

# Short Vita



**NAME:** Joaquin Dopazo

**ADDRESS:** Principe Felipe Research Center (CIPF),  
C/Eduardo Primo Yúfera, nº3, 46012, Valencia, Spain

**TEL:** (+34) 628156468

**EMAIL:** jdopazo@cipf.es / joaquin.dopazo@gmail.com

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## **NARRATIVE:**

Joaquín Dopazo obtained his PhD in Biology at the University of Valencia in 1989. After several appointments in different research centers and companies he worked for 5 years in Glaxo Wellcome (now Glaxo SmithKline) during the late nineties. There he was in charge of the Bioinformatics unit of the Spanish node, developing methods for bacterial genomic analysis and he participated in several bacterial and fungal genome sequencing projects. In particular, Dr. Dopazo coordinated the assembly and annotation of the bacterial pathogen *Streptococcus pneumoniae* (Dopazo, 20011, *Micr. Drug Res.*). In 2000 he moved to the Spanish National Cancer Center (CNIO), where he set up the Bioinformatics group. In the CNIO he designed the first Spanish microarray (the Oncochip) in 2000 and he developed the most used resource for microarray data analysis on the web (GEPAS, [www.gepas.org](http://www.gepas.org)) and the Babelomics ([www.babelomics.org](http://www.babelomics.org)), one of the most used resources for genomic data analysis and interpretation (cited more than 1500 times [http://bioinfo.cipf.es/docus/tools-citations/functional\\_profiling](http://bioinfo.cipf.es/docus/tools-citations/functional_profiling)). In 2005 Dr. Dopazo moved to the CIPF (Valencia) where he set up the Department of Computational Genomics (formerly Bioinformatics). He has been the Scientific director of the Center during 2012.

His scientific interests revolve around the study of disease mechanisms and drug action mechanisms, drug repositioning and the definition of mechanism-based biomarkers. The scope of his research has evolved in parallel to the introduction of "Big Data" in the life sciences. He has been working on genomic data integration and, specifically, during the last years, focusing on massive sequence data analysis. As an example of the impact of the developments of Dopazo's group, the software GenomeMaps ([www.genomemaps.org](http://www.genomemaps.org)) has been chosen as the genome viewer of the International Cancer Genome Consortium data analysis portal ([dcc.icgc.org](http://dcc.icgc.org)).

He has promoted and coordinated genomic projects such as the FutureClinic ([www.futureclinic.es](http://www.futureclinic.es)), to prepare the scenario for the introduction of the genome in the electronic health record, or the Medical Genome Project ([www.medicalgenomeproject.com](http://www.medicalgenomeproject.com)), to sequence 1000 patients of inherited diseases to search for new biomarkers and disease genes. He was also involved in international projects such as the MAQC and SEQC (best practices in the use of microarrays and NGS, respectively, for finding diagnostic biomarkers) or the START consortium to characterize the variability of the rat genome. He has been also promoter of the CitrusGen project to sequence more than 500 citric genomes for genetic improvement purposes. Dr. Dopazo also coordinates the HPC4Genomics (<http://www.hpc4g.org>) consortium, a joint initiative of the CIPF, several universities and companies that aim to combine genomic, bioinformatic and computing skills to address the new challenges posed by the technological advancement in genomics.

Dr. Dopazo's interests revolve around functional genomics, systems biology and development of algorithms and software for the analysis of high-throughput data (mainly, but not restricted to, Next Generation Sequencing) and its application to personalized and precision medicine, nutrigenomics and agro-genomics. He is particularly interested in studying disease mechanisms and drug action mechanisms by modeling complex cellular systems in which signaling, regulation and metabolism information are integrated (see an example with [pathways.babelomics.org/](http://pathways.babelomics.org/)).

Dr. Dopazo is especially interested on translational research and he is currently collaborating with numerous clinical groups. He has also several ongoing collaborative projects and grants with companies in the field of diagnostic and nutrigenomics.

In addition Dr. Dopazo is one of the founders of Genometra ([www.genometra.com](http://www.genometra.com)) a spin-off that provides advanced support and consultancy for the analysis of high-throughput genomic data.

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**EDUCATION:**

- Graduated in Chemistry, University of Valencia, 1985
- PhD in Biology, University of Valencia, 1989

**PRESENT POSITION:**

- Head of the Program of Computational Genomics at CIPF, Valencia, Spain

**OTHER SCIENTIFIC OR PROFESSIONAL ACTIVITIES**

- Scientific Director of the Principe Felipe Research Center (CIPF), Valencia, Spain, during 2012.
- Associated Director for Bioinformatics. Andalucian programme of Genetics, Fundación Progreso y Salud. Junta de Andalucía, 2009 - now.
- Director of the Bioinformatics node (U715), CIBERER, 2006 - now.
- Director of the Functional Genome node. Spanish National Bioinformatics Institute (INB), 2004 - now.

**PREVIOUS SCIENTIFIC OR PROFESSIONAL ACTIVITIES**

- Director of the Bioinformatics Unit, Centro Nacional de Investigaciones Oncológicas, 2000-2005.
- Researcher (Bioinformatician). Glaxo Wellcome S.A, 1997-2000.
- Head of R&D Bioinformatics, TDI S.A, 1995-1997.
- Researcher, Centro Nacional de Biotecnología, 1994-1995.
- Researcher, Instituto Nacional de Investigaciones Agrarias, 1990-1993.

**ACADEMIC ACTIVITIES**

- Teacher in PhD courses
- Organizer of the series "International Course on Massive Data Analysis" from 2005 to now in Valencia, Cambridge (UK), Lisbon (Portugal), Edinburgh (UK), Glasgow (UK) and Cape Town (South Africa)
- Coordinator of the Master on Bioinformatics of the University of Valencia
- Director of 7 Doctoral Theses.

**PROFESSIONAL MEMBERSHIPS**

- Member of the Science Advisory Board of the Centre of Excellence in Bioinformatics, Ghent University – VIB. Belgium.
- Member of the FGED advisory board: <http://www.mged.org/Board/advisory.html>
- Committee member of the "Infrastructure for Tools Integration" committee of the ELIXIR European initiative for the future of Bioinformatics in Europe. <http://www.elixir-europe.org/>
- Member of the PRACE prioritization panel
- Member of scientific committees of CAMDA, NNSP (IEEE), ISMB, ECCB, ECAI, Spanish Bioinformatics Group.

**EDITORIAL BOARD OF SCIENTIFIC JOURNALS**

- Associated editor of Bioinformatics (2006-2010), BMC Research notes, PLoS One and Journal of Data Mining in Genomics & Proteomics.
- Member of the Editorial Board in Advances in Bioinformatics, BMC Bioinformatics, BMC genomics, The Open Applied Informatics Journal, The Open Chemical and Biomedical Methods Journal, Clinical and Translational Oncology. The Open proteomics Journal. Recent Patents on Computer Science, The Open Systems Biology Journal

## COMMUNITY IDs

- ORCID: <http://orcid.org/0000-0003-3318-120X>
- Scopus Author ID: 18133480200
- <https://twitter.com/xdopazo>
- ResearcherID: <http://www.researcherid.com/rid/A-9270-2014>

## PUBLICATIONS

Total publications listed in PubMed: 224. Web of knowledge (10/02/2015): 9550 citations; Average citations per paper: 35.90; h-index: 52. Scholar Google: 12107 citations; h-index: 58.

Papers were published in international peer reviewed journals, including Nature Genetics, Nature Biotechnology, PNAS, Genome Research, NAR, etc., 14 international book chapters and one book edited.

## SELECTED PUBLICATIONS FROM THE LAST FIVE YEARS

1. Garcia-Alonso, L., Jiménez-Almazán, J., Carbonell-Caballero, J., Vela-Boza, A., Santoyo, J. Antiñolo, G. and Dopazo, J. 2014. The role of the interactome in the maintenance of deleterious variability in human populations. *Mol Syst Biol.* 10(9):752. IF: 11.340
2. Alemán A, Garcia-García F, Salavert F, Medina I, Dopazo J. 2014. A web-based interactive framework to assist in the prioritization of disease candidate genes in whole-exome sequencing studies. *Nucleic Acids Res.* 42:W88-93. IF: 8.808
3. Su Z, ..., Dopazo J, ... , Shi L. 2014. A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. *Nat Biotechnol.* 32, 903–914. IF: 39.08
4. Fernández RM, Bleda M, Luzón-Toro B, García-Alonso L, Arnold S, Sribudiani Y, Besmond C, Lantieri F, Doan B, Ceccherini I, Lyonnet S, Hofstra RM, Chakravarti A, Antiñolo G, Dopazo\* J, Borrego\* S. 2013. Pathways systematically associated to Hirschsprung's disease. *Orphanet J Rare Dis.* 8(1):187 \* Co-corresponding authors. IF: 5.074
5. Sebastián-León P, Carbonell J, Salavert F, Sanchez R, Medina I, Dopazo J. 2013. Inferring the functional effect of gene expression changes in signaling pathways. *Nucleic Acids Res.* 41:W213-7. IF: 8.026
6. Medina I, Salavert F, Sanchez R, de Maria A, Alonso R, Escobar P, Bleda M, Dopazo J. 2013 *Genome Maps*, a new generation genome browser. *Nucleic Acids Res.* 41:W41-6. IF: 8.026
7. García-Alonso L, Alonso R, Vidal E, Amadoz A, de María A, Minguez P, Medina I, Dopazo J. 2012 Discovering the hidden sub-network component in a ranked list of genes or proteins derived from genomic experiments. *Nucleic Acids Res.* 40(20):e158. A. IF: 8.026
8. Carbonell J, Alloza E, Arce P, Borrego S, Santoyo J, Ruiz-Ferrer M, Medina I, Jimenez-Almazan J, Mendez-Vidal C, Gonzalez-Del Pozo M, Vela A, Bhattacharya SS, Antinolo G, Dopazo J. 2012. A map of human microRNA variation uncovers unexpectedly high levels of variability. *Genome Med.* 4(8):62. IF: 4.94
9. Bleda M, Medina I, Alonso R, De Maria A, Salavert F, Dopazo J. 2012 Inferring the regulatory network behind a gene expression experiment. *Nucleic Acids Res.* 40:W168-72. A. IF: 8.026
10. Al-Shahrour F, Minguez P, Marqués-Bonet T, Gazave E, Navarro A, Dopazo J. (2010) Selection upon Genome Architecture: Conservation of Functional Neighborhoods with Changing Genes. *PLoS Comput. Biol.* 6 :e1000953. A. IF: 5.215

Complete list of publications: <http://www.ncbi.nlm.nih.gov/pubmed?term=%22dopazo%20j%22>