

Genomes, Genes, Proteins and Computers: Computational Molecular Biology and Bioinformatics Research in the BRL@UCY.AC.CY

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In my talk I will give a very brief overview of the multidisciplinary field of Computational Molecular Biology and follow with a description of ongoing research at the Bioinformatics Research Laboratory in the Department of Biological Sciences at the University of Cyprus.

More specifically, our research is oriented towards the interpretation of large scale genomic data and the use of computational methods in order to reveal the principles governing the Molecular Basis of Life. We are mainly interested in the elucidation of protein sequence to structure/function relationships using sequence similarity, statistical and machine learning techniques.

In particular, our research focuses on:

1. Sequence repeats, low complexity/compositionally biased regions: Investigation of their relation to protein structure and association to protein (mis)function. Study of the evolution of protein repeats.
2. Transmembrane and membrane-associated protein topology and structure prediction: Prediction of structural features of membrane proteins. Evolution of transmembrane protein topology/structure/function.
3. Sequence-based structural/functional classification of proteins
4. Study of bacterial genome evolution
5. Study of different metrics in biological sequence space for clustering protein and DNA sequences

I will present recent results (from our group and collaborators) on novel methodological approaches to filtering and protein sequence database search, and a novel cepstral coefficient-based approach to clustering protein sequences. Furthermore, I will illustrate how β -barrel outer membrane protein topology prediction is enhanced by the use of evolutionary information encoded in multiple sequence alignments.