











29 AUGUST, 10:30 AM HYBRID BIO21 AUDITORIUM / ZOOM

Prof. Jose-Maria Carazo

Biocomputing Unit, Head Instruct Spanish Center, Director Spanish National Center for Biotechnology, CNB-CSIC Madrid, Spain

Prof. Carazo studied Physics at the University of Granada, Spain, and obtained his PhD in Biology at University Autonoma, Madrid, Spain (1984). After his post-doc with Nobel Laureate Prof. Joachim Frank at the Wadsworth Center, New York State Department of Health (USA), he joined the National Center of Biotechnology as head of the Biocomputing Unit (1989), where he was appointed full professor of the Spanish National Research Council (CSIC) in 2005.



Professor Carazo has a vast experience in the field of 3-D Electron Microscopy under cryogenic conditions (cryo-EM), particularly in methods development. His laboratory has opened whole new areas in the field, such as the successful family of Maximum Likelihood algorithms (developed in Madrid, 2007-2011) or the much used EMDataBank (started from the European Union project "Bioimage" that he coordinated, 1996-1999). His laboratory also develops and supports software packages and web services; Xmipp and Scipion, have been actively used by more than 1,700 users in more than 13,000 projects throughout the world; the web service 3DBionotes, has close to 1,600 new users just in 2022. A version of Scipion, developed specifically for cryoEM facilities, is currently being used at the European Synchrotron (ESRF, Grenoble), and SciLab (Stockhom). He founded "Integromics", winner of the first National Prize of La Caixa Emprendedor XXI (2007) and the Frost & Sullivan award for the Most Innovative Bioinformatics Company in Europe (2008). Integromics was acquired by Perkin-Elmer in 2014. As recognition of his contributions to the EM field, his ability to form successful teams around him, and his international standing in Europe, his laboratory was selected as the Instruct Center for Image Processing in Structural Biology, which is part of the Strategic European Research Infrastructure INSTRUCT, starting in 2011. He is currently a member of several Scientific Advisory Boards in Spain and different countries; he has also served on the SAB of the former Uninvest venture capital firm.

CryoEM conformational landscapes: Directly accessing macromolecular flexibility

Electron Microscopy at cryogenic temperatures is currently a very well-known approach to solve the structure of biological macromolecules with sufficiently high resolution to obtain good structural models. Part of this success was the proposal of Maximum Likelihood approaches to disentangle macromolecular structural flexibility (first implemented in the software XMIPP and then in Relion) (1). However, it was then assumed that flexibility was discrete and that the user had to estimate the number of these discrete states, which clearly was not optimum. Nowadays, almost 15 years after this initial approach, new methods have been developed that allow us to consider continuous flexibility, opening the possibility to obtain conformational landscapes (2). In this context, Jose-Maria will present recent advances in his "Zernike3D" approach, showing how this can effectively access the whole range of macromolecular flexibility present in the cryoEM images without needing further estimations from the user.