

Ana Conesa, PhD

Synopsis

Publications: 123 Citations ¹ : > 22,000 h-index ¹ : 48 Conference Talks: 90	Projects as PI: 32 Lead-PI @ Multi-PI: 5 Total raised ~11M\$	PhD thesis completed: 6 Group members in the last 5 years: 31 Visiting students/post-docs last 5 years: 64 Active collaborations: 25 labs
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Scientific statement

I am Professor of Bioinformatics at the Microbiology and Cell Science Department of the University of Florida in Gainesville. 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). After a short appointment as bioinformatics project leader at the same institute, 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. In August 2014 I was recruited by the University of Florida through their Pre-eminence program to strengthen bioinformatics research and education at UF. I combined this appointment with my CIPF affiliation until August 2018.

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 thousand users world-wide. I have published over 120 research papers that have received more than 20,000 citations and I have an h-index of 46. My labs are well funded through private, national and international funding agencies including H2020, Marie Curie, NIH and USDA. I am leading PI of several EU and USA consortium projects: the STATegra (11 partners) project on multiomics data integration and the Marie Curie Action DEANN for creating a NGS network with American countries (16 partners). I am WP4 leader in ChromE Marie Curie ITN (12 partners) and I lead 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. My CIPF group was nominated the Valencia Node of the Spanish National Bioinformatics Institute (INB). I serve as scientific advisor in several European and USA scientific institutions, as associate editor of different specialized journals and as reviewer at research agencies world-wide.

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.

¹ Source: Google Scholar

Current scientific appointments

Pre-eminence Professor in Bioinformatics
Microbiology and Cell Science Department
University of Florida at Gainesville
aconesa@ufl.edu

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 *Leiden, The Netherlands*
Ph.D. Molecular Microbiology, June 2001.
Thesis: *Overproduction of Peroxidases by Filamentous Fungi.*
- Polytechnic University of Valencia *Valencia, Spain*
Agricultural Engineering Degree
Graduation Project: *Development of a plant breeding program in common bean (Phaseolus vulgaris)*
- 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)
Research Fellowship at the Valencia Institute for Agricultural Research (1992)
Erasmus Fellowship for international mobility of undergraduate students (1991)
- Positions** 2014-present, *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: Arjan Schot

1993-1994: *Institute for Plant Breeding (CPRO) Wageningen, The Netherlands*

Research Fellow at Molecular Flowering Department

Microsatellite markers in lilies

Supervisor: Hans Sandbrink

Software Developed

Functional Annotation

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)

Quality Control in NGS

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)

Statistical analysis of gene expression

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)

Multiomics data analysis

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)

MuliBac: Batch correction across omics (R package)

Funding as PI

Current

- 26.** 19-EXO19-0029 01.Feb.2020-31.Jan.2022
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**

Past

- 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 Aarhus (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

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

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

Pathogenomics: Development of transcriptional networks regulating virulence in filamentous fungi

Role: **PI**

1. BIO2008-05266-E/

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**

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| <p>4. Slovenian Institute of Biology
<i>Analysis and annotation of Solanum tuberosum Pacbio data</i>
Role: PI</p> | <p>01.Oct.2017</p> |
| <p>3. IGENOMIX
<i>Identificación de factores secretados y vinculados a alteraciones cromosómicas en embriones pre-implantacionales</i>
Role: PI</p> | <p>01.Oct.2014</p> |
| <p>2. IMEGEN
<i>Consulting RNA-seq data analysis</i></p> | <p>14.Mar.2014</p> |
| <p>1. ROSLIN Institute
Functional annotation of microarray data in livestock</p> | <p>08.Jun.2009</p> |

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](http://www.genometra.com)). The company ceased activity in 2018.

Publications

2020

129. *Newly assessed unconventional antimicrobial compounds for the control of Liberibacter asiaticus, the causative agent of citrus greening disease.*
Christopher L. Gardner, Danilo R. da Silva, Fernando A. Pagliai, Lei Pan, Kaylie A. Padgett-Pagliai, Ryan A. Blaustein, Marcelo L. Merli, Dan Zhang, Cécile Pereira, Max Teplitski, Jose X. Chaparro, Svetlana Y. Folimonova, **Ana Conesa**, Salvador Gezan, Graciela L. Lorca, Claudio F. Gonzalez.
Scientific reports, *Submitted*
128. *tappAS: a comprehensive computational framework for the analysis of the functional impact of differential splicing.*
Lorena de la Fuente¹, Ángeles Arzalluz-Luque, Manuel Tardáguila, Héctor del Risco, Cristina Martí, Sonia Tarazona, Pedro Salguero, Raymond Scott, Alberto Lerma, Ana Alastrue-Agudo, Pablo Bonilla, Jeremy R.B. Newman, Shunichi Kosugi, Lauren M. McIntyre, Victoria Moreno-Manzano, **Ana Conesa**

Genome Biology, *Revision submitted*.

- 127.** *Integrative analyses of TEDDY Omics data reveal lipid metabolism abnormalities, increased intracellular ROS and heightened inflammation prior to autoimmunity for type 1 diabetes.*
Leandro Balzano-Nogueir, Ricardo Ramirez, Tatyana Zamkovaya, Jordan Dailey, Alexandria N. Ardisson, Srikar Chamala, Michael J. Haller, Patrick Concannon, Mark A. Atkinson, Desmond A. Schatz, Eric W. Triplett, **Ana Conesa**.
Nature Communications, *under review*.
- 126.** *GAIT-GM: Galaxy tools for modelling metabolite changes as a function of gene expression.*
Lauren M. McIntyre, Francisco Huertas, Olexander Moskalenko, Marta Llansola, Vicente Felipo, Alison M. Morse, **Ana Conesa**.
Genomics, Proteomics and Bioinformatics, *submitted*.
- 125.** *Harmonization of Quality Metrics and Power Calculation in Multi-Omic Studies.*
Sonia Tarazona, David Gómez-Cabrero, Andreas Schmidt, Axel Imhof, Thomas Hankemeier, Jesper Tegnér, Johan A. Westerhuis, **Ana Conesa**.
Nature Communications, *second revision*.
- 124.** *MOSim: MultiOmics Simulation in R.*
Carlos Martínez, **Ana Conesa***, Sonia Tarazona.
BiorXiv 2018. <https://doi.org/10.1101/421834>. *Corresponding author
- 123.** *A multi-omics dataset of heat-shock response in the yeast RNA binding protein Mip6.*
Carmen Nuño, Manuel Ugidos, Sonia Tarazona, Alberto Ferrer, Susana Rodríguez-Navarro, **Ana Conesa**.
Scientific Data, 2020;7(1):69. Published 2020 Feb 27. doi:10.1038/s41597-020-0412-z.
- 122.** *MultiBaC: a strategy to remove batch effects from different omic data type.*
Ugidos M, Tarazona S, Prats-Montalbán JM, Ferrer A, **Conesa A**.
Statistical Methods in Medical Research. Published 2020 March 4
<https://doi.org/10.1177/0962280220907365>

2019

- 121.** *Making multi-omics data accessible to researchers.*
Ana Conesa, Stephan Beck.
Scientific Data, 2019 6:251. <https://doi.org/10.1038/s41597-019-0258-4>
- 120.** *Large expert-curated database for benchmarking document similarity detection in biomedical literature search.*
Brown P, RELISH Consortium (**Conesa, A**), Zhou Y.
Database, 2019, 1–67 doi: 10.1093/database/baz085
- 119.** *Mip6 binds directly to the Mex67 UBA domain to maintain low levels of Msn2/4 stress dependent mRNAs.*
Manuel Martín-Expósito, M^a Eugenia Gas, Nada Mohamad, Carme Nuño-Cabanes, Pau Pascual-García, Lorena de la Fuente, Belén ChavesArquero, Jonathan Merran, Jeffry Corden, **Ana Conesa**, José Manuel Pérez-Cañadillas, Jerónimo Bravo and Susana Rodríguez-Navarro
EMBO reports 2019, e47964

- 118.** *A Multiomic Study To Unravel The Effects Of Developmental Exposure To Endosulfan In Rats Molecular Explanation For Sex-Dependent Effects.*
Sonia Tarazona, Elena Bernabeu, Héctor Carmona, Belén Gómez-Giménez, Javier García-Planells, Pim Leonards, Stephan Jung, **Ana Conesa***, Vicente Felipo, Marta Llansola.
ACS Chem Neurosci. 2019 Sep 10. doi: 10.1021/acschemneuro.9b00304 (* Corresponding author)
- 117.** *STATegra: a comprehensive multi-omics dataset of B-cell differentiation in mouse.*
David Gomez-Cabrero, Sonia Tarazona, Isabel Ferreirós-Vidal, Ricardo N. Ramirez, Carlos Company, Andreas Schmidt, Theo Reijmers, Veronica von Saint Paul, Franscesco Marabita, Javier Rodríguez-Ubreva, Antonio Garcia-Gomez, Thomas Carroll, Lee Cooper, Ziwei Liang, Gopuraja Dharmalingam, Leandro Balzano-Nogueira, Vincenzo Lagani, Ioannis Tsamardinos, Michael Lappe, Dieter Maier, Johan A. Westerhuis, Thomas Hankemeier, Axel Imhof, Esteban Ballestar, Ali Mortazavi, Matthias Merckenschlager, Jesper Tegner, **Ana Conesa.**
Scientific Data, 2019, doi:10.1038/s41597-019-0202-7.
- 116.** *Building gene regulatory networks from scATAC-seq and scRNA-seq using Linked Self-Organizing Maps.*
Camden Jansen, Ricardo N. Ramirez, Nicole C. El-Ali, David Gomez-Cabrero, Jesper Tegner, Matthias Merckenschlager, **Ana Conesa**, Ali Mortazavi.
PLoS Computational Biology 15(11) e1006555. <https://doi.org/10.1371/journal.pcbi.1006555>
- 115.** *Differential modulation of Quorum-Sensing signaling through QsIA in Pseudomonas aeruginosa strains PAOI and PAI4.*
Sana T, Lomas R, Gimenez M, Laubier A, Soscia C, Chauvet C, **Cones A**, Voulhoux R, Iz D, Bleves S.
Journal of Bacteriology, 2019 Aug 12. pii: JB.00362-19
- 114.** *Feedforward regulation of Myc coordinates lineage-specific with housekeeping gene expression during progenitor cell differentiation.*
Ferreirós-Vidal I, Carroll T, Zhang T, Lagani V, Ramirez RN, Ing-Simmons E, Gómez-Valadés AG, Cooper L, Liang Z, Papoutsoglou G, Dharmalingam G, Guo Y, Tarazona S, Fernandes SJ, Noori P, Silberberg G, Fisher AG, Tsamardinos I, Mortazavi A, Lenhard B, **Conesa A***, Tegner J*, Merckenschlager M*, Gomez-Cabrero D.
PLoS Biol. 2019 Apr 12;17(4):e2006506 (* Corresponding authors)
- 113.** *Differences in gene expression profiling and biomarkers between histological colorectal carcinoma subsets from the serrated pathway.*
García-Solano J, Turpin-Sevilla MDC, García-García F, Carbonell-Muñoz R, Torres-Moreno D, **Conesa A**, Conesa-Zamora P.
Histopathology. 2019 Apr 26. doi: 10.1111/his.13889.

2018

- 112.** *Elucidating the role of chromatin state and transcription factors on the regulation of the Yeast Metabolic Cycle: a multi-omic integrative approach.*
Sánchez-Gaya V, Casaní Galdón S, Ugidos M, Kuang Z, Mellor J, **Conesa A**, Tarazona S.
Front. Genet., 30 November 2018 | <https://doi.org/10.3389/fgene.2018.00578>.
- 111.** *Transcriptional profiling of the mutualistic bacterium Vibrio fischeri and a hfq mutant under modeled microgravity.*

Alexandrea A. Duscher, **Ana Conesa**, Mary Bishop, Sergio D. Zubrizarreta, and Jamie S. Foster
Nature Microgravity 4, Article number: 25 (2018).

110. *Changes in the uterine metabolome of the cow during the first seven days after estrus.*
Tribulo P, Balzano L, **Conesa A**, Siqueira L, Hansen PJ.
Molecular Reproduction and Development, 2018, DOI: 10.1002/mrd.23082
109. *Two histologically colorectal carcinomas subsets from the serrated pathway show different methylome signatures and diagnostic biomarkers.*
García-Solano J, Turpin MC, Torres-Moreno D, Eduardo Estrada, Huertas-López F, Toumisto A, Makinen MJ, **Conesa A**, Conesa-Zamora P.
Clinical Epigenetics. 2018; 10: 141.
108. *Tumor Microenvironment-Targeted poly-L-glutamic acid-based Combination Conjugate for Enhanced Triple Negative Breast Cancer Treatment.*
Juan J Arroyo-Crespo, Ana Armiñan, David, Charbonnier, Leandro Balzano-Nogueira, Francisco Huertas-López, Cristina Marti, Sonia Tarazona, Jeronimo Forteza, **Ana Conesa**, María J. Vicent.
Biomaterials, Volume 186, December 2018, Pages 8-21.
107. *Gene expression profile and molecular pathway datasets resulting from benzo(a)pyrene exposure in the liver and testis of adult tilapia.*
Colli Dula RC, Fang X, Moraga-Amador D, Albornoz-Abud N, Zamora-Bustillos R, **Conesa A**, Zapata-Perez O, Moreno D, Hernandez-Nuñez E.
Data in brief, 2018 Sep 5;20:1500-1509.
106. *Overexpression of the vascular brassinosteroid receptor BRL3 confers drought resistance without penalizing plant growth.*
Fàbregas N, Lozano-Elena F, Blasco-Escámez D, Tohge T, Martínez-Andújar C, Osorio S, Bustamante M, Riechmann JL, **Conesa A**, Pérez-Alfocea F, Fernie A, Caño-Delgado A.
Nature Communications, volume 9, Article number: 4680 (2018).
105. *Event Analysis: using transcript events to improve estimates of abundance in RNA-seq data.*
Newman J, Concannon P, Tardaguila M, **Conesa A***, McIntyre L*.
G3 (Bethesda). 2018 Jul 18. pii: g3.200373.2018. doi: 10.1534/g3.118.200373
104. *Transcriptome Analysis Reveals Novel Insights Into the Response of Low-dose Benzo(a)pyrene Exposure in Male Tilapia.*
Colli Dula R, **Conesa A**, Moraga-Amador D, Moreno D, Albornoz-Abud N, Zapata-Perez O, Zamora-Bustillos R, FangX.
Aquatic Toxicology, 201 (2018) 162-173.
103. *Comparative Metagenomics Provides Insight into the Ecosystem Functioning of the Shark Bay Stromatolites, Western Australia.*
Babilonia J, Foster JS, **Conesa A**, Casaburi G, Pereira C, Louyakis A, Reid RP
Frontiers in Microbiology, 25 June 2018. <https://doi.org/10.3389/fmicb.2018.01359>
102. *Evidence of the Red-Queen hypothesis from accelerated rates of evolution of genes involved in biotic interactions in Pneumocystis.*
Delaye L, Ruiz-Ruiz S, Calderon E, Sonia Tarazona S, **Conesa A**, Moya A.
Genome Biol Evol. 2018 Jun 1;10(6):1596-1606

101. *Single-cell RNA-seq for the study of isoforms: how is that possible?*
Arzalluz-Luque A, **Conesa A**.
Genome Biology, 2018 19:110. <https://doi.org/10.1186/s13059-018-1496-z>.
100. *Integration of Multiomics data for Time Course Experiments*
Tarazona S, Balzano-Nogueira L, **Conesa A**
In: Comprehensive Analytical Chemistry, Volume 82, 2018, Pages 505-532.
99. *PaintOmics 3: a web resource for the pathway analysis and visualization of multi-omics data.*
Hernandez-de-Diego R, Tarazona S, Martinez-Mira C, Balzano-Nogueira L, Furió-Tarí P, Pappas G, **Conesa A**.
Nucleic Acid Research, May 25th 2018. <https://doi.org/10.1093/nar/gky466>
98. *The SAGA/TREX-2 subunit Sus1 binds widely to transcribed genes and affects mRNA turnover globally.*
García-Moliner V, García-Martínez J, Reja R, Furió-Tarí P, Antúnez O, Vinayachandran V, **Conesa A**, Pugh BP, Pérez-Ortín JE and Rodríguez-Navarro S.
Epigenetics Chromatin. 2018 Mar 29;11(1):13. doi: 10.1186/s13072-018-0184-2.
97. *SQANTI: extensive characterization of long read transcript sequences for quality control in full-length transcriptome identification and quantification.*
Tardaguila M, de la Fuente L, Marti C, Pereira C, del Risco H, Ferrell M, Mellado M, Macchietto M, Verheggen K, Edelmann M, Ezkurdia I, Vazquez J, Tress M, Mortazavi A, Martens L, Rodríguez-Navarro S, Moreno-Manzano V and **Conesa A**.
Genome Research, 2018. February 9, 2018, doi:10.1101/gr.222976.117.
- 2017
96. *GRAM-CNN: a deep learning approach with local context for named entity recognition in biomedical text.*
Zhu Q, Li X*, **Conesa A***, Pereira C.
Bioinformatics. 2017 Dec 20. doi: 10.1093/bioinformatics/btx815. * Corresponding author.
95. *Growth of Chlamydia pneumoniae is enhanced in cells with impaired mitochondrial function*
Käding N, Kaufhold I, Müller C, Szaszak M, Shima K, Weinmaier T, Lomas R, **Conesa A**, Schmitt-Kopplin P, Rattei T, Rupp J.
Frontiers in Cellular and Infection Microbiology. 2017 Dec 5; 7: Art. 499.
94. *Disease-specific biases in alternative splicing and tissue-specific dysregulation revealed by multi-tissue profiling of lymphocyte gene expression in type 1 diabetes.*
Newman JRB, **Conesa A**, Mika M, New FN, Onegut-Gumuscu S, Atkinson MA, Rich SS, McIntyre LM, Concannon P.
Genome Res. 2017 Nov;27(11):1807-1815.
93. *Identification and visualisation of differential isoform expression in RNA-seq time series.*
Nueda MJ, Martorell-Marugan J, Marti C, Tarazona S, **Conesa A**.
Bioinformatics. 2017 Sep 14. doi: 10.1093/bioinformatics/btx578.
92. *A benchmarking of workflows for detecting differential splicing and differential expression at isoform level in human RNA-seq studies.*
Merino GA, **Conesa A***, Fernandez EA*

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Conesa A, van De Velde F, van Rantwijk F, Sheldon RA, van Den Hondel CA, Punt PJ.
 J Biol Chem. 2001 May 25;276(21):17635-40.
1. *Studies on the Production of Fungal Peroxidases in Aspergillus niger*
Conesa A, van den Hondel CA, Punt PJ.
 Appl Environ Microbiol. 2000 Jul;66(7):3016-23.

Conferences and Seminars

90. *Bioinformatics tools for multi-omics integration and single molecule sequencing: application to human disease.*

(invited)

Topics in Cancer Seminar Series

Gainesville, December 6th, 2019

89. *Tools for transforming multi-omics data into disease models.*

(selected talk)

Advances in Computational Biology

Barcelona, November 28th, 2019

88. *From Long Reads to Transcript Function: Bioinformatics Tools for Iso-Transcriptomics Analysis*

(keynote)

North America PacBio Users Group Meeting

Delaware University, September 25th, 2019

87. *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

86. *Multiomics approaches to model development and disease*
(invited)

Institute for Integrative Systems Biology (I2SysBio)

Valencia, July 16th, 2019

85. *Multiomics and Third Generation Sequencing: at the forefront of genomics research*
(invited)

Barcelona Supercomputing center (BSC)

Barcelona, June 11th, 2019

84. *Multiomics and Third Generation Sequencing: at the forefront of genomics research*
(invited)

Centre for Research in Agro Genomics (GRAG)

Barcelona, June 11th, 2019

83. *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

82. *Multiomics and Third Generation Sequencing: at the forefront of genomics research*
(invited)

Animal Science Program, University of Florida

Gainesville, April 22th, 2019

81. *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

80. *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.

79. *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.

78. *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.

77. *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.

76. *Bioinformatics and Statistical Approaches for the Integration of Metabolomics and Transcriptomics Data (invited lecture).*

2018 SECIM Metabolomics Symposium

Gainesville, Florida, April 26th 2018.

75. *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

74. *SQANTI and TAPPAS: Making sense of Iso-seq data (invited lecture).*

SMRT Informatics Developers Conference @ PAG XVXXI

San Diego, January 17th 2018

73. *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

72. *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

71. *Unravelling novel transcriptome functional features*

Conference Lectures of the Bioinformatics Master of the University of Murcia

University of Murcia, May 19th, 2017.

70. *Multiblock integration of T1D gene expression and metabolomics data to study T1D progression*

TEDDY fall meeting

Tysons Corner, Virginia, November 8th, 2016.

69. *Developing statistical approaches for the integration of multi-omics data. (invited lecture)*

Frontiers in Genomics Program. Universidad Autónoma de Mexico.

Cuernavaca, 24th October 2016

68. *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

67. Functional Analysis at Isoform Resolution.

Pacbio industrial workshop. XXIV Plant and Animal Genome Conference

San Diego, California 12th January 2016.

66. 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

65. 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

64. Lessons and results of multi-omics data analysis (keynote speaker)

JOBIM 2015

Clermont-Ferrand, 6th- 9th July 2015

63. 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

62. STATegra: Statistical and Bioinformatics Resources for Analysis of Multi-Omics Projects

5th NGS Conference (distinguished speaker)

Boston, USA, 21st-22nd May 2015

61 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

59. 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

58. The STATegra NGS Experiment Management System

Computer Demo Session, **Plant and Animal Genome Conference XXIII**

San Diego, 14th January 2015

57. Functional Annotation of a mouse neural differentiation process (keynote speaker)

Australian Bioinformatics Conference

Melbourne, Australia, 11th October 2014

56. *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**

55. 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

54. 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

53. Nuevos retos de la medicina personalizada (invited conference)

MIT EmTech Valencia

Valencia, 5th November 2013

52. The STATegra project: new statistical methods and tools for integrative omics data analysis (invited seminar).

ALLBIO Meeting

Uppsala, 7th-8th October 2013

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

ISCB/GOBLET Meeting

Berlin 19th July 2013

50. The STATegra project: new statistical methods and tools for integrative omics data analysis (invited seminar).

Workshop in Translational Genomics

Barcelona, 26th April 2013

49. Pathway-based linear models (invited conference)

SeqAhead/STATegra High throughput and data integration workshop

Barcelona, 15th February 2013

48. Analysis of Fungal Transcriptomics with CLC Genomics Workbench and Blast2GO.

XXI Plant and Animal Genome Conference (invited conference)

San Diego, 15th January 2013

47. Transcriptome analysis with RNAseq: promises and biases (invited seminar)

Department of Genetics, Stanford University
Stanford, 28th September 2012

46. 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

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

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

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

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

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

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

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

38. Functional Genomics in the Next Generation Sequencing Era.
Conferencia de la Sociedad Española de Bioquímica y Biología Computacional.
Barcelona, 7th September 2011

37. 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

36. *Differential expression in RNASeq: a matter of depth* (conference)

Critical Assessment of Massive Data Analysis (CAMDA) 2011

Austria Center Vienna, 15th July 2011

35. *Ontología Génica y Anotación Funcional* (seminar)

AECID CYDET Curso Bioinformática y Genómica Vegetal

Cartagena de Indias, Colombia, 11th-13th July 2011

34. *Differential expression in RNAseq Studies* (seminar)

Practical Course on Bioinformatics and Network Biology.

Centro de Investigación del Cáncer, Salamanca, Spain, 23rd June 2011

33. *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

32. *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

31. *Differential expression with RNASeq: length and depth does matter* (conference)

Bioinformatics and High Throughput Sequencing 2011

Institute Pasteur Paris, France, 22nd March 2011

30. *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

29. *Biología cuantitativa ¿cuántos son dos más dos?* (conference)

Departamento de Matemáticas

Universitat de València, Spain, May 2010

28. *Pathway Analysis of Transcriptomics Data* (conference)

IX Jornadas Nacionales de Bioinformática

Calouste Gulbenkian Foundation, Lisbon, Portugal, 4th November 2009

27. *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

26. *Pathway Analysis of Transcriptomics Data* (conference)

XII Conferencia Española de Biometría

Universidad de Cádiz, Spain, 24th September 2009

25. *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

24. *B2G-FAR: The Blast2GO Functional Annotation Repository* (computer demo)

Plant and Animal Genome Conference, XVII

San Diego, USA, 14th January 2009

23. *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

22. *Finding relationships between high throughput data sources through multiway projection methods* (seminar)

MIPS, University of Munich

Munich, Germany, 4th March 2008

21. *Systems Level Analysis of Time Course Omics Data* (seminar)

Department of Statistics, University of Barcelona

Barcelona, Spain, November 2008

20. *Systems Level Analysis of Time Course Omics Data* (conference)

(EMBnet) Conference 2008: 20th Anniversary Celebration

Martina Franca, Italy, 19th September 2008

19. *Functional Genomics: Concepts, Databases and Methods* (seminar)

First International Course in Environmental Genomics

DISAV, University of Piemonte Orientale, Italy, 15th December 2008

18. *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

17. *Finding relationships between high throughput data sources through multiway projection methods* (conference)

Jornadas Nacionales de Bioinformática

Centro de Investigaciones Príncipe Felipe, 13th February 2008

16. *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

15. *High throughput functional annotation and analysis with the Blast2GO suite* (seminar)

EMBRACE Gene Ontology Workshop,
University of Bari, Italy 7th-9th November 2007

14. *Multi-way methods for integrating data and knowledge in genomics research* (conference)

XI Conferencia Española y Primer Encuentro Iberoamericano de Biometría
Universidad de Salamanca, Spain, 21st June 2007

13. *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

12. *Bioinformática en genómica vegetal: anotación de funciones génicas y análisis de respuestas transcripcionales* (seminar)

University of Malaga
Málaga, Spain, 4th May 2007

11. *Anotación funcional de secuencias en especies no modelo* (seminar)

Introduction to Bioinformatics
University of Alicante, Spain 19th December 2007

10. *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

9. *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

8. *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

7. *Applications of microarray technology to address biological questions* (seminar)

Instituto de Productos Lácteos de Asturias
Oviedo, Spain, 2005

6. *Analysis and interpretation of genome wide datasets: from sequence to function to biology* (seminar)

School of Biosciences, University of Birmingham

Birmingham, UK, 2005

5. *Finding significant differential gene expression profiles through maSigPro* (seminar)

Departamento de Estadística, Universidad de Barcelona

Barcelona, Spain, 2005

4. *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

3. *Functional genomics in citrus or the bioinformatics of non model species* (seminar)

TNO Nutrition and Food Research,

Zeist, The Netherlands, 3rd November 2005

2. *Blast2GO* (conference)

Gene Ontology Users Meeting

Bergen, Norway, 14th September 2005

1. *Blast2GO y maSigPro: herramientas bioinformáticas para Genómica Funcional en Investigación Agraria* (conference)

Segunda reunión de la red valenciana de genómica y proteómica

IATA, Valencia, 28th October 2004

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, submitted.
8. **Manuel Guerrero Ugidos.** *Desarrollo de métodos estadísticos para la Biología de Sistemas multiómica.* Universitat Politècnica de València, in progress.
9. **Francisco José Pardo Palacios.** *Desarrollo de métodos bioinformáticos y experimentales para el estudio del impacto funcional de las isoformas alternativas.* Universitat Politècnica de València, in progress.
10. **María Teresa Rubio Martínez-Abarca.** *Métodos de integración de datos multiómicos para el estudio de enfermedades.* Universitat Politècnica de València, in progress.

11. **Salvador Casaní Gabaldón.** *Bioinformatics methods to link metabolic and epigenetic regulation.* Universitat València, in progress.
12. **Tatyana Zamkovaya.** *Network analysis of Microbial Dark Matter.* University of Florida, in progress

Teaching

Organization and lecturer at specialized Bioinformatics courses

- 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
- Course in Automated Functional Annotation and Data Mining, Cape Town, December 2009
- Course in Automated Functional Annotation and Data Mining, 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
- Course in Transcript Assembly-Automated Functional Annotation and Data Mining, Oeiras, February 2011
- 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
- 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
- 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.

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 Technical University of Valencia, 2005
- Invited lecturer at the Master de Bioinformática, Universidad Complutense Madrid, 2005
- 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
- Director of over 30 graduation projects of Biotechnology, Biology, Bioinformatics and Computer Science.

Organization of Conferences.

1. Critical Assessment of Microarray Data Analysis Conference 2007 (CAMDA)
2. Jornadas Nacionales de Bioinformática, CIPF, January 2008
3. The Next NGS Challenge Conference, CIPF, May 2013 (Chair)
4. HiTSeq conference within ISMB, Boston (July 2014) and Dublin (July 2015), Orlando (July 2016), Prague (July 2017), Basel (July 2019)
5. SMODIA2015 Workshop, CIPF, September 2015 (Chair)
6. UF Genetics Institute Symposium 2019 2017
7. Organization Bioinformatics@Valencia, July 2018 (Chair)
8. UF Genetics Institute Symposium, November 2019 (Chair)
9. CSHL Genomics Informatics, November 2019 (Discussion leader)

Advisory activity

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 Study Section 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. Discussion Leader Genome Informatics CSHL Conference 2019
15. Genes Session Chair, ECCB 2020 Conference

Membership

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

Reviewer and editor activities

Reviewer of journals: 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), Natural Environment Research Council (UK), Institute of Computer Science Foundation for Research & Technology-Hellas (FORTH) (Greece), National Science Foundation (USA), National Institutes of Health (NIH), Alzheimer Research UK, NWO The Netherlands.

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

Editorial Commitments

- Editor of Scientific Data (Nature publishing)
- Editor of Genes (MDPI-Open Access)
- 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)