

The 9th NIBB Bio-Imaging Forum “Imaging of Physical Properties”

Organizer: Yasuhiro Kamei,
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January 26 (Mon) - 27 (Tue), 2015

Thirteen lectures (two from NIBB members) on temperature, kinetics, and molecular movement, as well as on how these forces affect biological research, drew a total of 49 participants. This led to broad multi-disciplinary discussions on the role of physics in living systems. These physical quantities still do not draw a lot of attention in the field of biology, but it was clear that many researchers feel we are closing in on the essence of biological activity from these processes. Many lectures from fields rooted in engineering were given, and for researchers of biological systems this active gathering with members of remarkably different fields led to fresh exchange and new perspectives. In addition, because it was the first symposium on biological systems in which heat and temperature were the main themes, there was hope from the speakers that more of these kinds of opportunities will become available going forward.

(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. In 2015 we held two training courses on Genome Informatics. The 3-day programs offer lectures and hands-on tutorials to introduce basic knowledge and skills to deal with large scale genomic data such as DNA sequence data generated by next-generation sequencing (NGS). The programs are specially designed for biologists who are not familiar with bioinformatics.

“Introduction to RNA-seq - from the basics of NGS to de novo analyses”

February 25 (Wed) -27 (Fri), 2015

- Organizer: Dr. Shuji Shigenobu (NIBB Core Research Facilities)
- Lecturers: Dr. Shuji Shigenobu, Dr. Ikuo Uchiyama, Dr. Masanao Sato, Dr. Katsushi Yamaguchi, Ms. Hiroyo Nishide, Dr. Taro Maeda
- Participants: 22 (including 3 from NIBB)
- Program:
 1. UNIX for beginners
 2. NGS basic data formats and NGS basic tools
 3. Introduction to statistics
 4. Introduction to “R”
 5. RNA-seq pipeline: genome-based and transcriptome-based approaches
 6. Multivariate statistics
 7. Exercises

“Introduction to RNA-seq - from the basics of NGS to de novo analyses”

September 9 (Wed) -11 (Fri), 2015

- Organizer: Dr. Shuji Shigenobu (NIBB Core Research Facilities)
- Lecturers: Dr. Shuji Shigenobu, Dr. Ikuo Uchiyama, Dr. Masanao Sato, Dr. Katsushi Yamaguchi, Ms. Hiroyo Nishide
- Participants: 22 (including 3 from NIBB)
- Program:

(as above)



The 3rd Bioimaging Analysis Training Course

The 3rd Bioimaging Training Course was held jointly by the Center for Novel Science Initiatives' Department of Imaging Science, 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". There were applications from 83 people for this course, which had a maximum capacity of 20 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 leading to fundamental image processing and analysis while obtaining the images to be used (workflows). In addition, we loaned the participants PCs pre-installed with ImageJ, a typical software package for biological image processing and analysis, and images to be used as teaching materials, which were used for practicing the basic operations and settings of image processing. In addition, lectures 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 possible 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)

December 7 (Mon) -9 (Wed), 2015

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



The NIBB Medaka Basic Training Course

The content of the course was decided through a questionnaire in the Medaka community's mailing list and out of the most requested topics we chose genome editing techniques using CRISPR/Cas9, microinjection techniques, rearing and anesthesia methods, and advanced imaging techniques as feasible subjects for NIBB. We originally planned to accept 8 participants, but as we had more than 20 applicants, we finally accepted 16. We also accepted two observers to learn skills for managing training courses, and asked a graduate student of Kyoto University for a presentation. The two-day course commenced with several lectures and hands on training. The course was tight-scheduled and may have been rather brief, but we believe we informed participants of the research potential of NIBB and of the support we can offer through collaborative programs including techniques needed in individual research projects. The questionnaire after the course revealed that the Medaka rearing methods were most appreciated.

August 6 (Thu) -7 (Fri), 2015

- Organizer: Dr. Yasuhiro Kamei (NIBB Core Research Facilities)
- Lecturers: Dr. Yasuhiro Kamei, Dr. Kiyoshi Naruse, Dr. Yusuke Takehana, Dr. Shigenori Nonaka
- Presentations: Mr. Ansai Satoshi (Kyoto Univ.), Dr. Shigenori Nonaka
- Participants: 16
- Program:
 1. Egg collection and outline of injection techniques
 2. Rearing and observation of embryos
 3. Anesthesia of the embryo
 4. Basics of genome editing techniques
 5. Microinjection
 6. Hatching enzyme treatment and sample preparation for microscopy
 7. Utilization of NMBR Medaka web pages
 8. Microscope handling and observation

