

**NSTDA Institute (NI)**  
**National Science and Technology Development Agency (NSTDA)**  
**Faculty of Graduate Studies, Mahidol University**

**Course Announcement**  
**GRID617 Hypercourse on Bioinformatics (2 credits)**  
**13-16 October 2009**

NSTDA Institute (NI), National Science and Technology Development Agency (NSTDA) in collaboration with Faculty of Graduate studies, Mahidol University will offer a hypercourse on Bioinformatics in the second semester of the academic year 2009. It is a 2-credit course, intended for graduate students and researchers in sciences, computer sciences and science-related disciplines from Mahidol University and other institutions.

**Course description**

Use of computers to store, retrieve, analyze biological information; implement and use web service workflow in bioinformatics; genomics-transcriptomics-proteomics, bioinformatics at DNA level; bioinformatics of gene cloning and expression, biological database and NCBI, sequence alignment and similarity searching, PCR primer and probe design, principle of nucleic acid analysis & sequence alignment algorithms, phylogenetic analysis, bioinformatics at SNP level; single nucleotide polymorphism and its' application, SNP database for investigation of human genome, pharmacogenomics/pharmacogenetics resources, an interactive SNP visualization tool, selection of SNP markers for disease association studies, bioinformatics at proteomics level; protein bioinformatics, protein expression, protein purification, introductory to proteomics, protein identification, proteomic modeling and drug design, chat room for hypercourse on bioinformatics.

**Course objectives**

1. To provide an opportunity in self education utilizing WWW resources so as to assist students in understanding the principle and concept of Bioinformatics.
2. To apply knowledge of bioinformatics (information and automation) to various problems e.g., genome projects.

**Prerequisites** : The student should be able to use Internet and must pass at least one course in biological sciences.

**Course format**

- Lecturer presentation and demonstration by using virtual multimedia simulation and interactive animation
- Self study by using WWW

**Duration and schedule** : The 4-day course will be offered during 13-16 October 2009  
at 8.30-17.00 h

**Venue** : Room L-02, Faculty of Science, Mahidol University

**Further information** : Please contact

Dr.Pintip Ruenwongsa <scprw@mahidol.ac.th>  
Institute for Innovative Learning  
Mahidol University, Rama 6 Rd, BKK 10400  
Tel (02) 4419020-4 # 1300-9 Fax (02) 4410479

National Science and Technology Development Agency (NSTDA)  
 Faculty of Graduate Studies, Mahidol University  
**GRID617 Hypercourse on Bioinformatics (2 credits)**  
 October 13-16, 2009. 9.00-17.00 h  
 at **Room L-02**, Faculty of Science, Mahidol University.

Date	Time	Lecture/Demonstration Topic	Lecturers/Instructors
Oct 13	<b>Lecture</b>		
	9.00-9.30	<b>Course orientation</b>	Wasun Chantratita (RAMA)
		Bioinformatics lecture tools; S* Alliance and ASEAN Virtual University in Science and Technology	Pintip Ruenwongsa (Fac. Science Mahidol)
		Bioinformatics tools; <ul style="list-style-type: none"> <li>BIO-IT (multimedia learning program of how to use bioinformatics tools, step by step)</li> <li>คู่มือสอนการใช้โปรแกรมชีวสารสนเทศเบื้องต้น (text book)</li> </ul>	
	9.30-10:30	<b>An Overview of Bioinformatics;</b>	
		Genomics-Transcriptomics-Proteomics	Wasun Chantratita (RAMA)
	10.30-10.45	<i>Break</i>	
	11.00-12.00	<b>Translational Bioinformatics;</b> <ul style="list-style-type: none"> <li>The development of storage, analytic, and interpretive methods to optimize the transformation of increasingly voluminous biomedical data, and genomic data in particular, into proactive, predictive, preventive, and participatory health.</li> </ul>	Wasun Chantratita (RAMA)
	12.00-13.00	<i>Lunch</i>	
		<b>Bioinformatics at DNA level</b>	
	13.00-15.00	<ul style="list-style-type: none"> <li>Principle of nucleic acid analysis &amp; sequence alignment algorithms</li> </ul>	Prasit Palittapongarnpim (Biotec)
	15.00-15.15	<i>Break</i>	
		<b>Demonstration</b>	
	15.15-15.45	Biological database and NCBI e-Utilities Web Service <ul style="list-style-type: none"> <li>NCBI tour</li> <li>Entrez</li> <li>Bioinformatics sequence formats</li> <li>Reference sequence</li> <li>How to get the interesting sequence/gene from the database</li> </ul>	Soranan Chantarangsu (Chula)
	15.45-16.30	Sequence alignment and similarity searching <ul style="list-style-type: none"> <li>BLAST</li> <li>Multiple alignment</li> <li>Consensus sequence</li> </ul>	Ekawat Pasomsub (RAMA)
	16.30-17.00	Taverna: Tool for designing and executing bioinformatics workflows	Ekawat Pasomsub (RAMA)
Oct 14	<b>Lecture</b>		
	9.00-10.00	Bioinformatics of gene cloning and expression	Wasun Chantratita (RAMA)
	10.00-10.10	<i>break</i>	
	10.10-12.00	Phylogenetic analysis	Sirawut Klinbunga (BIOTEC)
	12.00-13.00	<i>Lunch</i>	
		<b>Demonstration</b>	
	13.00-14.00	Phylogenetic tree reconstruction with Phylip	Ekawat Pasomsub (RAMA)
	14.00-15.00	PCR primer and probe design Primer check <ul style="list-style-type: none"> <li>BLAST</li> <li>OligoCalc</li> <li>OligoAnalyzer</li> </ul>	Ekawat Pasomsub (RAMA)
	15.00-15.15	<i>Break</i>	
	15.15-15.45	- Restriction enzyme analysis - Cloning analysis	Chuphong Thongnak (RAMA)
	15.45-16.30	Bioedit – Biological Sequence Alignment Editors	Chuphong Thongnak (RAMA)
	16.30-17.00	- DNA fragment assembly - Gene finding (ORF) - DNA translation	Soranan Chantarangsu (Chula)

Date	Time	Lecture/Demonstration Topic	Lecturers/Instructors
Oct 15	<b>Lecture</b>		
		<b>Bioinformatics at SNP level</b>	
	9.00-10.30	Overview: Single nucleotide polymorphism and its' applications <ul style="list-style-type: none"> <li>• SNP, LD bin and haplotype block, haplotype Tagging SNPs,</li> <li>• Linkage analysis and whole-genome disease association studies</li> </ul>	Surakameth Mahasirimongkol (Thailand MOPH)
		SNP genotyping; <ul style="list-style-type: none"> <li>• High throughput</li> <li>• Medium throughput</li> <li>• Low throughput</li> </ul>	
	10.30-10.45	<i>Break</i>	
	10.45-12.00	Genome Wide Association (GWAS) Data analysis	Soranan Chantarangsu (Chula)
	<b>12.00-13.00</b>	<i>Lunch</i>	
	<b>Demonstration</b>		
	13.00-14.30	SNP database for the investigation of the human genome (online): The browsers used to view the SNPs, linkage disequilibrium bins, and haplotype blocks across all populations <ul style="list-style-type: none"> <li>• dbSNP (SNP database from NCBI)</li> <li>• Perlegen (Perlegen Sciences, Inc)</li> <li>• HapMap and HapMart (The International HapMap Project)</li> <li>• SNPper (Retrieve known SNPs by position or by association with a gene)</li> </ul>	Chuphong Thongnak (RAMA), Ekawat Pasomsub (RAMA)
	14.30-15.00	An interactive SNP visualization tool (off-line tools); <ul style="list-style-type: none"> <li>• Genalys (powerful program which allows one to align multiple sequences)</li> <li>• SNPbrowsers (knowledge-guided selection of optimal sets of SNPs for association and fine mapping studies)</li> </ul>	Ekawat Pasomsub/ Soranan Chantarangsu (Chula)
	15.00-15.30	Sample size calculation tools (Minsage and Quanto) R-package for SNPs (handling genetic data)	Ekawat Pasomsub (RAMA)
	15.30-15.45	<i>Break</i>	
	15.45-16.30	An interactive SNP visualization tool (off-line tools); <ul style="list-style-type: none"> <li>• Haploview (simplify and expedite the process of haplotype analysis)</li> </ul>	Ekawat Pasomsub (RAMA)
	16.30-17.00	- Pharmacogenomics/Pharmacogenetics resources <ul style="list-style-type: none"> <li>• PharmGKB</li> </ul>	Soranan Chantarangsu (Chula)

Date	Time	Lecture/Demonstration Topic	Lecturers/Instructors
Oct 16	Lecture		
		<b>Clinical Genomics Level Seven (CGL7)</b>	
	9.00-10.00	<p>The Clinical Genomics Informatics System (CGIS)</p> <ul style="list-style-type: none"> <li>• Clinical genomics is an interdisciplinary field dealing with the use of genetic data in clinical practice, such as the prescription of drugs based on a patient's genetic profile.</li> <li>• Clinical Genomics Level Seven (CGL7) enables the exchange of clinical and personalized genomic data between interested parties. It is a set of Web services for clinical-genomics decision-support applications that follow the HL7® (Health Level 7®) Clinical Genomics standard for the representation and exchange of clinical genomics data.</li> <li>• CGIS is the Future-proof and audit trail system for pharmacogenomics projects and clinical trails <ul style="list-style-type: none"> <li>○ Applications will support Future Changes <ul style="list-style-type: none"> <li>▪ Applications are aware of future changes and gracefully adjust to changes in either the amount of services or in the exchange format. The application and the data exchange format support both extensions, removed elements and version controls. The system is to use XML with an XML Schema.</li> </ul> </li> <li>○ Application level audit trail allows us to track changes at the detailed level. With the database to build detailed records on changes, additions, and deletions at the database level.</li> </ul> </li> </ul>	Dr. Harold H. Hibbert (Bioinfogen)
		<b>Bioinformatics at Proteomics level</b>	
	10.00-12.00	<p>Overview: Protein bioinformatics</p> <ul style="list-style-type: none"> <li>• Database</li> <li>• Gene expression and webtools</li> <li>• Protein and webtools</li> <li>• Protein purification</li> </ul>	Sittiruk Roytrakul (Biotec)
		<p>Protein expression</p> <ul style="list-style-type: none"> <li>• Data retrieve</li> <li>• Prediction of posttranslational modification</li> <li>• Gene cloning</li> </ul>	
		<p>Protein purification</p> <ul style="list-style-type: none"> <li>• Physico-chemical of protein</li> <li>• Protein structure</li> <li>• Protein purification</li> </ul>	
		<p>Introductory to Proteomics</p> <ul style="list-style-type: none"> <li>• 2D-Gel and 2D-LC</li> <li>• Maldi-Tof and ESI Mass Spectrometer</li> <li>• Application</li> </ul>	
		<p>Protein Identification</p> <ul style="list-style-type: none"> <li>• Protein and proteome databases</li> <li>• Peptide Mass Fingerprint</li> <li>• De Novo sequencing</li> </ul>	
	12:00-13:00	Lunch	
	14:00-15:30	Proteomic modeling and drug design	Supa Hannongbua (Kaset)
	15:30-16.30	System Biology	Santitham Prom-on (KMITT)

**Intended Audience** : Graduate students and researchers in science and science-related disciplines from all universities and institutions. (registration fee = 1,800 baht)

**Registration** : Faculty of Graduate Studies, Mahidol University. Tel (02) 441-0182-3

**Audit registration for interested audiences**

Thailand Graduate Institute of Science and Technology (TGIST), NSTDA Building  
(Ms.Sunee Makvisai Tel (02) 6448150-4 ext. 127, e-mail : [sunee@nstda.or.th](mailto:sunee@nstda.or.th))

**Further information**

Contact Dr.Pintip Ruenwongsa, Institute for Innovative Learning, Mahidol University  
Tel (02) 4419020-4 # 1300-9, e-mail : [scprw@mahidol.ac.th](mailto:scprw@mahidol.ac.th)