

Special Course and Tutorial

Discovery Systems in Bioinformatics

July 10-14, 2006

University of Queensland, Building 83, Room C310

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Discovery Systems in Bioinformatics

Introduction: Bioinformatics comprises methods and techniques for acquisition, storage, retrieval, and analysis of biological data. With accumulation of biological data, bioinformatics is becoming necessary for dealing with large quantities of data and support of experimental research through selection of key experiments and experiment planning. Biological data come from multiple sources: public sequence databases (general and specialized), literature sources, patent databases, Web-accessible repositories, and private sources. These data provide rich sources of information and are used for discovery of new relevant patterns hidden in the data across multiple sources. These patterns, representing new knowledge, can be extracted by simulated experiments using computational models or through data mining techniques. This course will introduce participants to the discovery process and enable them to understand the use of bioinformatics for biological discovery. The contents of this course cover databases, bioinformatics tools, management of the discovery process, and the analysis of the results. The emphasis of the course is on practical applications of bioinformatics techniques.

Date: July 10-14, 2006

Venue: University of Queensland, Building 83, Room C310

Organisers: ACPFG node, University of Queensland (www.acpfg.com.au) and GENica (www.genica.net.au)

Course materials: <http://discovery.imb.uq.edu.au/courses/20060710>

Cost: No charge (sponsored by LAFS and ACPFG UQ). Participants need to arrange their own transport and accommodation.

Participants: This course is suitable for students and scientists who have background either in biology or computing. Due to the emphasis on practical applications, the attendance to the course is limited to a class of 20 participants. Preference will be given to the attendees from UQ, ACPFG, and CRC MPB (GENica partners).

Aim: This course is aimed to help attendees expand their knowledge and practical use of bioinformatics.

Lecturer/tutor: Prof. Vladimir Brusic, v.brusic@uq.edu.au

Course coordinator: Ping Zhang, p.zhang2@uq.edu.au

Texts and study materials: The texts and study materials will be handed to participants at the beginning of the course.

Registration: Opens on June 8. Please register by sending an email to Ping Zhang (p.zhang2@uq.edu.au)

Structure of the course: The course consists of five 5 hour sessions. Each session comprises of one hour introductory lecture followed by four hours of hands-on work by participants, under guidance of the tutor. Participants are expected to bring their own research topics to the course.

Timetable: Sessions 1-5

Monday July 10 – Friday July 14

9:00 – 10:00 lecture
10:00 – 10:45 hands-on tutorials
10:45 – 11:15 morning tea
11:15 – 12:00 hands-on tutorials
12:00 – 13:00 lunch
13:00 – 14:00 hands-on tutorials

Session 1, July 10

Scientific discovery – introduction
Selection of problem suitable for discovery
Data collection, cleaning, and enrichment

Session 2, July 11

Preliminary data analysis and identification of key issues
Sequence and structure analysis tools

Session 3, July 12

Practical applications of bioinformatics
Genome screening

Session 4, July 13

Pattern extraction I. Standard bioinformatic tools
Pattern extraction II. Specialist bioinformatic tools
Testing and validation, data mining, interpretation of results

Session 5, July 14

Web-enabled bioinformatics
Reports, scientific publications, patents and grants