

CBRC2006

CBRC symposium was started in 2005 as an opportunity to communicate research results from CBRC on a regular basis. In 2006, the 2nd symposium was held on September 28 and 29. The latest research results from CBRC were presented as well as results of research conducted in collaboration with The University of Tokyo and Waseda University. Many people attended the symposium and active discussion was held in each session.

Session 1 : The Front of Bioinformatics

CBRC' Research Topics



Dr. Tominaga

Dr. Kiryu

Dr. Kameda

Dr. Fujibuchi

"Gene expression time series analysis for cell array data"

Daisuke Tominaga (Research Scientist, Biology Network Team, CBRC)

"Development of methods for functional RNA discovery based on comprison of multiple DNA sequences"

Hisanori Kiryu (Research Scientist, Mathematical Model Team, CBRC)

"Molecular dynamics simulation of amyloid forming by generalized Born energy"

Tomoshi Kameda (Research Scientist, Molecular Modeling & DesignTeam, CBRC)

"Prediction of structures and functions of human cells"

Wataru Fujibuchi (Research Scientist, Sequence Analysis Team, CBRC)

Session 2 : Current of genome analysis

Collaboration with University of Tokyo



Dr. Hattori

Dr. Kin

Dr. Kato

Session place

"Analysis of the human intestinal metagenome"

Masahira Hattori (Professor, The Univ. of Tokyo)

Invitation lecture

"fRNAdb: a platform for mining/annotating functional RNA candidates from non-coding RNA sequences"

Taishin Kin (Research Scientist, Mathematical Model Team, CBRC)

"Drug resistance prediction from microarray data via network-based noise reduction"

Tsuyoshi Kato (The Univ. of Tokyo)

Session 3 : From the protein structure to the function

Collaboration with Waseda University



Dr. Wako

Dr. Sekijima

Dr. Shimizu

Dr. Yamada

"Fluctuation of three-dimensional structure of protein

- Approach with normal mode analysis"

Invitation lecture

Hiroshi Wako (Professor, Faculty of Science and Engineering, Waseda University)

"Free Energy Landscape Analysis of bio-molecules based on large-scale molecular dynamics simulation"

Masakazu Sekijima (Research Scientist, Protein Function Team, CBRC)

"Predicting protein disorder"

Kana Shimizu (AIST Research Staff, Protein Function Team, CBRC)

"PRIME: a program for multiple sequence alignment with piecewise linear gap cost"

Shinsuke Yamada (Faculty of Science and Engineering, Waseda University)

Bioinformatics Training Course Symposium

CBRC held a symposium to report the activities in the "Bioinformatics Training Course", supported by the Science and Technology Promotion and Adjustment Fund from the Ministry of Education, Culture, Sports, Science and Technology (MEXT). The symposium started September 29, 2005, at the AIST Tokyo Waterfront Bio-IT Research Building. Detailed summaries of the Bioinformatics Introductory Course I and II and Pharmaco-informatics Training Course were presented by instructors (Okada, Yokota, and Hirokawa, respectively). In addition, the learning experiences were reported by four working students. Future plans to improve the courses were also suggested.



Guest Greeting:
Mr. Horiuchi
(Science and Technology Policy Bureau, MEXT)



Opening Address:
Dr. Moriya
(Director, AIST Tokyo Waterfront)



Instructors: Dr. Hirokawa, Dr. Okada, Dr. Yokota
(From left)

Panel Discussion

*Hope for the next generation
bioinformatics engineer*



Panelists: Tomohisa ISHIKAWA (Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology)
Tsuguchika KAMINUMA (Tokyo Medical and Dental University)
Yukio TADA (Taiho Pharmaceutical Co., LTD.)
Hiroyuki TOH (Medical Institute of Bioregulation, Kyushu University)
Takatsugu HIROKAWA (Leader, Molecular & Modeling Design Team, CBRC)

Chairperson: Yutaka AKIYAMA (Director, CBRC)