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- [SAKURA](#) [Mass Sub](#)
- [Data Updates](#)
- [Search & Analysis](#)
- [ARSA](#) [getentry](#)
- [TXSearch](#)
- [FASTA](#) [BLAST](#)
- [SSEARCH](#) [HMMPFAM](#)
- [ClustalW](#)
- [WebAPI](#)
- [GIB](#) [GIB-V](#)
- [GTPS](#) [GTOP](#)
- [Breakdown Stats](#)
- [Download data](#)
- [DDBJ Release Note](#)
- [Release Information](#)
- [Q and A](#)
- [Doors for Info Bio](#)
- [Conference on Info Bio](#)
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Organized by the Center for Information Biology and DDBJ (CIB-DDBJ) at the National Institute of Genetics (NIG), Korean Bioinformatics Center (KOBIC) at the Korea Research Institute of Bioscience and Biotechnology (KRIBB), and Shanghai Center for Bioinformatics Technology (SCBIT).  
Supported by the Japan Science and Technology Agency (JST).

- Venue: International Center in Jeju University, Korea
- Dates: March 18th to March 21st, 2008
- Trainees: Ten trainees from each of the three countries, 30 in total.
- Language: English
- Note: This program is for a Japanese or a non-Japanese studying in Japan as a graduate school student or a post-doctoral fellow formally accepted by the Japanese university or institute. The non-Japanese applicants should hold the visa, or being permitted without visa, for entering to Korea.
- Reports of the past attendants will be helpful for your information. ([English](#)/[Japanese](#))

### Announcement

We are pleased to announce that "The 7th Japan-Korea-China Bioinformatic Training Course" will be held at the International Center in Jeju University, Korea, in March 18-21, 2008.

This time we will also organize a mini-symposium at which the lecturers of the training course talk about their original research topics. The trainees are expected to attend the mini-symposium, as well.

If you wish to participate in this training course as a trainee, please apply now (see below for application)!

The number of the trainees from Japan is limited to 10. The trainee is expected to be either a graduate student or a postdoc in bioinformatics or a related area who is fluent in English. In addition, the trainee is required to hold the passport which is valid for more than 6 months at the time of the training course. The deadline of the application is February 8, 2008.

The successful applicant is covered with travel expenses including air and train tickets, lodging and meals. He/She is also provided with a PC linked with Internet during the course.

➡ [Application:](#)

### Program

== Lecturers ==

Name (Affiliation)	Teaching topics
<b>Korea</b>	
Dr. Jong-Hwa Bhak (KOBIC) ; Dr. Sangsoo Kim (Soongsil U.) ; Dr. Namshin Kim (UCLA) :	
<b>Japan</b>	
Dr. Yoshio Tateno (NIG) : Fundamentals of Bioinformatics Dr. Takashi Gojobori (NIG) : Evolutionary Genomics Dr. Naruya Saitou (NIG) : Some examples of evolutionary genomics study Dr. Daron M. Standley (Osaka U.) :	
<b>China</b>	
Dr. Lei LIU (SCBIT) ; Dr. Yang ZHONG (Fudan U.) : Molecular Evolution Dr. Lu XIE (SCBIT) : Basic Mass Spectrometry Data Analysis in Proteomics	

KOBIC: [Korean Bioinformatics Center](#)  
Soongsil U.: [Soongsil University](#)  
UCLA: [University of California, Los Angeles](#)  
NIG: [National Institute of Genetics](#)  
Osaka U.: [Osaka University](#)  
SCBIT: [Shanghai Center for Bioinformatics Technology](#)  
Fudan U.: [Fudan University](#)

== Bioinformatics Training Course ==

#### Tuesday, March 18, 2008

17:00 - 18:00	Check in and Registration
18:00 - 18:10	Opening Address
18:10 - 18:20	Welcoming Speech
18:30 -	Reception

#### Wednesday, March 19, 2008

07:00 -	<i>Breakfast</i>
09:00 - 11:00	Fundamentals of Bioinformatics <span style="float: right;">Yoshio Tateno</span>
11:00 - 13:00	Structural bioinformatics tools at the Protein Data Bank Japan <span style="float: right;">Daron M. Standley</span>
13:00 - 14:00	<i>Lunch</i>
14:00 - 16:00	Basic Mass Spectrometry Data Analysis in Proteomics <span style="float: right;">Lu XIE</span>
16:00 - 18:00	Interactomics <span style="float: right;">Jong-Hwa Bhak</span>
18:30 -	<i>Dinner</i>

#### Thursday 20

07:00 -	<i>Breakfast</i>
09:00 - 11:00	Microarray Data Analysis <span style="float: right;">Lei LIU</span>
11:00 - 13:00	Molecular Evolution <span style="float: right;">Yang ZHONG</span>
13:00 - 14:00	<i>Lunch</i>
14:00 - 16:00	Genome Annotation <span style="float: right;">Namshin Kim</span>
16:00 - 18:00	Omics Data Integration Mining <span style="float: right;">Sangsoo Kim</span>
18:30 -	<i>Dinner</i>

#### Friday 21

07:00 -	<i>Breakfast</i>
09:00 - 11:00	Evolutionary Genomics <span style="float: right;">Takashi Gojobori</span>
11:00 - 13:00	Some examples of evolutionary genomics study <span style="float: right;">Naruya Saitou</span>
13:00 - 14:00	<i>Lunch and Closing Ceremony</i>

== Bioinformatics Conference: March 20(Thu), 2008 ==

Session	Time	Topic of Presentation	Speaker
1	10:00 - 10:30	Functional annotation of structural genomics targets by sequence-weighted structure alignments	Daron M. Standley
	10:30 - 11:00	Case studies of post-translational modification identification and prediction	Lu XIE
	11:00 - 11:30	Interaction network in biology	Jong-Hwa Bhak
	11:30 - 11:40	<i>Coffee Break</i>	
2	11:40 - 12:10	Alternative Splicing and Comparative Studies	Namshin Kim
	12:10 - 12:40	Sequence classification based on multidimensional scaling	Sangsoo Kim
	12:40 - 13:10	Comparison of network topology	Lei LIU
	13:10 - 14:00	<i>Lunch</i>	
3	14:00 - 14:30	Evolution of nervous system	Takashi Gojobori
	14:30 - 15:00	Construction of Tree of Life by Protein Domain Organizations	Yoshio Tateno
	15:00 - 15:30	Molecular phylogenetics based on multiple genes and genomic data	Yang ZHONG
	15:30 - 16:00	Evolution of highly conserved protein non-coding sequences in mammalian genomes	Naruya Saitou

### Others

➡ [Application:](#)

➡ Reports of the past attendants  
by [Fernando Encinas Ponce \(National Institute of Genetics\)](#) ([in English](#))  
by [Dr. Ryutaro Hirasawa \(National Institute of Genetics\)](#) ([in Japanese](#))

➡ Related Web Sites  
[6th \[2007.03.27-30\] - CHINA \(Japanese site\)](#)  
[5th \[2006.03.14-17\] - JAPAN](#)  
[4th \[2005.03.07-10\] - KOREA \(Japanese site\)](#)  
[3rd \[2004.03.16-19\] - JAPAN](#)  
[2nd \[2003.08.17-21\] - KOREA](#)  
[1st \[2003.03.15-18\] - JAPAN](#)  
[\[CIB-DDBJ, DDBJ, KRIBB, NGIC\]](#)

### Reports of the past attendants

Report of The 6th Japan-Korea-China Bioinformatics training course  
Fernando Encinas Ponce  
Researcher at Laboratory for Gene-Expression Analysis, National Institute of Genetics

#### \*I. Introduction

Since 2002, first Korea and Japan and later including China, the three countries have been organizing an annual bioinformatics training course. The initial idea to promote the field of bioinformatics, specially among young researchers, has become a very well established and formal "short-term" bioinformatics education on the basis that nowadays application of informatics along with diverse disciplines such as mathematics, statistics, chemistry and others are essential to carry out any research project in genomics, proteomics and other related fields in biology.

This year, The Sixth Sino-Japan-Korea Bioinformatics Training Course was held in the astonishing city of Shanghai under the organization of Shanghai Center for Bioinformatics Technology (SCBIT), the National Institute of Genetics (NIG, Japan) and the Korean Research Institute of Bioscience and Biotechnology (KRIBB).

#### \*II. General Information

Location: The training course took place in installations of Shanghai Jiaotong University, Minhang Campus in Shanghai, China. All participants were impressed by the splendid view of the campus and satisfied with all the facilities it includes, among others, the Guest House of the Academic Center where we stayed during the course.

At the moment of registration every participant was provided with all material necessary for the course and a kind gift from the organizers.  
Time: Basically the training was a 20 hour intensive course that extended from March 27th. to March 30th. Every day the sessions started at 8:00 and lasted until 18:45 with a main brake of 60 minutes for lunch.

Participants: The training course consisted of three different groups of participants:  
The organization group whose members were always kindly open to help and solve any inquire from the attendants, 10 lecturers from the three countries who were responsible to lead and present every session and 30 students (10 per country) whose background either related to biology or not, was not a limitation to make the best of this opportunity to experience the "taste" of the bioinformatics world.

#### \*III. Structure and contents

The course was divided by sessions, each at a time consisted of theoretical and practical contents. The theoretical content of each session was aimed to include in-depth coverage of subjects that support the development of research projects using genome-scale information or the construction of specific databases for storing specific kinds of data or if it was the case, the design of new software tools used for retrieval and analysis.

Immediately after, during the practical sessions, every student provided with a personal computer was encouraged to explore and use the methods and tools introduced by the lecturers using real biological examples.

Following is a brief summary of the topics covered during the training course:

• First day: Prof. Jong Bhak (KRIBB) made an interesting introduction to the field of bioinformatics and then described with many examples the perspectives of research on Single Nucleotide Polymorphism (SNPs) as the major genetic variation at genome level.

Following the first session, Prof. Zhiwei Cao (SCBT) reviewed some programs and methods used in genomic research such as gene prediction and gene annotation and described the strategies used to identify genes involved in microbial pathogenesis. Prof. Naruya Saitou (NIG) was in charge of the third session. He explained about the methods used to construct phylogenetic trees for comparative genomics and introduced many of his projects aimed to elucidate diverse evolutionary processes at sequence, genome and species level.

The closing session corresponding to the first day was presented by Prof. Yang Zhong from Fudan University. He made a concise review to the fundamentals of molecular evolution and during the practical session checked the packages developed to carry out phylogenetic analysis, specifically those used to detect positive selection between two sequences.

• Second day: The second day of the training course started with Prof. Haruki Nakamura from Osaka University who introduced the data, file formats, search engine and software developed at Protein Data Bank of Japan (PDB). He also described the role of PDB within the world wide PDB. During the practical session we had the opportunity to access PDB website and test some applications available there.

Prof. Sangsoo Kim from Soongsil University started immediately after and his presentation was aimed to stress the need and importance to integrate the huge amount of data accumulated in genomics and proteomics using a systems biology framework. He introduced many programs developed for this purpose and thus the practical session consisted in using a software package designed to integrate and analyze diverse data.

Starting from sequence retrieval to the use of molecular visualization tools, Prof. Sanguk Kim from Pohang University of Science and Technology explained the methods, use and perspectives of structural bioinformatics as a promising discipline to study membrane proteins and therapeutic development. Different applications for the identification of functional and structural analysis of proteins were introduced during the practical session.

Prof. Yoshio Tateno (NIG) closed the second day of the course. He focused his talk on the fundamentals of population genetics, the role of mutations as the driven force for evolution and the process and factors that govern changes in gene frequency. As a practical session, various related equations and exercises were solved during the class.

• Third day: This was our last day of training. A mixture of feelings was invading us. On one hand the satisfaction for having the work close to finish successfully, on the other hand, the sadness to leave behind such a beautiful experience.

Prof. Takashi Gojobori (NIG) started his lecture emphasizing the need to develop a new integrative biology way of thinking and research with all the opportunities provided by the huge amount of data available. Then he showed many examples of his work on different projects in comparative genomics and genome evolution.

Finally, Prof. Yu Shyr from Vanderbilt University was in charge of the very last session of the training course where he presented an in-depth explanation about the methods used for experimental designing, quality control assessment and analysis of high-throughput assays that render high dimensional data.

#### \*IV. Conclusions

The coverage of topics during the three days of activities was really broad and complete. This is quite important if we agree that bioinformatics is a very dynamic and competitive field that demands continuous learning, practice and updating.

Training courses such as this constitute fundamental steps in our formation as students or if we want to start a new project in this challenging field.

Useless to mention that in my case as an international student in Japan, I felt completely granted to participate in this course not only for the benefits to my current work but also for the perspectives in the field of bioinformatics in my country.

I would like to emphasize that the friendly environment surrounding the classes, the collaborative attitude of organizers and the kind consideration of lecturers to discuss with the students made from this course a complete success and a memorable experience for all of us.

Thank you Shanghai 2007!!!



\*\*\*\*\*

「日中韓合同バイオインフォマティクストレーニングコースに参加して」

平澤 竜太郎

国立遺伝学研究所・人類遺伝学部門

「初心者向けのバイオインフォマティクスの講習会があるよ。」

友人から聞いたそんな一言が参加のきっかけになった・・・。

主にマウスを用いた実験生物学を専門としている私にとって、バイオインフォマティクスは、生命現象を網羅的に捉えることが出来ると、統計学やコンピューターの高度な知識が必要とされる、敷居の高い学問という印象があった。しかし、近年では我々の研究分野でも、ゲノムワイドで網羅的な解析や考え方が要求されるものが多くなり、何か勉強をするきっかけが欲しい・・・、そんなことを考えていた矢先であった。せっかくの良い機会なのでバイオインフォマティクスという未知の分野に一度触れてみようと考え、この講習会に応募した。まずは、この講習会へ参加する機会を与えてくださった主催者のDDBJのスタッフおよび講師の先生方々に深く感謝したい。

講習会が行われた上海交通大学は中国でも有名な理系の総合大学であり、上海市内にくっつかのキャンパスがある。その中でも、会場となったMinhangキャンパスは、日本では考えられないほどの広大な敷地を持ち、同じキャンパス内にある宿泊施設から教室まではバスで15分ほどかかるほどの広さであった。受講生は日本・中国・韓国から各10人ずつの正式な参加者と上海交通大学の有志の学生を含めて、計40～50人ほどが参加していた。他の参加者と話してみた印象では、バイオインフォマティクスの関連分野を専攻している大学院生が多かった気もするが、初心者だという参加者も比較的多く見受けられた。

講義は2日半にわたり、計10人（日本4人・韓国3人・中国3人）の先生方によって行われ、様々な生命科学関連のデータベースの利用法を中心に、進化生物学やOmics（生命現象や生体物質の全体を網羅的に捉える学問の総称）といった実用的なバイオインフォマティクスまで幅広く学ぶことができた。講習会中は個人1台のパソコンを利用し、講義を聴きながらデータベースやデータ解析のためのウェブサイトを実際に使ってみるという形式で行われたが、講義内容は各分野の総論や研究紹介が中心であったため、初心者の私でも特に問題なく講義についていくことができた。1日10時間にもよぶ講義はとてもハードでタフなものであったが、幅広い分野を一度に学ぶことができ、大変有意義な3日間であったと思う。特に、今まで実験生物学を専攻していた私にとって、数学や統計学を用いて生命現象の全体像を網羅的に捉えるという考え方やその重要性に触れたことは、自分の研究を別の視点から見直すための良いきっかけとなった。

講習会の性質上、研究の即戦力となるような知識や技術を身に付けるような内容にはなっていないが、その分、幅広い内容の講義を聴くことができるので、初心者にとってはこの分野に触れる良いきっかけとなったのではないだろうか。また、既にこの分野の研究を行っている人にとっても、日中韓の最先端の研究者が講師として招かれているので、そのような先生方と直接議論できる良い機会となったのではないかと思う。

さらに、中国・韓国からの参加者との交流が持てたことは、この講習会においてとても思い出に残っていることの一つである。受講生の殆どが同世代の大学院生であることも手伝って、他の参加者ともすぐに打ち解けることができた。研究の話もとても興味深かったが、それ以上に大変印象に残っていることは、お互いの国の文化や言葉などに関する話をして交流を深めることができたことである。特に、現地の中国人学生の案内で、皆と一緒に大学周辺の街を歩いて、色々な物を見たり食べたりし、共に楽しい時間を過ごせたことは、私にとっても忘れがたい思い出になっている。

加えて、主催者であるDDBJスタッフの配慮もあり、講習会の2日前に現地入りして上海市内の観光をすることができ、講習会以外でもとても楽しい時間を過ごせた。今回は私を含め4人の大学院生が遠征団から参加しており、(女)の方のおまけで上海への滞在がより充実したのも因縁だった。特に講習会中はバイオインフォマティクスに不慣れな私をサポートしてくれた(女)らに、この場を借りて改めてお礼を言いたい。最後に、このような手記の執筆の機会を与えてくれたDDBJスタッフにも感謝の意を表すと共に、この駄文が来年度の参加を考えている学生の助けに少しでもなれば嬉しく思う。