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APRÍLOVÁ MINIKONFERENCE

BIOINFORMATICS, GENOMICS, GENOME ANNOTATION, GENE EXPRESSION DATA ANALYSIS, PROTEIN ENGINEERING, PREDICTION OF PROTEIN STRUCTURE, PHYLOGENETICS, COMPUTATIONAL CHEMISTRY, CHEMOINFORMATICS, HUMAN GENETICS, MICROARRAYS, SAGE, PROTEOMICS, DATA MINING, MOLECULAR GENETICS, CELL BIOLOGY, PROTEIN FOLDING, GENOTYPING, STRUCTURE-ACTIVITY RELATIONSHIP, RNAi, MOLECULAR DYNAMICS SIMULATION, COMPARATIVE GENOMICS, PROTEIN FOLDING, POSITIONAL CLONING, MULTIVARIATE STATISTICS, ENZYMATIC CATALYSIS, PROTEIN EXPRESSION

Pátek 1. dubna 2005 Svatý Jan pod Skalou

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Program

10:15 Zahájení (Jan Pačes)

Předsedající: Jan Pačes
10:30 Matej Lexa
Statisticka segmentacia biologickych sekvencii: cierna magia alebo krok spravnym smerom?

11:10 Zuzana Hořejší
Predikce funkční siRNA

11:50 Martin Mokrejš
IRESite - Databáze virových a buněčných IRES elementů

12:30 Oběd

Předsedající: Jiri Vondrašek
14:00 Mirek Janošík
Porucha sbalování a agregace jako prícina homocystinurie z deficitu cystathionin beta-synthasy

14:30 Vojtěch Spiwok
Enzymy aktivní při nízkých teplotách

14:00 Vojtěch Klusák
Hledani souvislosti mezi strukturou bilkoviny a jeji termostabilitou

15:30 Přestávka

Předsedající: Petr Divina
16:00 Jan Paul
Mitochondriomika: jak dýcháme

16:30 Marek Basler
i Železem regulovaný proteom a transkriptom Neisserie meningitidis
ii Analýza transkripčního profilu lidských endoteliálních buněk po interakci s Neisserii meningitides pomocí Affymetrix technologie

17:10 Jiří Vohradský
Recurrent neural network model of gene expression

Journal club, večeře, v sobotu výlet do okolí

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Statisticka segmentacia biologickych sekvencii: cierna magia alebo krok spravnym smerom?

Matej Lexa

Biologicke sekvencie sa skladaju s roznych elementov, ktore su usporiadane do vyssieho poriadku. Niektore pravidla takehoto usporiadania pozname, napriklad exony sa striedaju s intronmi, kodujucej casti genov predchadza oblast promotora a podobne. V tomto prispevku sa zaoberam moznostami odhalit strukturu, ktora nam je do znacnej miery zatial skryta, technikami statistiky. Biologicku sekvenciu prirovnavam k jazyku a skryte elementy k slovam biologickeho jazyka.

Prediction of functional siRNA sequence

Zuzana Hořejší

Introduction of short interfering RNA (siRNA) into a cell results in degradation of its homologous mRNA. This process is used for temporary knockdown of specific mRNA and therefore protein level in cell cultures and experimental animals. RNA interference involves recognition of the siRNA by a RNA-induced silencing complex (RISC), activation of the complex, recognition and subsequent cleavage of the target mRNA. It has been shown that the efficiency of mRNA degradation is highly dependent on the siRNA sequence. Based on datas previously published by other groups we tried to develop an algorithm susceptible to predict more precisely functional siRNA sequence.

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IRESite – The database of experimentally studied viral and cellular IRES elements

Martin Mokrejš

This project focuses on the IRES elements (Internal Ribosome Entry Site) which play important role in the initiation of translation in eukaryotes. The IRES elements were found in almost fifty distinct viruses, involving those which cause serious diseases of human being and animals. Recently the evidence also have appeared that IRES mediated translation initiation is not restricted only to transcripts of viral genomes. Although over the 70 different cellular IRES elements have been reported untill now, it is not yet clear whether the cellular IRESes are more widespread or not. There is a high demand to re-evaluate the very precious experimental data in current context, correlate the data in larger scale or even to find nifty details easily. Unfortunately, the data provided by printed publications are not accessible for efficient computer-based usage and analyses.

We are presenting the working database solution containing, as an example, the first data extracted from the publicly available scientific literature. The IRESite database records for every single experiment information about the nature and origin of the IRES elements, about their size, relative position in mRNA, reporter genes used to monitor their activity and about measured reporter-protein yields and/or activities. Further, the database records positive/negative controls used in every such experiment, presents known secondary structure of respective IRES element, records similarity to rRNA and presence of promoter-like elements in whole mRNA molecule studied, lists RNA-protein interaction if known, contains nucleotide sequence data of full-length mRNA and of IRES itself and also many other parameters including citation to primary literature. In total, IRESite keeps track of 92 biologically relevant features which were either extracted from literature or found by curator. By the end of May 2005 anyone will have the opportunity to insert new data into this curated database through its www interface at http://www.iresite.org. At the moment we finish the software development and continue to fill the database with first experimental data.

This work was supported by the Czech Grant Agency (Grant No. 204/03/1487), by the Grant Agency of Charles University (Grant No. 251/2004/B-BIO/PrF) and by the Ministry of Education (Grant No. MSM 0021620813).

Enzymy aktivní při nízkých teplotách

Vojtěch Spiwok

Enzymy organismů, adaptovaných na nízké teploty, představují atraktivní biokatalyzátory pro nízkoteplotní biotechnologie, protože při nízkých teplotách vykazují vysokou aktivitu. Kromě toho, výsledky výzkumu adaptace mikroorganismů na úrovni enzymů pomáhají objasnit zásadní otázky biochemie, jako je např. sbalování a stabilita proteinů, enzymová katalýza a další. Nejčastěji přijímaná teorie vysvětlující podstatu této adaptace předpokládá, že tyto enzymy mají ve srovnání s enzymy meso- a termofilních organismů vyšší strukturní flexibility (celkovou nebo lokalizovanou). S tím souvisí i jejich nižší tepelná stabilita. Přednáška srovnává tyto obecné představy o podstatě adaptace s výsledky komparativní simulace molekulové dynamiky. Simulace umožňuje srovnání flexibility a dalších vlastností mezi enzymy aktivními při nízkých teplotách a enzymy meso- nebo termofilních organismů.

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Mitochondriomics: What makes us breathe

Jan Paul

Mitochondrion is energy providing organelle of the eukaryotic cell, whose proteome arises from expression of two genomes, nuclear and mitochondrial. Mutation in any of these causes severe metabolic disorders with frequent fatal outcome. Bioinformatic approach has been recently applied in hunt for “nuclear-mitochondrial” genes in human genome which represent either possible target genes of nuclear DNA mutation caused mitochondrial disorders, or genes whose mutations and polymorphisms can complement mutations in mitochondrial or nuclear DNA. Methods based on prediction of protein targeting and localization, can tell us something about probability of protein being localized in mitochondria, and mitochondrial neighborhood analysis can successfully predict mitochondrial or “mitochondria-related” genes, using their gene expression signatures. At last but not least the genomic context of target gene can show us some hints concerning its “mitochondria-relatedness”.

Iron-regulated proteome and transcriptome of Neisseria meningitides

Marek Basler

The pathogenic Neisseria species produce a number of iron regulated proteins that are important in virulence. Here we analyzed the composition of the iron-regulated proteome and transcriptome of a local serogroup C invasive meningococcal isolate 10/96 on the whole genome level. The steady-state proteome of meningococci grown under iron-depleted and iron-replete conditions was analyzed by 2-D electrophoresis and the proteins exhibiting significantly enhanced or reduced expression levels at either condition were identified by MALDI-TOF MS analysis. In parallel, total RNA was isolated from the same cultures and screened for iron-regulated mRNA expression profiles using commercial spotted whole-genome DNA microarrays. In total, we identified 85 genes that were significantly up-regulated in cells from iron-replete cultures and 114 genes that were up-regulated upon growth in iron-depleted media. The overlap between the iron-regulated transcriptome and proteome data sets was, however, found to be rather low and only 18 open reading frames were detected by both methods as being subject to regulation in response to iron availability in the media. The various functional categories of iron-regulated genes and the possible physiologic consequences of adaptation to growth under iron-limited conditions will be outlined in the presentation.

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