

New! "Bioinformatics Training Course"

Our "Bioinformatics Training Course" proposal was adopted to the Promotion Fund for Science Technology by MEXT. It is a five year training project (FY2005-FY2009) designed for those working or will be working for the companies in bioinformatics research.

Outline of the course (for FY2006)

- ① Leader Training Course April 2006 ~ (A year OJT program)
- ② Bioinformatics Introductory Course I June ~ July, 2006 (9 days, 20 classes)
 Bioinformatics Introductory Course II October ~ November, 2006 (3 classes × 10 days, 30 classes)
- ③ Pharmaco-informatics Training Course August ~ September, 2006 (3 classes × 10 days, 30 classes)
 - A Molecular modeling
 - B Structure-based drug design (SBDD)
 - C Virtual screening



Enquiry

"Bioinformatics Training Course"
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The 4th Symposium on "AIST Upbringing Talents in Bioinformatics Course"

We had a symposium on *AIST Upbringing Talents in Bioinformatics Course* sponsored by MEXT promotion fund for science technology since 2001. This course has its final year in this fiscal year.



Scenes of the 3rd symposium in 2004

A panel discussion and introduction of the new training course were also given at this symposium.

- Date : Thu, 22nd Sep., 2005 (10:30 ~ 18:00)
- Venue : Mirai Can Hall, MeSci, Tokyo

The 4th "International Bio Expo"

The 4th International Bio Expo was held on 18th May through 20th May, 2005 at the Tokyo Big Sight and about 15,000 people visited over the three days. In the Academic Forum, Wataru Fujibuchi (Research Scientist) and Paul Horton (Team Leader) from the CBRC Sequence Analysis Team presented a talk on "CellMontage: System for Search and Analysis of a Microarray Database".



Top page of CellMontage (<http://cellmontage.cbrc.jp/>)



Talk by Dr. Fujibuchi, Research Scientist

The CellMontage, which was featured in Newsletter No. 10, is a "cell type" oriented gene expression profile analysis system that provides a fast profile-to-profile matching software and a catalogue of human cells with their profiles. More general co-expressed genes are constructed from the normal human cell profiles using eigenvalue decomposition, and the resulted gene clusters are provided for free upon request. Keyword search for easy access to profiles as well as the download page for all the profiles are also available.