

CURRICULUM VITAE

PERSONAL INFORMATION

Name: Ramón Díaz Uriarte
Date of birth: 30 October 1968
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EDUCATION

1998 – 2000: MSc Statistics, University of Wisconsin-Madison, USA.
1996 – 2000: PhD Zoology, University of Wisconsin-Madison, USA.
1993 – 1996: MSc Biometry, University of Wisconsin-Madison, USA.
1987 – 1993: Licenciatura con grado ($\approx BSc + MSc$) in Biology, Universidad Autónoma de Madrid, Madrid, Spain.

OTHER PROFESSION QUALIFICATIONS

- Fellow Royal Statistical Society (2002).
- GradStat, Royal Statistical Society (2002).

PROFESSIONAL EXPERIENCE

11/2006 – Present: Part-time Associate Professor of Bioinformatics, Universidad Autónoma de Madrid.

05/2002 – Present: Staff Scientist, Spanish National Cancer Center (CNIO, Centro Nacional de Investigaciones Oncológicas). Responsibilities:

- Analysis and design of cDNA and aCGH array experiments.
- Collaboration on the analysis of data from cancer research experiments.
- Development and implementation of statistical techniques for microarray experiments.
- Teaching of statistics.

08/2001 – 05/2002: Technical Knowledge Manager, Inner Strategic Research (Madrid, Spain). Responsibilities:

- Statistical consulting in marketing research.
- Teaching of statistics.
- Development, implementation, and adaptation, of statistical techniques of use in marketing research.

01/2001 – 07/2001: Data Mining Expert, NewKnow Network (Madrid, Spain). Responsibilities:

- Evaluation, comparison, and benchmarking of data mining algorithms.
- Combination and modification of data mining algorithms and statistical methods.

PUBLICATIONS

Author of over 34 peer-reviewed publications, including 25 in the areas of bioinformatics and genomics in the last five years (nine of those as corresponding author).

BIOINFORMATICS AND STATISTICS SOFTWARE

Developer and programmer of over nine applications and R packages for the analysis of genomic data (ADaCGH, Asterias, DNMAAD, FatiGO, GeneSrF, Pomelo and Pomelo II, RJaCGH, SignS, Tnasas), including analysis of differential expression, aCGH data, class prediction, and normalization. Most applications use parallel and distributed computing (with MPI) and have a web-based interface. Author also of programs for the analysis of phylogenetic data (PHYLOGR, contributions to PDAP), recording of behavioral data, and evaluation of evolutionarily stable strategies using genetic algorithms.

Main programming languages used for the above applications: R, C, C++, Python, Pascal, Reverse Polish Lisp.

Management of computational systems for bioinformatics and statistics

Systems administrator and manager of two Beowulf clusters of 30 nodes (one of them Intel Xeon based, the other AMD Opteron based) at CNIO (used both for research and application web-serving), including design of configuration, installation and maintenance of operating system, application migration, load balancing, and parallelization of computations (using MPI).

INVITED CONFERENCES AND COURSES

Invited conferences in statistical meetings (e.g., X Conferencia Española de Biometría), and teacher in several official master programs (Bioinformatics and Computational Biology, Molecular Oncology, Molecular Pathology, etc).

OTHER PROFESSIONAL ACTIVITIES AND AWARDS

- Ramón y Cajal researcher (December 2002)
- Two year scholarship from “Fundación La Caixa” (September 1993 – June 1995) for postgraduate work in the USA.
- **Member of** Royal Statistical Society, American Statistical Association, International Biometric Society.
- **Reviewer for** over 19 scientific journals, including Bioinformatics, IEEE Transactions in Computational Biology and Bioinformatics, Genome Biology, BMC Bioinformatics, Statistical Applications in Genetics and Molecular Biology, Journal of Multivariate Analysis, Electronic Journal of Statistics.

PARTICIPATION IN FUNDED SCIENTIFIC PROJECTS

Participation in 10 funded scientific projects, including two as PI.

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