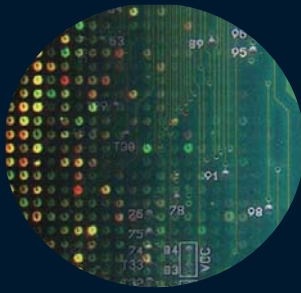
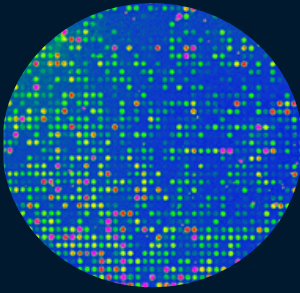


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K u a l a L u m p u r - M A L A Y S I A



ADVANCED COURSE

BIOINFORMATICS

- ❖ AN OVERVIEW OF BIOINFORMATICS
- ❖ SEQUENCE ALIGNMENTS
- ❖ CLUSTERING AND VISUALIZATION
- ❖ PHYLOGENETICS
- ❖ USE OF MARKOV MODELS
- ❖ PATTERN DISCOVERY AND RECOGNITION
- ❖ PROTEOMICS AND REGULATORY NETWORKS
- ❖ SELECTED EXAMPLES OF CURRENT RESEARCH

LECTURER:

Professor S. Halgamuge
The University of Melbourne,
Australia

LOCAL ADVISORS:

Assoc. Prof. Dr. G. R. A. Froemming
Institute for Medical Molecular Biotechnology (IMMB)
University Technology MARA (UiTM)
Malaysia

Dr. Mohd Shahir Shamsir
Faculty of Bioscience & Bioengineering
University Technology Malaysia (UTM)
Malaysia



VENUE:

THE RITZ CARLTON HOTEL KL

ORGANISED BY:

IRONIX- CONTINUING EDUCATION

www.ironix-conferences.com

COURSE OBJECTIVE

IRONIX CONTINUING EDUCATION

Bioinformatics is considered as one of the technologies that will revolutionize the mankind in the 21st Century. It is the integration of Computer Science and Engineering to help solving challenging problems encountered in Biology.

The influx of data generated by the various genome projects has led to a dramatic increase in research leading to very useful applications in Pharmaceutical industries and agriculture.

The 2-day intensive course is aimed at presenting theory, current methods and exciting R&D work in Bioinformatics highlighting applications useful in Drug Discovery and agriculture in a clear and easy to understand form.

THE COURSE CONSISTS OF:

LECTURES on Computational issues in Bioinformatics, methodologies (Multiple alignment methods in DNA and Protein Sequences, Hidden Markov Models, Dynamic Programming, Clustering and Classification) and applications

APPLICATION CASE STUDIES on Motif Search, Motif Discovery, Species Separation, metabolomic data analysis and Splice Site Detection

Course facilities at Ritz Carlton Hotel (KL) - Malaysia



BENEFITS OF ATTENDING THE COURSE

At the end of the course, participants will have thorough understanding of pattern recognition issues involved in Bioinformatics and a practical understanding of how to apply some of these methods to their own problems and domains. Participant will also benefit from the examples taken from cutting edge research.

WHO SHOULD ATTEND?

This course offers R&D personnel, lecturers, programme managers, computer scientists, engineers and technical specialists an opportunity to appreciate the emerging area of Bioinformatics and to learn the methodology for applying algorithms, tools and techniques to specific areas of Bioinformatics.

Participants are assumed to have knowledge of basic mathematics and in particular probability.

Some knowledge of Biology and computer programming is an advantage, and but not essential.

COURSE OUTLINE

IRONIX CONTINUING EDUCATION

1- AN OVERVIEW OF BIOINFORMATICS

- What is Bioinformatics, and why is it important?
- Primer on molecular biology and genetics
- DNA, RNA, genes, gene expression genetic
- What is System Biology?
- A brief history of Bioinformatics
- What areas in Mathematics and Computer Science are involved
- Biologically inspired computing

2 - SEQUENCE ALIGNMENTS

- Introduction to Dynamic Programming
- The Smith-Waterman algorithm
- Database searches
- Alignment scores and statistical significance of database searches;
- Multiple sequence alignment

3 - CLUSTERING AND VISUALIZATION

- Unsupervised Clustering Methods
- Dimensionality and Data Reduction
- Application Examples in Metagenomics: Species Separation with Clustering
- Micro Array Data Analysis

4 - PHYLOGENETICS

- Introduction to phylogenetics (distance based and character based)
- Phylogenetic trees;
- Distance matrix methods;
- Maximum likelihood approaches;
- Parsimony and ancestral sequences;
- Comparison of phylogenetic methods

5 - USE OF MARKOV MODELS

- Markov Models in Bioinformatics
- Hidden Markov models: Viterbi, forward, backward algorithms
- Application Examples

6 - PATTERN DISCOVERY AND RECOGNITION

- Gene finding
- Motif Search and discovery
- Gene structure, open reading frames and gene expression
- Alternative Splicing
- Microarrays

7 - PROTEOMICS AND REGULATORY NETWORKS

- Introduction to proteomics - protein structure; protein classification
- Protein and RNA structure prediction
- Protein folding
- An introduction to Regulatory Networks

8 - SELECTED EXAMPLES OF CURRENT RESEARCH

- Splice Site Detection with Markov models and Neural Networks
- Who has the best wheat?
- Semi-supervised Learning applied to Bioinformatics
- Locating CRISPR Sequences

A B O U T T H E L E C T U R E R

IRONIX CONTINUING EDUCATION

MORE ABOUT THE COURSE INSTRUCTOR:

Dr.-Ing Saman Halgamuge

http://www.mame.mu.oz.au/people/staff/saman_halgamuge.html



Dr. Halgamuge is a Professor in the Melbourne School of Engineering of The University of Melbourne and a member of the school wide initiative of Biomedical Engineering. He received Dipl.-Ing (1990) and Dr.-Ing (1995) degrees in Electrical Engineering from Technical University of Darmstadt, Germany.

He leads a group of postdoctoral fellows and PhD students working on Pattern Recognition and Optimization looking into problems in Bioinformatics and Sustainable Energy.

Dr. Halgamuge is the co-author of over 50 journal papers, 150 conference papers (h-index 18) and 15 book chapters. Among them are 6 top ranked journal papers based on ISI citations in their respective journals.

The 8 books edited by Dr. Halgamuge include: *Frontiers in the Convergence of Bioscience and Information Technologies* (IEEE Computer Society Press, 2007);

Classification and Clustering for Knowledge Discovery (Springer), 2005 and *Computational Intelligence for Modelling and Prediction* (Springer), 2005.

Dr. Halgamuge serves on the editorial boards of 6 journals, chaired about 12 conferences and served as a member of about 70 international program committees.

He has conducted international consultancies for UNDP and was an expert technical adviser to the Australian government Department of Health and Ageing.

REGISTRATION

IRONIX CONTINUING EDUCATION

(*) REGISTRATION INCLUDES :

- 2 full days course,
- Printed Course Materials,
- Course Certificate,
- 2 refreshments daily,
- Lunch at The Ritz Carlton Hotel (daily / 2 days).
- 10% discount voucher for the upcoming DSL2010 conference (Paris): www.dsl2010-paris.com
- 10% discount voucher for the upcoming ACE-X 2010 conference (Paris): www.ace-x2010.com

REGISTRATION FEE:

Early Bird Registration= 680 EUR (till 15/12/2009)

Late Registration= 980 EUR (after 15/12/2009)

CONTACT:

Dr. Meire Gomes

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University Technology Malaysia (UTM)

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shahir@fbb.utm.my

NOTE: this course is limited to a small number of participants, reserve your place soon!

**Special Rates (only for participants)
at Ritz Carlton Hotel - contact us!!!**



ADVANCED COURSE IN BIOINFORMATICS



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ADVANCED COURSE IN BIOINFORMATICS

Feb. 9-10, 2010 / Kuala Lumpur - Malaysia

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REGISTRATION FORM

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NIB: (Only for transfer inside of Portugal) 007900002608377210197

Credit Card:

() VISA () MASTER

Credit Card Number: _____

Expiration Date (Month/Year): _____

Signature / Date (AUTHORIZATION)

(*) Registration cancellations must be received by January 10 for a refund and note that a 100 EURO administrative fee is not refundable. Please note that refunds will be done after the EVENT for administrative reasons.