, suppl. 1, Jan. 2009.

The ongoing project is RNA-RNA interaction prediction and target discovery. In this work, we incorporate binding site profile of an antisense RNA to reduce the computation time of RNA-RNA interaction prediction. We use dynamic programming with binding site profile to predict secondary structure and interaction site(s) of target RNA. We also apply our algorithm to search for target RNA(s) of a given antisense RNA. The preliminary result has been published in Proceedings of The 15th Pacific Symposium on Biocomputing (PSB2010), page 98-107.

**Research objectives:**

The partner laboratory is Laboratory for Biocomputing and Informatics which belongs to the Department of Biology and Computer Science, Program in Bioinformatics, Boston University. The group leader is Associate Professor Gary Benson. This lab mainly focuses on development of algorithms and software tools for detection and analysis of novel repeats and reverses patterns in DNA sequences. The project that I will be involving is a collaborative research on developing an algorithm for mapping sequencing data to the human genome. The algorithm will take short fragments of DNA sequence from the sequencer machine as inputs. Since the input sequences contain some errors in general, the algorithm should be able to handle some erroneous sequences and map them to the human genome with reliability and effective computation time.

Plan (Continued)

Advantages that I expected to gain from participating ITP:

- Have a chance to study sequence analysis in genome-wide scale, which could be used to improve my recent research project. For example, enhance my algorithm so that it is able to search for RNA binding site in genome-wide scale.
- Apply algorithms that I have been used to model RNA sequences (Integer programming and Dynamic Programming) to the project that I will be participating in the partner laboratory.
- Improve my programming skill
- Acquire experience of working in a collaborative project.
- Improve English skill in communicating with native speakers, giving presentations as well as writing academic papers.