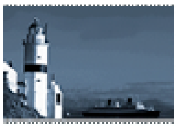

ISMB ECCB 2004

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JULY 31 - AUGUST 4, 2004 ■ GLASGOW, SCOTLAND, UK ■ SCOTTISH EXHIBITION AND CONFERENCE CENTRE

Submission Results

Poster Abstracts

Data Mining

A-1 A Bayesian Approach to Discover Sparse and Flexible Patterns in Biological Sequences

Kazuhito Shida, Makoto Ikeda, Atsuo Kasuya

> Patterns in biological sequences may have sparse design. However, the most flexible kind of such pattern (letter-composition at the sites and the length of the gaps are both variable) is scarsely investigated. A Bayesian automated detector of such patterns was deviced and tested successfully onsome of known examples.

Long abstract

A-2 ProtExt: a Web-based Protein-protein Interaction Extraction System for PubMed Abstracts

Chin-Lin Peng, Yung-Chung Lin, Hsuan-Cheng Huang, Cheng-Yan Kao, Shui-Tein Chen, Hsueh-Fen Juan

> ProtExt is a web-based software package, which automatically extracts information of protein-protein interactions from the literature abstracts available at the NCBI Entrez-PubMed system and present the extracted information graphically and intuitively. ProtExt is available at http://protext.csie.org.

Long abstract

A-3 Automatic Hidden Markov Model selection for clustering procedures

Schoenhuth, Alexander, Schliep, Alexander, Olof Persson, Christine Steinhoff

Long abstract

A-19 UVWORD: fast genome-scale analysis of DNA words on a PC

Vicente Arnau, Miguel Gallach, Francisco Ferri, Ignacio marín

We have developed a new algorithm that allows for the exhaustive determination of 1-14 nucleotides-long words in DNA sequences of any length. It is fast enough as to be used at a genomic scale running on a standard personal computer.

Long abstract

A-20 A cataloguing system for diverse biological datasets

T. G. Booth, A. J. Wood, P. Swift, B. Tiwari and D. Field.

Biologists produce many diverse datasets in the course of their research. We present a cataloguing system to capture and search descriptions of all data and sample sets associated with a research project. Our approach uses only freely available software, and can be easily adapted to suit any metadata capture need.

Long abstract

A-21 Analysing Patterns of DNA Methylation Associated With Clinical Outcome

Hall, J, Paul, J, Brown, R

Patterns of tumour CpG island DNA methylation associated with clinical outcome could aid disease management of patients, give insight into biological mechanisms and prioritiz future research areas. We investigated a supervised clustering methodology; initial results find associations but adequate power and validation are essential for correct interpretation of results.

Long abstract

A-22 Identification of candidate disease genes using text mining with controlled vocabularies

N. Tiffin, J. F. Kelso, A. R. Powell; P. Hong; V. B. Bajic; W.A. Hide

Complex-trait linkage analysis of a disease may identify hundreds of candidate disease-causing genes. Text-mining of Entrez-PubMed abstracts using eVOC ontology terms identifies tissues and cell types associated with the disease. Candidate genes expressed in these tissues may then be identified according to their expression profiles as defined by eVOC annotation.

WebLab, a protocol-based analysis platform with a user-friendly interface was developed using XML for program parameters and workflows. The applications are invoked with a job manager, and the data and analysis results are stored in a database and could be shared by users in the same group.

Long abstract

B-8 iCompare: a genome browser for displaying comparative genomics annotation

Syam S Tatineni, S Ribrioux, Adrian Bruengger, Markus John.

The iCompare genome browser is a web-based visualization tool displaying annotation tracks from different sources and species based on coordinate, keyword, and sequence searches. Its focus is on displaying comparative genomics annotations. iCompare accesses a generic Oracle database holding the annotation tracks and utilizes scalable vector graphics (SVG) for visualization.

Long abstract

B-9 CRAVE: Visualization of Phenotype Ontologies

G.V.Gkoutos, E.Green, A. Blake, S. Greenaway, A.-M. Mallon, J.M. Hancock, D. Davidson

Concept Relation Assay Value Explorer (CRAVE) is a visualization tool for viewing Phenotype Ontologies created according to recent proposals. CRAVE is available online at: http://www.mgu.har.mrc.ac.uk/servlet/browser.frameset

Long abstract

B-10 UVWORD-G: A graphical tool for the visualization of word counts in DNA sequences

José Vicente Martínez, Vicente Arnau, Ignacio Marín

We describe a JAVA program that determines all words of up to 14 nucleotides present in DNA sequences. It allows a varied repertoire of analyses, from descriptive studies of a sequence to comparative analyses between sequences. The program has a variety of graphical outputs that allow to comfortably visualize the results.

Long abstract

B-11 Feature Plots: Visualizing System Dynamics in Cyclic Processes

Anders Fausbøll, Thomas Skøt Jensen, Ulrik de Lichtenberg, Soren Brunak

Networks of thousands of genes and proteins are becoming available. Software exists for

Yuko Makita, Michiel J. L. de Hoon, Satoru Miyano and Kenta Nakai

> We used binding motif information and expression data for a genome-wide prediction of sigma factor regulation in B.subtilis. We confirm the sigma factor prediction by scanning the region upstream of the predicted transcription start site for binding sites of transcription factors known to be associated with the sigma factor.

Long abstract

D-17 UVCLUSTER: hierarchical cluster analysis of protein interaction data

Vicente Arnau, Sergio Mars, Ignacio Marín

> We have developed a new program, called UVCLUSTER, that uses iterative hierarchical clustering to analyze protein-protein interaction data. It allows the analysis of hundreds of interacting proteins, generating dendrograms that allows simple visualization of the degree of proximity among them.

Long abstract

D-18 Mechanism of redox regulation of TRPC3 channels

Christian Rosker, Michael Lukas, Klaus Groschner

> TRP channels have been suggested to serve as cellular redox sensors. We investigated the effects of oxidative stimuli on cellular localization and function of TRPC3. Our results indicate that TRPC3 is able to integrate redox and PLC-mediated signals, and interacts with membrane sterols as the basis of its redox sensitivity.

Long abstract

D-19 Locating cis-regulatory modules genome wide by comparative genomics

Kimmo Palin, Jussi Taipale

> We have developed a new method and a computational tool to discover cis-regulatory modules and functional transcription factor binding sites in genomic DNA. The method uses comparative genomics and binding site clustering to distinguish between functional and nonfunctional binding sites. The sofware is usable in genome-wide studies

Long abstract

D-20 Alternative Splicing in Eukaryotic Cells – Influence of SR proteins on Splice Site Selection

The conservation of mutation rates across lineages is a signature of common mutational pressures. We analyze such conservation in human, mouse, and rat. We find that substitution rates in gene silent-sites correlate overall between the species. Certain regions have extremely similar patterns of substitution, covarying over megabase length scales

Long abstract

H-23 Metazoan deep phylogenies – can the Cambrian explosion be resolved with molecular markers?

G. Fritzsch, M. Schlegel, P. Stadler

Fossils are our primary window to the history of life. The appearance and radiation within ten million years is referred to as the Cambrian explosion. We started a comprehensive multi-gene sequence analysis in order to contribute to the solution of this outstanding evolutionary phenomenon in metazoan evolution.

Long abstract

H-24 Comparative Genomics of Glutathione transferases

Antonio Marco, Ignacio Marín

Glutathione transferases (GSTs) are a highly heterogeneous group of detoxifying enzymes. In a phylogenetic analysis that involved 700 sequences, at least fourteen main groups of GSTs were found. A novel group includes the human gene GDAP1, involved in Charcot-Marie-Tooth disease. GDAP1 group proteins have unique structural features, including transmembrane domains.

Long abstract

H-25 Comparative genomics and proteomics of the septin gene family

Sergio Mars, Vicente Arnau, Ignacio Marín

We describe the phylogenetic relationships among septins, a group of proteins involved in cytokinesis and other processes. A comparative analysis of septin-interacting proteins in Saccharomyces cerevisiae and Drosophila melanogaster that suggests that septins are functioning differently in animals and fungi, is also presented.

Long abstract

H-26 Reconstructing Longitudinal Evolutional Phylogenetic Tree of HIV-1 Protease Gene under HAART by Linking Within-patient Orthologous Viral Population.