

From high-throughput structural bioinformatics to integrative systems biology: NETTAB 2014



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The NETTAB 2014 Workshop will be held in Torino, at the Molecular Biotechnology Centre, from 16 to 17 October 2014. It will be a joint event with the “2014: Crystal (c)Year” meeting¹, in the International Year of Crystallography 2014, and it will be followed by the annual meeting of the University of Torino’s Centre for Complex Systems in Molecular Biology and Medicine.



1 www.nettab.org/2014/CCY/

The workshop represents a virtual bridge between these two events, showing how to manage and elaborate structural and high-throughput proteomics data so that it may be integrated with information from other life science disciplines, aiming to reach a richer description and deeper understanding of mechanisms and interactions in the human being, in its physiological and pathological states. The workshop title, “*From high-throughput structural bioinformatics to integrative systems biology*”², reflects this scope.

The topics of the workshop will therefore relate to methods, tools, applications and perspectives on structural bioinformatics, proteomics and integrative systems biology. These issues are very relevant for several research communities, which are invited to join forces and create synergies for an interdisciplinary effort aimed at developing new tools at the interfaces of these disciplines. Contributions to the NETTAB 2014 workshop should, then, be focused on, but not limited to, the following non-exhaustive list of topics: bioinformatics methods, tools and applications for models, standards and management of high-throughput biological data, data integration, structural bioinformatics, functional proteomics, mass spectrometry, drug discovery, systems biology.

The workshop will run from the morning of Thursday 16 to the afternoon of Friday 17 October. It will include four keynote lectures, given by Wolfgang Marwan (Otto-von-Guericke Universität), Ram Samudrala (University of Washington), Torsten Schwede (University of Basel) and Ada Yonath (Weizmann Institute of Science). It will also include oral communications from selected contributions, open discussions and posters, as well as tutorials, which will be given on the premises of the [University of Torino’s Department of Computer Science](http://www.di.unito.it)³ on Wednesday 15 October.

Submissions are welcome, both for oral communications and for posters. All abstracts must be submitted through the NETTAB 2014 [EasyChair submission page](#)⁴. Abstracts for oral communications must not exceed four pages; those for posters must not exceed two pages. All abstracts

2 www.nettab.org/2014/

3 www.di.unito.it/

4 <https://www.easychair.org/conferences/?conf=nettab2014>

must be structured, and include an Introduction, as well as Methods, Results, Discussion and References sections. Two special issues will appear as supplements of BMC Bioinformatics and of BMC Systems Biology. The related Call for papers will be launched shortly after the workshop.

The workshop is held under the Patronage of the [International Society for Computational Biology](#)⁵ (ISCB), which has granted the status of ISCB Affiliated Conference to the workshop; the [Global Bioinformatics Network EMBnet](#)⁶; the

[Italian Society of Bioinformatics](#)⁷ (BITS); the [Polish Bioinformatics Society](#)⁸ (PTBI) and the [Rete Ligure di Bioinformatica](#)⁹ (ReLiB).



5 www.iscb.org/

6 www.embnet.org/

7 www.bioinformatics.it/

8 <https://www.linkedin.com/company/polish-bioinformatics-society>

9 <https://sites.google.com/site/reteliguredibioinformatica>