

# Call for Contributions

## Submission:

1. **Inform the Chair:** with the Title of your Contribution

2. **Submission URL:**

<https://www.ariasubmit.org/conferences/submit/newcontribution.php?event=BIOTECHNO+2018+Special>

Please select Track Preference as **NETomics**

Special track

## NETomics: Network Models for the Joint Analysis of Omics Data

### Chair and Coordinator

Ph.D. Antonino Abbruzzo, Department of Economics, Business and Statistics, University of Palermo, Italy  
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along with

BIOTECHNO 2018, The Tenth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies

May 20, 2018 to May 24, 2018 - Nice, France

<http://www.aria.org/conferences2018/BIOTECHNO18.html>

In recent years, the abundance of omics data has made data integration approaches increasingly popular. It has been assumed that a deep understanding of a biological system can come only from a joint analysis of all omics data. Omics data show distinct aspects of cellular functioning and the recent technological progress in high-throughput biology has facilitated their collection. Such analysis is often referred as network integration.

A network consists of nodes and links. In biological networks, nodes usually represent discrete biological objects at a molecular level (e.g., genes, proteins, metabolites, drugs, etc.) or phenotypic level (e.g. diseases), whereas edges describe physical, functional or chemical associations between pairs of objects. So far, networks have been one of the most widely used statistical tools for modeling and analyzing omics data and they have provided relevant biological knowledge from these different aspects of molecular machinery inside a cell. However, a more comprehensive understanding of a biological system is supposed to be achieved by a joint, integrative analysis of all these networks. To reach this purpose, data integration methodologies have to satisfy several challenges. These challenges arise due to different sizes, formats and dimensionalities of the data being integrated, as well as owing to their complexity, noisiness, information content and mutual concordance (i.e., the level of agreement between datasets). A number of current data integration methods meet some of these challenges to some extent, whereas the majority of them hardly meet any of them.

The main goal of this track is to explore network models that extract additional biological knowledge from multiple omics data that cannot be gained from any single dataset alone.

**Prospective authors** are invited to submit original papers on topics including, but not limited to:

- Network inference and functional linkage network construction
- miRNA-mRNA integrated analysis
- Protein function and protein-protein interaction prediction
- Disease gene prioritization and disease-disease association
- Patient-specific data integration

## **Important Datelines**

- Inform the Chairs: As soon as you decided to contribute
- Submission: February 7, 2018
- Notification: March 7, 2018
- Registration: March 21, 2018
- Camera ready: April 2, 2018

*Note: These deadlines are somewhat flexible, providing arrangements are made ahead of time with the chair.*

## **Contribution Types**

- Regular papers [in the proceedings, digital library]
- Short papers (work in progress) [in the proceedings, digital library]
- Posters: two pages [in the proceedings, digital library]
- Posters: slide only [slide-deck posted on [www.iaria.org](http://www.iaria.org)]
- Presentations: slide only [slide-deck posted on [www.iaria.org](http://www.iaria.org)]
- Demos: two pages [posted on [www.iaria.org](http://www.iaria.org)]

## **Paper Format**

- See: <http://www.iaria.org/format.html>
- Before submission, please check and comply with the editorial rules: <http://www.iaria.org/editorialrules.html>

## **Publications**

- Extended versions of selected papers will be published in IARIA Journals: <http://www.iariajournals.org>
- Print proceedings will be available via Curran Associates, Inc.: <http://www.proceedings.com/9769.html>
- Articles will be archived in the free access ThinkMind Digital Library: <http://www.thinkmind.org>

## **Paper Submission**

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## **Registration**

- Each accepted paper needs at least one full registration, before the camera-ready manuscript can be included in the proceedings.
- Registration fees are available at <http://www.iaria.org/registration.html>

## **Contacts**

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