

The 13th NIBB Bioimaging Forum “Behavioral and Recognition Research upon the Platform of Vision and Color-Recognition Studies and its Interdisciplinary Merging with Bioimaging”

Organizing Committee: Yasuhiro Kamei,
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February 12 (Tue)–13 (Wed), 2019

The 13th NIBB Bioimaging Forum was held in conjunction with the achievement briefing meeting conducted by the priority collaborative research project led by Prof. Fukamachi entitled "Toward Construction of a Research Platform of Vision and Color-Recognition Studies -Upon the Model of Medaka Whose Behaviors are Dominated by Vision- ". This collaborative research project was aimed at establishing methodologies for analyzing issues ranging from individual behaviors to molecular mechanisms of vision, which also use imaging technologies such as virtual reality and aerial imaging. As bioimaging aims to improve observation technologies, this joint meeting was viewed as a good opportunity for exchanging study results and other information.

In particular, rhodopsin (and other opsins) is a key substance combining the two participant groups. This is due to it being directly related to vision. It also can be used as a tool in optogenetics, itself a cutting-edge bioimaging methods. Additionally, Medaka have been used as a model organism for more than a hundred years in Japan, and have become popular as pets due to the many color variations they produce through cross-breeding.

We made this symposium open to public for the purposes of disseminating of knowledge on the research uses of Medaka and their history as a model organism, something which has likely benefitted historically. It was unfortunate that two of the invited speakers withdrew due to cancelling caused by an influenza epidemic, but their absence was covered by two young participants in a similar research field. This shows a large pool of researchers active in this field.

I would like to thank all the speakers and the project members for their contribution.

(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 2019, we held three sets of training courses on RNA-seq analysis. Each set 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 sequencing data. 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, Mr. Hiroki Sugiura (NIBB Core Research Facilities)

February 21 (Thu)–22 (Fri), 2019

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

- 30 participants (including 2 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 14 (Thu)–15 (Fri), 2019

(Practical Course) RNA-seq Analysis Pipeline

- 28 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. Introduction to Statistics
 5. RNA-seq Pipelines: Genome-Based and Transcriptome-Based Approaches
 6. Multivariate Statistics
 7. Functional Annotation and Gene Ontology
 8. Exercises