The 11th NIBB Bioimaging Forum "Pioneering New Bioimaging by Fusing Optics and Biology"

Organizers: Yasuhiro Kamei, Hideki Takami, Yutaka Hayano, Mitsuo Takeda, Hirotsugu Yamamoto, Masayuki Hattori, Takashi Murata, Shigenori Nonaka, Yosuke Tamada

February 14 (Tue) -15 (Wed), 2017

We held the 11th NIBB Bioimaging Forum on February 14th and 15th 2017. The subtitle for this meeting was "Pioneering New Bioimaging by Fusing Optics and Biology", and aimed at the development of new fields in bioimaging by inviting experts in various disciplines including optical engineering and astronomy to give lectures. Fifty four participants (8 were from NIBB, 46 from outside in which 24 were from private companies) from a wide variety of specialties, such as optics, engineering, mathematics, astronomy, biology, medicine, and agricultural science. The first session of the forum, therefore, included descriptions of characteristics of each field by specialists in biology, optical engineering, and astronomical optics to enhance understanding each other. The succeeding 4 sessions included 15 lectures (30 minutes each with 5 minutes discussion) and 10 posters. Dr. Mitsuo Takeda, a famous theoretical optics specialist, summarized at the end of the forum how we came to understand the "philosophy and condition" of each field, which is necessary to fuse different fields. Forums aiming to establish new methods of bioimaging by fusing different fields are still rare and we believe our forum is functioning well as a start point.

(Yasuhiro Kamei)

The NIBB Genome Informatics Training ourse

The NIBB Core Research Facilities organizes a series of training courses on up-to-date research techniques. The NIBB Genome Informatics Training Course (GITC) is specially designed for biologists who are not familiar with bioinformatics. In 2017, we held two sets of training courses on RNA-seq analysis, a UNIX learning course and a course on BLAST analysis. We provided the RNA-seq analysis course divided into two 2-day programs: one was a preparatory course to learn basics of UNIX and R and the other was a practical course to learn pipelines of RNA-seq analysis using next-generation sequence data. The UNIX learning course was a 2-day program for beginners who are starting bioinformatics. The BLAST analysis course was designed for advanced users aiming to enable participants to get familiar with a large scale sequence database search in the local environment using BLAST software in a robust and systematic manner. These GITC courses offered lectures and hands-on tutorials.

Introduction to RNA-seq – from the basics of NGS to *de novo* analyses

■Organizers: Dr. Shuji Shigenobu and Dr. Ikuo Uchiyama (NIBB Core Research Facilities)
■Lecturers: Dr. Shuji Shigenobu, Dr. Ikuo Uchiyama, Dr. Masanao Sato (Hokkaido Univ.), Mr. Tomoki Miwa, Dr. Katsushi Yamaguchi, Ms. Hiroyo Nishide, Mr. Takanori Nakamura (NIBB Core Research Facilities)

February 23(Thu)-24(Fri), 2017

(Preparatory Course) Basics of UNIX, R, and NGS
■Participants: 23 (including 4 from NIBB)
■Program:
1. UNIX for beginners
2. Introduction to "R"
3. NGS basic data formats and NGS basic tools
4. Text processing
5. Shell scripting
6. Exercises

March 9(Thu)-10(Fri), 2017

(Practical Course) RNA-seq analysis pipeline
■Participants: 21 (including 3 from NIBB)
■Program:
1. Introduction to statistics
2. RNA-seq for beginners: genome-based and transcriptome-based approaches
3. Multivariate statistics
4. Exercises

Introduction to UNIX for analyses of large scale biological data sets

June 22(Thu)-23(Fri), 2017

■Organizer: Dr. Ikuo Uchiyama (NIBB Core Research Facilities)
■Lecturers: Dr. Ikuo Uchiyama, Mr. Tomoki Miwa (Head of Technical Division), Ms. Hiroyo Nishide, Mr. Takanori Nakamura (NIBB Core Research Facilities)
■Participants: 22 (including 6 from NIBB)
■Program:
1. UNIX for beginners
2. Introduction to NGS data analysis
3. Text processing
4. Shell scripts
5. Usage of job management system
6. Exercises

Mastering BLAST, the essence of sequence analyses

September 14(Thu)-15(Fri), 2017

■Organizers & Lecturers: Dr. Shuji Shigenobu, Dr. Ikuo Uchiyama (NIBB Core Research Facilities)
■Participants: 21 (including 5 from NIBB)
■Program:
1. BLAST for beginners
2. Local BLAST search with command-line
3. BLAST inside – theoretical background of sequence search
4. Large scale BLAST search
5. Annotation of genes and ortholog analysis
6. Beyond BLAST

The 5th BioImage Analysis Training Course

Organizers: Dr. Kagayaki Kato, Dr. Yoshitaka Kimori, Dr. Yasuhiro Kamei, Dr. Hiroshi Koyama, Dr. Shigenori Nonaka, Dr. Takashi Murata.
Supervisors: Prof. Naoto Ueno, Prof. Toshihiko Fujimori.

November 20 (Mon) -22 (Wed), 2017

The 5th BioImage Analysis Training Course was held jointly by the Center for Novel Science Initiatives' Department of Imaging Science, JSPS KAKENHI Platforms for Advanced Bioimaging Support (ABiS), and NIBB. This course was designed for biologists who are relatively new to analyzing datum obtained through advanced microscopy. Therefore the focus of training was learning image processing and analytical techniques through "solving simple problems with image analysis" and "understanding appropriate methods and necessary preparation for consulting experts in technically advanced imaging challenges". 47 people applied for the course, which had a maximum capacity of 18 participants, this clearly suggests the height of the demand for courses on these subjects.

This course's lectures were conducted with the aim of training participants to keep in mind the series of steps essential to fundamental image processing and analysis while obtaining images to be used (workflows). In addition, we loaned the participants PCs pre-installed with ImageJ, a typical open-source software package for biological image processing and analysis, and images which were used for practicing the basic operations and settings of image processing. Also, lectures were given on how programming of simple "macro-programs" which use these workflows in ImageJ allows automation, which is essential for the large capacity and high-dimensional throughput of microscopic imaging which has become common in recent years.

At the conclusion of the course each of the students gave commentary and discussed the methods used with examples of actual images from their own research. Every year after the course, participants express feeling "pretty tired, and satisfied" as part of the questionnaire, and certainly there is a true benefit in terms of their image analysis by becoming more familiar with these techniques. In addition, we expect that this course will increase opportunities for joint research relating to biological image analysis.

(Kagayaki Kato)