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

July 5(Thu)-6(Fri), 2018

(Preparatory Course) Basics of UNIX, R, and NGS
■ Participants: 22 participants (including 1 from NIBB)

July 26(Thu)-27(Fri), 2018

(Practical Course) RNA-seq Analysis Pipeline
(Same participants as above)

Mastering BLAST: The Essence of Sequence Analyses

September 6(Thu)-7(Fri), 2018

■ Organizers & Lecturers: Dr. Shuji Shigenobu, Dr. Ikuo Uchiyama (NIBB Core Research Facilities)
■ Participants: 21 participants (including 1 from NIBB)
■ Program:
  1. BLAST Basics
  2. Local BLAST Search with Command-line
  3. BLAST Inside: Theoretical Background of Sequence Search
  4. Large Scale BLAST Search
  5. Sequence Database Functions
  6. Annotation of Genes and Ortholog Analysis
  7. Beyond BLAST
  8. Exercises

The 5th BioImaging Analysis Training Course

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

December 4 (Tue) -6 (Thu), 2018

The 5th Bioimaging Training Course was held jointly by the Exploratory Research Center on Life and Living Systems (ExCELLS), JSPS KAKENHI Platforms for Advanced Bioimaging Support (ABiS) and NIBB in December last year. This course was designed for biologists who are relatively new to analyzing datum obtained through advanced microscopy. Therefore, the focus of the training related to learning about 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". 40 people applied for the course, which had a maximum capacity of 17 participants. This clearly indicated the high demand for courses on these subjects.

This course's lectures were conducted with the aim of guiding participants towards keeping in mind the series of steps essential to fundamental image processing and analysis while obtaining images to be used (workflows). In addition, we loaned PCs pre-installed with ImageJ, a typical open-source software package for biological image processing and analysis, to the participants in addition to images which were used for practice. Also, lectures were given on how programming of simple "macro language", which uses these workflows in ImageJ allows automation; itself being a necessity 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, but satisfied". It certainly is beneficial in terms of their image analysis as they became 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)