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Πρόγραμμα Μεταπτυχιακών Σπουδών
ΤΕΧΝΟΛΟΓΙΕΣ ΠΛΗΡΟΦΟΡΙΚΗΣ
ΣΤΗΝ ΙΑΤΡΙΚΗ ΚΑΙ ΤΗ ΒΙΟΛΟΓΙΑ

ΔΙΕΠΙΣΤΗΜΟΝΙΚΟ ΣΕΜΙΝΑΡΙΟ

Modeling Noisy Data

with Applications in
Structural Bioinformatics

-- Frédéric Cazals --

*Algorithms-Biology-Structure,
INRIA Sophia-Antipolis, France*

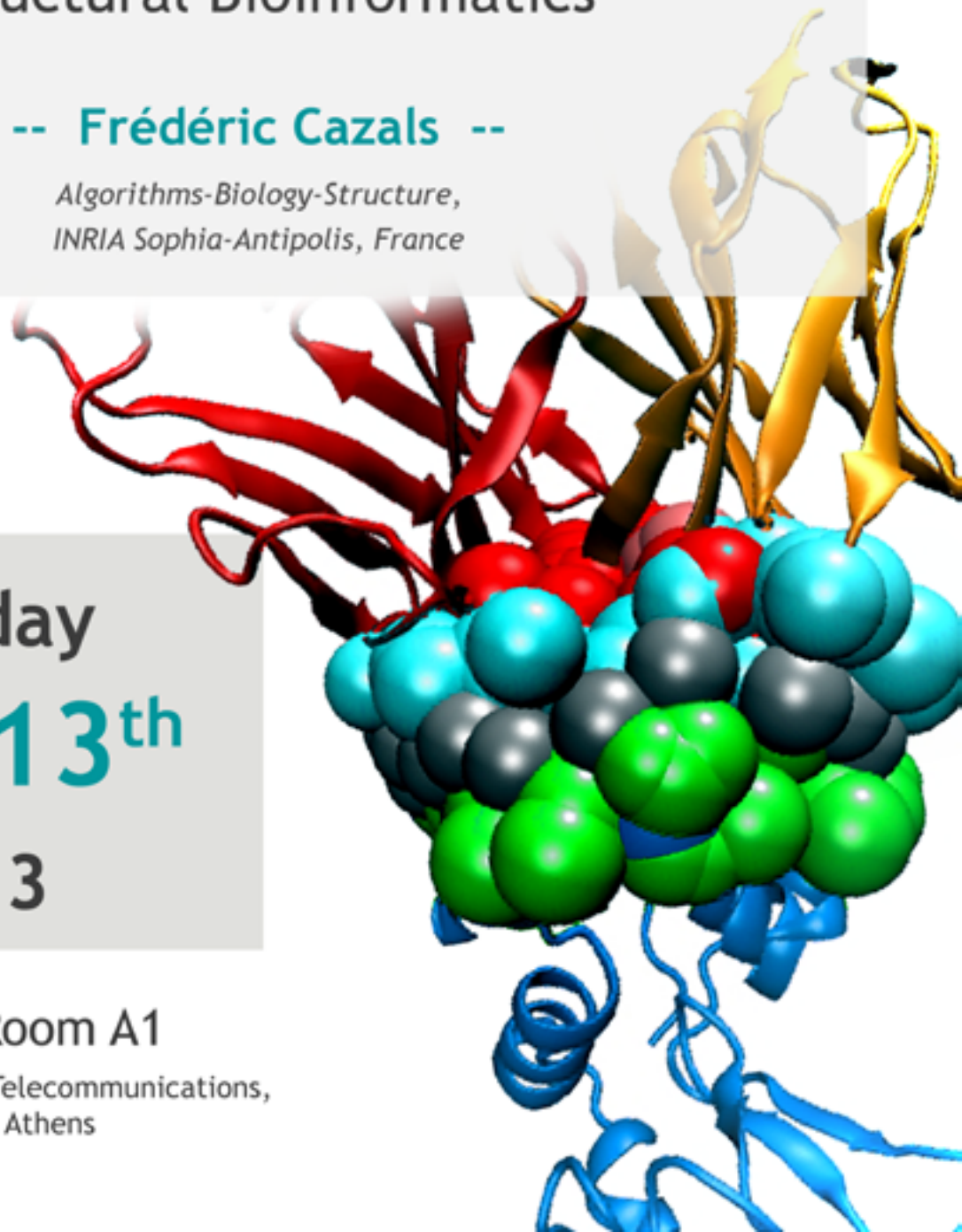
Monday

May 13th

2013

at 14:00, Room A1

Dept. of Informatics and Telecommunications,
University of Athens



Abstract:

Noisy data are common place in science and engineering, and the importance of developing robust non-parametric models for such data cannot be overstated.

In this talk, we shall review recent concepts and algorithms developed in computational geometry and computational topology for three seemingly unrelated problems in the realm of noisy data modeling, namely reconstructing sampled compact sets from \mathbb{R}^3 , modeling fuzzy (molecular) objects in \mathbb{R}^3 and, and investigating high dimensional terrains with applications in biophysics and non convex optimization.

Remarkably, we shall see that all solutions follow the same pattern, which consists of three steps, namely (i) defining a generalized distance function, (ii) constructing (a subset of) the Morse-Smale diagram of this function, and (iii) extracting stable features applying topological persistence on the Morse-Smale complex.

The benefits of using this framework will be illustrated on the problem of assessing the reconstruction of large protein assemblies.

Short CV:



Frédéric Cazals is research director at INRIA Sophia-Antipolis Mediterranee, France, where he leads the group Algorithms - Biology - Structure (ABS, <http://team.inria.fr/abs>). He holds an engineering degree in Biological Sciences from the Institut National Agronomique Paris-Grignon (Paris, France), a master degree in theoretical computer science from Ecole Normale Supérieure and Ecole Polytechnique (Paris, France), and a PhD in theoretical computer science from the University of Paris VII (Paris, France).

His research interests encompass computational structural biology (modeling protein complexes and assemblies, modeling the flexibility of proteins), as well as geometric and topological modeling (applied differential geometry, computational geometry, computational topology, shape learning).

He recently co-edited the book entitled Modeling in Computational Biology and Biomedicine (Springer), which pitches success stories at the interface biology/medicine - computer science - applied mathematics.

Frédéric Cazals will offer the short course “**MODELING MACRO-MOLECULAR COMPLEXES AND ASSEMBLIES**”, on:

- **Tuesday 14/05/2013**, 14:00-17:00, in Room A1 (Part 1) and
- **Wednesday 15/05/2013**, 10:00-13:00, in Room D (Part 2).

All students of the postgraduate program “Information Technologies in Medicine and Biology” are strongly encouraged to attend.

For more information visit the ITMB website: <http://itmb.di.uoa.gr>