

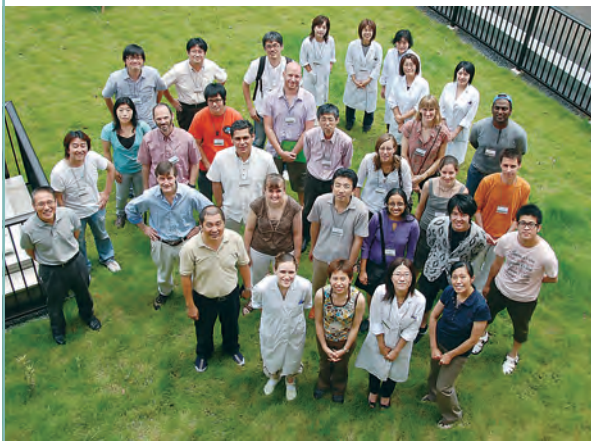
## The NIBB International Practical Course

The first NIBB International Practical Course was held in 2007 with the aim of providing young scientists around the world with opportunities to learn cutting-edge experimental skills and to communicate with experts in the field. The course replaced our Bioscience Training Course, which had been held for twenty years and which had, for the most part, accepted participants from universities and institutes in Japan. The Fourth International Practical Courses was held in 2009 as summarized below. The course was held in a laboratory provided by NIBB and equipped with the necessary instruments and tools and a good supply of experimental materials. We hope that the techniques and knowledge provided in these courses will prove useful in the future work of all of the participants.

### The Fourth International Practical Course: “2009 NIBB Laboratory Course and Workshops on *Physcomitrella patens*”

- Period: June 29 (Mon)- July 3 (Fri), 2009
- Participants: 17 (five from Japan, two from the UK, Germany, and Israel, and one each from Belgium, Czech, France, Sweden, Singapore, and India)
- Lectures:
  - Dr. Andrew C. Cuming (Univ. Leeds)
  - Dr. Yasuko Kamisugi (Univ. Leeds)
  - Dr. Tomoaki Nishiyama (Kanazawa Univ.)
  - Dr. Tetsuya Kurata (JST)
  - Dr. Yoshikatsu Sato (JST)
  - Dr. Yuji Hiwatashi (NIBB)
  - Dr. Minoru Kubo (JST)
  - Dr. Takashi Murata (NIBB)
  - Dr. Mitsuyasu Hasebe (NIBB)

Contents of the course: basic techniques including cultivation, observation of developmental processes at the cellular level, gene targeting, bioimaging, and bioinformatics used in the biology of the moss *Physcomitrella patens*



## The NIBB Training Course “How to translate results from microarray analysis”

NIBB started a series of training courses on up-to-date research techniques for researchers from mainly Japanese universities and institutions. In 2009 we held a bioinformatics training course on the statistical analyses of data obtained by microarray analyses.

- Period: August 19 (Wed) -21 (Fri), 2009  
September 8 (Tue) -10 (Thu), 2009
- Lecturers: Drs. Koji Kadota and Yuji Nakai (University of Tokyo)
- Participants:
  - August course: 16 (including 5 from NIBB)
  - September course: 17 (including 4 from NIBB)

Microarray analysis is one of the most frequently used comprehensive methods for researching gene expression. But it is not easy to properly translate results from microarray data for ordinary biologists who are not familiar with bioinformatics. The aim of this course was to give lectures on the fundamentals of microarray analysis using the statistical environment “R”, and practical methods for gene ontology analysis using free software.

1. Fundamentals of microarray analysis
2. How to use the statistical environment “R” for microarray analysis
3. Fundamentals of gene ontology analysis
4. Practical methods for gene ontology analysis

