



**POLITECNICO
DI TORINO**



Dipartimento di
Scienze Matematiche
G. L. Lagrange

ECCELLENZA 2018 • 2022

Tuesday the **05 February 2019** at 15:00

Politecnico di Torino, DISMA, Aula Buzano (third floor)

Pietro DI LENA

Assistant Professor at the University of Bologna

Protein inter-residue contact prediction and folding

Prof. Fabio Fagnani introduces the seminar

Abstract

The protein-folding problem is considered one of the “grand challenges” in computer science and computational biology, with significant medical implications. From a purely computational point of view, the folding problem consists of predicting the three-dimensional (3D) structure of proteins from their one-dimensional (1D) aminoacidic sequences. The state-of-the-art of structure modelling methods and related sub-problems are assessed every two years at the CASP experiments. Starting from the first CASP edition in 1994, the protein folding problem has attracted the attention of a large community of researchers from different fields, and important progress has been made in recent years.

In this talk, Prof. Di Lena will focus on inter-residue contact map representation of the protein structures and related research problems. Protein contact maps are square binary symmetry matrices that provide a two-dimensional (2D) rotation-invariant topological representation of the 3D protein structure. Protein contact map prediction is the CASP category that has registered the largest improvements in the most recent editions, due to the introduction of deep-learning approaches and novel statistical models based on Direct Coupling Analysis (DCA). In addition to the most relevant contact prediction approaches, he will discuss the application of predicted contacts to protein structure prediction and fold recognition.

Biography

Pietro Di Lena is Assistant Professor at the Department of Computer Science and Engineering at the University of Bologna from September 2012. He received his Master Degree (summa cum laude) in Computer Science in 2003, from the University of Bologna, and the PhD degree in Computer Science from the same University in 2007. Following his PhD studies, he was a postdoctoral fellow at the Department of Computer Science, University of Bologna (2007-2010), and at the Institute for Genomics and Bioinformatics, University of California, Irvine (2011-2012). His research interests include discrete dynamical systems, protein structure prediction and Next Generation Sequencing (NGS) data analysis.

Save the date for the next event: *March 06, 2019*

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