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## [Virtual BSC RS/Life Session Seminar: Non-globular proteins in the era of high accurate structure prediction](#)

### Objectives

**Abstract:** Protein structure prediction has long been considered the “Holy Grail” of structural biology. The recent success of AlphaFold has ushered in a new era of highly accurate structure prediction, bringing to light the secrets hidden in the three-dimensional structures of globular proteins. However, a large proportion of the proteomes from all domains of life are rich in sequences that do not fold into regular structures, commonly known as non-globular proteins (NGPs). NGPs comprise intrinsically disordered regions, repeats, low-complexity sequences, aggregation-prone and phase-separating sequences, and are implicated in a range of age-related diseases. Their heterogeneous structural states and low sequence complexity challenge current experimental structure determination techniques and machine learning (ML) methods for structure prediction, making the molecular understanding of their sequence-structure-dynamics-function relationship difficult. The aim of this talk is to show the current efforts in the NGP field led by our lab [BiocomputingUP](#) (Prof. Silvio Tosatto Lab) at the University of Padova, as well as the community efforts consolidated in different consortia and European projects related to NGPs.



Alexander Monzon got his Bioinformatics degree (BSc/MSc) in 2012, from the National University of Entre Ríos (Oro Verde, Entre Ríos, Argentina), and his PhD in Basic and Applied Sciences in 2018 from the National University of Quilmes (Buenos Aires, Argentina). After graduating, Alexander got the MSCA Seal of Excellence fellowship at the University of Padova and joined the group of Prof. Silvio Tosatto at the Department of Biomedical Sciences. After 4 years of postgraduate studies, Alexander obtained a Junior Faculty position in 2022, in the Department of Information Engineering at the University of Padova.

During his doctoral training he specialized in the area of Structural Bioinformatics, in the group of Dr. Gustavo Parisi, developing the CoDNaS database for the study of conformational diversity in the native state of proteins and contributing to this area with numerous publications in high impact journals. He continued his postdoctoral training in Prof. Silvio Tosatto's group, where he currently conducts his research in the field of non-globular (disordered and repetitive) proteins. His contributions in the area of Bioinformatics led him to co-author numerous important databases such as DisProt, RepeatsDB, MobiDB, PED and FuzDB, which represent the state of the art of what is known today in structural biology of non-globular proteins. In addition, he actively participates in different networks, scientific societies and international consortia, such as the ISCB student council, A2B2C, COST-action "NGP-net", MSCA RISE "[IDPfun](#)" and "[REFRACT](#)", and he is the main proposer of the recently funded COST action "ML4NGP". Google Scholar profile: <https://scholar.google.com.ar/citations?user=L--DUYwAAAAJ&hl=en>

## Speakers

**Speaker:** Alexander Monzon got his Bioinformatics degree (BSc/MSc) in 2012, from the National University of Entre Ríos (Oro Verde, Entre Ríos, Argentina), and his PhD in Basic and Applied Sciences in 2018 from the National University of Quilmes (Buenos Aires, Argentina).

**Host:** Alfonso Valencia, Life Sciences Department Director & Gonzalo Parra, Life Sciences - Computational Biology Life Sciences Group.  
Barcelona Supercomputing Center - Centro Nacional de Supercomputación

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