The 66th NIBB Conference / ABiS International Symposium "Cutting Edge Techniques of Bioimaging"

Organizers: Naoto Ueno (NIBB), Toshihiko Fujimori (NIBB), Junichi Nabekura (NIPS), Masanobu Kano (NIPS / The University of Tokyo)

February 17 (Sun)–18 (Mon), 2019

Imaging technology has been widely applied to areas ranging from molecules, cells, tissues and all the way up to individual organisms. It has consequently become an essential analytical tool in the field of life science research. The development of new probes, microscopes and quantitative analytical methods, as well as the ability of being able to extract biological information from images, has progressed at a remarkable pace. As a result, we can now observe both multiple objects and the spatial temporal dynamics of the subjects simultaneously at both high speed and resolution.

NIBB has taken on a major role within the field of bioimaging in Japan as evidenced by its involvement in the advancement of various activities. These roles have involved the development of new observation technology and bioimage analysis methods and their circulation through bioimaging training courses, conducting the NIBB collaborative research projects for integrative bioimaging, and taking on the role of core institute in coordinating the Advanced Bioimaging Support (ABiS) activities in conjunction with NIPS. Against this backdrop, the 66th NIBB Conference, entitled "Cutting Edge Techniques of Bioimaging", was held in cooperation with ABiS at the Okazaki Conference Center from February 17th to 18th.

This conference aimed to deepen discussion concerning cutting edge bioimaging as well as sharing information regarding this area. In particular, there was a focus on super high resolution and live cell imaging. Events included:

- Lectures conducted by both domestic and international researchers engaged in cutting edge projects in the above-mentioned fields
- Imaging related poster presentations
- Short talks about various posters chosen from those on display

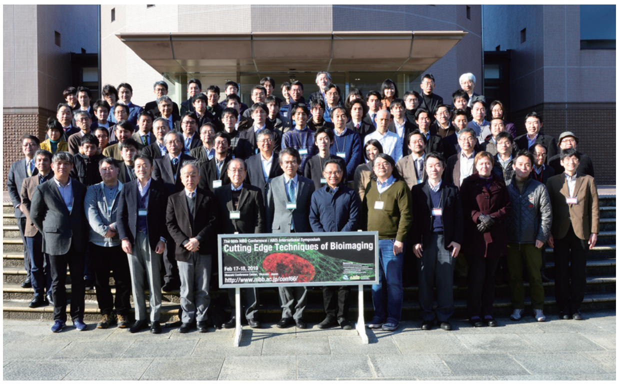
Additionally, much passionate discussion was also exchanged prior to the lecture's Q and A and poster sessions.

A total of 102 participants were able to obtain information on results and analytical techniques concerning the use of advanced bioimaging equipment. They were also able to think more deeply about the usage of advanced imaging techniques in their research. Furthermore, it was also a good opportunity to rethink cooperation in the field of bioimaging with other institutes and researchers.

Due to problems such as budgetary constraints, it is becoming progressively more difficult to introduce advanced equipment and operate it under suitable conditions. Network support activities such as ABiS, which was founded three years ago and has provided advanced bioimaging technologies, are necessary to support bioimaging research in Japan.

In closing, we would like to express our gratitude to the members of NIBB and NIPS for their efforts in hosting this conference.

Shoji Mano (NIBB /ABiS Administration Office)



Speakers

Chew, Teng-Leong (HHMI Janelia, USA), McDole, Kate (HHMI Janelia, USA)
Higashiyama, Tetsuya (Nagoya University, Japan), Okada, Yasushi (The University of Tokyo / RIKEN, Japan), Tamada, Yosuke (NIBB, Japan), Wake, Hiroaki (Kobe University, Japan), Watanabe, Naoki (Kyoto University, Japan)

The 67th NIBB Conference / The 6th Quest for Orthologs Meeting "Quest for Orthologs"

Organizers: Ikuo Uchiyama (NIBB), Christophe Dessimoz (UNIL), Toni Gabaldón Estevan (CRG), Erik Sonnhammer (SU), Paul D. Thomas (USC), Wataru Iwasaki (UTokyo), Shigehiro Kuraku (RIKEN BDR), Shuji Shigenobu (NIBB)

July 31 (Wed)–August 2 (Fri), 2019

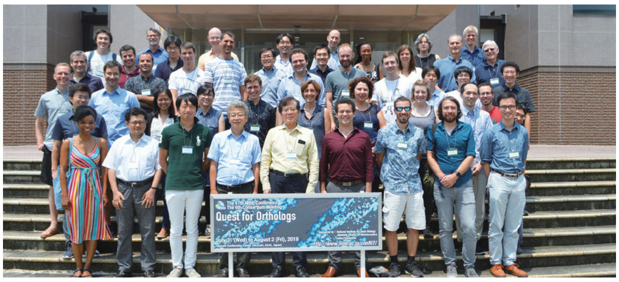
The 67th NIBB conference "Quest for Orthologs" was held with a focus on orthology analysis as a fundamental technology in the field of comparative genomics; something that is becoming more important as genomic technology is applied to a broader range of organisms. This meeting originated from the international consortium of the same name "Quest for Orthologs," which was established in 2009 by developers of orthology inference methods. Since then, the consortium has held a meeting biennially to discuss common subjects in the development of orthology inference methods such as benchmark tests for evaluating methods, a reference sequence set commonly used as input, and a common data format to represent orthology relationships, in addition to presenting the latest results from this field. This meeting, which marked the tenth anniversary of the abovementioned events being held, was hosted in Japan. This was the first time that it had been held outside of Europe and United States, and about half of the participants were from local institutions. As a part of the NIBB conference series, application of orthology inference methods to gene function predictions and/or evolutionary studies with application to biological studies using various organisms were also featured during this meeting.

The conference consisted of four sessions: the development of orthology inference methods and databases, application to function prediction, their application to evolutionary analysis, and new challenges in orthology inference issues. There were 22 invited speakers including 4 keynote lectures, as well as 8 oral presentations and 14 poster presentations by young researchers. During the round table discussion session held at the end of the second day, lively discussions were conducted between developers and users of orthology inference methods.

While this meeting was focused on the specific field of orthology inference methods, it covered a broad range of relevant studies from the basics to specific applications, and provided a good opportunity to review the current and future status of this field as a basis of various genomic studies. A large portion of the event's budget was used to financially support the travel expenses of students and young researchers, who themselves were active contributors to the discussions held during the conference.

We would like to thank all the presenters and participants for helping to stage this conference, the Japanese Society of Bioinformatics and Daiko Foundation for financial support, and the International Cooperation Group of the Research Enhancement Office for organizing the conference.

Ikuo Uchiyama (Laboratory of Genome Informatics)



Speakers

Altenhoff, Adrian (ETH Zurich / SIB Swiss Institute of Bioinformatics, Switzerland), Capella-Gutierrez, Salvador (Barcelona Supercomputing Center, Spain), Dessimoz, Christophe (University of Lausanne, Switzerland), Durand, Dannie (Carnegie Mellon University, USA), Ebersberger, Ingo (Goethe University Frankfurt, Germany), Hansen, Madison (American Museum of Natural History, USA), Jones, Tamsin (EMBL-EBI, UK), Kelly, Steven (University of Oxford, UK), Kriventseva, Evgenia (University of Geneva, Switzerland), Lecompte, Odile (ICUBE/University of Strasbourg, France), Linard, Benjamin (LIRMM, France), Mendes, de Farias Tarcisio (University of Lausanne, Switzerland), Moi, David (UNIL, Switzerland), Nevers, Yannis (ICube laboratory UMR7357, France), Ouangraoua, Aida (University of Sherbrooke, Canada), Patricio, Mateus (EMBL-EBI, UK), Pearson, William (University of Virginia, USA), Sonnhammer, Erik (Stockholm University, Sweden), Szklarczyk, Damian (SIB Swiss Bioinformatics Institute / University of Zurich, Switzerland), Thomas, Paul D. (University of Southern California, USA), Toni, Gabaldón (Centre for Genomic Regulation (CRG), Spain), Warwick, Vesztrocy Alex (University College London, UK), Chiba, Hirokazu (Research Organization of Information and Systems, Japan), Hara, Yuichiro (Nagoya University, Japan), Horiike, Tokumasa (Shizuoka University, Japan), Iwasaki, Wataru (The University of Tokyo, Japan), Kanehisa, Minoru (Kyoto University, Japan), Kuraku, Shigehiro (RIKEN BDR, Japan), Shigenobu, Shuji (National Institute for Basic Biology, Japan), Uchiyama, Ikuo (National Institute for Basic Biology, Japan)