Biologia Computazionale @ UniUD

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I componenti stabili del gruppo (in ordine alfabetico):

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Il gruppo collabora con:

- Istituto di Genomica Applicata
- NYU/Courant Bioinformatics Group
- Bioinformatics Milano Bicocca
- Center for Bioinformatics and Computational Biology NMSU
- Laboratory of Computational and Quantitative Biology CNRS Paris
- Bio-PEPA group University of Edimburgh
- ...

Alcuni Alumni

- Riccardo Vicedomini – CNRS Paris
- Tommaso Dreossi – Berkeley University
- Francesca Nadalin – CNRS Paris
- Giorgio Bacci – Aalborg University, Denmark
- Francesco Vezzi – Stockholm University
- Alexandru Tomescu – University of Helsinki
- Simone Scalabrin – IGA
- Luca Bortolussi – Università di Trieste

Di cosa ci occupiamo?

- definizione di modelli e linguaggi di interrogazione per la rappresentazione e lo studio di sistemi biologici
- metodi per la predizione della struttura terziaria di proteine
- algoritmi per l'assemblaggio e l'analisi di dati di sequenziamento

A.K.A. Systems Biology

H. Kitano – Science 2002

System-level understanding, the approach advocated in systems biology, requires a shift in our notion of "what to look for" in biology. While an understanding of genes and proteins continues to be important, the focus is on understanding a system's structure and dynamics.

Hiroaki Kitano is . . . [Wikipedia]

. . . head of the Systems Biology Institute (SBI); President and CEO of Sony Computer Science Laboratories; a Group Director of the Laboratory for Disease Systems Modeling at and RIKEN Center for Integrative Medical Sciences; and a professor at Okinawa Institute of Science and Technology (OIST).

He is known for developing the Systems Biology Markup Language (SBML). SBML is a representation format, based on XML, for communicating and storing computational models of biological processes. It is a free and open standard with widespread software support and a community of users and developers. SBML can represent many different classes of biological phenomena, including metabolic networks, cell signaling pathways, regulatory networks, infectious diseases, and many others. It has been proposed as a standard for representing computational models in systems biology today.

A.K.A. Systems Biology

P. Nurse –Nature 2003

An important part of the search for such explanations is the identification, characterization and classification of the logical and informational modules that operate in cells. For example, the types of modules that may be involved in the dynamics of intracellular communication include feedback loops, switches,timers, oscillators and amplifiers. Many of these could be similar in formal structure to those already studied in the development of machine theory, computing and electronic circuitry.

Paul Nurse is . . . [Wikipedia]

Sir Paul Maxime Nurse is an English geneticist, former President of the Royal Society and Chief Executive and Director of the Francis Crick Institute.He was awarded the 2001 Nobel Prize in Physiology or Medicine along with Leland Hartwell and Tim Hunt for their discoveries of protein molecules that control the division (duplication) of cells in the cell cycle.

Che differenza c'è?

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- Dimensione?
- Numero di variabili e parametri coinvolti?
- Numero di interazioni?
- Stocasticità?
- Controllabilità?
- Robustezza?
- Conoscenza del modello sottostante!