

Joaquim Aguirre-Plans

Network Medicine - Bioinformatics - Biotechnology

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Education

2017–2021	PhD Programme in Biomedicine Universitat Pompeu Fabra, Barcelona, Spain. <i>Mark: Excellent (Cum Laude)</i>
2015–2017	MSc in Bioinformatics for Health Sciences Universitat Pompeu Fabra, Barcelona, Spain. <i>Mark: 9.26/10</i>
2011–2015	BSc in Biotechnology Universitat Autònoma de Barcelona, Spain. <i>Mark: 7.62/10</i>

Research Experience

2021 - Present	Barabasi Lab. Northeastern University - <i>Postdoctoral Research Associate</i> Research on network medicine applied to understanding diseases and finding precise and personalized treatments. Supervised by Albert-Lazlo Barabasi.
2017 - 2021	Structural Bioinformatics Lab. Universitat Pompeu Fabra (UPF) - <i>PhD Thesis</i> Development and application of Network Medicine tools to study diseases and pharmacology (mechanism of action, repurposing, combinations, adverse reactions). Supervised by Baldo Oliva and Narcis Fernandez-Fuentes.
Jul - Aug 2017	Systems Biology of Small Molecules Group. Helmholtz Zentrum München - <i>Research Internship</i> Summer internship of 2 months working on the analysis of pharmacological data from clinicaltrials.gov. Supervised by Monica Campillos.
2016 - 2017	Structural Bioinformatics Lab. Universitat Pompeu Fabra (UPF) - <i>Master Thesis</i> Master thesis about the prediction of drug combinations and drug adverse effects using protein-protein interaction networks. Supervised by Baldo Oliva.
Feb - Jul 2015	Centre for Research into Animal Health (CReSA) - <i>Research Internship</i> Research project focused on the development of new vaccination strategies against the African Swine Fever Virus.
Jul - Aug 2014	Group of Applied and Environmental Microbiology. Universitat Autònoma de Barcelona (UAB) - <i>Research Internship</i> Internship in a laboratory working on the applicability of microbiology to veterinary. Analysis of food and environmental samples and evaluation of probiotics.

Code

Code	Python, R & Bash
Web/DB	Flask, PHP, JavaScript & MySQL
ML	Scikit-learn (Python) & caret (R)

Languages

Catalan	Mother tongue
Spanish	Mother tongue
English	Excellent (CAE-C1)

Selected Publications

Find a complete list at scholar.google.com/citations?user=9Oxu-5wAAAAJhl=es:

2021	Joaquim Aguirre-Plans , Janet Piñero, Terezinha Souza, Giulia Callegaro, Steven J Kunnen, Ferran Sanz, Narcis Fernandez-Fuentes, Laura I Furlong, Emre Guney, and Baldo Oliva. An ensemble learning approach for modeling the systems biology of drug-induced injury. <i>Biology direct</i> , 16(1):1–14, 2021a - <i>Peer-reviewed Journal</i>
	Joaquim Aguirre-Plans , Alberto Meseguer, Ruben Molina-Fernandez, Manuel Alejandro Marín-López, Gaurav Jumde, Kevin Casanova, Jaume Bonet, Oriol Fornes, Narcis Fernandez-Fuentes, and Baldo Oliva. Spserver: split-statistical potentials for the analysis of protein structures and protein–protein interactions. <i>BMC bioinformatics</i> , 22(1):1–13, 2021b - <i>Peer-reviewed Journal</i>
2020	Guillem Jorba*, Joaquim Aguirre-Plans *, Valentín Junet, Cristina Segú-Vergés, José Luis Ruiz, Albert Pujol, Narcís Fernández-Fuentes, José Manuel Mas, and Baldo Oliva. In-silico simulated prototype-patients using tpms technology to study a potential adverse effect of sacubitril and valsartan. <i>PLoS One</i> , 15(2):e0228926, 2020- <i>Peer-reviewed Journal</i>
	Joaquim Aguirre-Plans , Janet Piñero, Daniel Aguilar, Emre Guney, Ferran Sanz, Laura I Furlong, Narcis Fernandez-Fuentes, and Baldo Oliva. A review of network medicine approaches to understand comorbidity. In Leon V Berhardt, editor, <i>Advances in Medicine and Biology. Volume 158</i> , chapter 1, pages 1–42. Nova Science Publishers, New York, 2020- <i>Book Chapter</i>
2019	Joaquim Aguirre-Plans , Janet Piñero, Ferran Sanz, Laura I Furlong, Narcis Fernandez-Fuentes, Baldo Oliva, and Emre Guney. Guildify v2.0: A tool to identify molecular networks underlying human diseases, their comorbidities and their druggable targets. <i>Journal of molecular biology</i> , 431(13):2477–2484, 2019 - <i>Peer-reviewed Journal</i>
2018	Joaquim Aguirre-Plans , Janet Piñero, Jörg Menche, Ferran Sanz, Laura I Furlong, Harald HHW Schmidt, Baldo Oliva, and Emre Guney. Proximal pathway enrichment analysis for targeting comorbid diseases via network endopharmacology. <i>Pharmaceuticals</i> , 11(3):61, 2018 - <i>Peer-reviewed Journal</i>

Selected Conferences

2019	ISMB/ECCB 2019 , July 2019, Basel, Switzerland. Title: "An ensemble learning approach for modeling the systems biology of drug-induced injury in human liver". - <i>Peer-reviewed Conference - Short talk</i>
2019	ISMB/ECCB 2019 , July 2019, Basel, Switzerland. Title: "GUILDify v2.0: A tool to identify molecular networks underlying human diseases, their comorbidities and their druggable targets". - <i>Peer-reviewed Conference - Short talk</i>
2017	FEBS3+ , October 2017, Barcelona, Spain. Title: "Prediction of drug combinations using drug target and protein-protein interaction information". - <i>Peer-reviewed Conference - Short talk</i>

Grants & Awards

2019	CAMDA travel fellowship Travel award to present in the ISMB/ECCB 2019 conference.
2017	Erasmus + (Traineeships) Two months work placement in the Systems Biology of Small Molecules Group of the Helmholtz Zentrum München.