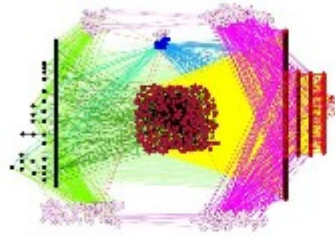


Unraveling the Complexity of Gene Networks: CRS4-Linkalab team among best performers at DREAM5 conference, Columbia University

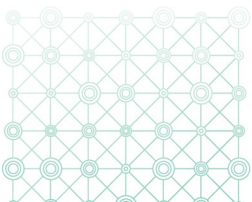
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The team composed by Andrea Pinna, Nicola Soranzo, Vincenzo De Leo and Alberto de la Fuente has qualified as one of the best performers in the "Network inference challenge" in the DREAM5 competition, whose results were presented at the prestigious venue of Columbia University, NYC, during the annual "3rd Joint Conference on systems biology, regulatory genomics and reverse engineering challenges". The team called "ALF" and led by Alberto de la Fuente from the Center for Advanced Studies, Research and Development in Sardinia (CRS4), received the award also thanks to his collaboration with the Laboratory for the study of complex systems Linkalab.



The "Joint Conference" at Columbia University provided computational and experimental scientists, working in the field of regulatory genomics and systems biology, with the chance to compare their study approaches, aiming at a shared understanding of gene regulation mechanisms. "DREAM" stands for "Dialogue for Reverse Engineering Assessments and Methods". The goal of the challenge, at its 5th edition, is quite interesting: "Biological network inference and quantitative modeling of biological systems", explains Alberto de la Fuente, "are only at a starting point: nobody can tell how adequate their methods are. As a consequence of that, DREAM aims at unbiased evaluation of the proposed methods".

"The approach taken by DREAM", adds Andrea Pinna, "is to organize a yearly competition that teams from all over the world can enter to present their algorithms". "The teams taking part in the challenge receive datasets from experiments and need to predict results that are known only by the challenge organizers", explains Nicola Soranzo: "by checking how well the predictions achieved by the participants coincide with the actual results, we can better understand which algorithms are most useful to obtain reliable models from genomic datasets".





CRS4 Bioinformatics Laboratory

CRS4 Bioinformatics is the computational biology laboratory of the Center for Advanced Studies, Research and Development in Sardinia. The research is directed towards the development of new computational models for the identification of disease-associated markers using functional genomic and systems biology approaches.

Relevant examples of the current research include: data management and integration of high-throughput datasets for the development of models for personalized-medicine; identification of biomarker candidates associated with sample stratification, disease susceptibility or clinical outcome and systems biology; inference of gene and protein networks in complex biological systems of biomedical interest and design and implementation of mathematical algorithm for the modeling of biological processes.



Laboratory for the study of complex systems Linkalab

During the last 10 years, Complex Network Theory has proved to be a valid approach to the analysis of the most diverse phenomena: scientific, social and technological. Linkalab mainly deals with the application aspects of Complex Network Theory, with a special attention on the computational side, the

optimization of calculation systems and the scientific cloud computing. With international quality standards, Linkalab developed theoretical and calculation tools in order to work as a research service for P.A.s and companies showing Complex Systems Analysis problems. Linkalab also develops web-groupware systems and last generation e-learning systems for knowledge management activities on web 2.0 platforms.

Further reading:

- The website of the conference
- The website of the DREAM project
- The website of CRS4 Bioinformatica
- The website of Linkalab
- Dr. Alberto de la Fuente's profile
- The poster describing the ALF team's approach
- The abstract of the work
- The official certificate

