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: Zhao Jin

Title: Comparative metagenomics analysis of microbial communities across bacteria

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

Partner institute of your choice：Bioinformatics Program, Boston University

Duration of your choice: January 16, 2012 ~ April 8, 2012

Plan：

Research Objectives:

I would like to apply for the ITP program for three months' study in Dr. Daniel Segre's laboratory, which belongs to Department of Biology & Department of Biomedical Engineering, Bioinformatics Program, Boston University.

There are various research interests in this partner laboratory which attract me very much, mainly using mathematical, computational and experimental approaches to study the dynamics and evolution of metabolism in individual microbes and in microbial ecosystems. They approach the questions of whether optimality principles are helpful in understanding the architecture and utilization of metabolic networks both in simplified artificial chemistries and in the global map of known biochemical reactions across all organisms; what role the metabolism played in the emergence of complex multicellular life (joint project with the NASA Astrobiology Institute (NAI) MIT team); the prediction of evolutionary trajectories of microbial metabolism; also the analysis on microbial community dynamics and synthetic ecology, and so on.

I used to focus on several bioinformatics studies such as oncogenic pathway characterization according to virus analysis and target prediction of viral miRNA. I believe this visiting would provide a great chance to apply and improve my research skills. Also during the communications with researchers and students joint with different programs from various countries, it will be beneficial to my professional vision and English communicating skills.

Research Plan:

Metagenomics is a rapidly growing field of research that aims at studying uncultured organisms to understand the true diversity of microbes, their functions, cooperation and evolution, in environments such as soil, water, ancient remains of animals, or the digestive system of animals and humans. Comparative analysis between metagenomes can provide additional insight into the function of complex microbial communities and their role in host health.

Plan (Continued)

Because bacteria species can be identified on the basis of 16S rRNA from the metagenomic datasets, our research would like to focus on the functional comparisons between metagenomes across bacteria made by comparing sequences against reference databases such as COG or KEGG, and tabulating the abundance by category and evaluating any differences for statistical significance in order to reveal the effect of habitat upon community structure and function. Besides, metagenomic sequencing is particularly useful in the study of viral communities, which could be applied in one of my past studies on virus. As viruses lack a shared universal phylogenetic marker (as 16S RNA for bacteria), the only way to access the genetic diversity of the viral community from an environmental sample is through metagenomics.

What's more, understanding metabolism is one of the major research interests in Dr. Daniel Segre's laboratory, they usually focus on microorganisms and try to model the metabolism through FBA (Flux Balance Analysis), which is a mathematical method for analyzing metabolism, to some extent. Therefore, the second plan during my stay is to understand the details of FBA and learn to work with this model, which may provide a new angle to my pathway research.

In conclusion, I will take part in not only researches but also events and communications actively during the three months' stay in Boston, trying to explore and experience various things that can only be obtained in this opportunity.