✍ Practical information

Place

The course takes place at Ghent University, campus Sterre, Krijgslaan 281, building S9, auditorium V2 on the 2nd floor & pc-room K. Zuse on the 3rd floor.

Time schedule

	Dates
Introductory sessions: -Biomolecular principles -Biostatistical principles	**23**/9, 25/9 2/10
M1: Bioinformatics	9/10, 16/10, 23/10, 30/10 & 6/11
M2: Biostatistics	13/11, 20/11, 27/11, 4/12 & 11/12

All dates mentioned above are Thursdays, except for Tuesday September 23rd.

Each session starts at 6 pm and lasts till 9.15 pm, with a coffee and sandwich break in between.

Lecturers

The lecturers in this course, all experts in the topics they will discuss, include:

?? *Prof.dr. Els Goetghebeur* - (UGent, Dep. Applied Mathematics & Computer Sciences)

?? *Prof. dr. Koen Goethals* - (UGent, Dep. Molecular Genetics)

?? *Dr. Kathleen Marchal* - (KULeuven: Dep. Electrical Engineering, ESAT/SISTA)

?? *Dr. Isabel Roldán-Ruiz* - (CLO: Plant Genetics & Breeding; UGent: Dep. Molecular Genetics)

?? *Prof.dr. Yves Van de Peer* - (UGent, Dep. Plant Systems Biology, Bioinformatics & evolutionary genomics)

?? *Dr. Marnik Vuylsteke* - (UGent-VIB: Dep. Plant Systems Biology, Functional Genomics)

?? *Prof. dr. Maria Ysebaert* - (UGent: Faculty of Science, Center for Statistics)

More detailed information about ICES, location and itineraries, the specific topics that will be discussed and the curriculum and research of the lecturers can be found at the ICES site:
http://allserv.UGent.be/~shoste/ICES/

✍ Registration fees

Registration is possible through use of the enclosed enrolment form. This form can also be found on our site.

Payment due within 30 days following receipt of invoice	Introductory sessions		1 module	Both modules[1] **(-10%)***
	Bio-molecular principles	Biostatistical principles		
Industry	€150	€75	€425	€765
Non-profit	€90	€45	€270	€486
Student	€70	€35	€225	€405

*Additional reduction
If 3 or more people from the same company enrol together for the full course, the reduction rises to 20%. This reduction does not apply to students.

This registration fee includes, course notes, lectures, coffee breaks and use of the auditoria and computers.
[1] People who enrol for both modules also receive the book 'Bioinformatics Sequence and Genome Analysis' by David W. Mount, Cold Spring Harbor Lab. Press, 2001

Cancelling is possible in writing until ten days before the start of the module, in which case 25% of the registration fee will be retained. In case of cancellation within 10 days before the start of the course the full registration fee is due.

WE ACCEPT THE TRAINING CHEQUES
WWW.OPLEIDINGSCHEQUES.BE

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✍ Further information

For more information about ICES and ICES courses:

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Phone: +32 (0)9 264 44 26 Fax: +32 (0)9 264 49 83
E-mail: Heidi.DeDobbelaere@UGent.be or
Isabel.DeZutter@UGent.be
Url: http://allserv.UGent.ac.be/~shoste/ICES/

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ices

Institute for
Continuing Education
in Science

Introductory course in
Bio–informatics
2003

2nd edition

including practical exercises

Faculty of Science

UNIVERSITEIT GENT

✍ Introduction

We live in a rapidly evolving technological society overrun by vast amounts of data and new information that reaches us in a fragmented and often incoherent way. To be able to structure these data into a meaningful whole, we must keep up with the latest advances in our society in the 21st century.

Bio-informatics is the field of research concerned with solving problems in molecular biology by computational techniques. It has gained enormous importance over the last decade, because of the exponential increase in genomic data. These data are stored in large databases from which the researcher can extract the necessary information using the right bioinformatics tools.

Fall 2003: Introductory course in Bioinformatics

The course consists of two optional modules:

Module 1: Bio-informatics

In the Introduction to Bio-informatics an overview of the link between bioinformatics and functional, structural and comparative genomics will be given.

The sessions on sequence alignment & homology searches address the basic principles of pair wise and multiple sequence alignment and heuristic homology searches (blast, Fast A). The power of these methodologies will be illustrated by an example.

Evolutionary analysis deals with the basic principles of phylogeny and gives an overview of different methodologies.

In the sessions on regulatory motif detection & pattern recognition an overview will be given of distinct motif representation (DNA & protein) and methodologies to search for statistically overrepresented motifs (HMM, Gibbs sampling, word counting.

In the final session comparative genomics and structural genomics will be illustrated by a number of concrete examples to show the strength of the techniques discussed in the previous sessions (gene prediction, phylogenetic footprinting, evolutionary genome analysis, genome wide detection of duplications)

Module 2: Bio-statistics

In the first session DNA-markers will be defined and some frequently used techniques for the generation of DNA-markers reviewed, highlighting some fields of application of DNA-fingerprinting in plant and human genetics.

Next, associations between a single marker and an observed phenotype (discrete or continuous) will be tested and the strength of any existing association measured with required confidence using standard statistical methods (linear and logistic regression and analysis of rxc tables)

Limitations of these methods are addressed in a following session and general solutions proposed in the form of maximum likelihood and permutation tests.

Finally, multiple markers will be tested with permutation methods as a solution to the multiple comparisons problem. Confounding & interaction will be discussed as a method to adjust for environmental factors in these datasets.

In the session on analysis of DNA chips & micro-arrays (clustering) an overview will be given of the customarily used techniques for data preprocessing and downstream analysis (clustering, classification) and their applications.

After a concise treatment of Mendel's laws, meiosis & recombination, the session on linkage analysis will deal with the following topics: the genetics of recombination, the estimation of recombination frequencies, the determination of linkage groups, and an introduction to mapping algorithms.

In Quantitative Trait Locus Analysis single marker QTL analysis and interval mapping QTL analysis will be discussed as well as an introduction to multiple QTL mapping.

✍ Intended audience

This course is aimed at researchers in both industry and academia wishing to gain some knowledge on or improve their knowledge of the techniques used in Bioinformatics, as well as the capabilities and use of these techniques.

✍ Required knowledge: Introductory sessions

The lectures are organised to be as self-contained as possible. The previous edition however has shown that basic knowledge of certain biomolecular, genetic and statistical terms is an advantage. Accordingly this course starts with a number of optional sessions, which introduce the specific terms, and principles that will be used in both modules.

Topics discussed in the introductory sessions are:

Bio-molecular sessions: DNA, genes, chromosomes, nucleic acid sequences, transcription, mRNA, tRNA, protein sequences, basic genetic principles, mutation, natural selection

Bio-statistical sessions: standard deviation, confidence interval, t-test, F-test, ?²-test, rxc tables, p-value & power, variance, linear & logistic regression, confounding & interaction

✍ New: practical exercises

Both modules incorporate practical exercises in the lectures, be it on a calculator or on computer. The number of participants is therefore limited to the number of computers.

✍ Exam

Participants who enrol for both modules are given the opportunity to take a written test at the end of the course. Participants who succeed in this exam receive a certificate of Ghent University. The course can be incorporated in the doctoral training program.