Dr. Brian Jiménez García

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Personal

Name: Brian Jiménez García

Born: October 5, 1984

Place of birth: Barcelona, Spain

Nationality: Spanish

Contact Address

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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)

Master, Biomedicine, 2010 - 2011

Ecole polytechnique fédérale de Lausanne (EPFL)

Stage, Biocomputing, 2007 - 2008

Universitat Politècnica de Catalunya (Barcelona Tech)

Engineering, Computer Science, 2002 – 2008

Work experience

Postdoctoral Researcher at Barcelona Supercomputing Center

July 2016 - Present (9 months)

Postdoctoral researcher at the Protein Interactions and Docking group and INB computational bioinformatics node. Protein-DNA docking tools in the MuG H2020 project (http://www.multiscalegenomics.eu).

Course Instructor at Universitat Oberta de Catalunya (UOC)

October 2015 - Present (1 year 6 months)

Programming for bioinformatics lecturer in the *Bioinformatics and Biostatistics* master's degree (http://estudis.uoc.edu/ca/masters-universitaris/bioinformatica-bioestadistica/presentacio).

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 Institute of Biomedical Innovation) and Protein interactions and Protein Interactions and Docking Group (Barcelona Supercomputing Center).

Software Engineer at CELLS (Spanish Synchrotron)

September 2008 - June 2010 (1 year 10 months)

Zope/Plone development

Sysadmin internship at Automatic Control Department BarcelonaTech

May 2005 - August 2006 (1 year 4 months)

Memberships

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

Grants and Awards

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

2012 - IUBMB-FEBS Sevilla 2012 international congress travel grant

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

2013 – AlgoSB Winter School travel grant

2015 – SEBBM travel grant

2016 – First conference of Research Software Engineers speaker travel grant

Courses

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)

2013

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

2014

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

2015

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

Publication list

Google Scholar: https://scholar.google.es/citations?hl=en&user=eVN1WVYAAAAJ

ORCID: orcid.org/0000-0001-7786-2109

2017

IRaPPA: Information retrieval based integration of biophysical models for protein assembly selection.

IH Moal, D Barradas-Bautista, B Jiménez-García, M Torchala et al.

Bioinformatics (Oxford, England)

2016

pyDock scoring for the new modeling challenges in docking: Protein–peptide, homo-multimers, and domain–domain interactions

C Pallara, B Jiménez-García, M Romero, IH Moal, J Fernández-Recio

Proteins: Structure, Function, and Bioinformatics

Prediction of homoprotein and heteroprotein complexes by protein docking and template-based modeling: A CASP-CAPRI experiment

MF Lensink, S Velankar, A Kryshtafovych, SY Huang et al.

Proteins: Structure, Function, and Bioinformatics 84 (S1), 323-348

2015

Updates to the integrated protein–protein interaction benchmarks: docking benchmark version 5 and affinity benchmark version 2

T Vreven, IH Moal, A Vangone, BG Pierce, PL Kastritis, M Torchala et al.

Journal of molecular biology 427 (19), 3031-3041

pyDockSAXS: protein–protein complex structure by SAXS and computational docking

B Jiménez-García, C Pons, DI Svergun, P Bernadó, J Fernández-Recio

Nucleic acids research 43 (W1), W356-W361

pyDock performance in 5th CAPRI edition: from docking and scoring to binding affinity predictions and other challenges

C Pallara, B Jiménez-García, M Romero, J Fernandez-Recio

BSC Doctoral Symposium (2nd: 2015: Barcelona), 99-100

CCharPPI web server: computational characterization of protein–protein interactions from structure

IH Moal, B Jiménez-García, J Fernández-Recio

Bioinformatics 31 (1), 123-125

2014

Blind prediction of interfacial water positions in CAPRI

MF Lensink, IH Moal, PA Bates, PL Kastritis, ASJ Melquiond, E Karaca et al.

Proteins: Structure, Function, and Bioinformatics 82 (4), 620-632

2013

Expanding the frontiers of protein–protein modeling: from docking and scoring to binding affinity predictions and other challenges

C Pallara, B Jiménez-García, L Pérez-Cano, M Romero-Durana et al.

Proteins: Structure, Function, and Bioinformatics 81 (12), 2192-2200

Community-wide evaluation of methods for predicting the effect of mutations on protein–protein interactions

R Moretti, SJ Fleishman, R Agius, M Torchala, PA Bates, PL Kastritis et al.

Proteins: Structure, Function, and Bioinformatics 81 (11), 1980-1987

pyDockWEB: a web server for rigid-body protein-protein docking using electrostatics and desolvation scoring

B Jiménez-García, C Pons, J Fernández-Recio

Bioinformatics, btt262

2012

Integration of protein-protein docking tools for multi-scale approach to complex structural prediction

B Jimenez-Garcia, J Fernandez-Recio

The Febs Journal 279, 532

A protein-RNA docking benchmark (II): Extended set from experimental and homology modeling data

L Pérez-Cano, B Jiménez-García, J Fernández-Recio

Proteins: Structure, Function, and Bioinformatics 80 (7), 1872-1882

2007

Centipede robot locomotion

B Jimenez, A Ikspeert

Master project, ecole polytechnique federale de Lausanne

Congress contributions

Posters

2016

B Jiménez-García, J Fernández-Recio (2016) High-performance computational tools for the characterization of protein-protein interactions. BIFI2016. Zaragoza (Spain).

B Jiménez-García, J Roel, J Fernández-Recio (2016) LightDock: a novel protein-protein docking framework for the new challenges in the interactomics era. 6th CAPRI evaluation meeting. Tel-Aviv (Israel).

2015

B Jiménez-García, J Fernández-Recio (2015) LightDock: a novel protein-protein docking framework for the new challenges in the interactomics era. SEBBM2015. Valencia (Spain).

2013

B Jiménez-García, C Pallara, D Triki, J Fernández-Recio (2013) PyDock version 3: improvements for high-performance docking and general applicability for non-peptidic molecules. CAPRI 5th. Utrecht (Netherlands).

2012

B Jiménez-García, C Pons, J Fernández-Recio (2012) pyDockWEB: a new web-server for energy-based protein-protein docking. XII Congress SBE. Barcelona (Spain).

B Jiménez-García, J Fernández-Recio (2012) Integration of protein-protein docking tools for multi-scale approach to complex structural prediction. IUBMB-FEBS. Seville (Spain).

Oral communications

2016

B Jiménez-García (2016) LightDock: a novel protein-protein docking framework for the new challenges in the interactomics era. Intelligent Pharma. Barcelona (Spain).

2015

B Jiménez-García (2015) Development and optimization of high-performance computational tools for protein-protein docking. Life Sciences Seminars (BSC). Barcelona (Spain).

B Jiménez-García (2015) LightDock: a novel protein-protein docking framework for the new challenges in the interactomics era. III Bioinformatics and Computational Biology Symposium (BIB). Barcelona (Spain).

2014

B Jiménez-García (2014) Swarm intelligence. Jornada d'Investigadors Predoctorals Interdisciplinària (JIPI). Barcelona (Spain).

B Jiménez-García (2014) Development and optimization of high-performance computational tools for protein-protein docking. BSC Days. Barcelona (Spain).

2013

B Jiménez-García (2013) Computational approaches to protein-protein docking. National Institute of Biomedical Innovation. Osaka (Japan).

Conference organization

- 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