

## The 10th NIBB Bioimaging Forum “Pioneering Bioimaging in the New Era”

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

We held the 10th NIBB Bioimaging Forum on February 16<sup>th</sup> and 17<sup>th</sup> 2016. The subtitle for this meeting was “Pioneering Bioimaging in the New Era”, and aimed at the development of new fields in bio-imaging by asking experts in various disciplines (optics, engineering, mathematics, astronomy, biology) to give lectures on new and anticipated imaging methods on the horizon. The forum was divided into 5 sessions; on the first day “The Present State and Problems of Imaging in the Fields of Biology and Astronomy” was addressed, followed by “Optical Theory Opening Up the Future of Imaging”, which covered the latest optical theory on holography and coherence, and the lecture “Creation of New Imaging Technology 1” on topics such as tomography was given. On the second day, we held the lecture “State-of-the-Art Image-Sensors and Devices” on cutting-edge camera technology and “Creation of new Imaging Technology 2” on the sparse modeling theory. There were 52 people in the audience, and more than 10 industry attendees. At the end of the forum a comprehensive discussion was held with all members, including the audience, and a consensus was reached on the necessity and difficulties of fusing the imaging fields. In addition, nearly 30 participants remained in the venue after the forum, and enthusiastic discussions and consultations on joint research took place. Although meetings aiming at establishing new bioimaging methods through fusion of different fields are uncommon in Japan the active interaction of participants at this forum lead to its success.

(Yasuhiro Kamei)



## The NIBB Genome Informatics Training Course

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 2016, we held two sets of training courses on RNA-seq analysis and one course on BLAST analysis. While we previously provided a 3-day program on RNA-seq analysis, we rearranged the course this year dividing it 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 new BLAST analysis course aimed to enable participants to get familiar with a large scale sequence database search in the local environment using BLAST software for systematic sequence data analyses. These GITC courses offered lectures and hands-on tutorials.

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

February 25(Thu)-26(Fri), 2016

(Preparatory Course) Basics of UNIX and R

■ Organizer: Dr. Ikuo Uchiyama (NIBB Core Research Facilities)

■ Lecturers: Dr. Ikuo Uchiyama, Dr. Shuji Shigenobu, Mr. Tomoki Miwa, Ms. Hiroyo Nishide, Mr. Takanori Nakamura (NIBB Core Research Facilities)

■ Participants: 22

■ Program:

1. UNIX for beginners
2. Introduction to “R”
3. Text processing
4. Shell scripting
5. Exercises



March 10(Thu)-11(Fri), 2016

(Practical Course) RNA-seq analysis pipeline

■ Organizer: Dr. Shuji Shigenobu (NIBB Core Research Facilities)

■ Lecturers: Dr. Shuji Shigenobu, Dr. Ikuo Uchiyama, Dr. Katsushi Yamaguchi, Ms. Hiroyo Nishide (NIBB Core Research Facilities), Dr. Masanao Sato (Keio Univ.)

■ Participants: 21 (including 1 from NIBB)

■ Program:

1. NGS basic data formats and NGS basic tools
2. Introduction to statistics
3. RNA-seq pipeline: genome-based and transcriptome-based approaches
4. Multivariate statistics
5. Exercises



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

August 25(Thu)-26(Fri), 2016

(Preparatory Course) Basics of UNIX, R, and NGS

■ Organizer: Dr. Shuji Shigenobu, Dr. Ikuo Uchiyama (NIBB Core Research Facilities)

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

■ Participants: 22 (including 3 from NIBB)

■ Program:

1. UNIX for beginners
2. Introduction to “R”
3. NGS basic data formats and NGS basic tools
4. Text processing in UNIX
5. Introduction to bias4 system
6. Exercises

September 8(Thu)-9(Fri), 2016

(Practical Course) RNA-seq analysis pipeline

■ Participants: 22 (including 3 from NIBB)

■ Program:

1. Review NGS basic data formats and NGS basic tools
2. Introduction to statistics
3. RNA-seq pipeline: genome-based and transcriptome-based approaches
4. Multivariate statistics
5. Exercises

## Mastering BLAST, the essence of sequence analyses

December 1(Thu), 2016

■ Organizers & Lecturers: Dr. Shuji Shigenobu, Dr. Ikuo Uchiyama (NIBB Core Research Facilities)

■ Participants: 20 (including 4 from NIBB)

■ Program:

1. BLAST for beginners
2. Local BLAST search with command-line
3. BLAST inside
4. Large scale BLAST search
5. Annotation of genes and ortholog analysis
6. Beyond BLAST



## The 4th Bioimaging Analysis Training Course

Organizers: Dr. Kagayaki Kato, Dr. Yoshitaka Kimori, Dr. Yasuhiro Kamei, Dr. Hiroshi Koyama, Dr. Shigenori Nonaka, Dr. Takashi Murata

December 5 (Mon) -7 (Wed), 2016

The 4th Bioimaging 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”. 58 people applied for the course, which had a maximum capacity of 21 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)

