



Applications for 2007-08 are welcomed after beginning of 2007. Further information: www.cs.helsinki.fi/mbi, bioinfo@cs.helsinki.fi

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formatics.

gy courses in MBI.

modelling and computationally feasible methods.

Information contained in biological measurements

has several special characteristics, e.g. the sequen-

tial nature of DNA, RNA, and proteins, which has

given rise to a new interdisciplinary field - bioin-



One of the MBI organisers, Professor Liisa Holm is an influential figure in protein bioinformatics. Urease enzyme is one of the protein



studied by Professor Holm's group.

professionals to work in research and development medicine, with computational means. The analysis tasks in biology and medicine. The degree also gives of measurement data is of vital importance in the excellent general background for graduate stud- modern research in biology and medicine. Underies in bioinformatics and in other related applied standing such data requires both robust statistical



Systems Vol. 15, No. 3 (2005) 163-179. of HERVs. The texts in the display are labels for current classifications of HERVs within each area. The differ similarities between all HERV sequences. It can be used to refine and complement the current classification

Merja Oja, Goran O. Sperper, Jonas Blomberg and Samuel Kaski. Self-organizing map-based discovery ence in color shade is proportional to the dissimilarity of neighboring areas.

and visualization of human endogenous retroviral sequence groups. International Journal of Neural



MBI MASTER'S DEGREE

PROGRAMME IN BIOINFORMATICS





Leading edge research and education in Finland and in Helsinki

its high-quality. This is exemplified by the facts that Finland continues at the top of OECD PISA reviews in mathematical literacy, outperforming USA, Ja-Established in 1640, University of Helsinki i University of Helsinki (UH) and the Helsinki Uni-leading European research universities. Helsinki University of Technology (TKK) is



Why graduate from MBI?

education in bioinformatics.

lence and they are central operators in the CoMBI,

carefully tailored to give sufficient background to Methodological principles (10 cr) data mining in genetics. Minor subject studies are science special module (20 cr) ics, biometrics, computational systems biology, and Biological or computer and information are biological sequences analysis, biomathemat- Thesis (30 cr) problem-settings. Examples of specialisation areas Elective studies (20 cr) with a strong emphasis on central bioinformatics Bioinformatics A3 (20 cr) tensive portion of general methodological studies Bioinformatics A2 (20 cr) Master's Degree in Bioinformatics consists of an ex- Master of Science in Technology (120 cr) What will you learn in MBI?

• The programme will start 3 September 2007

• Further information: www.cs.helsinki.fi/mbi

• Applications for 2007-08 are welcomed after

• The programme is aimed at full-time students

• Proficiency in English (TOEFL or equivalent) Mathematics, Statistics, or related biological field

• A Bachelor's degree in Computer Science,

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Admission requirements:

How to apply?

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Study plan (1 cr) Advanced internship (1-3 cr) (10 04) sisədT Biology or medicine Mathematics and statistics Computer science mi (10 04) seibuts toejdus roniM

Major subject studies in bioinformatics (30 cr) (12 021) Asience (120 cr)

and MSc (Tech.) in Bioinformatics. MBI offers two degrees: MSc in Bio



blue and red. Figure courtesy of Sarah Butcher and Juha Huiskonen, Institute of Biotechnology, University of Helsinki 46 mucleocapsid at 7.5 Å resolution, with the segmented icosadehrally-ordered capsomers coloured in brown, orange, green, yellow



Professor Esko Ukkonen is a pioneer in biological The teaching is given by people working in the cut-sequence analysis. His group has developed several ting edge of bioinformatics research. The organisers methods that belong to the core algorithmics of are members in three National Centres of Excel- approximate pattern matching and DNA sequence assembly. The currently standard formulation and the only Finnish graduate school offering PhD level algorithmic approach for assembling DNA sequences from short fragments is based on a paper by E. Ukkonen et al. from 1983.



–Liisa Holm

"The main interests of my research group are protein sequence-structurefunction relationships and computational analysis of gene regulation. We are developing computational methods to correlate specific sequence motifs with protein function, and to correlate co-regulated gene clusters from microarray experiments with biological processes and biochemical pathways."

Research in data mining started in Finland in the late 1980's when professor Heikki Mannila focused his research efforts into this area, among the first in the world. His group gave the first efficient algorithms for finding association rules. More recently, Heikki Mannila, together with professor Hannu Toivonen, defined the problem of finding episodes from sequences. The definitions and algorithms have turned out to be influential, for example, in medical genetics, where the group has participated in the discovery of genes related to diseases such as asthma and schizophrenia.

Professor Samuel Kaski is an internationall gnized researcher in machine learning and data analysis. "Bioinformatics is a perfect match to researchers interested in machine learning, modeling, or data mining on the one hand, and the fundamen tal problems in biology on the other. What could be teresting than being able to make sense of the functioning of a biological cell, given only i perfect measurement data, and with a little help from the wast databases of background data"

The Laboratory of Computer and Information Science of TKK is a <u>renowned</u> research center in loarning and nottone discourse it liachnie learning and pattern discovery, with th his Self-Organizing Mane

. Organizing Map

