Abstract Submission and Registration - Workshop Bringing Maths to Life, Naples, 19-21 October 2015

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http://www.biometricsociety.net/2015/06/19/abstract-submission-and-registration-workshop-bringing-maths-to-life-naples-19-21-october-2015/

Dear Colleague,

It is a pleasure to invite you for the **2nd edition of the Workshop Bringing Maths to Life (BMTL)**, which will be held October 19-21, 2015, in Naples at the Centro Congressi Federico II. This workshop lets biologists and mathematicians join forces to address key areas in biology that face demanding mathematical challenges. Discussing existing cases to identify gaps or to share existing solutions should help these disciplines in successfully linking up.

Important deadlines:

June 30th, 2015 – Early registration and booking accommodation

June 30th, 2015 – Submission of abstracts

Topics include:

(i) **Dynamics of genomes –** Technological advances that facilitate whole-genome and whole-population sequencing, coupled with experiments that 'watch' evolution in action, have brought insights into studies of mutation rates and genome evolution. In this session, we discuss the molecular mechanisms and evolutionary processes that shape the structure and function of genomes and that govern genome dynamics.
(ii) **Dynamics of pattern recognition –** Motif searching in DNA, RNA and proteins is a key process to discover emergent properties of cells, tissues and organisms. It requires always more complex and comprehensive algorithms that can incorporate the growing up to date information from experimental sets. This session will provide an overview on current methods for motif searching and experimental validation.
(iii) **Dynamics of biological networks –** Networks representing complex biological functions and activities are useful to interpret physiological processes in the cell, pathological states, and to investigate the potential effects of drug therapies, to name a few. Several mathematical models and algorithms are available for the different tasks involved in their integration, analysis and characterization, although difficulties arise in case of big data and dynamic systems, both at local and global scale.
(iv) **Dynamics of genetic variation –** Routine production of large data set resulted in a comprehensive catalogs of genetic variability and the knowledge of functional units of genomes improved thanks to the combination of effective prediction tools and large validation sets. In this session we want to provide examples of in silico prediction of functional consequences of mutations and experimental validation of genomic features.

Invited speakers include:

Chris Bowler, France
Marco Cosentino Lagomarsino, France
Giuseppe Jurman, Italy
Sebaastian Meijsing , Germany
Morgane Thomas-Chollier, France
Panos Pardalos, United States
Peter Van Loo, United Kingdom

For details and regular updates:

www.bmtl.it

Register at:

https://secure.webol.info/bmtl/en/register-here.php

Abstract info:

http://www.bmtl.it/en/abstract-info.php?Preview=ok

Abstract submission:

http://www.bmtl.it/en/abstract-submission.php

Please feel free to forward this mail to interested colleagues!

We look forward to meet you in Naples.

Kind regards,

The BMTL Organising Committee

Vincenza Colonna, IGB – CNR

Mario Guarracino, ICAR – CNR

Alessandra Rogato, IBBR – CNR

Valeria Zazzu, IGB – CNR