

若手研究者国際ショナル・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
ワークショップ参加レポート

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Title: IBSB 2012 Participation Report

Workshop Report:

As an oral presenter, I had a great opportunity to participate in 12th International workshop on Bioinformatics and Systems Biology (IBSB) July 22-26, 2012 in Boston University. This was revisiting of the place as a part of ITP after an interval of 3 years, and thus it was very emotive to see people and atmosphere there again.

The workshop took place over 5 days including the first day of reception and the last day of faculty presentation that was the first attempt in this workshop from this year. There were 29 presentations either in oral or poster from members in Boston, Japan, Germany and newly participating Austria. In poster session, I spent more time on explaining my research. It was a quit hard but fruitful practice to get my research across to several people with different background within limited time, and it was nicer that they didn't just listen to but responded to me many times. Unfortunately, I couldn't find any presentations close to my research field, but I found that many people were working for application of microarray and next-generation sequence data especially on human-diseases and having tight connections to experimental laboratories. Other people were more toward system biological aspect of a cell or even larger scope of biological units and showing their models with solid mathematical backgrounds, but basically all the presentations covered a wide range of topics.

Regarding oral presentation, both presenters and audiences actively argued. I gave a talk entitled "Comparative analysis of antigenic variant gene families of *Plasmodium* species". I introduced both commonality and peculiarity found in this type of gene families compared with other multigene families and discussed how these characteristics were important in term of evolutionary framework in host-parasites

interaction. Having questions from 5 people, I was mainly pointed out about the methods I used, which may or may not be very crucial but something I had never considered. Another was suggestion to investigate the possibility that these families were under different types of genomic modifications I didn't mentioned and was actually pertinent.

The rest of the time during the workshop was very nicely coordinated and refreshing. Every night was stuffed with some exciting activities.

Finally, I express my gratitude for Minoru Kanehisa, Susumu Goto and Hiroshi Mamitsuka who gave me such a precious and valuable chance, and also thank all the participants and organizers in Boston University who kindly devoted to make our stay very exciting.

