

The NUS/TLL/NIBB Joint Practical Workshop “Genetics, Genomics and Imaging in Medaka and Zebrafish”

- Period: July 22(Sun) - July 31(Tue), 2012
- Participants: 16 (3 from Germany, 2 from China, 2 from India, 2 from Italy, one each from Australia, Austria, Canada, France, Japan, Norway, and USA)
- Venue: Natl. Univ. Singapore (NUS) and TLL, Singapore
- Lecturers:
 - Dr. Kiyoshi Naruse (NIBB)
 - Dr. Atsuko Shimada (Univ. Tokyo)
 - Dr. Suresh Jesuthasan (Duke-NUS NRP, Singapore)
 - Dr. Zhiyuan Gong (NUS)
 - Dr. Thorsten Wohland (NUS)
 - Dr. Dipanjan Bhattacharya (NUS)
 - Dr. Paul Matsudaira (NUS)
 - Dr. Tom Carney (Inst. Mol. Cell Biol., Singapore)
 - Dr. Vladimir Korzh (Inst. Mol. Cell Biol., Singapore)
 - Dr. Atsuko Sehara-Fujisawa (Kyoto University)
 - Dr. Yasuhiro Kamei (NIBB)
 - Dr. Hiroyuki Takeda (Univ. Tokyo)
 - Dr. Tetsuaki Kimura (NIBB)
 - Dr. Sinnakarupan Mathavan (Genome Inst. Singapore)
 - Dr. Sudipto Roy (Inst. Mol. Cell Biol., Singapore)

■ Course Staff:

Dr. Mireia Perez Camps, Dr. Takuya Kaneko, Dr. Toru Kawanishi, Dr. Karuna Sampath, Dr. Anand Singh, Dr. Sahar Tavakoli, Dr. Yan Tong, Dr. Yin Wang, Dr. Christoph Winkler, Dr. Chang Woei

■ Contents of the course:

Somite transplantation, Cell transplantation, Cryopreservation of Medaka sperm: In-vitro fertilization, TALENs: Targeted gene modification in zebrafish, Establishment of BAC transgenic medaka, IR-LEGO, SPIM



The NIBB Genome Informatics Training Course

NIBB organizes a series of training courses on up-to-date research techniques for researchers from mainly Japanese universities and institutions. In 2012 we held two training courses on Genome Informatics. The two-day programs offer lectures and hands-on tutorials to introduce basic knowledge and skills to deal with genomic scale large data such as next-generation sequences (NGS). The programs are specially designed for biologists who are not familiar with bioinformatics.

“Introduction to Transcriptome Data Analysis”

March 22 (Thu) -23 (Fri), 2012

- Organizer: Dr. Shuji Shigenobu(NIBB Core Research Facilities)
- Lecturers: Dr. Ikuo Uchiyama, Dr. Masanao Sato, Dr. Katsushi Yamaguchi, Dr. Shuji Shigenobu
- Participants: 19 (including 6 from NIBB)
- Program:
 - 1. Overview: Transcriptome data analysis
 - 2. Introduction to statistics
 - 3. Introduction to “R”
 - 4. RNA-seq analysis pipeline
 - 5. Basic format of mapping data and basic tools
 - 6. Expression data analysis I: Normalization, differential expression analysis
 - 7. Expression data analysis II: Multivariate analysis
 - 8. Excercise

“Introduction to Next-generation DNA Sequence Data Analysis”

September 6 (Thu) -7 (Fri), 2012

- Organizer: Dr. Shuji Shigenobu(NIBB Core Research Facilities)
- Lecturers: Dr. Ikuo Uchiyama, Mr. Tomoki Miwa, Dr. Katsushi Yamaguchi, Dr. Shuji Shigenobu
- Participants: 16 (including 1 from NIBB)
- Program:
 - 1. Overview: NGS data analysis
 - 2. UNIX for beginners
 - 3. NGS basic data formats
 - 4. NGS basic tools I: Mapping
 - 5. NGS basic tools II: Visualization tools
 - 6. NGS basic tools III: Samtools
 - 7. Methods for text data processing
 - 8. Excercise

