David Mas-Ponte

Bioinformatics - Genomics - Biotechnology

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Education

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

Research Experience

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 (*drift*) or adaptive (*selection*) 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 *in situ* hybridization and in recombinant DNA techniques for CRISPR/Cas9 set up. **Gerardo Jimenez's Lab**

Code

+3 years	Python, Bash, nextflow, git & R
1-2 years	HTML, SQL & LaTeX

Publications

Lead author in bold

2020

Joana Carlevaro-Fita, Andrés Lanzós, Lars Feuerbach, Chen Hong, David Mas-Ponte, Jakob Skou Pedersen, PCAWG Drivers and Functional Interpretation Group, Rory Johnson, and PCAWG Consortium. Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. *Communications Biology*, 3(1):56, February 2020. ISSN 2399-3642. doi: 10.1038/s42003-019-0741-7 - *Peer-reviewed Journal*

2019

Marina Salvadores, David Mas-Ponte, and Fran Supek. Passenger mutations accurately classify human tumors. *PLOS Computational Biology*, 15(4), April 2019. doi: 10.1371/journal.pcbi.1006953 - *Peer-reviewed Journal*

Irene Franco, Hafdis T. Helgadottir, Aldo Moggio, Malin Larsson, Peter Vrtačnik, Anna Johansson, Nina Norgren, Pär Lundin, David Mas-Ponte, Johan Nordström, Torbjörn Lundgren, Peter Stenvinkel, Lars Wennberg, Fran Supek, and Maria Eriksson. Whole genome DNA sequencing provides an atlas of somatic mutagenesis in healthy human cells and identifies a tumor-prone cell type. *Genome Biology*, 20(1):285, 2019. ISSN 1474-760X. doi: 10.1186/s13059-019-1892-z - *Peer-reviewed Journal*

2018

André Flores-Bello, David Mas-Ponte, Miruna E. Rosu, Elena Bosch, Francesc Calafell, and David Comas. Sequence diversity of the Rh blood group system in Basques. *European journal of human genetics: EJHG*, 26(12):1859–1866, 2018. ISSN 1476-5438. doi: 10.1038/s41431-018-0232-1 - *Peer-reviewed Journal*

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. *Rna*, 23(7):1080–1087, 2017. Publisher: Cold Spring Harbor Lab - *Peer-reviewed Journal*

Conferences

Presenting author in bold

2019

David Mas-Ponte and Fran Supek. HyperMut: a method to detect localized hypermutation with stringent control for confounders. In *ISMB/ECCB*, Basel, Switzerland, July 2019 - *Peer-reviewed Conference - Presentation*

2018

I Franco, H Helgadottir, A Moggio, M Larsson, P Vrtacnik, A Johansson, N Norgren, P Lundin, D Mas-Ponte, J Nordstrom, and others. Basal and mutagen-driven somatic mutagenesis shape the genome of healthy human cells. In *ESHG Conference*, Gothenburg, Sweden, June 2018 - *Peer-reviewed Conference - Presentation*

David Mas-Ponte and Fran Supek. Association of localized hypermutation patterns with transcription programs of tumor samples. In *EMBL Conference: From Functional Genomics to Systems Biology*, Heidelberg, Germany, November 2018 - *Peer-reviewed Conference - Poster*

Marina Salvadores, David Mas-Ponte, and Fran Supek. Passenger mutations but not drivers accurately classify human tumors. In *EMBL Conference: From Functional Genomics to Systems Biology*, Heidelberg, Germany, November 2018 - *Peer-reviewed Conference - Poster*

2016

Andre Flores-Bello, David Mas, Miruna Rosu, and David Comas. Genetic analysis and evolution of Rh blood group system in basques. In *6th international conference of the series: DNA Polymorphisms in Human Populations, Musée de l'Homme*, Paris, France, December 2016 - *Peer-reviewed Conference - Poster*

Other scientific contributions

2018-2019 | **ENABLE 2019** - *Scientific Organizing Committee*
ENABLE is an international scientific conference for Ph.D. Students from all over the world co-organized by 4 European research centers (IRB Barcelona, RIMLS, CPR, and SEMM) funded by the European Union Horizon 2020 program. The third edition was held in the city of Nijmegen in the Netherlands with a total of 229 Ph.D. students and postdocs coming from 26 different countries.

Scholarships & Awards

2018-2021 | FPI - Severo Ochoa - *Fellowship*

I was awarded with a FPI Severo-Ochoa from the Institute for Research in Biomedicine in the international Ph.D. call to pursue my graduate studies in Fran Supek's Lab.

2015-2016 | JAE - CSIC + MECD - COLAB - *Fellowship*

I was awarded with a JAE INTRO fellowship in Institute of Evolutionary Biology by Consejo Superior de Investigaciones Cientificas (CSIC) and the COLAB fellowship by MECD (UPF) to collaborate in David Comas' Lab.

2014-2015 | UAB + AGAUR Exchange - *Scholarship*

I was awarded with an scholarship from my university and from the Catalan government for my Exchange Academic Experience in CANADA.

Courses

Jul 2019 | Recent Advances in Statistical Methods and Computational Algorithms for Single-Cell Omics Analysis - ISMB 2019 Tutorial
Jan 2018 | How to be an Effective Researcher (Soft Skills) - BIST - VITAE
Sep 2017 | Nextflow, Reproducibility in silico Genomics - courses CRG

Languages

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