Postgraduate Student: **Maria Paraskevopoulou**

Thesis Title:

Computational prediction of microRNA targets on long non coding RNAs

Abstract

microRNAs (miRNAs) are small endogenous RNA molecules (~22nt) that belong in the wide ncRNA family. They play a major role in a plethora of biological processes and especially act as post-transcriptional gene regulators. lncRNAs, on the other hand, are long non coding transcripts, larger than 200 nucleotides. They are identified either on intergenic regions, or in genomic locations that exhibit overlap with protein-coding genes. Possible interactions of lncRNAs-microRNAs can indirectly regulate gene expression.

Aim of this study, is to explore microRNA – lncRNA putative functional interactions, based on high-throughput experimental data, as well as on state of the art in silico target predictions. Moreover, it provides for the first time, a comprehensive annotation of microRNA (miRNA) targets on human and mouse lncRNAs. miRNA targets of large collections of lncRNA transcripts have not yet been extensively studied through experimental data analysis, and there are only few lncRNA-miRNA interactions reported in the available literature.

The first part of the study includes the collection of the available lncRNA resources, derived from the most recently updated biological databases and the relevant literature. Subsequently, miRNA targets on lncRNAs have been identified with the analysis of high-throughput data, and more precisely HITS/PAR-CLIP experimental data. Morever, one of the best target prediction algorithms in terms of sensitivity and specificity, DIANA-microT-CDs, has been utilized for computational detection of miRNA targets on lncRNAs. Finally, miRNA/lncRNA-related information, as well as experimentally verified and in silico predicted miRNA-lncRNA interactions have populated a novel database named DIANA-LncBase. The experimentally supported entries available in DIANA-LncBase correspond to more than 5,000 interactions, while the computationally predicted interactions exceed 10 million. DIANA-LncBase is an extensive repository of miRNA-lncRNA interactions that can provide high quality data for numerous analyses and future research projects throughout the community.

Examining Committee

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