qenvio's resume

Enrique (Quique) Vidal

Aside

Contact Info

- qenvio@gmail.com
- github.com/qenvio

Skills

- R
- Bash
- SQL
- Python

Disclaimer

Last updated on 2019-12-20.

Main

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

Universidad Autónoma de Madrid

PhD. in Epidemiology

Madrid, Spain

2011

Anisotropic models to study cancer mortality around poullutant sources

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Thesis text and slides (in Spanish)

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Universitat de València

Degree in Statistics

Valencia, Spain

2006

Universitat de València

Degree in Physics

Valencia, Spain

2005

Consulting Experience

Statistics and bioinformatics

Ferrer Corporate

Barcelona, Spain

2019

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- Multiclass classifier for prediction of tumor origin
- Implementation of a workflow for mutation detection

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Research Experience

Postdoctoral Researcher

Center for Genomic Regulation (CRG)

Barcelona, Spain

Now - 2015

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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

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dryhic R package

for genome structure data. It includes OneD bias correction method using GAMs

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Postdoctoral Researcher

Bellvitge Biomedical Research Institute (IDIBELL)

Barcelona, Spain

2015 - 2012

- Integrative analysis of epigenomic data

Postdoctoral Researcher

Principe Felipe Research Center (CIPF)

Valencia, Spain

2012 - 2011

- Implementation of the platform to analyze exomes for rare diseases (CIBERER-BIER)

Bioinformatician / Biostatistician

Principe Felipe Research Center (CIPF)

Valencia, Spain

2011 - 2009

- Network analysis and multilevel modeling in the context of signaling pathways

Biostatistician

National Center for Epidemiology

Madrid, Spain

2009 - 2006

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- Analysis of mortality time-trends
- Disease mapping (spatio-temporal smoothing)
- Assement of risk factors associated with pollution

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Teaching Experience

Biostatistics, Epidemiology and Public Health

Instructor

Castellón, Spain

2017 - 2016

Universitat Jaume I

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Medical degree

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Basic Epidemiology

Coordinator and instructor

Valencia, Spain

2011

Valencian School for Health Studies (EVES)

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Professional training

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Biostatistcis and Epidemiology

Instructor

Madrid, Spain

2009 - 2008

National School of Public Health, ISCIII

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M.S. Public Health

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Statistical analysis with R (2 editions)

Coordinator and Instructor

Madrid, Spain

2009 - 2008

Carlos III Institute of Health (ISCIII)

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Professional training

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Selected talks

Simple statistical models for complex 3D genome data

Statistical Methods for Post Genomic Data

Barcelona, Spain

2019

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Slides

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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

2019

Awarded with **"Outstanding presentation prize"**

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Poster

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Segmented Poisson models

The R User Conference

Dortmund, Germany

2008

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Slides

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Selected publications

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Full list of publications accesible here

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First author publications in peer-reviewed journals

Hormone-control regions mediate steroid receptor–dependent genome organization

doi.org/10.1101/gr.243824.118

Genome Research

2019

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

2018

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

2017