Postgraduate Student: **Ioannis Vlachos**

Thesis Title:

Computational Tools for the Identification of the Functional Role of Experimentally Validated microRNA Gene – Targets.

Abstract:

microRNAs are small non coding RNA species (~23bp), which actively regulate gene expression. They are esteemed as central regulators for a large number of biological processes and human pathologies.

Aim of the present study is to actively link for the first time experimentally validated microRNA targets with molecular pathways. This connection will be established via the formation of highly specific algorithms and applications to microRNA centered research. An imperative perquisite for achieving this goal is the design and implementation of 2 distinct applications: a new data base collecting significantly more experimentally validated targets than any other available today; as well as a web application allowing the accurate determination of the functional role of microRNAs in molecular pathways. The interconnection between these two on-line applications will significantly extend their functionality and usefulness to the research community.

Initially, the largest available microRNA gene target dataset was manually extracted from the available literature. A text mining assisted curation pipeline was implemented, in order to optimize the laborious manual process. The collected targets represent a 16.5 to 175 – fold increase, compared to all available manually curated databases available today. This wealth of information was inserted in TarBase v6.0, an online version of our database, in order to be freely accessible to the public.

Following the creation of a database capable of supporting the project's aim, a series of highly specific tools and algorithms were implemented enabling the identification of microRNA regulated molecular pathways. All these modules were incorporated to DIANA-miRPath v2.0, the second version of the miRPath werb server, which was redesigned from the ground up to meet the project's specifications. This application is the first available to include predicted, as well as experimentally validated microRNA targets. It was especially designed to offer tools and functionalities highly specific to the detection and analysis of microRNA – pathway interactions. DIANA-miRPAth v2.0 offers a plethora of novel tools, such as clustering of microRNAs and pathways based on their interactions, design of microRNA vs pathways heat maps and more.

The integration of these two implementations can support a large number of different use case scenarios and research pipelines by sophisticated statistics and relevant algorithms, while offering for the first time essential tools to the research community. These tools can significantly assist researchers examine and understand data relevant to microRNA nature and function.

Examining Committee:

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