BCB Seminar

Time: Wednesday, May 7, 2003, 4:00 - 6:30 pm
Place: Humboldt University of Berlin, Dept. of Computer Science
Rudower Chaussee 25 (IV 101), 12489 Berlin

Rolf Backofen, University of Jena
RNA Sequence Structure Properties

Previously, RNA was more or less considered to be just an intermediate step in the translation from DNA to protein. But recently, RNA gained more interested since it was found that it has much more functionality This was the reason that research on small RNAs was cited as past year scientific breakthrough.

Hence, one is especially interested in finding conserved RNA-motifs. It has been shown that structure is more conserved than sequence when considering RNA-motifs. Hence, all sequence-based methods for finding RNA-motifs such as multiple sequence alignment will fail.

We will shortly give an overview over existing approaches for finding RNA-motifs, before we consider some problems (such as finding the consensus structure) in more detail.

- coffee break -

Christian Piepenbrock, Epigenomics AG Berlin
Epigenomics - Large Scale Microarray Analysis for DNA Methylation

Bioinformatics at Epigenomics faces three challenges:
1) enable genome-wide DNA methylation analysis;
2) support large scale microarray studies from experimental design to data interpretation;
3) integrate data from multiple assay formats and technologies for product development.

The talk will provide an overview of bioinformatics for DNA methylation analysis including the medical applications and then focus on maintaining and controlling data quality in large scale microarray studies. The effective identification of problems is an essential prerequisite for improving chip experiments. Traditionally, the influence of data quality problems can only be minimized by expensive repeated measurements, because a detailed understanding of all relevant parameters seems impossible. However, when experiments are standardized enough, then process dependent alterations are relatively rare events. Therefore, instead of reducing these effects by repetitions one should rather detect problematic chips or chip batches and repeat only those. This can only be achieved by controlling process stability. We demonstrate the power of our approach on 3 large sets of DNA methylation microarray data.

- coffee break -

Jörg Hakenberg, Humboldt University of Berlin

Statistical approaches to analyze positional dependencies in protein domains

MOTIVATION: Protein domains are usually identified by conserved regions in the primary amino acid structure. Protein functions are dependent on the 3-dimensional structure and biochemical properties of the amino acids. 3-Dimensional structures are stabilized by interactions between amino acids which are not necessarily adjacent in the primary structure. To preserve the structure, even if certain residues of the sequence are mutated, similar interactions must be possible. This property has to be reflected by positional dependencies between residues of positions crucial for such interactions. We use statistical approaches to identify positional dependencies in aligned protein sequences of the death domain family and the homeodomain.

RESULTS: A 12 amino acid region with high correlations in the death domain and in the CARD but not in the DED could be identified. Most positions with known mutations in death domain family members showed a strong correlation with other positions in the protein. The correlated positions identified in the homeodomain were distributed over the whole sequence. Point mutations in the positions of the homeodomain leading to a defect were either correlated or conserved, i.e. showed a low entropy.

Guests are welcome !

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