

Prof. Dr. Julio Saez-Rodriguez



Head of Research group and Director of Institute for
Computational Biomedicine – Bioquant, Heidelberg University –
Faculty of Medicine, Heidelberg University Hospital, Heidelberg

Role in LiSyM-Cancer

- Project leader in C-TIP-HCC
- Methods to build dynamic models from large-scale functional data, esp. logic-based models, functional analysis of genomics data in pathway and network-based models
- Mechanistic models for integrating phospho-proteomic, transcriptomic and metabolomic data with networks

Expertise

- functional analysis of transcriptomics data: single-cell and spatial data, multi-omics integration, and understanding multi-cellular communication
- focus is on cancer, autoimmune diseases, and conditions of the kidney and heart
- interrogation of large biological data sets with mathematical models to unveil the molecular basis of disease as a means to develop novel therapies
- use of existing knowledge of biological processes to support computational analysis
- developing open-source computational tools and co-organization of the DREAM challenges

Degrees

- 2002-2007, PhD summa cum laude in Process Engineering; Max-Planck-Institute for Dynamics of Complex Technical Systems and University of Magdeburg, Germany (Advisor: E. D. Gilles)
- 2000-2001, Exchange Erasmus student at the University of Stuttgart, Germany
- 1996-2001, 'Licenciatura' (MS), in Chemical Engineering University of Oviedo, Spain, finished with the best academic record of the year

Professional Experience

- Since 2018, Group Leader at EMBL - University Hospital Heidelberg Molecular Medicine Partnership Unit (MMPU)
- Since 2018, Full (W3) Professor of Medical Bioinformatics and Data Analysis & Director of the Institute for Computational Biomedicine Heidelberg University, Faculty of Medicine, Germany
- 2015-2018, Full (W3) Professor of Computational Biomedicine & Director of the Institute for Computational Biomedicine I, RWTH-Aachen University, Faculty of Medicine, Germany
- 2015-2018, Visiting group leader at the European Bioinformatics Institute, European Molecular Biology Laboratory (EMBL-EBI)
- 2010-2015, Group Leader at the European Bioinformatics Institute, European Molecular Biology Laboratory (EMBL-EBI), with a joint appointment in the EMBL Genome Biology Unit in Heidelberg
- 2010-2015, Senior fellow at Wolfson College (Cambridge, UK)
- 2008-2010, Scientific Coordinator of the NIH-NIGMS Cell Decision Process Center, Cambridge, MA, USA
- 2007-2010, Postdoctoral Fellow, Harvard Medical School and MIT, Boston USA
- 2002-2007, Research Assistant, Max Planck Institute, Magdeburg, Germany
- 2001-2002, Research assistant, University of Stuttgart, Institute of Biochemical Engineering, Germany, and Insilico Biotechnology, Germany

Publications

2025-11-18	OmniPath: integrated knowledgebase for multi-omics analysis <i>Nucleic Acids Research</i>
2025-09-01	From cirrhosis to cancer: α-SMA+ CAF and CD68+ macrophage rewiring in the cirrhosis–HCC transition <i>79. Jahrestagung der DGVS mit Sektion Endoskopie Jahrestagung der Deutschen Gesellschaft für Allgemein- und Viszeralchirurgie mit den Arbeitsgemeinschaften der DGAV und Jahrestagung der CACP</i>
2025-05-22	Comprehensive evaluation of phosphoproteomic-based kinase activity inference <i>Nature Communications</i>
2025-02-01	NetworkCommons: bridging data, knowledge, and methods to build and evaluate context-specific biological networks <i>Bioinformatics</i>
2025-01-01	TGF-β critically determines the activation state of both, the macrophage subpopulation that is particularly recruited in the context of MASH progression, as well as of TAMs <i>41. Jahrestagung der Deutschen Arbeitsgemeinschaft zum Studium der Leber</i>
2024-12-21	Comparison and evaluation of methods to infer gene regulatory networks from multimodal single-cell data
2024-11-19	PhosX: data-driven kinase activity inference from phosphoproteomics experiments <i>Bioinformatics</i>
2024-07-02	Comprehensive evaluation of phosphoproteomic-based kinase activity inference (preprint) <i>bioRxiv</i>
2024-01-01	Progression of MASLD goes along with significant changes of a recruited and TGFβ sensitive macrophage population <i>Zeitschrift für Gastroenterologie</i>
2023-11-10	Expanding the coverage of regulons from high-confidence prior knowledge for accurate estimation of transcription factor activities <i>Nucleic Acids Research</i>
2023-06-26	Gene regulatory network inference in the era of single-cell multi-omics. <i>Nat Rev Genet</i>
2023-02-01	Phosphoproteomic analysis of metformin signaling in colorectal cancer cells elucidates mechanism of action and potential therapeutic opportunities <i>Clinical and Translational Medicine</i>
2023-01-01	Hepatocytes reprogram liver macrophages involving control of TGF-β activation, influencing liver regeneration and injury <i>Hepatology Communications</i>