

CURRICULUM VITAE

PERSONAL INFORMATION

Name: Ramón Díaz Uriarte
Year of birth: 1968
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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 ($\approx BSc + MSc$) 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

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

54. Fernandez-Navarro P1, Gonzalez-Neira A, Pita G, Diaz-Uriarte R, Tais Moreno L, Ederra M, Pedraz-Pingarron C, Sanchez-Contador C, Vazquez-Carrete JA, Moreo P, Vidal C, Salas-Trejo D, Stone J, Southey MC, Hopper JL, Perez-Gomez B, Benitez J, Pollan M. 2015. Genome wide association study identifies a novel putative mammographic density locus at 1q12-q21. **Int J Cancer**, 136 (10): 2427–36.
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 Zolypsis. **BMC Cancer**, 14: 281.
52. Diaz-Uriarte, R. 2014. ADAcGH2: parallelized analysis of (big) CNA data. **Bioinformatics**, 30 (12): 1759–61.
51. Landa I, Boullosa C, Inglada-Perez L, Sastre-Perona A, Pastor S, Velazquez A, Mancikova V, Ruiz-Llorente S, Schiavi F, Marcos R, Malats N, Opocher G, Diaz-Uriarte R, Santisteban P, Valencia A, Robledo M. 2013. An Epistatic Interaction between the PAX8 and STK17B Genes in Papillary Thyroid Cancer Susceptibility. **PLoS ONE**, 8(9):e74765.
50. Rueda OM, Rueda C, Diaz-Uriarte R. 2013. A Bayesian HMM with random effects and an unknown number of states for DNA copy number analysis. **Journal of Statistical Computation and Simulation**, 83 (1): 82–96.
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**,.
48. Montes-Moreno S, Martinez N, Sanchez-Espiridion B, Diaz Uriarte R, Rodriguez ME, Saez A, Montalban C, Gomez G, Pisano DG, Garcia JF, Conde E, Gonzalez-Barca E, Lopez A, Mollejo M, Grande C, Martinez MA, Dunphy C, Hsi ED, Rocque GB, Chang J, Go RS, Visco C, Xu-Monette Z, Young KH, Piris MA. 2011. MicroRNA expression in diffuse large B-cell lymphoma treated with chemoimmunotherapy. **Blood**, 118: 1034–1040.
47. Subirana I, Diaz-Uriarte R, Lucas G, Gonzalez JR. 2011. CNVassoc: Association analysis of CNV data using R. **BMC Medical Genomics**, 4: 47.
46. Babel I, Barderas R, Diaz-Uriarte R, Moreno V, Suarez A, Fernandez-Aceñero MJ, Salazar R, Capellá G, Casal JI. 2011. Identification of MST1/STK4 and SULF1 proteins as autoantibody targets for the diagnosis of colorectal cancer by using phage microarrays. **Molecular & Cellular Proteomics**, :M110.001784.
45. Fuxjager MJ, Foufopoulos J, Diaz-Uriarte R, Marler CA. 2011. Functionally opposing effects of testosterone on two different types of parasite: implications for the immunocompetence handicap hypothesis. **Functional Ecology**, 25: 132–138.
44. Carro A, Rico D, Rueda OM, Diaz-Uriarte R, Pisano DG. 2010. waviCGH: a web application for the analysis and visualization of genomic copy number alterations. **Nucleic Acids Research**, 38: W182–W187.
43. Rueda OM, Diaz-Uriarte R. 2010. Finding Recurrent Copy Number Alteration Regions: A Review of Methods. **Current Bioinformatics**, 5: 1–17.
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.
41. Rueda OM, Diaz-Uriarte R. 2009. RJaCGH: Bayesian analysis of aCGH arrays for detecting copy number changes and recurrent regions. **Bioinformatics**, 25: 1959-1960
40. Babel I, Barderas R, Diaz-Uriarte R, Martínez-Torrecuadrada JL, Sánchez-Carbayo M, and Casal JI. 2009. Identification of tumour-associated autoantigens for the diagnosis of colorectal cancer in serum using high-density protein microarrays. **Molecular & Cellular Proteomics**, 8: 2382-2395.
39. Morrissey E, Diaz-Uriarte, R. 2009. Pomelo II: finding differentially expressed genes. **Nucleic Acids Research**, 37: W581-W586.

38. Sequeira-Mendes J, Diaz-Urriarte R, Apedaile A, Huntley D, Brockdorff N, Gomez M. 2009. Transcription Initiation Activity Sets Replication Origin Efficiency in Mammalian Cells. **PLoS Genetics**, 5: e1000446.
37. Infante A, Laresgoiti U, Fernández-Rueda J, Fullaondo A, Galán J, Diaz-Urriarte R, Malumbres M, Field SJ, Zubiaga AM. 2008. E2F2 represses cell cycle regulators to maintain quiescence. **Cell Cycle**, 7: 3915-3927.
36. Urdinguio RG, Lopez-Serra L, Lopez-Nieva P, Alaminos M, Diaz-Urriarte R, Fernandez AF, Esteller, M. 2008. Mecp2-Null Mice Provide New Neuronal Targets for Rett Syndrome. **PLoS ONE**, 3: e3669.
35. Alibés A, Cañada A, Diaz-Urriarte R. 2008. PaLS: filtering common literature, biological terms and pathway information. **Nucleic Acids Research**, 36: W364-W367.
34. Diaz-Urriarte R. 2008. SignS: a parallelized, open-source, freely available, web-based tool for gene selection and molecular signatures for survival and censored data. **BMC Bioinformatics**, 9: 1-11.
33. Rueda OM, Diaz-Urriarte 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.
32. Collado M, Garcia V, Garcia JM, Alonso I, Lombardía L, Diaz-Urriarte R, López LA, Zaballos A, Bonilla F, Serrano M. 2007. Genomic Profiling of Circulating Plasma RNA for the Analysis of Cancer. **Clinical Chemistry**, 53, 1860-1863.
31. Diaz-Urriarte R. 2007. GeneSrF and varSelRF: a web-based tool and R package for gene selection and classification using random forest. **BMC Bioinformatics**, 8: 328-343.
30. Castilla AM, Dhondt AA, Diaz-Urriarte 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.
29. Diaz-Urriarte R, Rueda OM. 2007. ADaCGH: a parallelized web-based application and R packages for the analysis of aCGH data. **PLoS ONE**, 8: 394-400.
28. Rueda OM, Diaz-Urriarte R. 2007. Flexible and accurate detection of genomic copy-number changes from aCGH. **PLoS Computational Biology**, 3: 1115-1122.
27. Diaz-Urriarte R, Alibés A, Morrissey ER, Cañada A, Rueda OM, Neves ML. 2007. Asterias: integrated analysis of expression and aCGH data using an open-source, web-based, parallelized software suite. **Nucleic Acids Research**, 35: W75-W80.
26. Alibés A, Yankilevich P, Cañada A, Diaz-Urriarte R. 2007. IDconverter and IDClight: Conversion and annotation of gene and protein IDs. **BMC Bioinformatics**, 8: 1-9.
25. Moneo V, Serelde BG, Leal JFM, Blanco-Aparicio C, Diaz-Urriarte R, Aracil M, Tercero JC, Jimeno J, Carnero A. 2007. Levels of p27kip1 determine Aplidin sensitivity. **Therapeutics**, 6: 1310-1316.
24. Rodríguez A, Villuendas R, Yáñez L, Gómez ME, Diaz-Urriarte R, Pollán M, Hernández N, de la Cueva P, Marín MC, Swat A, Ruiz E, Cuadrado MA, Conde E, Lombardía L, Cifuentes F, Gonzalez M, García-Marco JA, Piris MA. 2007. Molecular heterogeneity in chronic lymphocytic leukemia is dependent on BCR signaling: clinical correlation. **Leukemia**, 21: 1984-1991.
23. Alibés A, Morrissey E, Cañada A, Rueda O, Casado D, Yankilevich P, Diaz-Urriarte, R. 2007. Asterias: a parallelized web-based suite for the analysis of expression and aCGH data **Cancer Informatics**, 3: 1-9.
22. Diaz-Urriarte R, Alvarez de Andrés S. 2006. Gene selection and classification of microarray data using random forest. **BMC Bioinformatics**, 7:3.

21. Vaquerizas J, Conde L, Yankilevich P, Cabezon A, Minguez P, Diaz-Uriarte R, Al-Shahrour F, Herrero J, Dopazo J. 2005. GEPAS, an experiment-oriented pipeline for the analysis of microarray gene expression data **Nucleic Acids Research**, 33: W616-W620.
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18. Alvarez de Andrés S, Diaz-Uriarte R, Osorio A, Barrosa A, Paz MF, Honrado E, Rodríguez R, Urioste M, Valle L, Diez O, Cigudosa JC, Dopazo J, Esteller M, Benítez J. 2005. A predictor based on the somatic changes of the BRCA1/2 breast cancer tumors identifies the non-BRCA1/2 tumors with BRCA1 promoter hypermethylation. **Clinical Cancer Research**, 11: 1146-1153.
17. Meléndez B, Diaz-Uriarte R, Martínez-Ramírez A, Fernández-Piqueras J, Rivas C, Dopazo J, Martínez-Delgado B, Benítez J. 2004. Gene expression analysis on chromosomal regions of gain or loss in genetic material detected by comparative genomic hybridization. **Genes Chromosomes and Cancer**, 41: 353-365.
16. Vaquerizas J, Dopazo J, Diaz-Uriarte R. 2004. DNMAID: 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.
14. Al-Shahrour F, Diaz-Uriarte R, Dopazo J. 2004. FatiGO: a web tool for finding significant associations of Gene Ontology terms with groups of genes. **Bioinformatics** 20: 578-580.
13. Martinez-Delgado B, Meléndez B, Cuadros M, Alvarez J, Castrillo JM, Ruiz de la Parte A, Mollejo M, Bellas C, Diaz-Uriarte R, Lombardía L, Al-Shahrour F, Domínguez O, Cascon A, Robledo M, Rivas C, Benitez J. 2004. Expression Profiling of T-Cell Lymphomas Differentiates Peripheral and Lymphoblastic Lymphomas and Defines Survival Related Genes **Clinical Cancer Research** , 10: 4971-4982.
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.
11. Herrero,J, Al-Shahrour F, Diaz-Uriarte R, Mateos A, Vaquerizas JM, Santoyo J, Dopazo J. 2003. GEPAS, a web-based resource for microarray gene expression data analysis **Nucleic Acids Research**, 31: 3461-3467.
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.
8. Diaz-Uriarte R. 2002. Incorrect analysis of crossover trials in animal behaviour research. **Animal Behaviour**, 63: 815-822.
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.
1. Diaz JA, Diaz-Uriarte R, Rodríguez A. 1996. Influence of behavioral thermoregulation on the use of vertical surfaces by Iberian wall lizards, *Podarcis hispanica*. **Journal of Herpetology**, 30: 548–552.

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, 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 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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