

Topology of Manifolds, Lisbon

By Gustavo Granja*

The conference Topology of Manifolds, Lisbon was held at the National Museum of Science and Natural History of the University of Lisbon, from June 27th to July 1st 2016. The event was partially supported by the following institutions: *National Science Foundation* (U.S.A.), *Centro de Análise Matemática, Geometria e Sistemas Dinâmicos* (IST, Universidade de Lisboa), *Fundação Calouste Gulbenkian, Fundação para a Ciência e Tecnologia* and *Centro Internacional de Matemática*.

The conference brought together 120 experts on Algebraic and Geometric Topology, mostly from the United States and Europe. The program consisted of 11 invited talks and 14 contributed talks. The scientific committee of the conference consisted of G. ARONE (University of Virginia), A. RANICKI (University of Edinburgh) and U. TILLMANN (Oxford University) and the organizing committee consisted of P. BOAVIDA (IST, University of Lisbon), S. GALATIUS (Stanford University), G. GRANJA (IST, University of Lisbon) and P. LAMBRECHTS (Université Catholique de Louvain).

The conference was an opportunity to celebrate the 60th anniversary of MICHAEL S. WEISS, one of the foremost contributors to the subject of the conference in the last 35 years. Michael Weiss holds the Alexander von Humboldt Professur at the Westfälische Wilhelms-Universität Münster since 2012, having joined Münster from the University of Aberdeen. His contributions to homotopy theory and geometric topology include outstanding work on Automorphisms of Manifolds and its relation to Algebraic K-theory (with Bruce Williams) [1], the development of Homotopy Functor Calculus (specifically Orthogonal Calculus [2] and Calculus of Embeddings [3]) now called Goodwillie-Weiss Calculus. He is perhaps most famous for the solution (with Ib Madsen, in 2002) of the Mumford Conjecture on the stable homology of the mapping class group [4]. Weiss received the



Michael S. Weiss. Picture by A. Ranicki

Fröhlich Prize of the London Mathematical Society in 2006.

The circle of ideas involved in the Madsen-Weiss solution of the Mumford conjecture has exploded into a new and very active field of Algebraic and Geometric Topology — the study of moduli spaces of manifolds and cobordism categories [5] — which was heavily represented in the program of the conference. There were also many talks on the related and extremely active field of homological stability, as well as talks on the more classical subjects of surgery and Algebraic K and L-theory.

Highlights of the conference included Michael Weiss' own talk proving the existence of exotic Pontryagin classes for topological bundles of Euclidean spaces and Alexander Kupers' talk proving the finite generation of the homotopy groups of the diffeomorphism

groups of disks relative to their boundary (in dimensions not equal to 4, 5 and 7) drawing on Galatius and Randal-Williams's work on parametrized surgery [6] as well as Goodwillie-Weiss calculus.

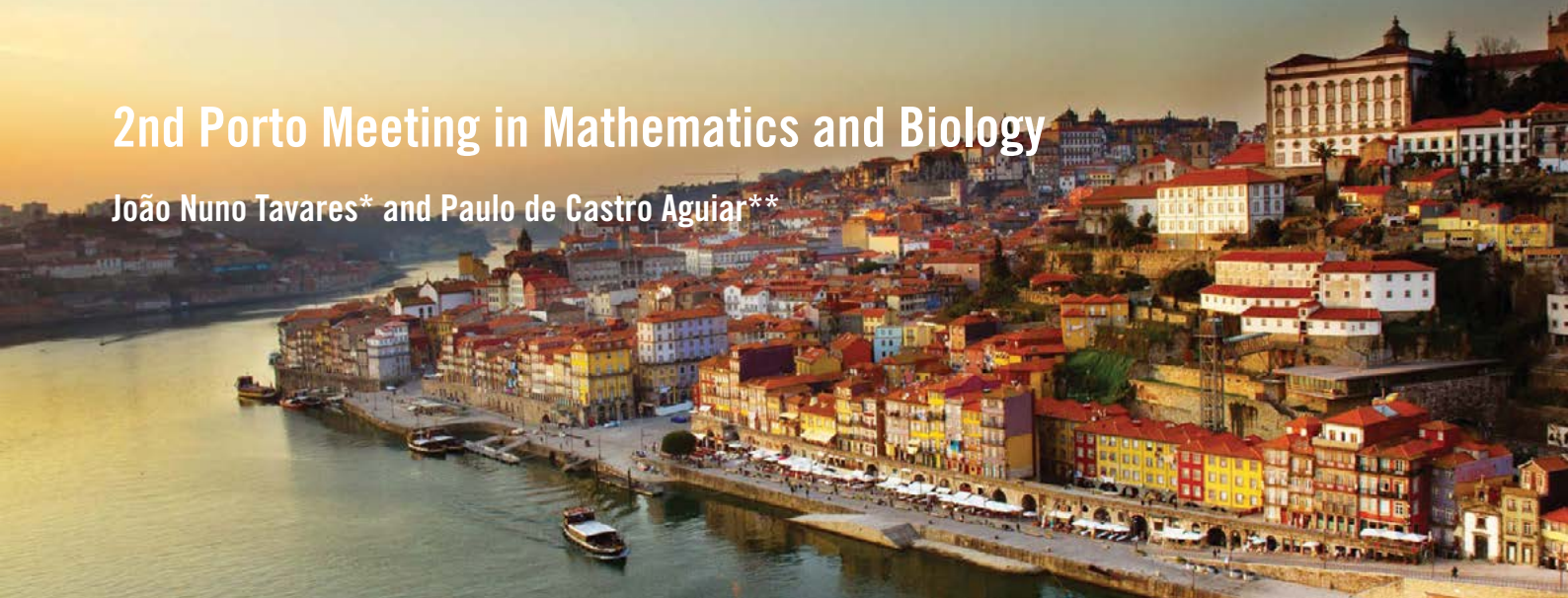
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2nd Porto Meeting in Mathematics and Biology

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In the past days 15 to 17 June 2016, held the second edition of the so entitled *Porto Meetings in Mathematics and Biology*, with the promoting of the *Faculty of Sciences of University of Porto*, the *Institute for Research and Innovation in Health (i3s)*, the *Mathematics Center of the University of Porto (CMUP)*, and also counted with the sponsorship of the CIM.

The purpose of this second meeting (the first was held on 23 and 24 June 2015) was to promote interaction between mathematicians, physicists, engineers, statisticians, biologists and clinicians to discuss the application of quantitative analysis methods to biological problems. More specifically this year's edition was dedicated to the theme *Systems Biology*.

Systems Biology is a new methodological paradigm that transformed 21st century research in Biology. Biology has become increasingly cross-disciplinary as biologists, computer scientists, engineers, mathematicians, physicists and physicians, work together to develop the high throughput technologies and computational/mathematical tools required for this new biology — all driven by the contemporary needs of biology and medicine. The systemic approach to biology is not new, but recently gained new impact, mainly due to the remarkable progress of experimental and computational (Bioinformatics) methods, each time most ingenious and powerful. We have now a golden opportunity to uncover the essential principles of biological systems that enable us to understand them in their entirety by investigating: (1). the structure of the systems, such as genes, metabolism, and signal transduction networks and physical structures, (2). the dynamics of such systems, (3). methods to control them, and (4.) methods to design and modify them for desired properties.

This conference was part of a set of initiatives that are designed to promote scientific interactions between math-

ematicians, biologists and clinicians (epidemiologists, immunologists, etc.) to facilitate the multidisciplinary research on topics of common interest.

The conference has consisted of the following 4 courses: *Introduction to Dynamic Mathematical Modelling in Systems Biology*, by Brian Ingalls (Department of Applied Mathematics, University of Waterloo); *Metabolic Network Modelling: Genome-scale Reconstruction, Flux Balance Analysis, and Applications to *Caenorhabditis elegans* Metabolism* by Lutfu Safak Yilmaz (Walhout Lab, Program in Systems Biology, Department of Biochemistry and Molecular Pharmacology, University of Massachusetts Medical School, USA); *Introduction to modelling noise and cell-to-cell variability in signaling networks* by Maciej Dobrzynski (Systems Biology Ireland, Conway Institute Belfield, Dublin, Ireland); *Optimization and parameter estimation (with COPASI)* by Pedro Mendes (Director of Mendes Research Group, School of Computer Science, Manchester Institute of Biotechnology, UK), and of the following Plenary lectures *Aging, Cancer and Neurodegenerative diseases* by Lloyd Demetrius (Max Planck Institute for Molecular Genetics at Berlin, Germany, and the Department of Organismic and Evolutionary biology, Harvard University); *Patterns of gene expression across multiple tissues and individuals* by Pedro G Ferreira (i3S, Porto); *In silico metabolic engineering* by Miguel Rocha (Departamento de Informática da Escola de Engenharia da Universidade do Minho, and finally *Using time series data to reconstruct gene signaling networks* by Joel Arrais (DEI/FCTUC, University of Coimbra).

All the information's are available in the conference website <http://cmup.fc.up.pt/cmup/biomath/>

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