UNIVERSIDAD DE GRANADA

Máster Universitario en
Investigación y Avances
en Inmunología
Molecular y Celular

The Functional Isotranscriptomics paradigm or long read sequencing applied to transcriptome research

23/03/2022

Seminarios en el PTS: "The Functional Isotranscriptomics paradigm or long read sequencing applied to transcriptome research"
Dra. Ana Conesa. Institute for Integrative Systems Biology (CSIC), Valencia.

Día: Wednesday, 23th March, 2022
Hora: 12:00 pm
Lugar: Salón de Actos de GENYO

Contacto: Pedro Carmona:
pedro.carmona@genyo.es
José Camacho: josecamacho@go.ugr.es

Bioskecht.

Ana Conesa is Research Professor at the Institute for Integrative Systems Biology (CSIC) in Valencia (Spain) and Courtesy Professor at the University of Florida. She graduated as Agricultural Engineer at the Polytechnical University of Valencia in 1993 and did her PhD in at the University of Leiden in the Netherlands. After a short appointment as bioinformatics project leader at TNO Quality of Life (The Netherlands) she obtained a Ramon y Cajal award and joined the Valencia Agricultural Research Institute in 2003. She held positions as group leader at the Principe Felipe Research Center (2007-2018), and as full professor at the University of Florida (2014-2020). In 2022 she became member of the Spanish Royal Academy of Engineer and of the Board of Directors of the International Society for Computational Biology. Ana Conesa's lab is interested in understanding functional aspects of gene expression at the genome-wide level and across different organisms. Her group has developed

http://masteres.ugr.es/inmunologia/

statistical methods and software tools that analyze the dynamics aspects transcriptomes, integrate these with other types of molecular data and annotate them functionally, with a special focus on Next Generation Sequencing (NGS) data. A strong drive in her research is helping the genomics community to bridge the gap between data and knowledge by creating bioinformatics tools that everybody can use. Some of our popular software tools are Blast2GO, PaintOmics, maSigPro, NOISeq, Qualimap, SQANTI, tappAS, etc. She has led international projects such as STATegra and DEANN where European and American scientists developed new tools for the analysis of sequencing data. She is organizer of major international conferences in Computational Biology, has delivered over 50 keynote lectures and regularly acts as scientific advisor for funding agencies, research institutions and companies worldwide. She is also co-founder of Biobam Bioinformatics, a start-up that provides bioinformatics tools for biologists. She has published 143 research papers that have received more nearly 30.000 citations.