# CURRICULUM VITAE

## PERSONAL INFORMATION

**Name:** Ramón Díaz Uriarte
**Year of birth:** 1968
**Nationality:** Spanish
**Address:** Dept. Biochemistry, Universidad Autonoma de Madrid, Arzobispo Morcillo 4, E-28029, Madrid (Spain)
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## PROFESSIONAL EXPERIENCE

**07/2011 – Present:** Associate Professor, Dept. of Biochemistry, Universidad Autónoma de Madrid, Spain.
**11/2006 – 06/2011:** Part-time Assistant Professor, Dept. of Biochemistry, Universidad Autónoma de Madrid, Spain.
**05/2002 – 06/2011:** Staff Scientist, Centro Nacional de Investigaciones Oncológicas (Spanish National Cancer Research Centre, CNIO), Madrid, Spain.
**08/2001 – 05/2002:** Technical Knowledge Manager, Inner Strategic Research (Madrid, Spain).
**01/2001 – 07/2001:** Data Mining Expert, NewKnow Network (Madrid, Spain).

## 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 (≈ $BSc+MSc$) in Biology, Universidad Autónoma de Madrid, Madrid, Spain.

## OTHER PROFESSION QUALIFICATIONS

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

## PUBLICATIONS

### Articles in peer-reviewed journals

59. Diaz-Uriarte, R. and Vasallo, C. 2019. Every which way? On predicting tumor evolution using cancer progression models. **PLoS Computational Biology** 15(8).

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57. Diaz-Uriarte, R. 2018. Cancer Progression Models And Fitness Landscapes: A Many-To-Many Relationship. **Bioinformatics**, 34(5): 836–844.

56. Diaz-Uriarte, R. 2017. OncoSimulR: genetic simulation with arbitrary epistasis and mutator genes in asexual populations. **Bioinformatics**, 33(12): 1898–99.

55. Diaz-Uriarte, R. 2015. Identifying restrictions in the order of accumulation of mutations during tumor progression: effects of passengers, evolutionary models, and sampling. **BMC Bioinformatics**, 16:41

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53. Moneo V, Serelde BG, Blanco-Aparicio C, Diaz-Uriarte R, Aviles P, Santamaria G, Tercero JC, Cuevas C, Carnero A. 2014. Levels of active tyrosine kinase receptor determine the tumor response to Zalypsis. **BMC Cancer**, 14: 281.

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49. Barderas R, Babel I, Diaz-Uriarte R, Moreno V, Suarez A, Bonilla F, Villar-Vazquez R, Capella G, Casal JI. 2012. An optimized predictor panel for colorectal cancer diagnosis based on the combination of tumor-associated antigens obtained from protein and phage microarrays. **Journal of Proteomics**,.

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47. Subirana I, Diaz-Uriarte R, Lucas G, Gonzalez JR. 2011. CNVassoc: Association analysis of CNV data using R. **BMC Medical Genomics**, 4: 47.

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42. Rueda OM, Diaz-Uriarte R. 2009. Detection of recurrent copy number alterations in the genome: taking among-subject heterogeneity seriously. **BMC Bioinformatics**, 10: 308.

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33. Rueda OM, Diaz-Uriarte R. 2007. A response to Yu et al. 'A forward-backward fragment assembling algorithm for the identification of genomic amplification and deletion breakpoints using high-density single nucleotide polymorphism (SNP) array', BMC Bioinformatics 2007, 8: 145. **BMC Bioinformatics** 2007, 8: 394-400.

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30. Castilla AM, Dhondt AA, Diaz-Uriarte R, Westmoreland D. 2007. Predation in ground nesting birds: an experimental study using natural egg-color variation. **Avian Conservation and Ecology - Écologie et conservation des oiseaux**, 2.

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25. Moneo V, Serelde BG, Leal JFM, Blanco-Aparicio C, Diaz-Uriarte R, Aracil M, Tercero JC, Jimeno J, Carnero A. 2007. Levels of p27kip1 determine Aplidin sensitivity. **Therapeutics**, 6: 1310-1316.

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16. Vaquerizas J, Dopazo J, Diaz-Uriarte R. 2004. DNMAD: web-based diagnosis and normalization for microarray data. **Bioinformatics**, 20: 3656-3658.

15. Herrero J, Vaquerizas J, Al-Shahrour F, Conde L, Mateos A, Santoyo J, Diaz-Uriarte R, Dopazo J. 2004. New challenges in gene expression data analysis and the extended GEPAS. **Nucleic Acids Research**, 32: W485–W491.

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12. Moreno-Bueno G, Sánchez-Estévez C, Cassia R, Rodríguez-Perales S, Diaz-Uriarte R, Domínguez O, Hardisson D, Andujar M, Prat J, Matias-Guiu X, Cigudosa JC, Palacios J. 2003. Differential Gene Expression Profile in Endometrioid and Nonendometrioid Endometrial Carcinoma: STK15 Is Frequently Overexpressed and Amplified in Nonendometrioid Carcinomas. **Cancer Research**, 63: 5697-5702.

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10. Herrero J, Diaz-Uriarte R, Dopazo J. 2003. An approach to inferring transcriptional regulation among genes from large-scale expression data. **Comparative and Functional Genomics**, 4: 148-154.

9. Herrero J, Diaz-Uriarte R, Dopazo J. 2003. Gene Expression Data Preprocessing. **Bioinformatics**, 19: 655-656.

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7. Diaz-Uriarte R. 2001. Territorial intrusion risk and antipredator behaviour: a mathematical model. **Proceedings of the Royal Society of London**, Series B, 268: 1165–1173.

6. Diaz-Uriarte R. 1999. Anti-predator behaviour changes following an aggressive encounter in the lizard *Tropidurus hispidus*. **Proceedings of the Royal Society of London**, Series B, 266: 2457–2464.

5. Garland T Jr, Diaz-Uriarte R. 1999. Polytomies and independent contrasts: an examination of the bounded degrees of freedom approach. **Systematic Biology**, 48: 547–558.

4. Diaz-Uriarte R, Garland T Jr. 1998. Effects of branch length errors on the performance of phylogenetically independent contrasts. **Systematic Biology**, 47: 654–672.

3. Bauwens D, Diaz-Uriarte R. 1997. Covariation of life-history traits in lacertid lizards: a comparative study. **The American Naturalist**, 149: 91–111.

2. Diaz-Uriarte R, Garland T Jr. 1996. Testing hypotheses of correlated evolution using phylogenetically independent contrasts: sensitivity to deviations from Brownian motion. **Systematic Biology**, 45: 27–47.

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### Book chapters and books

7. Rueda O.M., Diaz-Uriarte R., Caldas C. 2013. Finding Common Regions of Alteration in Copy Number Data. In: Banerjee D., Shah S. (eds), **Array Comparative Genomic Hybridization. Methods in Molecular Biology (Methods and Protocols)**, vol 973. Humana Press, Totowa, NJ.

6. Diaz-Uriarte R. 2005. Supervised methods with genomic data: a review and cautionary view. Pp. 193–214 in F. Azuaje, and J.Dopazo (eds.), **Data analysis and visualisation in genomics and proteomics**, John Wiley & Sons, New York.

5. Diaz-Uriarte R, Al-Shahrour F, Dopazo J. 2003. Use of GO terms to understand the biological significance of microarray differential gene expression data. Pp. 233-247 in K. F. Johnson and S. M. Lin (eds.), **Methods of microarray data analysis** (CAMDA 2002), Kluwer Academic Press, New York.

4. Al-Shahrour F, Herrero J, Mateos Á, Santoyo J, Diaz-Uriarte R, Dopazo J. 2003. Using Gene Ontology on genome-scale studies to find significant associations of biologically relevant terms to group of genes. pp. 43-52 in **Neural Networks for Signal Processing, XIII**, IEEE Press, New York.

3. Garland T Jr, Martin KLM, Diaz-Uriarte R. 1997. Reconstructing ancestral trait values using squared-change parsimony: plasma osmolarity at the origin of amniotes. Pp. 425–501 in: S. S. Sumida & K. L. M. Martin (eds.), **Amniote origins: completing the transition to land**, Academic Press, San Diego.

2. Diaz-Uriarte R. 2001. The analysis of cross-over trials in animal behavior experiments: review and guide to the statistical literature. Samizdat Press (`http://samizdat.mines.edu`).

1. Diaz-Uriarte R, Díez I. 1985. Las Aves Urbanas. Editorial Penthalon. Madrid.

## BIOINFORMATICS AND STATISTICS SOFTWARE

Developer and programmer of over nine applications and R/BioConductor packages for the analysis of genomic data (ADaCGH, Asterias, DNMAD, FatiGO, GeneSrF, OncoSimulR, Pomelo and Pomelo II, RJaCGH, SignS, Tnasas), including analysis of differential expression, aCGH data, class prediction, and normalization and simulation of evolution in asexual populations. Most applications use parallel and distributed computing (with MPI) and several have a web-based interface. Author also of programs for the analysis of phylogenetic data (PHYLOGR, contriutions 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 clusters of computing including design of configuration, installation and maintenance of operating system, application migration, load balancing, and parallelization of computations (using MPI).

## 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.
- **Reviewer for** over 19 scientific journals, including Bioinformatics, BMC Bioinformatics, Electronic Journal of Statistics, eLife, Genome Biology, IEEE Transactions in Computational Biology and Bioinformatics, Journal of Multivariate Analysis, Journal of Biopharmaceutical Statistics, Journal of Statistical Software. Nature Biotechnology, Statistical Applications in Genetics and Molecular Biology,
- **Associate editor** of BMC Bioinformatics, **former Associate editor** of Journal of Statistical Software.

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