Francisco García García

I am a biostatistician working in the Computational Genomics Department of the Prince Felipe Research Center (CIPF) in Valencia, Spain, where our goal is to apply translational bioinformatics to personalized medicine integrating genomic and clinical data.

Research interests

Statistical methods development for analysis and **omic data integration** from a Systems Biology perspective.

Software development that allow converting data produced by the new high-throughput technologies (NGS, proteomics, metabolomics) into valuable, meaningful biomedical information that can be used for diagnostic, and prognostic purposes.

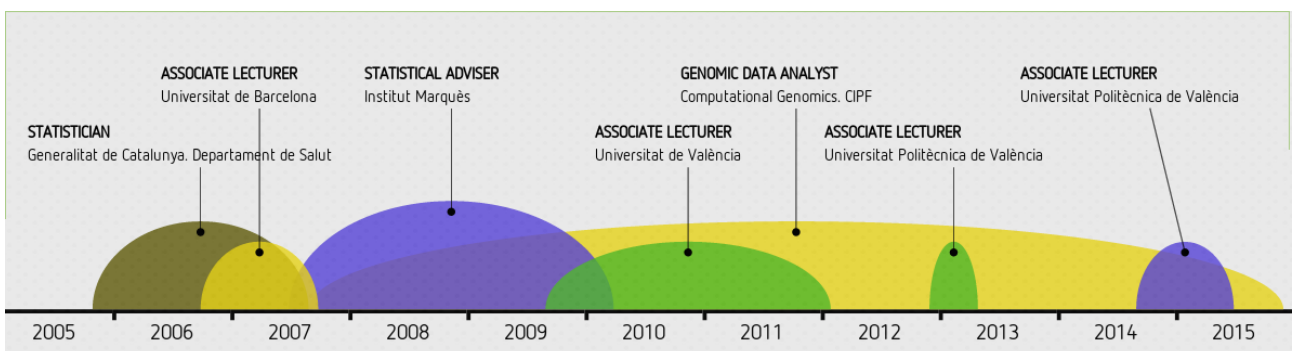Characterization of **genetic variation in human populations** by NGS.

Education

2012   **Master in Biostatistics**, *Universitat de Valencia*, Spain.
2005   **BSc in Statistical Techniques and Sciences**, *Universitat de Valencia*, Spain.
2001   **Diploma in Statistics**, *Universitat de Barcelona*, Spain.
.

Experience

STATISTICIAN
Generalitat de Catalunya. Departament de Salut

ASSOCIATE LECTURER
Universitat de Barcelona

STATISTICAL ADVISER
Institut Marquès

ASSOCIATE LECTURER
Universitat de València

GENOMIC DATA ANALYST
Computational Genomics. CIPF

ASSOCIATE LECTURER
Universitat Politècnica de València

ASSOCIATE LECTURER
Universitat Politècnica de València

2005   2006   2007   2008   2009   2010   2011   2012   2013   2014   2015

Languages

English	**intermediate level**
French	**basic level**
Catalan	**fluent level**
Spanish	**native**

Computer skills

Statistical software: **R, SPSS, Stata**

Operating Systems: **Linux, Mac OS X, Windows**

Others: **Bioinformatics tools, LaTex, Bash**

Teaching
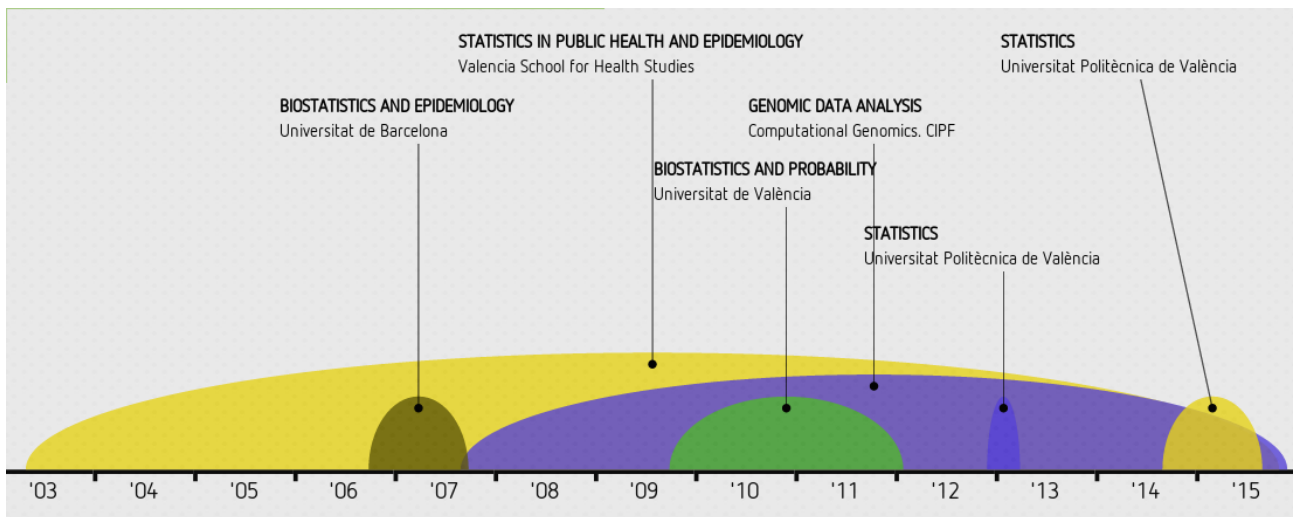
Last publications

2015

Integrating transcriptomic and metabolomic analysis to understand natural leaf senescence in sunflower. Authors: Moschen, Sebastian; Bengoa Luoni, Sofía; Di Rienzo, Julio; Caro, Maria; Tohge, Takayuki; Watanabe, Mutsumi; Hollmann, Julien; González, Sergio; Rivarola, Máximo; **García-García, Francisco**; Dopazo, Joaquin; Hopp, H.; Hoefgen, Rainer; Fernie, Alisdair; Paniego, Norma; Fernández, Paula; Heinz, Ruth. Plant Biotechnology Journal 2015 Jul 1. doi: 10.1111/pbi.12422.

Deregulation of key signaling pathways involved in oocyte maturation in FMR1 premutation carriers with Fragile X-associated primary ovarian insufficiency.. Authors: Alvarez-Mora MI, Rodriguez-Revenga L, Madrigal I, **Garcia-Garcia F**, Duran M, Dopazo J, Estivill X, Milà M. Gene. 2015 Jun 18. pii: S0378-1119(15)00748-9. doi: 10.1016/j.gene.2015.06.039.

Babelomics 5.0: functional interpretation for new generations of genomic data. Authors: Alonso R, Salavert F, **Garcia-Garcia F**, Carbonell-Caballero J, Bleda M, et al. Nucl. Acids Res. (2015) doi: 10.1093/nar/gkv384.

Whole Exome Sequencing Reveals ZNF408 as a New Gene Associated With Autosomal Recessive Retinitis Pigmentosa with Vitreal Alterations. Authors: A Avila-Fernandez; R Perez-Carro; M Corton; MI Lopez-Molina; L Campello; A Garanto; L Fernandez-Sanchez; L Duijkers; MA Lopez-Martinez; R Riveiro-Alvarez; L Rodrigues Jacy da Silva; R Sanchez-Alcudia; E Martin-Garrido; N Reyes; **F Garcia-Garcia**; J Dopazo; B Garcia-Sandoval; RW Collin; N Cuenca; C Ayuso. Human Molecular Genetics 2015; doi: 10.1093/hmg/ddv140.

BRCA1 alternative splicing landscape in breast tissue samples. Authors: Romero A, **García-García F**, López-Perolio I, Ruiz de Garibay G, García-Sáenz JA, et al. BMC Cancer, Apr 2015; 15. DOI: 10.1186/s12885-015-1145-9.

2014

Permanent Cardiac Sarcomere Changes in a Rabbit Model of Intrauterine Growth Restriction. Authors: I Torre, A González-Tendero, P García-Cañadilla, F Crispi, **F García-García**, B Bijnens, I Iruretagoyena, J Dopazo, I Amat-Roldán, E Gratacós. PLoS ONE 9(11): e113067. doi:10.1371/journal.pone.0113067, 17 Nov 2014.

The activation of the Sox2 RR2 pluripotency transcriptional reporter in human breast cancer cell lines is dynamic and labels cells with higher tumorigenic potential. Authors: Iglesias JM, Leis O, Pérez Ruiz E, Gumuzio Barrie J, **Garcia-Garcia F**, et al. Front. Oncol., 04 November 2014 | doi: 10.3389/fonc.2014.00308., Nov 2014.

A web tool for the design and management of panels of genes for targeted enrichment and massive sequencing for clinical applications. Authors: Aleman, A; **Garcia-Garcia, F**; Medina, I; Dopazo, J. Nucleic Acids Res. 2014 May 26. pii: gku472.

A web-based interactive framework to assist in the prioritization of disease candidate genes in whole exome sequencing studies. Authors: Aleman, A; **Garcia-Garcia, F**; Salavert, F; Medina, I; Dopazo, J. Nucleic Acids Research. 2014 May 6. PMID: 24803668.

Programmed cell death activated by Rose Bengal in Arabidopsis thaliana cell suspension cultures requires functional chloroplasts. Authors: J Gutiérrez, S González-Pérez, **F García-García**, CT Daly, O Lorenzo, JL Revuelta, PF McCabe, JB Arellano. Journal of Experimental Botany, April 2014, doi:10.1093/jxb/eru151.

Capturing the biological impact of CDKN2A and MC1R genes as an early predisposing event in melanoma and non melanoma skin cancer. Authors:Puig-Butille JA, Escámez MJ, **Garcia-Garcia F**, Tell-Marti G, Fabra À, et al. Oncotarget, Vol 5, No 6, March 2014.

Full list of publications in PubMed.

Networks: *ResearchGate*, *Linkedin*, *ResearcherID (B-1929-2014)*.