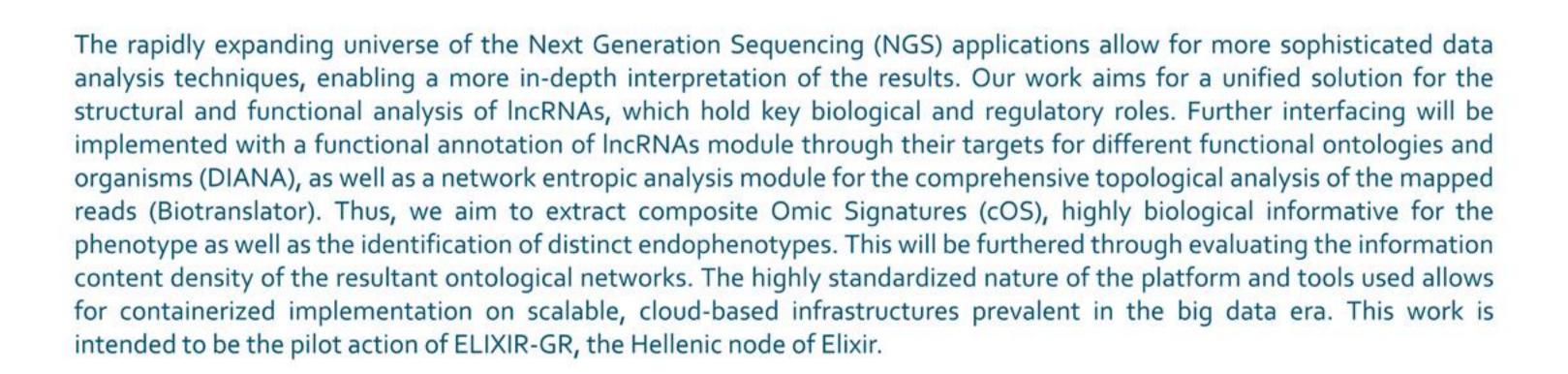
ELIXIR – GR: Development of an integrated functional network analysis and composite signature derivation pipeline for ncRNAs RNA-seq data

Irene Liampa 1,2, Hector-Xavier de Lastic 1,2, Eleftherios Pilalis 3, Aristotelis Chatziioannou 1,3

Affiliations:

- Metabolic Engineering and Bioinformatics Group, Institute of Biology, Medicinal Chemistry and Biotechnology, Hellenic Research Foundation NHRF, Athens, Greece
 Department of Molecular Biology and Genetics, Democritus University of Thrace, Dragana, Greece.

e-NIOS Applications Private Company, Kallithea-Athens, Greece



Mapping of ncRNAs to genes

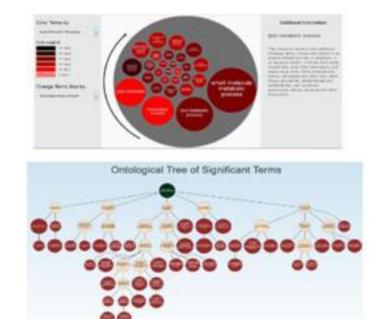
Composite signatures

- Integration module to support ncRNA, RNAseq analysis
- Integration of multiple datasets
- Functional annotation of ncRNAs through their targets for different functional ontologies and organisms

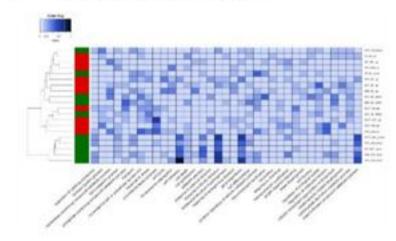
Topological analysis

(BioTranslator)

- Network entropic analysis module
- Ranked genes & pathways



- Comparative analysis for different datasets
- Measurement of information captured
- Multiple classification methodologies bundled (SVM, Random Forests, Neural Networks, etc)
- Discriminative gene sets
- PCA analysis
- Classification module



Galaxy-based node architecture

DATABASE (Creation/Maintenance) ncRNAs (miRNAs, IncRNAs) Reference data Target gene expression (exome) Other layers SNPs, CNVs,

- Galaxy

Distinct biological layer Analysis Module

- Read Alignment
- Annotation-based Assembly/ De novo Assembly
- Transcript-level/Gene-level Quantification
- Differential Expression
- Non-coding potential evaluation
- Noise filtering

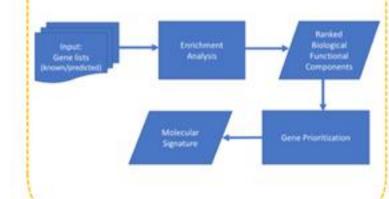
Integrative Analysis Module

Association Analysis

- Identification of putative ncRNA targets
- Identification of promoter regions and TFs of miRNA transcripts
- Alternative splicing, polyA and RNAediting sites
- Epigenetic modifications

Biotranslator

- Derivation of composite Omic Signatures (cOS)
- Endophenotypes construction
- **Gene Prioritization**
- Functional Annotation expressed transcripts and their interactions



- Powerful user management mechanism
- · User friendly
- Data sharing
- Integration of large SQL and noSQL databases
- Integration with BioTranslator through its Galaxy operators:
 - ✓ Pathway analysis operator
 - ✓ Gene prioritization operator
 - Comparative analysis
 - ✓ Network analysis

Contact

Irene liampa: eliampa@eie.gr Hector-Xavier de Lastic: hector.xavier.de.lastic@gmail.com Aristotelis Chatziioannou: achatzi@eie.gr Eleftherios Pilalis: epilalis@eie.gr

We acknowledge support of this work by the project "ELIXIR-GR: Hellenic Research Infrastructure for the Management and Analysis of Data from the Biological Sciences" (MIS 5002780) which is implemented under the Action "Reinforcement of the Research and Innovation Infrastructure", funded by the Operational Programme "Competitiveness, Entrepreneurship and Innovation" (NSRF 2014-2020) and co-financed by Greece and the European Union (European Regional Development Fund).



OPERATIONAL PROGRAMME

ENTREPRENEURSHIP

INNOVATION





