

Proyecto: Novel methodologies for multi-omics integrative analysis with cutting-edge sequencing technologies (novelMO)

Plaza ofertada: Ayudas para contratos predoctorales para la formación de doctores

Código de la plaza ofertada: PFI2024 - novelMO (PID2023-152976NB-I00)

Descripción del proyecto:

La comunidad de genómica ha ido adoptando enfoques multiómicos (MO) para estudiar sistemas biológicos complejos y modelar circuitos reguladores. Los avances en tecnologías de secuenciación ofrecen mediciones a nivel de célula individual (SC) con resolución espacial (ST), y la Secuenciación de Tercera Generación (TGS) permite el análisis de moléculas largas individuales. Estas innovaciones se están integrando rápidamente para investigar redes reguladoras específicas de tipo celular, resueltas espacialmente. Aunque existen numerosos métodos para analizar datos MO NGS, las técnicas para SC, ST o TGS para MO todavía están en desarrollo.

El objetivo del proyecto novelMO es desarrollar nuevos métodos estadísticos y herramientas bioinformáticas para analizar datos MO de SC, ST y TGS para entender mejor la regulación del ARN. Nuestra idea es crear nuevas metodologías o modificar los existentes para construir redes reguladoras de múltiples capas, teniendo en cuenta los aspectos únicos de los datos de célula individual. Además, planeamos integrar datos de transcriptómica espacial en estos marcos reguladores MO y desarrollar métodos novedosos para el análisis de datos de MO de molécula única. Finalmente, incorporaremos estos nuevos métodos en paquetes de R o Python, y los implementaremos en nuestras suites existentes de PaintOmics y tappAS, mejorando su facilidad de uso y accesibilidad para una amplia gama de usuarios y tecnologías.

Palabras clave: multi-ómica, single cell, long reads, spatial transcriptomics, bioinformática

Plan de formación:

El estudiante pre-doctoral se incorporará a un equipo constituido por dos grupos de investigación, que son co-IPs del proyecto novelMO: el grupo de Genómica de la Expresión Génica en el I2SysBio (liderado por la Dra. Ana Conesa) y el grupo BiostatOmics de la UPV (liderado por la Dra. Sonia Tarazona) para desarrollar su tesis en el contexto de la generación de nuevas herramientas bioinformáticas para el análisis de datos multi-ómicos de secuenciación de célula única, transcriptómica espacial y/o lecturas largas.

Las dos co-IPs del proyecto han colaborado durante muchos años en diversos proyectos y su colaboración ha dado como fruto importantes resultados científicos gracias a la complementariedad de su formación y experiencia investigadora. A continuación se resume el historial científico-técnico de ambas, sus líneas de investigación y los principales proyectos en los que están participando.

CVA Dra. Conesa

Section A. PERSONAL DATA

Name and Surname	Ana Victoria Conesa Cegarra		
DNI	22973218J	Age	56
Researcher's identification number	Researcher ID	A-9559-2014	
	ORCID	0000-0001-9597-311X	

A.1. Current professional situation

Institution	Spanish National Research Council		
Dpt. / Centre	Institute for Integrative Systems Biology		
Address	Catedrático Agustín Escardino 9, Paterna, Spain		
Phone	+34963544771	Email	ana.conesa@cisc.es
Professional category	Research Professor	Start date	2021
Keywords	Bioinformatic, multi-omics, long-read sequencing		

A.2. Academic education (Degrees, institutions, dates)

Bachelor/Master/PhD	University	Year
Molecular Microbiology	University of Leiden	2001
Agricultural Engineering Degree	Polytechnic University of Valencia	1993

A.3. General quality indicators of scientific production

Publications: **164**; Citations [Google Scholar]: aprox.**40,000**; h-index [Google Scholar]: **62**; Software tools created: **22**. Conference Talks: **151**; Projects as PI: **40**; Lead-PI at Multi-PI projects: **12**; Total raised funds ~**15M\$**. PhD thesis completed: **13**; in progress: **9**.

Section B. SUMMARY OF THE CURRICULUM

I am Research Professor at the Institute for Integrative Systems Biology (CSIC) and *courtesy professor* at the University of Florida (USA). I currently hold positions as Director of the I2SysBio Theoretical and Computational Systems Biology Programme, Coordinator of the CSIC network for Computational Biology and Bioinformatics, member of the CSIC VIDA committee, and member of the Board of Directors of the International Society for Computational Biology. Moreover, I am Member of the Spanish Royal Academy of Engineering, Honorary Member of the Spanish Society for Bioinformatics and Computational Biology, and Fellow of the International Society for Computational Biology.

My lab is 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 and Third Generation Sequencing 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 led multiple large international research consortium projects, including STATegra (EU FP7,

11 partners, on multiomics data integration), DEANN (Marie Curie Action, 16 partners, for bioinformatics science exchange), LRGASP (15 labs, benchmarking Long-reads methods) and LongTREC (Marie Curie Action Doctoral Network, 12 partners, long reads bioinformatics tool development). I serve as SAB member of national and international research institutes. 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 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, single-molecule and spatial transcriptomics sequencing data.

Section C. MOST RELEVANT MERITS (ordered by typology)

C.1. Publications (total 164 publications)

- 1** **Scientific paper (AC)**. Pardo-Palacios F, ..., **Conesa A***, Brooks A*. *Systematic assessment of long-read RNA-seq methods for transcript identification and quantification*. **Nature Methods**. 2024 Jun 7. doi: 10.1038/s41592-024-02298-3
- 2** **Scientific paper (AC)**. Pardo-Palacios F, ..., **Conesa A**. *SQANTI3: curation of long-read transcriptomes for accurate identification of known and novel isoforms*. **Nature Methods**. 2024 Mar 20. doi: 10.1038/s41592-024-02229-2.
- 3** **Scientific paper (AC)**. Mestre-Tomás J, ..., **Conesa A**. *SQANTI-SIM: a simulator of controlled transcript novelty for lrRNA-seq benchmark*. **Genome Biology**. 2023 Dec 11;24(1):286.
- 4** **Scientific paper (AC)**. Arzalluz-Luque A, Salguero P, Tarazona S, **Conesa A**. *Acorde: unraveling functionally interpretable networks of isoform co-usage from single-cell data*. **Nature Communications**. 2022 Apr 5;13(1):1828.
- 5** **Scientific paper (AC)**. Balzano-Nogueira L, ..., **Conesa A**. Integrative analyses of TEDDY Omics data reveal lipid metabolism abnormalities, increased intracellular ROS and heightened inflammation prior to autoimmunity for type 1 diabetes. **Genome Biology**. 2021, 22(1):39.
- 6** **Scientific paper (AC)**. Tarazona, S; Balzano-Nogueira, L; Gómez-Cabrero, D; et al; **Conesa, A**. 2020. Harmonization of quality metrics and power calculation in multi-omic studies. **Nature Communications**. 11-1, pp.3092-3092.
- 7** **Scientific paper (AC)**. de la Fuente, L; Arzalluz Á; Tardáguila, M; et al; **Conesa, A**. 2020. tappAS: a comprehensive computational framework for the analysis of the functional impact of differential splicing. **Genome Biology**. 21-1, pp.119.
- 8** **Scientific paper**. Fàbregas, N; Lozano-Elena, F; **Conesa A**, et al; Caño-Delgado, A 2018. Overexpression of the vascular brassinosteroid receptor BRL3 confers drought resistance without penalizing plant growth. **Nature Communications**. 9-1, pp.4680.
- 9** **Scientific paper (AC)**. Tardáguila, M, et al; **Conesa, A**. 2018. SQANTI: extensive characterization of long read transcript sequences for quality control in full-length transcriptome identification and quantification. **Genome Research**. 28-3, pp.396.
- 10** **Scientific paper (AC)**. Arzalluz-Luque, A; **Conesa, A**. 2018. Single-cell RNAseq for the study of isoforms: how is that possible? **Genome Biology**. 19, Article nb: 110.

C.2. Participation in R&D and Innovation projects in the las 10 years (total 40 projects as PI)

- 1** HubBCB: The CSIC Bioinformatics and Computational Biology Connection. CSIC, **Coordinator, \$200.000**

- 2 Cells2Spine: Spatial Transcriptomics and Cell Communication Models applied to tissue regeneration and treatment in Spinal Cord Injury with Precision Nanomedicine. PROMETEO-CIPROM/2022/25. Valencia Government. **Coordinator, \$600.000**
- 3 LongTREC: The Long Reads European Transcriptomics Consortium. The next generation transcriptome biology revealed by single molecule sequencing technologies. MSCA-DN-2021-101072892. **Coordinator, \$2.700.000**
- 4 Integrating multi-omics data for the inference of multi-layered disease models (MO4D). Spanish Ministry of Science and Innovation. PID2020-119537RB-100 **PI €260.000**
- 5 Development of methods for transcript quantification and differential expression analysis using long-read sequencing technologies. National Institutes of Health **NIH (USA); PI. 01/09/2020-31/08/2022. \$405.007**
- 6 Microbial Dark Matter. **NASA (USA); co-PI. 01/02/2020-31/01/2022. \$266.435**
- 7 Integrative Analysis of TEDDY data to improve T1D diagnosis Helmsley Charitable Trust. (Helmsley Foundation). 01/09/2015-31/08/2017. **\$550.000**
- 8 Novel methods for the new challenges in the analysis of High-throughput sequencing data. **MINECO; PI 01/01/2016- 31/12/2018. €220.000.**
- 9 Developing a European- American NGS network (DEANN). **MC-IRSES-H2020; Coordinator. 01/01/2014-31/12/2017. €900.000.**
- 10 User-driven development of statistical methods for experimental planning, data gathering, and integrative analysis of next generation sequencing, proteomics and metabolomics data. **FP7 programme; Coordinator. 01/10/2012- 01/10/2015. €6.000.000.**

C.3. Relevant talks and seminars (out of 151 items)

- 1 *Third-generation long-read transcriptome sequencing for unraveling transcriptome complexity (keynote).* **7th Denmark Bioinformatics Symposium.** Aarhus (Denmark) 7th September, 2023
- 2 *Long-read sequencing for the analysis of the transcriptome (keynote).* **Annual Symposium of Polish Bioinformatics Society.** Gliwice, Poland, September 13th, 2023
- 3 *Third-generation sequencing technologies to investigate the complexity of transcriptomes. (keynote).* **SysReg COSI at ISMB/ECCB 2023** Lyon July 26th, 2023
- 4 *The bioinformatics of multiomics data integration and modeling (keynote).* **7th European Student Council Symposium 2022/ECCB2022.** Sitges, September 18th, 2022
- 5 *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
- 6 *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
- 7 *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
- 8 *Unravelling novel transcriptome functional features by NGS technologies (opening keynote).* **VI Argentinian Conference in Bioinformatics and Computational Biology.** Bahia Blanca, Argentina, 14th-16th October 2015.
- 9 *Lessons and results of multi-omics data analysis (keynote speaker).* **JOBIM 201.** Clermont-Ferrand, France, 6th- 9th July 2015.
- 10 *Functional Annotation of a mouse neural differentiation process (keynote).* **Australian Bioinformatics Conference.** Melbourne, Australia, 11th October 2014

C.4. Technology transfer merits

- 1 Co-Founder of Biobam Bioinformatics, a CIPF spin-off on bioinformatics software, 2010

- 2 Co-Founder of Genometra, a CIPF spin-off on bioinformatics services, 2011 (Discont. in 2016)
- 3 Developer of 23 software tools for the genomics and bioinformatics community (*Blast2GO*, *IsoAnnot*, *spongeScan*, *Qualimap*, *NOISeq*, *SQANTI3*, *SQANTI-SIM*, *maSigPro*, *ASCA-genes*, *SEA*, *tappAS*, *acorde*, *STATegraEMS*, *Paintomics*, *RGmatch*, *MOSim*, *MORE*, *MultiBac*, *Padhoc*, *MirCure*, *DeCovid*, *MAMBA*, *SQANTI-SIM*)

C.5. Completed thesis in the last 10 years (9 additional on-going thesis)

- 1 Angeles Arzalluz-Luque. *Understanding isoform expression and alternative splicing biology through single-cell RNAseq*. Universitat Politècnica de València. **March 26th 2024**
- 2 Manuel Guerrero Ugidos. *Desarrollo de métodos estadísticos para la Biología de Sistemas multiómica*. Universitat Politècnica de València. **March 29th 2023**
- 3 Rocío Amorín. *Elucidating the role of microbial dark matter in microbialite-forming ecosystems*. University of Florida. **September 18th 2023**.
- 4 María Teresa Rubio Martínez-Abarca. *Métodos de integración de datos multiómicos para el estudio de enfermedades*. Universitat Politècnica de València, **June 30th 2022**.
- 5 Salvador Casaní Gabaldón. *Bioinformatics methods to link metabolic and epigenetic regulation*. Universitat València. **February 8th 2021**.
- 6 Tatyana Zamkovaya. *Network analysis of Microbial Dark Matter*. University of Florida. **November 13th 2020**.
- 7 Pedro Furió Tarí. *Development of bioinformatic tools for massive sequencing analysis*. Universitat Politècnica de València, **March 30th 2020**.
- 8 Lorena de la Fuente. *Development of a Bioinformatics Approach for the Functional Analysis of Alternative Splicing*. Universitat Politècnica de València, **July 20th 2019**
- 9 Rafael Hernández. *Development of Bioinformatics Resources for the Integrative Analysis of Next Generation Omics Data*. Universitat Politècnica de València, **June 5th 2016**
- 10 Sonia Tarazona. *Statistical methods for transcriptomics: from microarray to RNA-seq*. Universitat Politècnica de València, **November 23th 2014**

C.6. SAB Memberships and Honors (out of 14 items)

- 1 Member of the Spanish Royal Society of Engineering
- 2 Member of the Board of Directors of the International Society of Computational Biology.
- 3 Fellow of the International Society of Computational Biology.
- 4 Honorary Member of the Spanish Society of Bioinformatics and Computational Biology
- 5 Scientific Advisory Board (SAB) member of the French Bioinformatics Institute (IFB).
- 6 SAB member of the Center for Biotechnology and Plant Research (CBPR-CSIC)
- 7 SAB member of the Instituto Biosanitario de Granada
- 8 SAB member Informatics Institute, University of Florida
- 9 SAB member Scientific Computing Program, University of Florida
- 10 SAB member of IMAGING VLC, 2023

C.7. Institutional positions and service (out of 17 items)

1. Member I2SysBio Scientific Committee
2. Director of the I2SysBio Theoretical and Computational Systems Biology Programme.
3. Chair of the Sustainability Committee at I2SysBio
4. Member of the Sustainability Committee at CSIC
5. Member of the ISCB GreenISCB group
6. Member of the VIDA Programme Committee at CSIC

7. COSI representative at the Board of Directors of the International Society for Computational Biology
8. Engineering and Health working group Spanish Royal Academy of Engineering
9. Associated Editor of Scientific Data (Nature publishing) and Genome Biology (BMC)
10. Chair of HitSeq ISCB Community of Special Interest group.

C.8. Conference and course organization (out of 48 items)

1. Scientific Committee Chair of the 1st Conference of the Spanish Society for Bioinformatics and Computational Biology
2. European Conference in Computational Biology 2020 (GENES track chair) and 2022 (Chair Proceedings)
3. UF Genetics Institute Symposium 2019-2017 (Organizing Committee member and Chair)
4. Course in Long-reads transcriptomics methods (6 editions in different countries, 2020-2022)
5. CSHL Genomics Informatics, November 2019 (Discussion leader)
6. Course of Automated Functional Annotation and Analysis (19 editions in 12 countries)
7. HitSeq and ISMB Conference (yearly since 2014).
8. SMODIA2015 Workshop, CIPF, September 2015 (Chair)
9. The Next NGS Challenge Conference, CIPF, May 2013 (Chair)
10. Organizer Critical Assessment of Microarray Data Analysis Conference (2007)

C.9. Evaluator R&D

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 (NSF), French National Research Agency (France), Novo-Nordisk Foundation Center for Biosustainability (Denmark), King Abdullah University of Science and Technology (South Arabia)

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.

CVA Dra. Tarazona

Sonia Tarazona is an Associate Professor in the Department of Applied Statistics and Operations Research and Quality at the Universitat Politècnica de València (UPV), where she has been teaching statistics and machine learning since 2005. She currently leads the BiostatOmics group at UPV, which is part of the Multivariate Statistical Engineering Group (GIEM).

Sonia Tarazona has led the Genomics of Gene Expression Group (GGE) with Dr. Ana Conesa since July 2018 till January 2024, and she has been part of the group since 2008, where she started her research career in Bioinformatics in 2008 under the supervision of Dr. Ana Conesa at Centro de Investigación Príncipe Felipe in València (CIPF). She worked at the CIPF until 2019, when she became a full-time lecturer at the UPV. In 2014, Sonia got her PhD in Statistics and Optimization (Cum Laude) with International Mention, co-supervised by Dr. Ana Conesa and Dr. Alberto Ferrer. Her thesis title was "Statistical Methods for Transcriptomics: From microarrays to RNA-seq", which got the Extraordinary Thesis Award at the UPV and rendered the R/Bioconductor NOISeq package published in NAR, and one of the seminal papers (in Genome Research) highlighting the impact of sequencing depth on differential expression.

Since her participation in the STATegra European project, Sonia specialized in the development of statistical methods and software for the integrative analysis of multi-omics (MO) experiments and has been involved in several research projects to study the regulation of gene expression and its relationship with phenotype. She has analyzed omic datasets obtained with many different techniques: microarrays, RNA-seq, CHIP-seq, ATAC-seq, smallRNA-seq, Methyl-seq, microbiome, etc., and also studied the limitations of each modality by designing the R/GitHub MultiPower package to estimate the power of a MO dataset (published in Nature Communications). Sonia has contributed to implementing many software tools (Qualimap, maSigPro, tappAS, PaintOmics, etc.). Under her supervision, other useful MO have been created: RGmatch, a flexible Python tool to associate genomic regions to their closest genes (<https://bitbucket.org/pfurio/rgmatch/>), published in BMC Bioinformatics; the first batch effect correction method for MO experiments (Bioconductor/R package MultiBaC), published in Bioinformatics and Statistical Methods for Medical Research; the CRAN/R package coxmos for the survival analysis of high-dimensional and multi-block data including efficient variable selection and functionalities for results interpretation (paper in preparation); the Bioconductor/R package MOSim, the first tool for the simulation of MO regulatory networks from bulk or single-cell sequencing data (bioRxiv 421834); and MORE, a R/GitHub package for the inference of multi-layer regulatory networks from any omics combination that offers network visualization and interpretation (bioRxiv 577162). Her expertise in MO analysis has been gathered in the book chapter "Multiomics Data Integration in Time Series Experiments" (Elsevier, 2018) and in a perspective article in Nature Computational Science.

Sonia also supervised a pioneer tool for creating networks of isoform co-usage from single-cell data, the R/GitHub *acorde* package (published in Nature Communications). Her active participation in a COST action on optimizing machine learning (ML) methods for microbiome to predict disease resulted in 2 publications in Frontiers in Microbiology. Another ML-based study was a PLoS ONE paper for mortality risk prediction in COVID-19 patients.

All these developments have been framed within the different research projects Sonia has participated in and has succeeded thanks to the work of her collaborators and students. Sonia has supervised 14 final year projects, 14 Final Master theses, and 6 PhD theses. She is currently supervising 2 final year projects, 3 Final Master Thesis and 5 PhD theses.

Sonia's research has resulted so far in more than 40 publications (total number of citations: 8593, 5931 since 2019; H index: 24; I10 index: 39) and many contributions in conferences. Her research is currently focused on the development or adaptation of statistical strategies for the integration of different omic modalities generated, not only by NGS techniques but also by other novel sequencing techniques such as single-cell, single-molecule or spatial omics, to build informative regulatory networks to model the mechanisms underlying different phenotypes. Related to this research line, she is co-PI of a national project on the development of MO models for single cell and spatial technologies and PI of a European project for the study of response to treatment in ovarian cancer by creating MO signatures with transcriptomics, proteomics and phosphoproteomics data.

Publications

1. Liu T; Salguero P; Petek M;...; Tarazona S; Conesa A. 2022. PaintOmics 4: new tools for the integrative analysis of multi-omics datasets supported by multiple pathway databases. Nucleic Acids Research. DOI: <https://doi.org/10.1093/nar/gkac352>. [9/10]
2. Ugidos M, Nueda MJ, Prats-Montalbán JM, Ferrer A, Conesa A, Tarazona S. 2022. MultiBaC: An R package to remove batch effects in multi-omic experiments. Bioinformatics. doi: 10.1093/bioinformatics/btac132. PMID: 35238331.
3. Arzalluz-Luque, A., Salguero, P., Tarazona, S., Conesa A. 2022. *acorde* unravels functionally interpretable networks of isoform co-usage from single cell data. Nature Communications, 13, 1828. <https://doi.org/10.1038/s41467-022-29497-w>
4. Tarazona, S., Arzalluz-Luque, A., Conesa, A. 2021. Undisclosed, unmet and neglected challenges in multi-omics studies. Nature Computational Science, 1(6), 395-402.
5. Tarazona S; Carmona H; Conesa A; Llansola M; Felipo V. 2020. A multi-omic study for uncovering molecular mechanisms associated with hyperammonemia-induced cerebellar function impairment in rats. Cell Biology and Toxicology, 37(1), 129-149. <https://doi.org/10.1007/s10565-020-09572-y>.
6. Tarazona, S; Balzano-Nogueira L; Gómez-Cabrero D;...; Conesa A. 2020. Harmonization of quality metrics and power calculation in multi-omic studies.

Nature Communications, 11:3022. <https://doi.org/10.1038/s41467-020-16937-8>. [1/9]

7. Sánchez-Gaya; Casaní-Galdón; Ugidos, M; Kuang; Mellor; Conesa A.; Tarazona, S. 2018. Elucidating the Role of Chromatin State and Transcription Factors on the Regulation of the Yeast Metabolic Cycle: A Multi-Omic Integrative Approach. *Frontiers in Genetics*, 9:578. doi: 10.3389/fgene.2018.00578
8. Hernandez-De Diego, R*; Tarazona, S*; Martínez-Mira, C; Balzano-Nogueira, L; Furió-Tarí, P; Pappas, G.; Conesa, A. 2018. PaintOmics 3: a web resource for the pathway analysis and visualization of multi-omics data. *Nucleic Acids Research*, 46, pp.503-509. DOI: 10.1093/nar/gky466.
9. Tarazona, S; Furió-Tarí, P; Turrà, D; Di Pietro, A; Nueda, MJ; Ferrer, A; Conesa, A. 2015. Data quality aware analysis of differential expression in RNA-seq with NOISeq R/Bioc package. *Nucleic Acids Research*, 43(21):e140. DOI: 10.1093/nar/gkv711.
10. Tarazona, S; García-Alcalde F; Dopazo J; Ferrer, A; Conesa, A. 2011. Differential expression in RNA-seq: A matter of depth. *Genome Research*, 21, pp.2213-2223. DOI: 10.1101/gr.124321.111.

Congress

1. ORAL PRESENTATION. *Uncovering Multi-Omic Regulatory Networks with MORE*. Congreso SEBiBC 2024. M. Aguerralde-Martin, C. Monzó, A. Conesa, S. Tarazona
2. POSTER. *The challenges of multi-omics survival analysis: a use-case in ovarian cancer*. ECCB 2024 (Turku, Finland). P. Salguero, M. Aguerralde-Martin, A. Conesa, S. Tarazona.
3. POSTER. *Exploring Parkinson's Disease at the Cellular Level Across Different Brain Regions*. Jornadas Andaluzas de Bionformática (Granada), 25/06/2024. J.A. Tejedor-Serrano, Á. Arzalluz-Luque, S. Tarazona, J. Martorell-Marugan.
4. ORAL PRESENTATION. *¿Cómo abordar la selección de variables en una situación de multicolinealidad? Impacto y soluciones en la inferencia de redes regulatorias multi-ómicas*. XL Congreso Nacional de Estadística e Investigación Operativa (Elche), 10/11/2023. M. Aguerralde-Martin; C. Monzó; A. Conesa; S. Tarazona.
5. ORAL PRESENTATION. *Power calculation in multi-omic studies*. XXXVIII Congreso Nacional de Estadística e Investigación Operativa (Alcoi), 06/09/2019. S. Tarazona; D. Gómez-Cabrero; J. Westerhuis; A. Conesa.
6. ORAL PRESENTATION. *Measuring isoform co-expression in single-cell RNAseq successfully decodes splicing coordination as a key determinant of neural cell type identity*. ISMB/ECCB (Basel, Switzerland), 25/07/2019. A. Arzalluz-Luque; S. Tarazona; A. Conesa.

7. ORAL PRESENTATION. *Integrative multi-omics analysis to explain immune alterations in minimal hepatic encephalopathy patients*. XIV Symposium on Bioinformatics (Granada), 16/11/2018. T. Rubio; V. Felipo; C. Montoliu; S. Tarazona; A. Conesa.
8. ORAL PRESENTATION. *Inferring significant pathway regulators from the integration of multi-omics NGS data in Generalized Linear Models*. XIII Symposium on Bioinformatics (València), 13/05/2016. S. Tarazona; M. Clemente-Císcar; P. Sebastián-León; A. Conesa.
9. ORAL PRESENTATION. *Integrated variable selection from multi-omics experiments using machine learning*. International Work-Conference on Bioinformatics and Biomedical Engineering (Granada), 17/04/2015. S. Tarazona; M. Clemente-Císcar; A. Conesa.
10. ORAL PRESENTATION. *Differential Expression in RNA-seq: A Matter of Depth*. X Jornadas de Bioinformática (Málaga), 27/10/2010. S. Tarazona; F. García-Alcalde; J. Dopazo; A. Ferrer; A. Conesa.

Research projects

1. novelMO. *Novel Methodologies for Multi-Omics Integrative Analysis with Cutting-Edge Sequencing Technologies*. Ministerio de Ciencia, Innovación y Universidades. PIs: S. Tarazona & A. Conesa. 01/09/2024-31/08/2027. 275.000 €.
2. Cell2Spine. *Spatial Transcriptomics and Cell Communication Models applied to tissue regeneration and treatment in Spinal Cord Injury with Precision Nanomedicine*. Generalitat Valenciana (Prometeo 2022). PI: A. Conesa. 01/09/2023-31/08/2026. 597.364€.
3. OVA-PDM. *Personalising the clinical decision making in ovarian cancer through patient-derived in vitro models*. European Agency through FCAECC & ISCIII (ERA PerMed, JTC 2022). PI: S. Tarazona. 01/04/2023-31/03/2026. 144.600€ (FCAECC) + 165.891€ (ISCIII).
4. MO4D. *Integración de datos multi-ómicos para la inferencia de modelos multi-capa de enfermedad*. Ministerio de Ciencia e Innovación. PIs: S. Tarazona & A. Conesa. 01/09/2021-31/08/2024. 242.000 €.
5. MIMARISCA-2. *Detección de una firma de MiRNAs como bioMARCadores predictivos de daño ISquémico CArdíaco*. UPV-La Fe (INBIO 2021). PIs: S. Tarazona & I. Ontonia. 01/10/2021-01/10/2022. 15.000 €.
6. CA18131. *Statistical and machine learning techniques in human microbiome studies*. European Agency (COST Action). PI: M. Claesson (University College Cork, Ireland). 22/02/2019-21/06/2023. Role: Management Committee, WP3 co-leader.

7. BIO2015-71658-R. *Nuevos métodos para los retos emergentes en el análisis de datos de secuenciación masiva*. Ministerio de Economía y Competitividad. PIs: A. Conesa (CIPF) & S. Tarazona (UPV). 01/01/2016-31/12/2019. 220.000 €. Role: Work team (< 07-2018) & PI (> 07-2018).
8. PROMETEO 2016/093. *The Next Systems Biology: desarrollo de métodos estadísticos para la biología de sistemas multiómica*. Generalitat Valenciana. PI: A. Conesa (CIPF). 01/01/2016-31/12/2018. 192.164 €. Role: Research team & co-supervisor PhD student.
9. BIO2012-40244. *Desarrollo de recursos computacionales para la caracterización y anotación funcional de ARN no codificante*. Ministerio Economía y Competitividad. PI: A. Conesa (CIPF). 01/01/2013-31/12/2005. Role: Research team.
10. FP7-306000. *STATegra: User-driven Development of Statistical Methods for Experimental Planning, Data Gathering and Integrative Analysis of Next Generation Sequencing, Proteomics and Metabolomics*. European Agency, FP7-HEALTH 2007–2013. PI: A. Conesa (CIPF). 01/10/2012-30/09/2015. 7.856.483 €. Role: Employed by the project.