

ENRIQUE (QUIQUE) VIDAL

From physics and statistics to bioinformatics and genomics through epidemiology. Data scientist helping to ask and answer questions quantitatively. R'ing all the way from data processing to modeling and visualizing. Non-stop-learner.



EDUCATION

- 2011 • **Universidad Autónoma de Madrid**
PhD. in Epidemiology 📍 Madrid, Spain
Anisotropic models to study cancer mortality around pollutant sources
- 2006 • **Universitat de València**
Degree in Statistics 📍 Valencia, Spain
- 2005 • **Universitat de València**
Degree in Physics 📍 Valencia, Spain



CONSULTING EXPERIENCE

- 2019 • **Statistics and bioinformatics**
Ferrer Corporate 📍 Barcelona, Spain
 - Multiclass classifier for prediction of tumor origin
 - Implementation of a workflow for mutation detection



RESEARCH EXPERIENCE

- Now | 2015 • **Postdoctoral Researcher**
Center for Genomic Regulation (CRG) 📍 Barcelona, Spain
Acting as head of computational biology for the 4DGenome Unit:
 - Implemented a reproducible workflow for genome structure samples
 - Developed a bias-correction method for genome structure data
 - Visualization tools based on shiny
 - Context-specific analysis for the study of the dynamics of genome structure
- 2015 | 2012 • **Postdoctoral Researcher**
Bellvitge Biomedical Research Institute (IDIBELL) 📍 Barcelona, Spain
 - Integrative analysis of epigenomic data
- 2012 | 2011 • **Postdoctoral Researcher**
Príncipe Felipe Research Center (CIPF) 📍 Valencia, Spain
 - Implementation of the platform to analyze exomes for rare diseases (CIBERER-BIER)
- 2011 | 2009 • **Bioinformatician / Biostatistician**
Príncipe Felipe Research Center (CIPF) 📍 Valencia, Spain
 - Network analysis and multilevel modeling in the context of signaling pathways

CONTACT INFO

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🐙 github.com/qenvio

Thesis [text](#) and [slides](#) (in Spanish)

SKILLS

R
Bash
SQL
Python

dryhic R package

for genome structure data. It includes [OneD](#) bias correction method using GAMs

Last updated on 2019-09-16.

- 2009
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2006
- **Biostatistician**
National Center for Epidemiology 📍 Madrid, Spain
 • Analysis of mortality time-trends • Assessment of risk factors
 • Disease mapping (spatio-temporal associated with pollution smoothing)



TEACHING EXPERIENCE

- 2017
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2016
- **Biostatistics, Epidemiology and Public Health**
Instructor 📍 Castellón, Spain Medical degree
Universitat Jaume I

2011

 - **Basic Epidemiology**
Coordinator and instructor 📍 Valencia, Spain Professional training
Valencian School for Health Studies (EVES)

2009
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2008

 - **Biostatistics and Epidemiology**
Instructor 📍 Madrid, Spain M.S. Public Health
National School of Public Health, ISCIII

2009
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2008

 - **Statistical analysis with R (2 editions)**
Coordinator and Instructor 📍 Madrid, Spain Professional training
Carlos III Institute of Health (ISCIII)



SELECTED TALKS

- 2019
- **Simple statistical models for complex 3D genome data**
Statistical Methods for Post Genomic Data 📍 Barcelona, Spain [Slides](#)

2019

 - **OneD: increasing reproducibility of Hi-C samples with abnormal karyotypes**
Keystone Symposia: Chromatin Architecture and Chromosome Organization; ISCB Next Generation Sequencing Conference 📍 Whistler, British Columbia, Canada [Poster](#)
Awarded with "Outstanding presentation prize"

2008

 - **Segmented Poisson models**
The R User Conference 📍 Dortmund, Germany [Slides](#)



SELECTED PUBLICATIONS

First author publications in peer-reviewed journals

- 2019
- **Hormone-control regions mediate steroid receptor-dependent genome organization**
doi.org/10.1101/gr.243824.118 📍 Genome Research Full list of publications accesible [here](#)

2018

 - **Transcription factors orchestrate dynamic interplay between genome topology and gene regulation during cell reprogramming**
doi.org/10.1038/s41588-017-0030-7 📍 Nature Genetics

- 2018 ● **OneD: increasing reproducibility of Hi-C samples with abnormal karyotypes**
doi.org/10.1093/nar/gky064 📍 Nucleic Acids Research
- 2017 ● **Copy number rather than epigenetic alterations are the major dictator of imprinted methylation in tumors**
doi.org/10.1038/s41467-017-00639-9 📍 Nature Communications
- 2017 ● **A DNA methylation map of human cancer at single base-pair resolution**
doi.org/10.1038/onc.2017.176 📍 Oncogene