The 12th NIBB Bioimaging Forum
"The Future of Bioimage Analysis Explored by AI"

Organizing Committee: Yasuhiro Kamei, Yoshitaka Kimori, Kagayaki Kato, and Natsumaro Kutsuna

The 12th NIBB Bioimaging Forum was held on March 26th 2018. We have previously held a series of forums on advanced bioimaging technologies such as novel techniques of image analysis, the application of adaptive optics to light microscopy, the imaging of physical properties *etc*. However, this time we picked artificial intelligence (AI), an area that has been growing rapidly in recent years, as the main subject of the forum.

We organized the forum so that the participants could understand how AI will affect the field of bioimaging in the near future and feel "the future of bioimage analysis explored by AI". The importance of imaging in biology is continually increasing, but at the same time we have come to feel the presence of its various limitations. For example, as the spatial and the temporal resolution of microscopic images has increased, the size of the data has vastly expanded to the point where we require computer science to analyze it. As AI will most likely play a key role in future data analysis, there must be a mutual understanding and collaboration between biology and computer science so we can be prepared for the future.

While this forum included an introduction to the cutting edge of AI technologies and lectures conducted by image analysis professionals, it also featured lectures held by biologists on how they are trying to apply AI to the analyses of biological phenomena. At the end of the forum we had general discussions and provided an opportunity for mutual understanding between image analysis professionals and lecturers from IT industries.

From last year, this forum has been supported by the Grant-in-Aid for Scientific Research on Innovative Areas - Platforms for Advanced Technologies and Research Resources "Advanced Bioimaging Support (ABiS)". We would like to thank members of the ABiS image analysis support team for their lectures.

(Yasuhiro Kamei)

The NIBB Genome Informatics Training Course

The NIBB Core Research Facilities regularly 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 2018, we held two sets of training courses on RNA-seq analysis and a course on BLAST analysis. The entirety of the RNA-seq analysis course was made up of two 2-day programs: one was a preparatory course concerning the basics of UNIX and R, and the other was a practical course to learn the pipelines of RNA-seq analysis using next-generation sequence data. The BLAST analysis course was designed for advanced users and aimed at enabling participants to become more familiar with large scale sequence database searches in a 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.), Dr. Katsushi Yamaguchi, Ms. Hiroyo Nishide, Mr. Takanori Nakamura, Mr. Takahiro Bino (NIBB Core Research Facilities)

February 22(Thu)-23(Fri), 2018

(Preparatory Course) Basics of UNIX, R, and NGS
- 22 participants (including 1 from NIBB)
- Program:
  1. UNIX for Beginners
  2. Editor and Scripts
  3. Introduction to "R"
  4. NGS Basic Data Formats and NGS Basic Tools
  5. Text Processing
  6. Exercises

March 8(Thu)-9(Fri), 2018

(Practical Course) RNA-seq Analysis Pipeline
(Same participants as above)
- Program:
  1. Introduction to RNA-seq
  2. NGS Basic Data Format and Basic Tools
  3. Visualization of NGS Data
  4. Introduction to Statistics
  5. RNA-seq Pipelines: Genome-Based and Transcriptome-Based Approaches
  6. Multivariate Statistics
  7. Functional Annotation and Gene Ontology
  8. Exercises