Ana Conesa, PhD

Synopsis

Publications: 163 Citations[1]: > 38,000 h-index[1]: 61 Conference Talks: 146	Projects as PI: 38 Lead-PI @ Multi-PI: 9 Total raised ~15M$ Software tools: 22	PhD thesis completed: 13; in progress: 9. Group members in the last 5 years: 33. Visiting students/post-docs last 5 years: 64.

Scientific statement

I am Research Professor at the Spanish National Research Council (CSIC) I graduated as Agricultural Engineer at the Polytechnical University of Valencia in 1993 and obtained my PhD in Molecular Microbiology at the University of Leiden in the Netherlands with a research project at the Microbiology Department of the Dutch Institute for Food Research (TNO). I obtained a Ramon y Cajal award and joined the Valencia Agricultural Research Institute (Spain) in 2003 to develop bioinformatics tools for citrus genomics. I moved into CIPF in 2007 and became Senior Group Leader in 2010, creating the Genomics of Gene Expression Laboratory. From August 2014 to May 2021, I was Full professor at the Microbiology and Cell Science Department and Genetics Institute of the University of Florida. On May 2021, I joined the CSIC Institute for Integrative Systems Biology (I2SysBio) and became courtesy faculty of the University of Florida. In January 2022, I was elected Member of the Spanish Royal Academy of Engineering.

I am interested in understanding functional aspects of gene expression at the genome-wide level, across different organisms and in relation to pathological processes. My group has developed 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. I am creator of popular bioinformatics software such Blast2GO, Paintomics, maSigPro, NOISeq, Qualimap, SQANTI, tappAS, with tens of thousands of users world-wide, and pioneered the methodologies for transcriptome analysis using single-molecule sequencing technologies. My research has been well-funded through national and international funding agencies including Horizon Europa, H2020, Marie Curie Actions, NIH, NASA, and USDA, as well as by private foundations such as Santander, JDRF and Helmsley. I have lead multiple international research consortium projects, including STATegra (EU FP7, 11 partners, 8 countries, €6M, on multiomics data integration), DEANN (Marie Curie Action, 16 partners, 14 countries, €0.9M, for bioinformatics science exchange), LongTREC (Marie Curie Action Doctoral Network, 12 partners, 10 countries, €2.7M, long-read bioinformatics tool development), and a team of 6 PIs at UF to develop multi-omics models for Type 1 Diabetes progression. I have (co)-organized numerous bioinformatics and NGS conferences –including the major conference in the Computational Biology field ISMB- and delivered specialized bioinformatics courses in over 10 countries in 5 continents with over 500 attendants. I am co-founder and scientific advisor of Biobam Bioinformatics, a company operating since 2010 to create bioinformatics solutions for biologists.

My most current research interests are the development of statistical methods for multiomics data integration for systems biology, the creation of tools for the analysis of third-generation sequencing data, and the understanding microbial interactions through community modeling.

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[1] Source: Google Scholar

Current research position
Research Professor
Institute for Integrative Systems Biology-
Spanish National Research Council
ana.conesa@csic.es

web: http://conesalab.org
google scholar https://scholar.google.es/citations?user=KMTiIH4AAAAJ&hl=es&oi=ao
ORCID code: 0000-0001-9597-311X

Education	University of Leiden/ TNO Ph.D. Molecular Microbiology, June 2001. Thesis: Overproduction of Peroxidases by Filamentous Fungi.	*Leiden, The Netherlands*
	Polytechnic University of Valencia Agricultural Engineering Degree Graduation Project: *Development of a plant breeding program in common bean (Phaseolus vulgaris)*	*Valencia, Spain*
Languages	Spanish (Mother tongue) English (Correct at Reading, Oral and Writing) Dutch (Correct at Reading, Oral and Writing) Italian (Good at Oral and Reading)	
Awards and Fellowships	El Mundo Award Best start up in Valencia 2013 to Biobam Mobility Grant Castillejo – Four-month sabbatical at UC-Berkeley (2012) Mobility Grant GA – Two month visit to Copenhagen University (2008) Ramón y Cajal Award for international talent attraction (2003-2008) Comett Fellowship for international mobility of graduate students (1993-1994) Undergraduate research grant, Polytechnical University of Valencia (1993) Research Fellowship at the Valencia Institute for Agricultural Research (1992) Fellowship at Interlegsa Breeding Company, Valencia (1992) Erasmus Fellowship for international mobility of undergraduate students (1991)	

Honors

Jul 2023	**Fellow of the International Society for Computational Biology**
Dec 2022	**Member of the “Científicas e Innovadoras” platform of the Spanish Ministry of Science and Innovation**
Dec 2022	**Honorary Member of the Spanish Society for Bioinformatics and Computational Biology**
Oct 2022	**Member of the Spanish Royal Academy of Engineering**

Scientific Appointments

Jan 2022 to date	COSI representative at the Board of Directors of the International Society for Computational Biology (ISCB)
Jan 2022 to date	Member of the I2SysBio Scientific Committee
Oct 2022 to date	Chair of the I2SysBio Sustainability Committee
Feb 2023 to date	Member of ISCB Membership Taskforce
Feb 2023 to date	Member of the ISCB GreenScience Committee
Mar 2023 to date	Member of the CSIC VIDA Programme Committee
May 2023 to date	Node of the Spanish National Bioinformatics Institute – ELIXIR-Spain
Sep 2023 to date	Coordinator CSIC Network in Bioinformatics and Computational Biology
Sep 2023 to date	Member of the CSIC Sustainability Committee
Oct 2023 to date	Director of the I2SysBio Theoretical and Computational Biology Programme

Positions

2021- present, **CSIC** *Valencia, Spain*
Research professor, I2SysBio

2021- present, *University of Florida* *Gainesville, Florida, USA*
Courtesy faculty, Microbiology and Cell Science

2014-2021, *University of Florida* *Gainesville, Florida, USA*
Professor Dept. Microbiology and Cell Science

2010-2018: *Centro de Investigación Príncipe Felipe* *Valencia, Spain*
Head Genomics of Gene Expression Laboratory

2008-2010: *Centro de Investigación Príncipe Felipe* *Valencia, Spain*
Junior PI at Bioinformatics Department (permanent position)
Development of bioinformatics tools for functional genomics

2007- 2008: *Centro de Investigación Príncipe Felipe* *Valencia, Spain*
Ramon y Cajal Fellow at CIPF
Development of bioinformatics tools for functional genomics

2003- 2007: *Valencia Institute for Agricultural Research* *Valencia, Spain*
Ramon y Cajal Fellow at Plant Genomics Center
Develop supporting bioinformatics research for the Citrus Genome Project

2001-2003: TNO Nutrition and Food Research Institute Zeist, The Netherlands
Project Leader Bioinformatics
Setup the bioinformatics infrastructure for microarray gene expression analysis at the Department of Toxicology.

1996-2001: *TNO Nutrition and Food Research Institute* *Zeist, The Netherlands*
PhD student at Molecular and Applied Microbiology Department
Synthetic biology for the industrial production of peroxidases enzymes in fungal cellular factories.

Supervisor: Cees van de Hondel and Peter Punt

1994-1995: *Institute for Plant Pathology (IPO) Wageningen, The Netherlands*
Research Fellow at Monoclonal Antibodies Laboratory
Plantibodies to infer resistance to cyst nematodes in potato
Supervisor: Jack Stockkermans

1993-1994: *Institute for Plant Breeding (CPRO) Wageningen, The Netherlands*
Research Fellow at Molecular Flowering Department
Microsatellite markers in lilies
Supervisor: Hans Sandbrink

1992 July-August: *Instituto VALENCIANO DE Investigación Agraria*
Introduction to Research grant from Valencian Goverment
Molecular Markers in tomato
Supervisor: María José Asíns

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Software Developed

<u>Functional Annotation</u>
Blast2GO. Functional annotation & analysis of novel sequence data (Java desktop)
isoAnnot: Functional annotation with isoform resolution (Python)
spongeScan. Search for miRNA Multiple Recognition Elements in lncRNAs (Web)
<u>Quality Control in NGS</u>
Qualimap. Quality analysis of mapped NGS data (Java desktop)
NOISeq. Differential expression analysis of NGS data (R package)
SQANTI. Structural and Quality Analysis of Transcripts Isoforms (Python script)
SQANTI-SIM: Simulation of long read transcript models (Python script)
<u>Statistical analysis of gene expression</u>
maSigPro. Analysis of time-series gene expression data (R package)
ASCA-genes. Analysis of multifactorial gene expression data (R package)
SEA. Analysis of serial gene expression data (Web site)
tappAS. Functional profiling at the isoform resolution (Java desktop)
acorde. Network analysis of isoform co-expression at single cells (R package)
<u>Multiomics data analysis</u>
STATegraEMS. Experiment Management System for multiomics (Java desktop)
Paintomics. Integration of multiple omics on KEGG pathways (Web site)
RGmatch. Linking genomics regions to gene models by NGS data (Python script)
MOSim. Simulation of multiomics datasets (R package)
MORE: Multiomics regulatory models (R package)
MultiBac: Batch correction across omics (R package)
Padhoc: Pathway Reconstruciton on the fly (Python)
MirCure: Quality control of microRNA annotations (Shiny app)
DeCovid: Analysis of COVID19 disease map gene expression (Shiny app)
MAMBA: Multi-omics Flux-Balance Analysis (Matlab)

Funding as PI

Current

34. PID2023-152976NB-I00 01.Sep 2024-31.Aug.2027
MCIU
Novel methodologies for multi-omics integrative analysis with cutting-edge sequencing technologies
Role: **PI**

33. INFRA2024 01.Jun 2024-31.May.2026
CSIC
Impulsando la presencia del CSIC dentro de la ESFRI ELIXIR
Role: **PI-Coordinator**

32. HubBCB 01.Sep.2023-31.Ago.2025
CSIC
Conexión CSIC en Biología Computacional y Bioinformática.
Role: **Coordinator**

31. PROMETEO-CIPROM/2022/25 01.Jul.2023-31.Dec.2026
Generalitat Valenciana
Cells2Spine: Spatial Transcriptomics and Cell Communication Models applied to tissue regeneration and treatment in Spinal Cord Injury with Precision Nanomedicine.
Role: **Coordinator**

30. MSCA-DN-2021-101072892 01.Oct.2022-3.Sep.2026
Horizon Europa
LongTREC: The Long Reads European Transcriptomics Consortium. The next generation transcriptome biology revealed by single molecule sequencing technologies.
Role: **Lead-PI**

29. PID2020-119537RB-100 01.Sep.2021-31.Aug.2024
Integración de datos multi-ómicos para la inferencia de modelos multi-capa de enfermedad.
Role: **PI**

28. NSF 01.Feb.2020-31.Jan.2024
Identifying the determinants of high protein content in seeds of Phaseolus
Role: **Co-PI** (PI: Eduardo Vallejos)

Past

27. 1R21HG011280-01 01.Sep.2020-31.Aug.2022
NIH

Development of methods for transcript quantification and differential expression analysis using long-read sequencing technologies
Role: **PI**

26. 19-EXO19-0029 01.Feb.2020-31.Jan.2024
NASA
Microbial Dark Matter
Role: **Co-PI** (PI: Jamie Foster)

25. FSGC 08 TO No NNX15_033 01.Aug.2019-31.Jul.2020
Florida Space Research Program
Facilitating knowledge exchange between microbiology and computer science students: a computationally intensive approach to discover new adaptation genes in extreme environment
Role: **PI**

24. 2-SRA-2019-805-S-B 01.Jul.2019-30.Jul.2021
JDRF-PILOT STUDIES FOR MECHANISMS OF T1D DISEASE PATHOGENESIS
Genotype by Environment interaction analysis to understand mechanisms of T1D pathogenesis
Role: **PI**

23. R01DK116954 28.Feb.2018-27.Feb.2022
NIH(R01).
Critical role for alternative splicing in conferring risk for T1D
Role: **Co-PI** (PI: Concannon)

22. RFA-RM-17-001 19. Sep.2017-19.Sep.2020
NIH(R03)
Galaxy platform for integrative metabolomics and transcriptomics analysis
Role: **PI**

21. 2015-70016-23029 01.Oct.2015-30.Sep.2022
USDA
A Novel Antimicrobial Approach To Combat Huanglongbing
Role: **Co-PI (**PI: Lorca**)**

20. UF Start-up funds 01.Sep.2014-31.Dec.2019
Developing the Functional Iso-Transcriptomics framework.
Role: **PI**

19. 2018 SECIM 01.Jul.2018-30.Jul.2019
U24DK097209 NIH Common Fund metabolomics program
Development of multiomics methods for the integrative study of the Yeast Metabolic Cycle
Role: **PI**

18. PT17/0009/0015

ISCIII
Plataformas de apoyo a la investigación en ciencias y tecnologías de la salud de la convocatoria 2017 de la Acción Estratégica en Salud.
Role: **PI Nodo Valencia**

17. UFII Seed Funds 2017
University of Florida Informatics Institute
Understanding the functional role of alternative splicing in crop traits
Role: **PI**

16. PROMETEO/2016/093
The Next Systems Biology: statistical methods for multiomics systems biology
Generalitat Valenciana
Role: **Lead PI**

15. BIO2015-1658-R
MINECO
Novel methods for new challenges in the analysis of high-throughput sequencing data (NOVELSEQ)
The goal of this project is the development of new methods in the massive data analysis sequencing.
Role: **PI**

14. MSCA-ITN-2015. 2016-2019
Horizon 2020
CHROME
Computational methods for the integration of ChIP-seq, metabolomics and RNA-seq data to model chromatin metabolism.
Role: **WP4 leader**

13. Proyectos sinérgicos CIPF
Identification and modelling of molecular and cellular events of the immune response associated to the appearance of minimal hepatic encephalopathy in cirrhotic patients
Role: **PI**

12. Ayuda Complementaria Jeronimo Forteza
Desarrollo de métodos estadísticos para la integración de múltiples datos ómicos y de secuenciación masiva.
Generalitat Valenciana
Support finalization STATegra project.
Role: **Lead PI**

11. TEDDY
Helmsley Charitable Trust
Integrative Analysis of TEDDY data to improve T1D diagnosis.

Integration of multiomics, nutritional, demographic and clinical data from a cohort of 1.000 T1D patients to find Type 1 Diabetes triggers.
Role: **Lead PI**

10. BIO2012-40244
MINECO
Development of Computational Approaches for the characterization and functional annotation of long-non-coding RNA (Annot-lncRNA)
The goal of this project is the development of computational approaches to unravel function of long non-coding RNAs
Role: **PI**

9. GA-612583
EU Marie Curie IRSES
Developing a European American NGS Network (DEANN)
Scientific network of European and Latin America researchers in the field of Next Generation Sequencing (DEANN) applied to the analysis of variation in human and natural endemic populations
Role: **Lead PI**
Partners: TGAC(UK), UCL(UK), SLU(Sweden), Udine University(Italy); UPF(Spain), CIPF(Spain), IMEGEN(Mexico), CINVESTAV(Mexico), Brasilia Univ. (Brazil), INTA (Argentina), CONICET (Argentina), INACH (Chile)

8. GA-30600
FP7 HEALTH
User-driven development of statistical methods for experimental planning, data gathering, and integrative analysis of next generation sequencing, proteomics and metabolomics data
Statistical methods for multiomics data integration
Role: **Lead PI**
Partners: Imperial College(UK), IDIBELL(Spain), Karolinska Institute(Sweden), FORTH(Greece); CIPF(Spain), University Munich (Germany), Biomax(Germany), University Amsterdam (Holland), University Leiden (Holland), Qiagen Aahrus (Denmark), University California (USA)

7. ACOMP/2012/058
Generalitat Valenciana 2012 complementary actions
Complementing Grant for Pathogenomics- Metabolomics and Interactomics of the relationship host-pathogen
RNA-seq analysis in pathogenic bacteria
Role: **PI**

6. FPA/2013
Jerónimo Forteza 2012 Programme
Supporting technician for the Project "Development of transcriptional networks regulating virulence in filamentous fungi"
RNA-seq analysis in fungi

Role: **PI**

5. 16ER
GentxGent 2012 20,500€
Analysis of discordant twins to investigate correlation of gene expression changes and DNA methylation in Lupus
RNA-seq y Methyl-seq analysis in a rare disease
Role: **PI** and **Scientific Coordinator**
Partners: CIPF (Spain) and Idibell (Spain)

4. PIB2010AR-00266
Acción Internacional MICINN
Genomics and Transcriptomics of detoxification pathways in Drosophila
NGS-based genomic and transcriptomics analysis of natural fly strains fed under different nutritional conditions
Role: **PI** and **Scientific Coordinator**
Partners: CONICET (Argentina), UPF (Spain) and CIPF (Spain)

3. BIO2009-10799
MICINN Proyectos de Investigación Fundamental 2009 130,000€
Exploring novel genome-transcriptome relationships by Next Generation Sequencing approaches
Desarrollo de plataformas informáticas para el estudio de la regulación genómica mediante técnicas de ultrasecuenciación
Role: **PI**

2. BIO2008-04638-E
MICINN, Acciones Complementarias -ERA-NETs 2009 92,000€
Pathogenomics: Development of transcriptional networks regulating virulence in filamentous fungi
Role: **PI**

1. BIO2008-05266-E/ 136,000€
MICINN, Acciones Complementarias -ERA-NETs 2009
Pathomics: Metabolomics and Interactiomics of the relationship host-pathogen
Role: **PI**

Research Contracts

5. Kwait University 01.January.2018
KFAS
Identification of Novel Drought-responsive Genes in the Date Palm (Phoenix dactylifera L.) Using a Combination of Illumina and Pacbio NGS-based RNA-seq Technologies
Role: **PI**

4. Slovenian Institute of Biology 01.Oct.2017

Analysis and annotation of Solanum tuberosum Pacbio data
Role: **PI**

3. IGENOMIX 01.Oct.2014
Identificación de factores secretados y vinculados a alteraciones cromosómicas en embriones pre-implantacionales
Role: **PI**

2. IMEGEN 14.Mar.2014
Consulting RNA-seq data analysis

1. ROSLIN Institute 08.Jun.2009
Functional annotation of microarray data in livestock

Technology Transfer

1. **Co-founder and Scientific Advisor of Biobam Bioinformatics S.L.** 2010. Biobam is a leading bioinformatics solution provider which accelerate research in disciplines such as agricultural genomics, microbiology and environmental NGS studies, amongst others. Biobam is committed to the development of user-friendly software solutions for biological research. Our mission is to transform complex data analysis procedures into an attractive and interactive task. Biobam is devoted to close the gap between experimental work, bioinformatics analysis and applied research. (http://biobam.com)
2. **Co-founder of Genometra S.L.** 2011. Genometra is a service provider company for the bioinformatics analysis of high-throughput genomics data (http://www/genometra.com). The company ceased activity in 2018.

Publications

2024

170. *MOSim: bulk and single-cell multi-layer regulatory network simulator.*
Carolina Monzó, Carlos Martínez-Mira, Ángeles Arzalluz-Luque, **Ana Conesa***, Sonia Tarazona*
bioRxiv 2024.421834; doi: https://doi.org/10.1101/421834. *Corresponding author

169. *MORE interpretable multi-omic regulatory networks to characterize phenotypes*
Maider Aguerralde-Martin, Mónica Clemente-Císcar, Luis López Cárcel, **Ana Conesa***, Sonia Tarazona*
bioRxiv 2024.01.25.577162; doi: https://doi.org/10.1101/2024.01.25.577162

168. *MAMBA: a model-driven, constraint-based multiomic integration method*
Manuel Ugidos, Carme Nuño-Cabanes, Sonia Tarazona, Alberto Ferrer, Lars Keld Nielsen, Susana Rodríguez-Navarro, Igor Marín de Mas, **Ana Conesa**.
bioRxiv 2022.10.09.511458; doi: https://doi.org/10.1101/2022.10.09.511458

167. *Evaluation of strategies for evidence-driven genome annotation using long-read RNA-seq*

Alejandro Paniagua, Cristina Agustín-García, Francisco Pardo Palacios, Klaus Lubinus, Maite De María, Nancy D. Denslow, Margaret E. Hunter, Camila Mazzoni, **Ana Conesa**.
Genome Research (under revision)

166. *New challenges posed by long-read sequencing for the study of transcriptional diversity and genome annotation*
   Carolina Monzó, Adam Frankish, **Ana Conesa**.
   Genome Research (invited perspective under revision)

165. *Single-molecule sequencing epigenomics advancing towards long-read multi-omics method*
   Tianyuan Liu, **Ana Conesa**.
   Nature Genetics (invited review under revision)

164. *A Roadmap for Translational Research on mRNA Splicing in Cancer*
   Olga Anczuków, Brittany Angarola, Douglas Black, Angela Brooks, Chonghui Cheng, **Ana Conesa**, Edie Crosse, Ernesto Guccione, Sydney Lu, Karla Neugebauer, Priyanka Sehgal, Xiao Song, Zuzana Tothova, Juan Valcárcel Juarez, Eduardo Eyras, Kevin Weeks, Gene Yeo, Andrei Thomas-Tikhonenko, and Frederic Allain.
   Nature Reviews Cancer (under revision, minor)

163. *scMaSigPro: Differential Expression Analysis along Single Cell Trajectories.*
   Priyansh Srivastava, Marta Benegas Coll, Stefan Goetz, María José Nueda and **Ana Conesa**
   Bioinformatics, 8, July 2024, btae443, https://doi.org/10.1093/bioinformatics/btae443

162. *Systematic assessment of long-read RNA-seq methods for transcript identification and quantification.*
   Pardo-Palacios FJ, Wang D, Reese F, Diekhans M, Carbonell-Sala S, Williams B, Loveland JE, De María M, Adams MS, Balderrama-Gutierrez G, Behera AK, Gonzalez Martinez JM, Hunt T, Lagarde J, Liang CE, Li H, Meade MJ, Moraga Amador DA, Prjibelski AD, Birol I, Bostan H, Brooks AM, Çelik MH, Chen Y, Du MRM, Felton C, Göke J, Hafezqorani S, Herwig R, Kawaji H, Lee J, Li JL, Lienhard M, Mikheenko A, Mulligan D, Nip KM, Pertea M, Ritchie ME, Sim AD, Tang AD, Wan YK, Wang C, Wong BY, Yang C, Barnes I, Berry AE, Capella-Gutierrez S, Cousineau A, Dhillon N, Fernandez-Gonzalez JM, Ferrández-Peral L, Garcia-Reyero N, Götz S, Hernández-Ferrer C, Kondratova L, Liu T, Martinez-Martin A, Menor C, Mestre-Tomás J, Mudge JM, Panayotova NG, Paniagua A, Repchevsky D, Ren X, Rouchka E, Saint-John B, Sapena E, Sheynkman L, Smith ML, Suner MM, Takahashi H, Youngworth IA, Carninci P, Denslow ND, Guigó R, Hunter ME, Maehr R, Shen Y, Tilgner HU, Wold BJ, Vollmers C, Frankish A, Au KF, Sheynkman GM, Mortazavi A, **Conesa A**, Brooks AN.
   Nat Methods. 2024 Jun 7. doi: 10.1038/s41592-024-02298-3.

161. *SQANTI3: curation of long-read transcriptomes for accurate identification of known and novel isoforms.*
   Pardo-Palacios FJ, Arzalluz-Luque A, Kondratova L, Salguero P, Mestre-Tomás J, Amorín R, Estevan-Morió E, Liu T, Nanni A, McIntyre L, Tseng E, **Conesa A.**
   Nat Methods. 2024 May;21(5):793-797. doi: 10.1038/s41592-024-02229-2

160. *Nucleotide-level distance metrics to quantify alternative splicing implemented in TranD.*
   Nanni A, Titus-McQuillan J, Bankole KS, Pardo-Palacios F, Signor S, Vlaho S, Moskalenko O, Morse AM, Rogers RL, **Conesa A**, McIntyre LM.
   Nucleic Acids Res. 2024 Feb 10:gkae056

2023

159. *SQANTI-SIM: a simulator of controlled transcript novelty for lrRNA-seq benchmark.*
Jorge Mestre-Tomas, Tianyuan Liu, Francisco Pardo-Palacios, **Ana Conesa**
Genome Biol. 2023 Dec 11;24(1):286.

158. *Integration of multi-omics data to characterize keystone unknown taxa within microbialite-forming ecosystems.*
Rocío Amorin, **Ana Conesa***, Jamie Foster*.
Front. Microbiol., 28 July 2023mVolume 14 - 2023 | *Corresponding author

157. *Identification of food and nutrient components as predictors of Lactobacillus colonization.*
Thompson SC, Ford AL, Moothedan EJ, Stafford LS, Garrett TJ, Dahl WJ, **Conesa A**, Gonzalez CF, Lorca GL.
Front Nutr. 2023 Apr 21;10:1118679.

156. *Differences in uterine and serum metabolome associated with metritis in dairy cows.*
Figueiredo CC, Balzano-Nogueira L, Bisinotto DZ, Ruiz AR, Duarte GA, **Conesa A**, Galvão KN, Bisinotto RS.
J Dairy Sci. 2023 May;106(5):3525-3536

2022

155. *New roles for JUNB in cell cycle control and tumorigenic cell invasion via regulation of cyclin E1 and TGF-alpha2*
Pérez-Benavente B, Fathinajafabadi A, de la Fuente L, Gandía C, Martínez-Férriz A, Pardo-Sánchez JM, Milián L, **Conesa A**, Romero OA, Carretero J, Matthiesen R, Jariel-Encontre I, Piechaczyk M, Farràs R.
Genome Biol. 2022 Dec 9;23(1):252.

154. *Palmitate impairs circadian transcriptomics in muscle cells through histone modification of enhancers.*
Pillon NJ, Sardón Puig L, Altıntaş A, Kamble PG, Casaní-Galdón S, Gabriel BM, Barrès R, **Conesa A**, Chibalin AV, Näslund E, Krook A, Zierath JR.
Life Sci Alliance. 2022 Oct 27;6(1):e202201598.

153. *The absence of the queuosine tRNA modification leads to pleiotropic phenotypes revealing perturbations of metal and oxidative stress homeostasis in Escherichia coli K12.*
Pollo-Oliveira L, Davis NK, Hossain I, Ho P, Yuan Y, Salguero García P, Pereira C, Byrne SR, Leng J, Sze M, Blaby-Haas CE, Sekowska A, Montoya A, Begley T, Danchin A, Aalberts DP, Angerhofer A, Hunt J, **Conesa A**, Dedon PC, de Crécy-Lagard V.
Metallomics. 2022 Sep 24;14(9):mfac065.

152. *ECCB2022: the 21st European Conference on Computational Biology.*
Capella-Gutierrez S, Alloza E, Rubinat-Ripoll L; ECCB2022 Organising Committee, the ECCB2022 Programme Committee, the ECCB2022 Steering Committee, **Conesa A**, Valencia A.
Bioinformatics. 2022 Sep 16;38(Supplement_2):ii1-ii4.

151. *A roadmap for the functional annotation of protein families: a community perspective*

de Crécy-Lagard V, Amorin de Hegedus R, Arighi C, Babor J, Bateman A, Blaby I, Blaby-Haas C, Bridge AJ, Burley SK, Cleveland S, Colwell LJ, **Conesa A**, Dallago C, Danchin A, de Waard A, Deutschbauer A, Dias R, Ding Y, Fang G, Friedberg I, Gerlt J, Goldford J, Gorelik M, Gyori BM, Henry C, Hutinet G, Jaroch M, Karp PD, Kondratova L, Lu Z, Marchler-Bauer A, Martin MJ, McWhite C, Moghe GD, Monaghan P, Morgat A, Mungall CJ, Natale DA, Nelson WC, O'Donoghue S, Orengo C, O'Toole KH, Radivojac P, Reed C, Roberts RJ, Rodionov D, Rodionova IA, Rudolf JD, Saleh L, Sheynkman G, Thibaud-Nissen F, Thomas PD, Uetz P, Vallenet D, Carter EW, Weigele PR, Wood V, Wood-Charlson EM, Xu J
Database (Oxford). 2022 Aug 12;2022:baac062. doi: 10.1093/database/baac062.

150. *Independent phenotypic plasticity axes define mammalian metabolic and obesity sub-types*
Yang CH, Fagnocchi L, Apostle S, Wegert V, Casaní-Galdón S, Landgraf K, Panzeri I, Dror E, Heyne S, Wörpel T, Chandler DP, Lu D, Yang T, Gibbons E, Guerreiro R, Bras J, Thomasen M, Grunnet LG, Vaag AA, Gillberg L, Grundberg E, **Conesa A**, Körner A; PERMUTE, Pospisilik JA.
Nat Metab. 2022 Sep;4(9):1150-1165

149. *Transcriptional responses are oriented towards different components of the rearing environment in two Drosophila sibling specie*
De Panis D, Dopazo H, Bongcam-Rudloff E, **Conesa A**, Hasson E
BMC Genomics. 2022 Jul 16;23(1):515. doi: 10.1186/s12864-022-08745-9.

148. *A high resolution single molecule sequencing-based Arabidopsis transcriptome using novel methods of Iso-seq analysis*
Zhang R, Kuo R, Coulter M, Calixto CPG, Entizne JC, Guo W, Marquez Y, Milne L, Riegler S, Matsui A, Tanaka M, Harvey S, Gao Y, Wießner-Kroh T, Paniagua A, Crespi M, Denby K, Hur AB, Huq E, Jantsch M, Jarmolowski A, Koester T, Laubinger S, Li QQ, Gu L, Seki M, Staiger D, Sunkar R, Szweykowska-Kulinska Z, Tu SL, Wachter A, Waugh R, Xiong L, Zhang XN, **Conesa A**, Reddy ASN, Barta A, Kalyna M, Brown JWS
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Lectures, Seminars and Talks

146. *El ConesaLab o la Bioinformática para el análisis transcriptómico*
(invited speaker)
V Congreso de Bioinformática de Perú
Remote lecture, July 25th

145. *Bias analysis for long-reads transcriptomics multi-sample datasets*
(selected talk)
iRNA COSI at ISMB2024
Montreal, 12th-16th July 2024

144. *Using long reads to understand complexity and specificity of the transcriptomes*
(keynote)
Norwich Single-cell Symposium
Earlham Institute, Norwich, June 26th-27th June 2024

143. *Novel insights in transcriptional complexity through single-molecule sequencing.*
(invited speaker)
PacBioPRISM24
Lisbon, Portugal, April 24th, 2024

142. *Quantifying isoform expression and transcriptome complexity by single-molecule sequencing.*
(selected talk)
ABGT 2024
Orlando, Florida, USA, February 6th, 2024

141. *Assessing transcriptome complexity by high-throughput single-molecule sequencing.*
(invited speaker).
PacBio Day UCL London
London, UK, November 21st, 2023

140. *Long-read sequencing for the analysis of the transcriptome.*
(invited speaker).
Therapeutic targeting of mRNA splicing in cancer
Asilomar, California, USA, September 21st, 2023

139. *Long-read sequencing for the analysis of the transcriptome.*
(keynote).
Annual Symposium of Polish Bioinformatics Society

Gliwice, Poland, September 13th, 2023

138. *Using long reads technologies to reveal new insights into the functional complexity of the transcriptomes.*
(keynote).
Grapedia Annual Meeting
Valencia September 11th, 2023

137. *Third-generation long-read transcriptome sequencing for unraveling transcriptome complexity.*
(keynote).
7th Denmark Bioinformatics Symposium
Aarhus (Denmark) 7th September, 2023

136. *Las tecnologías de secuenciación de tercera generación nos revelan nuevos aspectos de la biología de los transcriptomas.*
(keynote).
Octavo Sysmposio Argentino de Jóvenes Investigadores en Bioinformática
Virtual August 3rd, 2023

135. *Third-generation sequencing technologies to investigate the complexity of transcriptomes.*
(keynote).
SysReg COSI at ISMB/ECCB 2023
Lyon July 26th, 2023

134. *Herramientas transcriptómicas para el modelado de sistemas biologicos complejos.*
(invited seminar).
Congreso Biotec 2023 de la Sociedad Española de Biotecnología
Madrid July 17th, 2023

133. ***Análisis integrativo de datos multiómicos***
(invited seminar).
CSIC symposium in Computational Biology, IA and Data Science.
Madrid July 3rd, 2023

132. *Assessing long-read transcriptomics data for isoform identification and genome annotation.*
(invited seminar).
European Reference Genomes Archive plenary.
Virtual June 20th, 2023

131. *Benchmarking of multiple long reads sequencing methods and platforms for transcriptome analysis.*
(invited seminar).
Instituto Valenciano de Biomedicina

Valencia February 24th, 2023

130. *Single molecule, long reads sequencing for the characterization of the transcriptome* (keynote speaker).
Jornadas de Bioinformática Granada
Virtual February 23rd, 2023

129. *Benchmarking of multiple long reads sequencing methods and platforms for transcriptome analysis.*
(invited seminar).
Barcelona Supercomputing Center
Lisbon February 16th, 2023

128. *Benchmarking of multiple long reads sequencing methods and platforms for transcriptome analysis.*
(invited seminar).
PRBB Barcelona
Lisbon February 16th, 2023

127. *Long-read sequencing to unravel the functional impact of alternative splicing* (invited seminar).
Olissipo Winter School
Lisbon February 10th, 2023

127. *Long-read sequencing to unravel the functional impact of alternative splicing* (invited seminar).
Olissipo Winter School
Lisbon February 10th, 2023

126. *Multiomics tools to model dynamic cellular systems in health and disease* (invited seminar).
Olissipo Winter School
Lisbon February 9th, 2023

125. *Lessons and perspectives learnt from the LRGASP project on long reads transcriptome sequencing* (invited seminar).
European Bioinformatics Institute
Huxton, Cambridge January 27th, 2023

124. *Benchmarking of multiple long reads sequencing methods and platforms for transcriptome analysis* (invited speaker).
Festival of Genomics 2023
London, January 25th -26th, 2023

123. *SQANTI3: A Set of Tools for Curation, Annotation and Quantification of Long Reads RNA Sequencing (lrRNA-seq) Data*

XXX Plant and Animal Genome Conference
San Diego, January 13th -18th, 2023

122. *PaintOmics, a Tool for the Integrative Analysis and Visualization of Multi-Omics Data*
XXX Plant and Animal Genome Conference
San Diego, January 13th -18th, 2023

121. *Benchmarking of transcriptomics long reads technologies for transcript identification: the LRGASP project* (invited speaker).
X Genomics and Bioinformatics Symposium
University of Valencia, December 15th -16th, 2022

120. *Multi-omic integration to model dynamic biological systems* (invited speaker).
International Food Data Science Workshop
Instituto de Tecnología de Alimentos (Valencia), November 30th – December 2nd, 2022

119. *Diseño, análisis e interpretación de datos multiómicos en desarrollo y enfermedad* (opening lecture).
Seminarios de la Sociedad Española de Bioinformática y Biología Computacional
Online, November 21st, 2022

118. *Benchmarking of transcriptomics long reads technologies for transcript identification: lessons from the LRGASP project* (invited speaker).
Long Reads Uppsala Workshop
University of Uppsala, October 31st – November 2nd, 2022

117. *The Conesa Lab: genomics tools for the people* (invited).
LASER TALKS, Universitat Politècnica de Valéncia
Center Cultural del Carmen, October 21st, 2022

116. *From multi-omics data to multi-layered systems models: challenges and solutions* (invited speaker).
Tri-Omics Summit, invited Speaker
Thistle Marble Arch Hotel, London, October 18th, 2022

115. *The bioinformatics of multiomics data integration and modeling* (keynote).
7th European Student Council Symposium 2022/ECCB2022
Sitges, September 18th, 2022

114. *Leveraging Long Reads Sequencing for Developing a Functional Iso-Transcriptomics Analysis Framework* (invited speaker).
Computational Challenges in Very Large-Scale 'Omics'.
University of California at Berkeley, United States, July 18th to 21th, 2022

113. *The integration of multiomics data to infer multi-layered systems biology models*

(keynote)
SysMod COSI at the Intelligent Systems for Computational Biology Conference
Madison, United States, July 10th to 14th 2022

112. *Tools for transforming long reads into functional insights about isoform expression* (invited speaker)
Long-reads sequencing workshop. The Jackson Laboratory for Genomic Medicine
Farmington, Connecticut May 19th 2022

111. *Multiomics integration and third-generation sequencing boost biomedical research with new tools for data analysis* (invited speaker).
Cabimer (Sevilla)
May 13th, 2022

110. *The Functional Iso-transcriptomics paradigm or long read sequencing applied to transcriptome research* (invited speaker).
Genyo (Granada)
March 23rd 2022

109. *From multiomics data to multilayered systems biology models: do´s and don´ts.* (invited speaker)
University of Granada, Department of Computer Science,
March 22rd, 2022

108. *Single molecule long reads sequencing as a new paradigm in transcriptomics research* (keynote speaker)
Australian Mathematical Sciences Institute BioInfoSummer 2021.
Virtual meeting, December 2nd 2021,

107. *Multi-omics integration and third-generation sequencing boost biomedical research with new tools for data analysis* (keynote speaker)
Argentina Bioinformatics Conference.
Virtual meeting, November 17th 2021.

106. *Statistical and bioinformatics methods for the integration of multi-omics data to understand disease mechanisms* (invited speaker)
School of Medicine, Virgina University
27th October 2021

105. *Interpretable integration of multiomics data to unravel disease mechanisms* (invited speaker)
Cross disciplinary Study of Post-transcriptional and Post-translational modifications.
NSF sponsored workshop
Virtual meeting, 18th October 2021

104. *Multi-OMICs modelling of T1D links lipid impairment with T1D onset*

(invited speaker)
Ask the Expert. Sugar Science
Virtual meeting, 23rd September 2021

103. *Challenges and solutions in for the integrative analysis of multi-omics data* (invited speaker)
Belgrade Bioinformatics Conference 2021,
Virtual meeting, 23rd June 2021

102. *Considerations for quality control, quantification and differential expression analysis using lrRNA-seq* (invited speaker)
Earlham Institute Long Read RNA Symposium 2021
Virtual meeting, 16th June 2021

101. *Methods and tools for the integration of multi-omics data to model biological processes*
Mechanisms of Oncogenesis program,
UF Cancer Institute, 25th January 2021

100. *The Functional Iso-Transcriptomics toolset to leverage long reads sequencing for unravelling isoform transcriptional networks from single cells* (keynote).
iRNA COSI at the European Conference in Computational Biology 2020, Tutorial
Virtual meeting, 13th July 2020

99. *Full-Length RNA-Seq Analysis using PacBio long reads: from reads to functional interpretation*
European Conference in Computational Biology 2020, Tutorial
Virtual meeting, 12th July 2020

98. *The functional iso-transcriptomics pipeline: from long reads to biological insights*
SMRT Informatics Leiden,
May 2020

97. *Leveraging long reads to unravel isoform-expression networks in single cells.* (keynote)
SMRT Informatics Leiden
Online, May 2020

96. *Bioinformatics tools for multi-omics integration and single molecule sequencing: application to human disease.* (invited speaker).
Topics in Cancer Seminar Series
Gainesville, December 6th, 2019

95. *Tools for transforming multi-omics data into disease models.* (selected talk)
Advances in Computational Biology
Barcelona, November 28th, 2019

94. *From Long Reads to Transcript Function: Bioinformatics Tools for Iso-Transcriptomics Analysis* (keynote)
North America PacBio Users Group Meeting
Delaware University, September 25th, 2019

93. *Tools for transforming multiomics data into disease models* (flash presentation)
EMBO | EMBL Symposium: Multiomics to Mechanisms - Challenges in Data Integration
EMBL Heidelberg, September 13th, 2019

92. *Multiomics approaches to model development and disease* (invited)
Institute for Integrative Systems Biology (I2SysBio)
Valencia, July 16th, 2019

91. *Multiomics and Third Generation Sequencing: at the forefront of genomics research* (invited)
Barcelona Supercomputing center (BSC)
Barcelona, June 11th, 2019

90. *Multiomics and Third Generation Sequencing: at the forefront of genomics research* (invited)
Centre for Research in Agro Genomics (GRAG)
Barcelona, June 11th, 2019

89. *From long reads to functional analysis of isoforms: bioinformatics tools to understand differential isoform expression in neural differentiation* (invited)
ENCODE Long reads meeting
Barcelona, June 9th- 10th, 2019

88. *Multiomics and Third Generation Sequencing: at the forefront of genomics research* (invited)
Animal Science Program, University of Florida
Gainesville, April 22th, 2019

87. *Multi-omics and third generation sequencing strategies for the future of genome research. The functional transcriptomics story* (keynote)
#20YEARSOFGENOMICS,
École normale supérieure, Paris, March 28th, 2019

86. *From biomarkers to systems models: methods and software for multi-omics data integration (*keynote talk*)*
Challenges and perspectives in integrative bioinformatics
Paris, France, September 17th 2018.

85. *SQANTI: extensive characterization of long-read transcript sequences for quality control in full-length transcriptome identification and quantification (*highlight talk*)*
European Conference in Computational Biology, ECCB2018.
Athens, Greece, September 11th 2018.

84. *Bioinformatics methods for the integrative analysis of multi-omics and third generation sequencing data (invited lecture)*
Spetses ChroMe summer school.
Spetses Greece, August 26th 2018.

83. *Integrative analysis of multiomics TEDDY data reveals dysregulation at molecular events up to 12 months before seroconversion (invited lecture)*
TEDDY project meeting
Washington DC, May 2nd 2018.

82. *Bioinformatics and Statistical Approaches for the Integration of Metabolomics and Transcriptomics Data (invited lecture).*
2018 SECIM Metabolomics Symposium
Gainesville, Florida, April 26th 2018**.**

81. Functional Profiling of Alternative Isoform expression on Mouse Neural Differentiation using Single Molecule Sequencing and tappAS
Bermuda Principles. Impact on Splicing. 2nd Annual Conference.
Bermuda, February 21st-25th, 2018

80. SQANTI and TAPPAS: Making sense of Iso-seq data (invited lecture).
SMRT Informatics Developers Conference @ PAG XVXXI
San Diego, January 17th, 2018

79. Multiomics data integration to unravel local gene regulatory networks (invited lecture).
International Workshop in Environmental Omics Integration and Modeling
CosmoCaixa, Barcelona, Spain, October 20th 2017

78. The STATegra road map for the design and analysis of multiomics perturbation experiments (invited lecture).
Leeds Advanced Statistical Research 2017/ Mimomics Workshop
University of Leeds, June 29th 2017

77. Unravelling novel transcriptome functional features
Conference Lectures of the Bioinformatics Master of the University of Murcia
University of Murcia, May 19th, 2017.

76. Multiblock integration of T1D gene expression and metabolomics data to study T1D progression.
TEDDY fall meeting
Tysons Corner, Virginia, November 8th, 2016.

75. Developing statistical approaches for the integration of multi-omics data. (invited lecture)
Frontiers in Genomics Program. Universidad Autónoma de Mexico.
Cuernavaca, 24th October 2016

74. Functional transcriptomics in the post-NGS era: multiomics integration and new technologies (Plenary lecture).
Third International Conference of Computational Biomedicine, CBM 2016
Gainesville, Florida 25th-27th February 2016

73. Functional Analysis at Isoform Resolution.
Pacbio industrial workshop. XXIV Plant and Animal Genome Conference
San Diego, California 12th January 2016.

72. Unravelling novel transcriptome functional features by NGS technologies (opening lecture).
VI Argentinian Conference in Bioinformatics and Computational Biology.
Bahia Blanca, Argentina, 14th-16th October 2015

71. Comparison of temporal gene expression profiles with other omics to understand gene expression regulation.
Workshop on Statistical Methods for Omics Data Integration and Analysis.
Valencia, Spain. 14th-16th September 2015

70. Lessons and results of multi-omics data analysis (keynote speaker)
JOBIM 2015
Clermont-Ferrand, 6th- 9th July 2015

69. ***Integration of multi-omics data to study B-cell differentiation: experimental design and analysis issues (keynote speaker)***
ABS4NGS Workshop
Paris, France, 22nd-23rd June 2015

68. STATegra: Statistical and Bioinformatics Resources for Analysis of Multi-Omics Projects
5th NGS Conference (distinguished speaker)
Boston, USA, 21st-22nd May 2015

67 Functional Alternative Isoform Expression Analysis Using Long Read Technologies.
Post-transcriptional Gene Regulation Workshop, **Plant and Animal Genome Conference XXIII**
San Diego, January 11th, 2015

66. Functional Alternative Isoform Expression Analysis Using Long Read Technologies.
Centro de Investigación Príncipe Felipe

Valencia, January 30th, 2015

65. The STATegra Initiative Develops Novel Methodologies for the Integrative Analysis of Multiple Types of NGS & Omics Data
Bioinformatics Workshops, **Plant and Animal Genome Conference XXIII**
San Diego, January 13th, 2015

64. The STATegra NGS Experiment Management System
Computer Demo Session, **Plant and Animal Genome Conference XXIII**
San Diego, 14th January 2015

63. Functional Annotation of a mouse neural differentiation process (keynote speaker)
Australian Bioinformatics Conference
Melbourne, Australia, 11th October 2014

62. The STATegra project: new tools for analysis and integration of multi-omics data (keynote speaker)
Conference of the Australasian Genomics Technologies Association
Melbourne, Australia, 13th October 2014

61. The STATegra project: new statistical tools for analysis and integration of diverse omics data (invited lecture).
EpiConcept Workshop 2014
Gran Canarias, Spain, 8th May 2013

60. NGS in Functional Genomics. NGS data integration (invited seminar)
SeqAhead Workshop: NGS after the Gold Rush
Norwich, UK, 6th May 2014
Bioinformatics for the Diverse Life Sciences (invited seminar)
Genetics Institute, University of Florida
Gainesville, Florida, USA, 17th February **2014**

59. A Tour Though Data Integration Approaches at the GGE Lab.
Centro de Investigación Principe Felipe
Valencia, January 24th, 2014

58. Nuevos retos de la medicina personalizada (invited conference)
MIT EmTech Valencia
Valencia, 5th November 2013

57. The STATegra project: new statistical methods and tools for integrative omics data analysis (invited seminar).
ALLBIO Meeting
Uppsala, 7th-8th October 2013

56. Multidisciplinary multi-institutional PhDs (invited seminar).

ISCB/GOBLET Meeting
Berlin 19th July 2013

55. The STATegra project: new statistical methods and tools for integrative omics data analysis (invited seminar).
Workshop in Translational Genomics
Barcelona, 26th April 2013

54. Pathway-based linear models (invited conference)
SeqAhead/STATegra High throughput and data integration workshop
Barcelona, 15th February 2013

53. Analysis of Fungal Transcriptomics with CLC Genomics Workbench and Blast2GO.
XXI Plant and Animal Genome Conference (invited conference)
San Diego, 15th January 2013

52. Transcriptome analysis with RNAseq: promises and biases (invited seminar)
Department of Genetics, Stanford University
Stanford, 28th September 2012

51. Pathway based methods to unravel functional relationships: application to pathway network inference and drug repurposing (invited seminar)
UCB Statistics and Genomics Seminars
Berkeley, 27th September 2012

50. NGS of a transdifferentiation system and other RNA-seq tricks (invited conference)
Joining Forces Symposium
Zurich, 22nd June 2012

49. Functional Annotation of Sequence Data (seminar)
COST Action SeqAhead Course in Next Generation Sequencing
Uppsala, 31st May 2012

48. Next generation sequencing in transcriptomics: new views on the genome and much confusion (invited conference)
Langebio Institute, CINVESTAV
Irapuato, Mexico, 8th May 2012

47. Transcriptional networks controlling virulence in filamentous fungal pathogen.
Joint Status Seminar of the ERA-Net PathoGenoMics
Tenerife, 23rd January 2012

46. Sequencing the Snake Venom Transcriptome for Its Applications in Biomedicine.
Plant and Animal Genome Conference XX
San Diego, California, 15th January 2012

45. Differential expression with RNA-seq: new potentials and new concerns (invited seminar)
Instituto Valenciano de Biomedicina.
Valencia, 18th November 2011

44. NOISeq: a RNA-seq differential expression method robust for sequencing depth biases.
COST SeqAhead meeting.
Brussels, 8th November 2011

43. Aplicaciones de las nuevas tecnologías de secuenciación masiva al studio de la relación genoma-proteoma.
Conferencia de la Sociedad Española de Bioquímica y Biología Computacional.
Barcelona, 7th September 2011

42. Differential expression in RNASeq: a matter of depth (conference)
Conference of the International Society of Computational Biology/ European Conference in Computational Biology (ISCB/ECCB)
Austria Center Vienna, 18th July 2011

41. Differential expression in RNASeq: a matter of depth (conference)
Critical Assessment of Massive Data Analysis (CAMDA) 2011
Austria Center Vienna, 15th July 2011

40. Ontología Génica y Anotación Funcional (seminar)
AECID CYDET Curso Bioinformática y Genómica Vegetal
Cartagena de Indias, Colombia, 11th-13th July 2011

39. Differential expression in RNAseq Studies (seminar)
Practical Course on Bioinformatics and Network Biology.
Centro de Investigación del Cáncer, Salamanca, Spain, 23rd June 2011

38. Blast2GO: A Gene Ontology annotation, visualization and analysis tool for functional genomics projects (seminar)
Practical Course on Bioinformatics and Network Biology.
Centro de Investigación del Cáncer, Salamanca, Spain, 23rd June 2011

37. Introduction to NGS technology (seminar)
Data analysis workshop for massive sequencing data
E.T.S. de Ingenierías Informática y de Telecomunicación
University of Granada, Spain, 13th June 2011

36. Differential expression with RNASeq: length and depth does matter (conference)
B**ioinformatics and High Throughput Sequencing 2011**
Institute Pasteur Paris, France, 22nd March 2011

35. High performance sequencing and gene expression quantification (conference)

RES Scientific Seminar of Supercomputing and Next Generation Sequencing
Parque Tecnológico de Andalucía, Málaga, Spain, 17th March 2011

34. Variable Selection for Multifactorial Genomic Data
XXXII Congreso Nacional de Estadística e Investigación Operativa y VI Jornadas de Estadística Pública
Universidad Da Coruña, September 17th, 2010

33. Biología cuantitativa ¿cuántos son dos más dos? (conference)
Departamento de Matemáticas
Universitat de Valéncia, Spain, May 2010

32. Pathway Analysis of Transcriptomics Data (conference)
IX Jornadas Nacionales de Bioinformática
Calouste Gulbenkian Foundation, Lisbon, Portugal, 4th November 2009

31. Pathway Analysis of Transcriptomics Data (conference)
Séptima reunión de la red valenciana de genómica y proteómica
Facultad de Farmacia de la Universitat de València, Spain, 12th November 2009

30. Pathway Network Analysis in Systems Biology (conference)
XII Conferencia Española de Biometría
Universidad de Cádiz, Spain, 24th September 2009

29. The Joined GEPAS, Babelomics and Blast2GO Suites: Statistical and Functional Analysis of Genomics Data on the Web (computer demo)
Plant and Animal Genome Conference, XVII
San Diego, USA, 14th January 2009

28. B2G-FAR: The Blast2GO Functional Annotation Repository (computer demo)
Plant and Animal Genome Conference, XVII
San Diego, USA, 14th January 2009

27. PLS Analysis with Gene Ontology data: inferring the phenotype from the function of genes (conference)
11th Conference on Chemometrics in Analytical Chemistry
Montpellier SupAgro, Montpellier, France, 3rd July 2008

26. Finding relationships between high throughout data sources through multiway projection methods (seminar)
MIPS, University of Munich
Munich, Germany, 4th March 2008

25. Systems Level Analysis of Time Course Omics Data (seminar)
Department of Statistics, University of Barcelona
Barcelona, Spain, November 2008

24. Systems Level Analysis of Time Course Omics Data (conference)
(EMBnet) Conference 2008: 20th Anniversary Celebration
Martina Franca, Italy, 19th September 2008

23. Functional Genomics: Concepts, Databases and Methods (seminar)
First International Course in Environmental Genomics
DISAV, University of Piemonte Orientale, Italy, 15th December 2008

22. An approach to the characterization of the date palm genome (conference)
II Congreso Internacional Oasis y Turismo Sostenible
La Tribuna del Agua de Expo Zaragoza, 9th August 2008

21. Finding relationships between high throughput data sources through multiway projection methods (conference)
Jornadas Nacionales de Bioinformática
Centro de Investigaciones Príncipe Felipe, 13th February 2008

20. Partial Least Squares on Gene Functional Classes (conference)
Critical Assessment of Gene Expression Data Analysis (CAMDA Conference)
Centro de Investigación Príncipe Felipe, Valencia, Spain, 14th December 2007

19. High throughput functional annotation and analysis with the Blast2GO suite (seminar)
EMBRACE Gene Ontology Workshop,
University of Bari, Italy 7th-9th November 2007

18. Multi-way methods for integrating data and knowledge in genomics research (conference)
XI Española y Primer Encuentro Iberoamericano de Biometría
Universidad de Salamanca, Spain, 20st June 2007

17. N-way methods to functional genomics: can we integrate all data in a multidimensional box? (conference)
Systems Biology Symposium
Universidad Complutense de Madrid, Spain, 8th June 2007

16. Bioinformática en genómica vegetal: anotación de funciones génicas y análisis de respuestas transcripcionales (seminar)
University of Malaga
Málaga, Spain, 4th May 2007

15. Anotación funcional de secuencias en especies no modelo (seminar)
Introduction to Bioinformatics
University of Alicante, Spain 19th December 2007

14. Blast2GO v2.0: A comprehensive functional annotation and analysis tool for the genomics of non-model species (computer demo)
Plant and Animal Genome Conference, XV
San Diego, USA, 15th January 2007

17. *A multi-way strategy for the integrative analysis of high dimensionality 'omics' data*
7th Spanish Symposium on Bioinformatics and Computational Biology
Zaragoza, November 22nd, 2006

16. Blast2GO: Conceptos de anotación funcional automática y su aplicación en una herramienta bioinformática (seminar)
BiT-Lab. Departamento de Arquitectura de Computadores, Universidad de Málaga,
Málaga, Spain, 6th October 2006

15. Blast2GO: Conceptos de anotación funcional automática y su aplicación en una herramienta bioinformática (seminar)
Foro de Biotecnología de Plantas, Taller Bioinformática
Universidad de Murcia, Spain, 28th September 2006

14. maSigPro: A method to identify significantly differential expression profiles in time-course microarray experiments (póster)
X Conferencia Española de Biometría
Oviedo, Spain, 27th May 2006

13. Vitamin: an Ontology-driven information System for Mutant Annotation
4th European Conference on Computational Biology
Madrid, Spain, 28th September to 1st October 2005

12. Blast2GO: A universal Gene Ontology annotation, visualization and analysis framework for th egenomics research of non-model species
4th European Conference on Computational Biology
Madrid, Spain, 28th September to 1st October 2005

11. Aplicación de la Genómica Funcional como Respuesta a Problemas Biológicos (seminar)
Instituto de Productos Lácteos de Asturias
Oviedo, Spain, May 25th, 2005

10. Analysis and interpretation of genome wide datasets: from sequence .... to function .... to biology (seminar)
School of Biosciences, University of Birmingham
Birmingham, UK, 2005

9. Finding significant differential gene expression profiles through maSigPro (seminar)
Departamento de Estadística, Universidad de Barcelona
Barcelona, Spain, 2005

8. Functional genomics in citrus or the bioinformatics of non model species (seminar)
Department of Molecular Biology, University of Groninghem.
Groninghem, The Netherlands, 28th November 2005

7. Functional genomics in citrus or the bioinformatics of non model species (seminar)
TNO Nutrition and Food Research,
Zeist, The Netherlands, 3rd November 2005

6. Blast2GO (conference)
GO Users Meeting organized by EMBL-EBI
Bergen, Norway, 14th September 2005

5. maSigPro: a method to identify significantly diferencial expresion profiles in time-course microarray experiments (póster)
5th Annual Spanish Bioinformatics Conference
UPC, Barcelona, 29th November – 2nd December 2004

4.Blast2GO: a universal annotation and visualization tool for functional genomics reserach (póster)
5th Annual Spanish Bioinformatics Conference
UPC, Barcelona, 29th November – 2nd December 2004

3.*Blast2GO y maSigPro: herramientas bioinformáticas para Genómica Funcional en Investigación Agraria* (conference)
Tercera reunión de la red valenciana de genómica y proteómica
IATA, Valencia, 28th October 2004

2. *Expression of Caldariomyces fumago chloroperoxidase in Aspergillus niger*
VII International Fungal Biology Conference
Groningen, Netherlands, August, 1999

1. Expression of the heme-peroxides in Aspergillus (oral presentation)
Symposium NvvM section Mycology (oral presentation)
Wageningen, October 29th, 1998

Thesis as supervisor

1. **Maria José Nueda Roldán**. *Statistical methods for Time Course Microarray data*. Universitat Politècnica de València, 2009.
2. **Sonia Prado López**. Efectos del oxígeno en la expresión genética y diferenciación de líneas de células madre embrionarias humanas (hESC). Universitat de València, 2009.
3. **Stefan Goetz.** *Functional characterization of genome-wide sequence data: development of methods and tools for high-throughput analysis.* Universitat Politècnica de València, 2010.
4. **Sonia Tarazona Campos**. *Statistical methods for transcriptomics: from microarray to RNA-seq.* Universitat Politècnica de València, 2014

5. **Rafael Hernández de Diego**. *Development of Bioinformatics Resources for the Integrative Analysis of Next Generation Omics Data*. Universitat Politècnica de València, 2016.
6. **Lorena de la Fuente**. *Development of a Bioinformatics Approach for the Functional Analysis of Alternative Splicing.* Universitat Politècnica de València, 2019.
7. **Pedro Furió Tarí**. *Development of bioinformatic tools for massive sequencing analysis*. Universitat Politècnica de València, 2020
8. **Tatyana Zamkovaya**. *Network analysis of Microbial Dark Matter.* University of Florida, 2020
9. **Salvador Casaní Gabaldón**. *Bioinformatics methods to link metabolic and epigenetic regulation.* Universitat València, defense on February 8th 2021.
10. **María Teresa Rubio Martínez-Abarca**. *Métodos de integración de datos multiómicos para el estudio de enfermedades.* Universitat Politècnica de València, June 30th 2022.
11. **Manuel Guerrero Ugidos**. *Desarrollo de métodos estadísticos para la Biología de Sistemas multiómica.* Universitat Politècnica de València. 2023
12. **Rocío Amorín**. *Elucidating the role of microbial dark matter in microbialite-forming ecosystems.* University of Florida. September 18th, 2023.
13. **Angeles Arzalluz-Lopez.** *Understanding isoform expression and alternative splicing biology through single-cell RNAseq*. Universitat Politècnica de València. March 26th, 2024.
14. **Francisco José Pardo Palacios**. *Desarrollo de métodos bioinformáticos y experimentales para el estudio del impacto funcional de las isoformas alternativas*. Universitat Politècnica de València, September 2024.
15. **Pedro Salguero,** Universitat Politècnica de València, in progress.
16. **Luidmyla Kondratova,** University of Florida, in progress.
17. **Alejandro Paniagua,** Universitat de València, in progress.
18. **Priyansh Srivastava,** Universitat de València, in progress.
19. **Tianyuan Liu,** Universitat de València, in progress.
20. **Fabian Jatzinger,** Universitat de València, in progress.
21. **Enrique Vidal,** Universitat Politècnica de València, in progress.
22. **Maider Aguelarre,** Universitat Politècnica de València, in progress.

Member of PhD thesis defense committees

26. Sonia García Ruiz.
    UCL Great Ormond Street Institute of Child Health.
    Assessing splicing accuracy and its determinants across human tissues using RNA sequencing.
    September 7th, 2023

25. Joanna Ficek-Pascual.
    LMU Munich.
    Computational methods for dissecting cancer heterogeneity using multi-modal data: from bulk to spatial resolution.
    Augustus 17th, 2023

24. Sharon Thompson.

Microbiology and Cell Science Department, University of Florida.
Investigation of the impact of diet on the probiotic organism lactobacillus johnsonii n6.2.
2023

23. Adrian Barry Sousa. *Microbial communites of the upper Floridan aquifer, U.S.A.: composition, structure, and contributions to biogeochemical cycling.*
    Microbiology and Cell Science Department, University of Florida.
    2023

22. Adelena Nanni.
    Genetics and Genomics Doctoral Programme, University of Florida.
    Insights into the regulation of expression and quantification of Transcripts using modern analytical approaches.
    2022

21. Alexandra L. Wiscovitch Bonilla.
    Genetics and Genomics Doctoral Programme, University of Florida.
    Single-cell sexual dimorphisms in non-sexual organs
    2022

20. Katheleen Miller.
    Microbiology and Cell Science Department, University of Florida.
    Exploring adaptation to pressure extremes relevant to earth and mars via growth, transcriptomic, and epigenetic modulation within the genus carnobacterium
    2022

19. Christina Davis.
    Microbiology and Cell Science Department, University of Florida.
    Ecology of subglacial lake microbial communities in west antarctica
    2022

18. Richard Kuo
    College of Medicine and Veterinary Medicine. The University of Edinburgh
    Identifying Long Non-Coding RNA in the Chicken Transcriptome
    July 28th, 2022

17. Luis Ferrández Peral
    Departament de ciències experimentals i de la salut. Universitat Pompeu Fabra.
    Evolution of the transcriptomic regulation in the primate lineage
    June 8th, 2022

16. Alvaro Montesinos.
    Departamento de Bioquímica y Biología Molecular y Celular, **Universidad de Zaragoza.**
    Dynamics of almond (Prunus amygdalus (L.) Batsch, syn. P. dulcis (Mill.)) tree architecture and scion/rootsock interaction

February 17th, 2022

15. Jordi Martorell.
Centro Pzifer, Universidad de Granada
Computational and statistical methods for integrated analysis of biomedical data
Abril 27th, 2021

14. Julia Betancourt.
Genetics and Genomics Doctoral Programme, University of Florida.
Single-cell analysis reveals targets of an endocrine disruptor in the developing genitalia
2021

13. Isabel Betegón Putze.
Animal Biology, Plant Biology and Ecology Department. Universitat Autonoma de Barcelona
Spatiotemporal analysis of brassinosteroid signaling in the vascular stem cells.
November 10th, 2020

12. Kelsey s. Aadland.
Genetics and Genomics Doctoral Programme, University of Florida
Conservation of early miRNA biogenesis in animal and plant lineages
2020

11. Krishna Bhattarai.
Horticultural Sciences Department, University of Florida
Genetic mapping and next-generation sequencing ot identify quantitative trait loci and candidate genes for powdery mildew resistance in gerbera (Gerbera hybrida)
2020

10. Joany Bablilonia.
Microbiology and Cell Science Department, University of Florida.
Comparative metagenomics and metabolomics for characterizing stromatolite ecological community function
2019

9. Morgan Smith.
Genetics and Genomics Doctoral Programme, University of Florida.
The Characterization of Sirpγ and its role in Type I Diabetes
2019

8. Stefanos Fafalios.
Computer Science Department, Creta University.
Towards a universal molecular classifier
December, 2019

7. Jordi Durban i Sánchez
Facultat de Biològiques, Universidad de Valencia

Aplicacions de Next Generation Sequencing en organismes no model : caracterització dels transcriptomes de verins de serps
2015

6. Stanley Kimbung
University of the Western Cape
2014

5. Tamara Garrido Gómez
Facultad de Medicina, Universidad de Valencia
Estudio proteómico del endometrio humano
May 29th, 2012

4. Patricia Díaz Gimeno
Departamento de Pediatría, Obstetricía y Ginecología, Universidad de Valencia
Desarrollo de una herramienta molecular diagnóstica de la Receptividad endometrial
2011

3. Rubén Noglas Cadenas
Facultad de Informática, Universidad Complutense de Madrid
2010

2. Laura Pascual Bañuls
Departamento de Biotecnología, Universidad de Valencia
2010

1. Aureliano Bombarely Gómez
Departamento de Biología y Bioquímica, Universidad de Málaga
2007

Supervision of graduate and master thesis

29. Enrique Sapena Ventura.
Master en Bioinformática. Universitat de Valencia
LRGASP: OpenEBench implementation
2023

28. Alejandro Escobar Simón
Master en Biomedicina y Biotecnologia, Universitat de Valencia
Estudio de la inestabilidad transcripcional asociada a envejecimiento, desarrollo y/o enfermedad mediante tecnologías de secuenciación de tercera generación.
2023

27. Alessandra Martínez
Master en Bioinformática, Universitat de Valencia

Development of isoannot: a new pipeline for Transcriptome functional annotation at isoform Resolution
2023

26. Idoia Alvarez
Master en Bioinformática, Universitat de Valencia
Anotación de sitios de unión de miRNA y señales de localización celular en isoformas
2023

25. Cristina Araiz
Grado de Biotecnología, Universitat Politècnica de Valencia
Analisis multiómico con MAMBA
2023

24. Eva Navarre
Grado de Biotecnología, Universitat Politècnica de Valencia
Análisis multiómico de datos circadianos
2022

23. Isidro Sobrino
Grado de Biotecnología, Universitat Politècnica de Valencia
Análisis multiómico de datos circadianos
2022

22. Enrique Sales
Grado de Biotecnología, Universitat Politècnica de Valencia
Análisis multiómico de datos circadianos
2022

21. Alejandro Paniagua
Máster de Bioinformática, Universidad de Valencia
Evidence-driven annotation of the Trichechus manatus latirostris genome using long-reads
2022

20. Jorge Mestre
Máster de Bioinformática, Universidad de Valencia
SQANTISIM: a simulator of controlled novelty and degradation of transcripts sequenced by long-reads
2022

19. Pedro Salguero
Máster de Bioinformática, Universidad de Valencia
tappAS: marco computacional para el análisis del impacto funcional del splicing alternativo.
2019

18. David Richard Toole

M.S. Microbiology and Cell Science, University of Florida
Picrust2 and Tax4fun2: a comparison of bacterial functional predictions tools in Southwest Florida soils
2018

17. Hector Carmona Salido
Máster de Bioinformática, Universidad de Valencia
Multi-omics integration to elucidate the effects of hyperamonemia in minimal hepatic encephalopathy.
2018

16. Victor Sanchez Gaya
Licenciatura biotecnología, Universidad Politécnica de Valencia
Estudio del efecto de la exposición a pesticidas en el neurodesarrollo mediante la integración de datos ómicos.
2017

15. Francisco Huertas López
Master de Bioinformática, Universidad de Murcia
DNA Methylation and Metagenomic sequencing data integration in a colorectal cancer study.
2017

14. Jordi Martorell
Licenciatura biotecnología, Universidad Politécnica de Valencia
Análisis de expresión alternativa de isoformas en el tiempo mediante datos de RNA-seq.
2015

12. Rodrigo García Valiente
Máster de Bioinformática, Universidad de Valencia
Desarrollo de recursos computacionales para la anotación y caracterización funcional del ARN largo no codificante en especies no modelo.
2015

12. Rafael Hernández de Diego
Licenciatura biotecnología, Universidad Politécnica de Valencia
Caracterización funcional de lncRNAs a partir de datos de NGS.
2012

11. David Jovani Sales
Licenciatura biotecnología, Universidad Politécnica de Valencia
Estudio de la organización funcional de los genes humanos y la regulación de la expresión de sus funciones en distintos tejidos mediante técnicas de secuenciación de nueva generación.
2012

10. Aaron Weimann
Master Program in Bioinformatics, Saarland University (Germany)

Functional Profiling and Quantitative Comparison of Microbial Communities.
2012

9. Federico Jose García López
Licenciatura biotecnología, Universidad Politécnica de Valencia
Desarrollo de un método bioinoformático de integración y visualización de datos de t. transriptómica y metabolómica.
2009

8. Jorge Ruiz Otera
Licenciatura biotecnología, Universidad Politécnica de Valencia
Análisis funcional del splicing alternativo mediante técnicas de ultrasecuenciación.
2010

7. Óscar David Sánchez Jiménez
Departamento de Física Aplicada, Universidad de Valencia
Técnicas del modelado conceptual aplicadas a la información biológica
2007

6. María José Nueda Roldán
Tesina. Politechnical University Valencia, Spain
Departamento de Estadística e Investigación Operativa Aplicadas y Calidad
Métodos estadísticos aplicados a la transcriptómica
2005

5. María Teresa Peralta
Escuela de Ingeniería de Telecomunicaciones
Graduation Project (TFG) Politechnical University Valencia, Spain
Normalización de datos de microarrays
2004

4. Stefan Goetz
Departamento de Física Aplicada
Graduation Project (TFG) Politechnical University Valencia, Spain
Blast2GO: An universal annotation tool for the functional annotation of sequece data
2004

3. Paul Roepman
Graduate Msc student tesis. University of Wageningen, The Netherlands
cDNA microarray analysis. Effects of querciting on colon cancer cells
2002

2. J.J.H.P Bartels
Fontys Hogeschool Eindhove, The Netherlads
The production of linging peroxidase in Aspergillus niger
2000

1. Gerri Weelink
Hogeschool Drenthe, Emmen, The Netherlands
The trans activity of the chloroperoxidase pro-peptide in Aspergillus niger
1999

Teaching

<u>Organization and lecturer at specialized Bioinformatics courses</u>

- Microarray Data Analysis, CIPF, Valencia, March 2008
- Microarray Data Analysis, CIPF, Valencia, March 2009
- Course in Automated Functional Annotation and Data Mining, Valencia, September 2009
- Course in Automated Functional Annotation and Data Mining, Florida, October 2009
- I Jornada de Tecnologías para la Salud, Valencia, November, 2009 (Only lecturer)
- Course in Automated Functional Annotation and Data Mining, Cape Town, December 2009
- Course in Automatic Functional Annotation and Data Mining, Oeiras, May 2010
- Microarray Data Analysis using GEPAS and BABELOMICS, Oeiras, May 2010
- Massive Data Analysis, CIPF, Valencia, June 2010
- Course in Automated Functional Annotation and Data Mining, Valencia, October 2010
- Course in Automated Functional Annotation and Data Mining, Florida, November 2010
- Course in Automated Functional Annotation and Data Mining, Cape Town, December 2010
- Massive Data Analysis, CIPF, Valencia, March 2011
- Course in Automated Functional Annotation and Data Mining, Davis, July 2011
- Course in Automated Functional Annotation and Data Mining, Valencia, October 2011
- Transcriptómica y modelización de proteínas empleando Supercomputación, Castilla y León, November, 2011
- Course in Transcriptome Assembly, Automated Functional Annotation and Data Mining, Oeiras, February 2012
- Course in Automated Functional Annotation and Data Mining, Irapuato. Mexico, May 2012
- Course in Automated Functional Annotation and Data Mining, Davis, July 2012
- Course in Automated Functional Annotation and Data Mining, Valencia, October 2012
- Course in Blast2GO and Babelomics, Portici, Italy, November 2012
- Course in Automated Functional Annotation and Data Mining, Brisbane, Australia, January 2013
- IX International Course of Massive Data Analysis, Valencia, March 2013
- Course in Automated Functional Annotation and RNA-seq, Oeiras, March 2013
- Course in Automated Functional Annotation and Data Mining, Valencia, October 2013
- Course in Automated Functional Annotation and Data Mining, Sao Paulo, November 2013
- Course in RNA-seq and Functional Annotation, Buenos Aires (Argentina), November 2013
- Course in Automated Functional Annotation and Data Mining, La Paz (México), January 2014
- NGS Course in transcriptomics, Cancun (México), April 2016
- Multiomics and Integrative Analysis of Gene Expression, Valencia, January 2017.
- Workshop in Multiomics Data Integration and Technology Transfer, Mexico City, November 2017.

- Bioinformatics III (Multiomics Technologies) at ChroMe ETN Network, Stockholm, December 2017.
- Multiomics and Integrative Analysis of Gene Expression, Valencia, March, 2018.
- Full-Length RNA-Seq Analysis using PacBio long reads: from reads to functional interpretation, Virtual ISMB2020 Conference, July 2020
- Full-Length RNA-Seq Analysis using PacBio long reads: from reads to functional interpretation, Virtual ECCB2020 New Trends in Bioinformatics, September 2020
- PacBio Iso-Seq Workshop Online UCDavis, September 30th – October 2nd, 2020

Regular Teaching

- R for Functional Genomics, University of Florida, 3 Credits, 2015-17
- Human Genetics, University of Florida, 3 Credits, 2017
- Invited lecturer at the Polytechnical University of Valencia, 2004-2007
- Invited lecturer at the Master de Bioinformática, Universidad Complutense Madrid, 2007-2008
- Invited lecturer at the Master de Bioinformática, Universidad Valencia, 2013
- Invited lecturer at the Master de Bioinformática, Universidad Murcia, 2013
- Invited lecturer at the Master de Bioinformática, Polytechnical University of Valencia, 2018
- Member of 32 UF graduate student committees
- Supervisor 10 undergrad student internships, Polytechnic University of Valencia, 2004-2017
- Supervisor 3 undergrad student internships, University of Valencia, 2006-2017
- Supervisor undergraduate student theses, Polytechnic University of Valencia, 2004

Organization of Conferences.

1. Critical Assessment of Microarray Data Analysis Conference 2007 (CAMDA)
2. Jornadas Nacionales de Bioinformática, CIPF, January 2008
3. SeqAhead Workshop on High Performance Computing for Next Generation Sequencing Analysis (HPC4NGS), 2012
4. The Next NGS Challenge Conference, CIPF, May 2013 (Chair)
5. HiTSeq conference within ISMB, Boston (July 2014) and Dublin (July 2015), Orlando (July 2016), Prague (July 2017), Basel (July 2019), Virtual formats (July 2020 and July 2021), Madison (2022)
6. SMODIA2015 Workshop, CIPF, September 2015 (Chair)
7. UF Genetics Institute Symposium 2019-2017
8. Organization Bioinformatics@Valencia, July 2018 (Chair)
9. UF Genetics Institute Symposium, November 2019 (Chair)
10. CSHL Genomics Informatics, November 2019 (Discussion leader)
11. European Conference in Computational Biology 2020 (GENES track chair) and 2022 (Chair Proceedings)

Advisory activity and institutional service

1. Scientific Advisory Board member of the Instituto Biosanitario de Granada, Spain
2. Member of the Scientific Advisory Board of the Interdisciplinary Center for Biotechnological Research, University of Florida
3. Scientific Advisory Board member of the Informatics Institute, University of Florida
4. Scientific Advisory Board member of the Bioinformatics Core ICBR, University of Florida

5. Scientific Advisory Board member of the Scientific Computing Program, University of Florida
6. Scientific Advisory Board member of the French Bioinformatics Institute (IFB).
7. Committee member Juan de la Cierva Postdoctoral awards, Spanish Ministry of Economy and Competitiveness, 2016
8. Panel Member at the "Relationship between genome and epigenome" Workshop organized European Commission's Directorate General for Research and Innovation (DG RTD) and Cooperation in Science and Technology (COST), Brussels, 14th-15th February 2013.
9. Panel Member at the "Big data in health research: an EU action plan" Workshop organized European Commission's Directorate General for Research and Innovation (DG RTD), Luxemburg 30th October 2015.
10. Evaluation Committee member BioExcel H2020 project 2016-2017
11. Member Biotechnology Evaluation Committee Plan Nacional (Spain), 2017
12. Member NSF Advances in Biological Informatics (ABI) Career Panel, 2017
13. Senior Programme Committee Member as HiTSeq COSI Chair, ISMB Conference 2018
14. Member of Barcelona Supercomputing Center Access Committee, 2017-2019
15. Member of Scientific Committee of I2SysBio, from 2022
16. Member of HPC Advisory Committee of I2SysBio, from 2022
17. Chair of Sustainability Committee of I2SysBio, from 2022
18. Evaluator for EU ESFRI Landmarks projects, 2023
19. Scientific Advisory Board member of IMAGING VLC, 2023
20. Expert Evaluator of the EU ESFRI Landmark Elixir, 2023
21. Scientific Advisory Board Member of the Plant Biotechnology and Genomics Center (Centro de Biotecnología y Genómica de Plantas, CBGP, UPM-INIA/CSIC), 2023
22. Expert Evaluator of the Department of Molecular Life Sciences, University of Zurich, 2023.
23. Chair of GreenISCB, from 2023

Membership

1. International Society of Computational Biology (ISCB)
2. Green Science Working Group ISCB
3. Chair HitSeq
4. Sociedad Iberoamericana de Bioinformática (SoiBio)
5. Sociedad Española de Biotecnología (Sebio)
6. GOBLET, global organization for Bioinformatics training
7. American Association for Advance in Science

Reviewer and editor activities

<u>Reviewer of journals</u>: Nature Methods, Nature Protocols, Nature Biotechnology, Scientific Reports, Nature Communications, Genome Research, Genome Biology, Bioinformatics, BMC Bioinformatics, BMC Systems Biology, BMC Genomics, BMC Research Notes, BMC Neuroscience, PLoS ONE, Nucleic Acid Research, Genomics, Journal of Genomics, Journal of Chemometrics, Bioinformatics and Biology insights, JZUS-B (Biomedicine & Biotechnology), International Journal of Plant Genomics.

Reviewer for funding agencies: ANEP (Spain), The Executive Agency for Higher Education, Research, Development and Innovation Funding (Romania), European Commission, European COST Action, Natural Environment Research Council (UK), Institute of Computer Science Foundation for Research & Technology-Hellas (FORTH) (Greece), UK Fight for Sight, Argentina Science, Technology and Productive Innovation Agency, National Science Foundation (USA), National Institutes of Health (NIH), Alzheimer Research UK, NWO The Netherlands, European Science Foundation, French National Research Agency (France), Novo-Nordisk Foundation Center for Biosustainability (Denmark), King Abdullah University of Science and Technology (South Arabia)

Reviewer at Conferences: CAMDA, Jornadas de Bioinformática, Bioinformatics Italy 2012, Bioinformatics 2014, ISMB conferences, Genome Informatics

Editorial Commitments

- Associated Editor of Scientific Data (Nature publishing)
- Associated Editor of Genes (MDPI-Open Access)
- Associated Editor of G3
- Editor of Scientific Data Multiomics Collection (Nature publishing)
- Editor of BMC System Biology Special Issue in Data Integration (BioMed Central)
- Editor of BMC Bioinformatics Special Issue in Multiomics analysis (BioMed Central)
- Guest Editor of Genome Research Special Issue in Long reads Methods (2023)