



CIBB 2015: 12th International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics,

CNR Research Area, Naples, Italy, 10-12 September 2015

<http://bioinfo.na.iac.cnr.it/cibb2015/>

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**CALL FOR PAPERS – Special Session on
Regularization methods for genomic data analysis**

Aims and scope

The incredible development of high throughput technologies has called for new statistical methodologies dedicated to high dimensional data-sets. In this setting, where the number of parameters is close or greater than the number of observations, standard statistical tasks, like regression, clustering, classification or testing can not be performed using standard tools. Regularization methods have shown to be very efficient by controlling the complexity of the chosen models with respect to the ratio between the number of observations and the number of parameters. Many regularization methods are now available, like the lasso and its associated methods. Moreover, new strategies have consisted in incorporating prior information in the penalization scheme, in order to regularize the model in a more efficient manner, leading to structured sparsity.

The aim of this special session is to gather works dedicated to the development of statistical methodologies based on regularization and dedicated to genomic data.

Organisers

Dr. Franck Picard (CNRS, Univ. Lyon)
Prof. Vivian Viallon (Univ. Lyon)

Invited Speaker:

Prof. Julien Chiquet (INRA, Univ. Evry):
Title of the talk: *Fast tree inference with weighted fusion penalties*

Submissions

Conference papers must be prepared following the guidelines illustrated on the CIBB website, which include the requirement of being between 4 and 6 pages in length and having five sections:

1. Scientific background
2. Material and methods
3. Results
4. Conclusion
5. References (no more than 10)

These papers should be submitted in PDF format on the Easy Chair conference system (it is necessary to select this special session in the submission system).

A second submission after the conference, in an extended version, is required to be considered for publication in the Springer's Lecture Notes in Bioinformatics (LNBI) series (<http://www.springer.com/computer/lncs?SGWID=0-164-6-73658-0>). Moreover, as it has been the case in previous CIBB conferences, we are planning to publish the best papers of CIBB 2014 in an extended form in a special issue of an international scientific journal, including special session papers.

Important dates

Paper submission deadline:	May 30, 2015
Abstract submission deadline:	May 30, 2015
Notification of Acceptance:	June 19, 2014
Final papers due:	July 20, 2015 (*)
Conference:	September 10-12, 2015

(*) for the inclusion in the CIBB15 conference proceeding

About the organisers

Dr. **Franck Picard** (CNRS, Univ. Lyon) is a statistician working on genomic data analysis. He developed methods for copy number variation detections based on change-points models, and also contributed to the analysis of biological networks by developing model-based clustering methods for random graphs. His recent work concern the analysis of sequencing data with application to the study of human replication origins, and the development of functional models for NGS data analysis. He recently created the High Dimensional Statistics for Genomics group <https://lbbe.univ-lyon1.fr/-Equipe-Statistique-en-Grande-.html?lang=en>.

Prof. **Vivian Viallon** (Univ. Lyon) is an Associate Professor of Statistics. He studied various aspects of L1-penalized methods, such as safe feature elimination prior to solving the lasso or the robustness of the generalized fused lasso to prior mis-specification. He also studied regularized methods for binary graphical models, multi-task learning as well as the assessment of categorical effect modification.