

David Mas-Ponte

Bioinformatics - Genomics - Biotechnology

david.mas.p@gmail.com
Barcelona, Spain



github://davidmasp 
linkedin://davidmasponte 
davidmasp.github.io

Education

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| 2015–2017 | M.Sc. in Bioinformatics for Health Sciences Universitat Pompeu Fabra, Barcelona, Spain. <i>Specialization in Genomics - GPA: 9 / 10</i> |
| 2014 | Exchange Student McGill University, Montreal, Canada. <i>Academic international exchange</i> |
| 2011–2015 | B.Sc. in Biotechnology Universitat Autònoma de Barcelona, Spain. <i>GPA: 8.5 / 10</i> |

Research Experience

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| 08 2017 - | Institute for Research in Biomedicine - Ph.D. Student My Ph.D. project is enclosed in the field of computational genetics, studying how mutational processes shape the eukaryotic genomes. We use statistical and machine learning techniques to extract patterns from massive genomic data sets. In particular, we are interested in unraveling mechanisms of local hypermutation both somatically and in populations. Fran Supek's Lab (AGENDAS). |
| 2016 - 2017 | Centre for Genomic Regulation (CRG) - Master Science Research Thesis My Master Thesis was focused in the link between lncRNAs' subcellular localization and their function. I have also developed a web-based DB using R and SQL to make subcellular expression data available to the scientific community. Roderic Guigo's Lab, tutored by Rory Johnson. |
| 2015-2016 | Institute of Evolutionary Biology (IBE) - Part time Research Internship I studied the evolutionary processes surrounding the RHD gene in Western Mediterranean populations in order to unravel demographic (<i>drift</i>) or adaptive (<i>selection</i>) processes. David Comas' Lab |
| 06-08 2014 | Molecular Biology Institute of Barcelona (IBMB) - Research Internship I took part in the study of the CIC (CapICua) protein in Drosophila development. I gained research skills in fruit fly genetics, in <i>in situ</i> hybridization and in recombinant DNA techniques for CRISPR/Cas9 set up. Gerardo Jimenez's Lab |

Code

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| Good | Python, SQL & R |
| Fair | Perl, Shell, git & L ^A T _E X |

Publications & Conferences

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| 2018 | André Flores-Bello, Mas-Ponte, David , Miruna E Rosu, Elena Bosch, Francesc Calafell, and David Comas. Sequence diversity of the rh blood group system in basques. <i>Eur J Hum Genet</i> , Aug 2018. doi: 10.1038/s41431-018-0232-1 - <i>Peer-reviewed Journal</i> |
| 2017 | David Mas-Ponte , Joana Carlevaro-Fita, Emilio Palumbo, Toni Hermoso Pulido, Roderic Guigo, and Rory Johnson. Lncatlas database for subcellular localization of long noncoding rnas. <i>Rna</i> , 23(7):1080–1087, 2017 - <i>Peer-reviewed Journal</i> |
| | Joana Carlevaro-Fita, Andres Lanzos, Lars Feuerbach, Chen Hong, David Mas-Ponte , Roderic Guigo, Jakob Skou Pedersen, Rory Johnson, et al. Unique genomic features and deeply-conserved functions of long non-coding rnas in the cancer lncrna census (clc). <i>bioRxiv</i> , page 152769, 2017 - <i>Preprint (under review)</i> |
| 2016 | Andre Flores-Bello, David Mas , Miruna Rosu, and David Comas. Genetic analysis and evolution of rh blood group system in basques. In <i>6th international conference of the series: DNA Polymorphisms in Human Populations, Musée de l'Homme, Paris</i> , December 2016 - <i>Peer-reviewed Conference - Poster</i> |

Languages

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| Catalan | Mother tongue |
| Spanish | Bilingual Proficiency |
| English | Fluent (FCE 2011) |

Scholarships & Awards

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| 2015-2016 | MECD - COLAB - <i>Fellowship</i> |
| | I was awarded with the Beca de Colaboracion (Collaboration Fellowship) in Department of Experimental and Health Sciences UPF by Ministerio de Educacion, Cultura y Deporte to collaborate in David Comas Lab. |
| 09-10 2015 | JAЕ INTRO - CSIC - <i>Fellowship</i> |
| | I was awarded with a JAЕ INTRO fellowship in Institute of Evolutionary Biology by Consejo Superior de Investigaciones Cientificas (CSIC) to collaborate in David Comas Lab. |
| 2014-2015 | UAB + AGAUR Exchange - <i>Scholarship</i> |
| | I was awarded with an scholarship from my university and from the Catalan government for my Exchange Academic Experience in CANADA. |