

Brian Jiménez-García, PhD

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Personal

Name: Brian Jiménez García
Born: October 5, 1984
Place of birth: Barcelona, Spain
Nationality: Spanish

Contact

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Languages

- Mother tongues: Spanish and Catalan
- Fluent in English
- Basic knowledge: French, Japanese

Education

Universitat de Barcelona (University of Barcelona)

Doctor of Philosophy (PhD), Bioinformatics and Computational Biology, 2011 - 2016
(*Cum Laude*)

Universitat de Barcelona (University of Barcelona)

MSc, Biomedicine, 2010 - 2011

École Polytechnique Fédérale de Lausanne (EPFL)

Stage, Biocomputing, 2007 - 2008

Universitat Politècnica de Catalunya (BarcelonaTech)

Engineering, Computer Science, 2002 - 2008

Work experience

Postdoctoral Researcher at Bonvin Lab (Utrecht University)

May 2018 - Present

Postdoctoral researcher at Bonvin Lab (bonvinlab.org). EOSC-Hub (eosc-hub.eu) and BioExcel2 (bioexcel.eu) EU H2020 projects. New HADDOCK v2.4 server (wenmr.science.uu.nl/haddock2.4). New developments of the LightDock protocol for macromolecular docking, protein-peptide and protein-DNA.

Postdoctoral Researcher at Barcelona Supercomputing Center

July 2016 – April 2018

Postdoctoral researcher at the Protein Interactions and Docking group and INB computational bioinformatics node. Development of protein-protein and protein-DNA docking tools for the MuG H2020 project (multiscalegenomics.eu).

Course Instructor at Universitat Oberta de Catalunya (UOC)

October 2015 - Present

Programming for bioinformatics lecturer in the *Bioinformatics and Biostatistics* master's degree.

PhD Candidate at Barcelona Supercomputing Center

June 2010 - July 2016 (6 years 2 months)

PhD student at the Protein Interactions and Docking Group.

Student visitor at National Institute of Biomedical Innovation

May 2013 – August 2013 (4 months)

Collaboration between Mizuguchi Laboratory (National Institutes of Biomedical Innovation, Health and Nutrition) and the Protein Interactions and Docking Group (Barcelona Supercomputing Center).

Software Engineer at CELLS (Spanish Synchrotron)

September 2008 - June 2010 (1 year 10 months)

Python and Zope/Plone software development.

Sysadmin internship at Automatic Control Department-BarcelonaTech

May 2005 - August 2006 (1 year 4 months)

GNU/Linux administrator, user support.

Memberships

- Python Software Foundation
- Spanish Society for Biochemistry and Molecular Biology (SEBBM)
- MDPI Journals reviewer

Grants and Awards

2019 – SEBBM conference travel grant (Madrid, Spain)

2018 – Seal of excellence awarded to ProtDNADockChallenge "Addressing Protein-DNA Interactions Docking Challenges" proposal and submitted under the Horizon 2020's Marie Skłodowska-Curie actions call H2020-MSCA-IF-2017

2016 – First conference in Research Software Engineers speaker travel grant (Manchester, UK)

2015 – SEBBM conference travel grant (Valencia, Spain)

2013 – Short Stays for Research Staff – FPI (Spanish Ministry of Economy and Competitiveness)

2013 – AlgoSB Winter School travel grant (Toulouse, France)

2012 – FPI pre-doctoral grant (4 years, Spanish Ministry of Economy and Competitiveness)

2012 – IUBMB-FEBS 2012 international congress travel grant (Sevilla, Spain)

Teaching Experience

Universitat Oberta de Catalunya (UOC)

October 2015 - Present

Programming for bioinformatics course instructor and original course material. Twice per year.

Utrecht University

Fall 2018

Structural Bioinformatics & Modelling laboratory instructor (bonvinlab.org/education/molmod). Once per year.

Courses

2019

- Defensive Programming and Debugging (PRACE MOOC, online)

2015

- Programming Distributed Computing Platforms with COMPSs (Barcelona, Spain)

2014

- 13th VI-HPS Tuning Workshop @ BSC (Barcelona, Spain)
- PATC Programming ARM based prototypes (Barcelona, Spain)

2013

- Algorithms in Structural Biology Winter School (Toulouse, France)

2011

- NVIDIA Programming and Tuning Massively Parallel 2011 Systems summer school (Barcelona, Spain)
- Stanford-Sweden multiresolution Molecular simulation 2011 workshop (Uppsala, Sweden)
- HPC-PRACE Winter School (Nicosia, Cyprus)

Conference organization

- Course instructor of the EMBO practical course on “Integrative modelling of biomolecular interactions”, Izmir, Turkey, July 2020.
- Course instructor of the EMBO practical course on “Integrative modelling of biomolecular interactions”, Barcelona, Spain, July 2-6, 2018.
- Course instructor of the EMBO practical course on “Integrative modelling of biomolecular interactions”, Barcelona, Spain, July 4-9, 2016.
- Bioinformatics section chairman of the “1st Biomed PhD Day Symposium”, Barcelona, Spain, December 7, 2016.

Universitat Oberta de Catalunya (UOC)

2019

Diseño y desarrollo de un nuevo algoritmo basado en la naturaleza para la resolución del problema del vendedor ambulante

I García de las Cuevas, B Jiménez-García, MJ Marco Galindo

<http://hdl.handle.net/10609/90526>

2018

VCFWeb: Aplicación web para el filtrado de variantes en formato VCF y diseño de estrategias para su priorización e integración con distintos tipos de datos

A Martín Lázaro, B Jiménez-García, MJ Marco Galindo

<http://hdl.handle.net/10609/81670>

Representació tridimensional de les proteïnes amb Panda 3D

J Escofet Figueras, B Jiménez-García, MJ Marco Galindo

<http://hdl.handle.net/10609/81706>

Programación de una librería de Python capaz de leer ficheros PDB para representar proteínas en 3D

A Cabrelles Muñoz, B Jiménez-García, MJ Marco Galindo

<http://hdl.handle.net/10609/81729>

Implementación de un algoritmo basado en la naturaleza para la predicción de la estructura péptido-proteína conociendo el sitio de unión

E Delgado Rodríguez, B Jiménez-García, MJ Marco Galindo

<http://hdl.handle.net/10609/81448>

Diseño y desarrollo de un visualizador de moléculas en formato PDB para Android

J González Salinas, B Jiménez-García, MJ Marco Galindo

<http://hdl.handle.net/10609/73545>

2017

Development, optimization, and integration of molecular fitting tools and models in UCSF Chimera

P Solar Rodríguez, B Jiménez-García, MJ Marco Galindo

<http://hdl.handle.net/10609/64387>

Comparación de resultados de dos técnicas de biología de sistemas para la aplicación de un análisis de reposicionamiento de fármacos

E Gabarrón Romero, B Jiménez-García, MJ Marco Galindo

<http://hdl.handle.net/10609/64326>

Ant colony optimization for predicting gene interactions from expression data

E Moncho Escriva, B Jiménez-García, MJ Marco Galindo

<http://hdl.handle.net/10609/64285>

Análisis de la relación entre cambios en la isomería de las cadenas R y la constante de disociación en la formación de complejos proteicos

FJ Lobo Cabrera, B Jiménez-García, MJ Marco Galindo

<http://hdl.handle.net/10609/64627>

2016

Explorando la relación entre expresión génica y propiedades topológicas de la red de interacción de Arabidopsis thaliana

S Giménez Santamarina, B Jiménez-García, MJ Marco Galindo

<http://hdl.handle.net/10609/60525>

Uso de algoritmos de aprendizaje automático aplicados a bases de datos genéticos (HapMap)

J Pulido Lozano, B Jiménez-García, MJ Marco Galindo

<http://hdl.handle.net/10609/59950>

Barcelona Supercomputing Center (BSC)

2015

Inclusion of Flexibility in Protein-Protein Docking

J Roel-Touris, B Jiménez-García, J Fernández-Recio

<https://www.upf.edu/web/bioinformatics/projects-2015-2016>

Utrecht University (UU)

2019

Optimising the integration of crosslinking mass spectrometry data into data-driven docking

R Pendavingh, B Jiménez-García