The NIBB Genome Informatics Training Course

The NIBB Core Research Facilities regularly organizes a series of training courses on the most recently developed research techniques. The NIBB Genome Informatics Training Course (GITC) is specially designed for biologists who are unfamiliar with bioinformatics. In 2020, we held two sets of training courses on RNA-seq analysis. Each version of the RNA-seq analysis course was basically made up of two 2-day programs: one being a preparatory course (Introduction to NGS Analysis) concerning the basics of UNIX and R, and the other a practical course (Introduction to RNA-seq) for learning about the pipelines to RNA-seq analysis using next-generation sequencing data. These GITC courses offered lectures and hands-on tutorials. This year, we initially held a practical course on RNA-seq analysis, that had been postponed due to the COVID-19 pandemic, only. However, we subsequently held a full version of the training course. All courses were held online to prevent the spread of COVID-19 infection.

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. Hiroki Sugiura (NIBB Core Research Facilities)

June 4 (Thu)–5 (Fri), 2020

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

Introduction to NGS Analysis: Basics of UNIX, R, and NGS

November 26 (Thu)–27 (Fri), 2020

■ 32 participants and 9 auditors (including 3 from NIBB)
■ Program:
1. UNIX for Beginners
2. Introduction to "R"
3. Introduction to Statistics
4. NGS Basic Data Formats and NGS Basic Tools
5. Editor and Scripts
6. Text Processing
7. Exercises

Introduction to RNA-seq: RNA-seq Analysis Pipeline

March 10 (Wed)–11 (Thu), 2021

(This program was the same as the above listed practical course)
■ 31 participants and 10 auditors (including 2 from NIBB)

The Bio-imaging Data Analysis Training Course 2020

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

December 9 (Wed)–11 (Fri), 2020

The 8th Bio-imaging Data Analysis Training Course was jointly held by the Exploratory Research Center on Life and Living Systems (ExCELLS), 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 the training was related to learning about image processing and analytical techniques through solving simple problems with image analysis, and understanding appropriate methods and necessary preparation when consulting experts in technically advanced problems concerning imaging. 114 people applied for the course, which had an announced capacity of 16 participants. Given the high demand for courses on these subjects, we accepted 18 participants.

This course's lectures were conducted with the aim of guiding participants towards an awareness of the series of steps essential for fundamental image processing and analysis while also obtaining images for eventual use (workflows). In addition to this, participants independently worked on practical image analysis exercises using ImageJ; a typical open-source software package for biological image processing and analysis. Lectures were also given on how the programming of simple "macro language", which uses the aforementioned workflows in ImageJ, allows for automation; a necessity for the large capacity and high-dimensional throughput of microscopic imaging which has more become common over recent years.

Upon the course's conclusion, each student offered commentary about and discussed the methods taught by providing examples of images gleaned from their own research.

Unfortunately, although this year's course was held online due to issues associated with COVID-19, we utilized technological innovations within the lectures and exercises, such as a chat service to support individual participants, so as to allow them to feel as if the course was being held as an in-person event.

Every year following the course's completion, participants often report feeling pretty tired, but satisfied. In a similar vein, we believe that this course is beneficial to its participants thanks to the associated increase in their familiarity with image analysis techniques Thus, we expect that this course will increase opportunities for joint research relating to biological image analysis moving forward.

(Kagayaki Kato)

Advanced Bioimaging Support (ABiS)

The demand for bioimaging has increased in recent years in the field of life science. However, due to advances in imaging technologies, such as the diversification and specialization of imaging equipment, increasingly complex operations, increased equipment and running costs, as well as the growing need for image data analysis, individual research institutes and universities are increasingly encountering difficulties related to the introduction, maintenance, and operation of imaging equipment.

ABiS was launched as one of the designated "Platforms for Advanced Technologies and Research Resources" during fiscal year (FY) 2016 under the new framework of the Grant-in-Aid for Scientific Research on Innovative Areas (Leader: Prof. Masanobu KANO, NIPS/The University of Tokyo). This program aims to contribute to the further development of academic research in Japan through the provision of cutting-edge equipment and methodologies to individual KAKENHI (Grants-in-Aid for Scientific Research) research projects by the Ministry of Education, Culture, Sports, Science and Technology (MEXT) under the Grant-in-Aid for Scientific Research on Innovative Areas (FY2016-FY2021).

Cooperating with domestic partner organizations that own and operate multiple types of advanced specialized imaging equipment, ABiS provides cutting-edge instruments for light microscopy, electron microscopy, magnetic resonance imaging, and other methods through its network. It aims to provide comprehensive support for advanced imaging in the field of life science. NIBB, together with NIPS, contributes as a core institute in the ABiS network. Among the various support activities that ABiS performs, NIBB is tasked with the following:

■ Light microscopy
  • 4D microscopy administered by Prof. Toshihiko FUJIMOIRI
  • IR-LEGO microcopy administered by Assoc. Prof. Yasuhiro KAMEI
  • DSLM administered by Assoc. Prof. Shigenori NONAKA
■ Imaging analysis
  • Development of image processing/analysis algorithms for biological data administered by Prof. Naoto UENO, Assist. Prof. Kagayaki KATO and Assist. Prof. Yusaku OHTA.
■ Training
  • Training for image analysis administered by Prof. Naoto UENO and Assist. Prof. Hiroshi KOYAMA.

To organize and coordinate ABiS activities, two secretariat offices were established at NIBB (Assoc. Prof. Shoji MANO) and NIPS, respectively, under the control of the general support group (Individuals in charge at NIBB; Director-general Prof. Kiyokazu AGATA, Prof. Naoto UENO, Prof. Shinji TAKADA, and Assoc. Prof. Shoji MANO). General support provided includes budget planning and management of ABiS activities. In particular, we promote ABiS activities via its associated website and other media, so that KAKENHI researchers make full use of the ABiS platform to accelerate their research projects. In addition, we organize technology training sessions, workshops, and symposia to disseminate advanced imaging technologies and share information about them.