

Jordi Abante Llenas

Universitat de Barcelona
Department of Biomedical Sciences
Department of Mathematics and Computer Science
Casanova, 143 · 08036 Barcelona, Catalonia

jordi.abante@ub.edu
<https://jordiabante.github.io>
Skype: jordi.abante1
Phone: +1 (979) 739-2083

RESEARCH INTERESTS Machine Learning, Computational Genomics, Epigenetics.

LANGUAGES Catalan (native), Spanish (native), English (proficient), French (basic).

PROGRAMMING julia, python, R, bash, perl, C++, Matlab, L^AT_EX.

EDUCATION & TRAINING **Universitat de Barcelona** 1/2023 - Present
Barcelona, Catalonia, Spain

- Postdoctoral research fellow
- Department of Biomedical Sciences
- Department of Mathematics and Computer Science

Stanford University 9/2021 - 1/2023
Stanford, California, U.S.

- Postdoctoral research fellow at the Salzman lab
- Department of Biomedical Data Science
- Center for Computational, Evolutionary & Human Genomics

Johns Hopkins University
Baltimore, Maryland, U.S.

- Ph.D., Electrical and Computer Engineering 8/2016 - 8/2021
- M.S.E., Applied Mathematics and Statistics 8/2016 - 12/2018
- Teaching Institute Certificate 6/2020 - 3/2021

Texas A&M University
College Station, TX, U.S.

- M.S., Electrical and Computer Engineering 8/2014 - 5/2016
- Business Management Certificate 5/2015 - 6/2015

Polytechnic University of Catalonia

Barcelona, Catalonia, Spain

- Llicenciatura, Industrial Engineering 9/2008 - 5/2014
- Major: Power Electronics

RESEARCH
EXPERIENCE

Research Assistant

9/2016 - 6/2021

Whitaker Biomedical Engineering Institute (CIS)

Johns Hopkins University, Baltimore MD, U.S.

- Genomics & epigenetics data modeling & analysis
- Statistical inference & machine learning

Research Assistant

9/2014 - 1/2015, 6/2015 - 5/2016

Center for Bioinformatics and Genomic Systems Engineering

Texas A&M University, College Station, TX, U.S.

- Genome & transcriptome data modeling & analysis
- Statistical inference & machine learning

Team Captain & Member

8/2012 - 8/2014

ETSEIB Motorsport Formula Student Team

Polytechnic University of Catalonia

Barcelona, Catalonia, Spain

- Power electronics R&D
- Electric vehicle R&D

PEER
REVIEWED
JOURNAL
ARTICLES

J. Abante, P. L. Wang, J. Salzman. “DIVE: a reference-free statistical approach to diversity-generating and mobile genetic element discovery”. *Genome Biology* (Minor review).

Y. Fang, Z. Ji†, W. Zhou†, **J. Abante**†, M.A. Koldobskiy, H. Ji, and A.P. Feinberg. “DNA methylation entropy is associated with DNA sequence features and developmental epigenetic divergence”. *Nucleic Acids Research* (2023), gkad050. † Equal contribution.

J. Abante, S. Kambhampati, A.P. Feinberg, J. Goutsias. “Estimating DNA methylation potential energy landscapes from nanopore sequencing data”. *Scientific Reports* (2021), 11-21619.

M.A. Koldobskiy, G. Jenkinson, **J. Abante**, V.A. Rodriguez DiBlasi, W. Zhou, E. Pujadas, ..., H. Ji, J. Goutsias, and A.P. Feinberg. “Converging genetic and epigenetic drivers of paediatric acute lymphoblastic leukaemia identified by an information-theoretic analysis”. *Nature Biomedical Engineering* 5.4 (2021), 360-376.

J. Abante, Y. Fang, A.P. Feinberg, J. Goutsias. “Detection of haplotype-dependent allele-specific DNA methylation in WGBS data”. *Nature Communications* 11, 5238 (2020). **Nature Comms Editors’ Highlights**.

C. Qiu, H. Jin, I. Vvedenskaya, **J. Abante**, T. Zhao, I. Malik, S. Schwartz, P. Cui, P. Cabart, K. Hoo, R.P. Metz, C.D. Johnson, S. Sze, B.F. Pugh, B.E. Nickels, C.D. Kaplan. “Universal promoter scanning by Pol II during transcription initiation in *Saccharomyces cerevisiae*”. *Genome Biology* (2020), 21:132.

M. Koldobskiy, **J. Abante**, G. Jenkinson, E. Pujadas, A. Tetens, F. Zhao, R. Tryggvadottir, A. Idrizi, A. Reinisch, R. Majeti, J. Goutsias, and A. P. Feinberg. “A Dysregulated DNA Methylation Landscape Linked to Gene Expression in MLL-Rearranged AML”. *Epigenetics* (2020), 1-18.

M. P. Menden, D. Wang, M. J. Mason, B. Szalai, K. C. Bulusu, Y. Guan, J. Kang, M. Jeon, R. Wolfinger, T. Nguyen, M. Zaslavskiy, **J. Abante**, et al. “Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen.” *Nature Communications* 10, 2674 (2019).

G. Jenkinson, **J. Abante**, M. Koldobskiy, A. P. Feinberg, J. Goutsias. “Ranking genomic features using an information-theoretic measure of epigenetic discordance”. *BMC Bioinformatics* (2019), 20:175.

G. Jenkinson, **J. Abante**, A. P. Feinberg, J. Goutsias. “An information-theoretic approach to the modeling and analysis of whole-genome bisulfite sequencing data”. *BMC Bioinformatics* (2018), 19:87.

J. Abante, N. Ghaffari, C.D. Johnson, A. Datta. “HiMMe: using genetic patterns as a proxy for genome assembly reliability assessment.” *BMC Genomics* (2017), 18:694.

PREPRINT
PAPERS

Y. Fang, Z. Ji, W. Zhou, **J. Abante**, M. Koldobskiy, H. Ji, A. P. Feinberg. (2022). “DNA methylation entropy is associated with DNA sequence features and developmental epigenetic divergence”. *bioRxiv*, 2022-12.

J. Abante, P. L. Wang, J. Salzman. “DIVE: a reference-free statistical approach to diversity-generating and mobile genetic element discovery”. *bioRxiv* (2022), 495703.

J. Abante, S. Kambhampati, A.P. Feinberg, J. Goutsias. “Estimating DNA methylation potential energy landscapes from nanopore sequencing data”. *bioRxiv* (2021), 431480.

J. Abante, J. Goutsias. “CpelTdm.jl: a Julia package for targeted differential DNA methylation analysis”. *bioRxiv* (2020), 343020.

C. Qiu, H. Jin, I. Vvedenskaya, **J. Abante**, T. Zhao, I. Malik, A.M. Visbisky, S.L. Schwartz, P. Cui, P. Čabart, K.H. Han, W.K.M. Lai, R.P. Metz, C.D. Johnson, S.H. Sze, B.F. Pugh, B.E. Nickels, C.D. Kaplan. “Promoter scanning during transcription initiation in *Saccharomyces cerevisiae*: Pol II in the “shooting gallery””. *bioRxiv* (2019), 810127.

N. Ghaffari, **J. Abante**, R. Singh, P. D. Blood, L. Pipes, C. Mason, C. D. Johnson. “What are the most influencing factors in reconstructing a reliable transcriptome assembly?”. *bioRxiv* (2017), 220269.

PEER
REVIEWED
CONFERENCE
PROCEEDINGS

P. Blood, N. Ghaffari, A. S. Seetharam, L. Pipes, R. Singh, **J. Abante**, A. Severin, C. D. Johnson, C. Mason. “Fast, flexible, and free: enabling large-scale genome assembly and analysis with the Bridges supercomputer”. *In Plant and Animal Genome XXVI Conference*, San Diego, CA, U.S., 2018.

N. Ghaffari, **J. Abante**, R. Singh, P. D. Blood, C. D. Johnson. “Computational considerations in transcriptome assemblies and their evaluation, using high quality human RNA-Seq data”. *XSEDE16: Extreme Science and Engineering Discovery Environment 2016 Conference*, Miami, FL, U.S., 2016.

INVITED
TALKS

Single-cell analysis of neurodevelopment in Huntington’s disease @ Barcelona Computational, Cognitive and Systems Neuroscience meeting (BARCCSYN), 5/2023.

Nanopore-derived epigenetic landscapes and reference-free analysis of microbial evolution @ Biomedical Sciences, Universitat de Barcelona, 9/2022.

On the estimation of epigenetic energy landscapes from nanopore sequencing data @ MLCSB + ISMB + ECCB 2021, 7/2021.

An information-theoretic approach to allele-specific DNA methylation analysis
@ Salzman Lab, Stanford University, 11/2020

@ Yosef Lab, Berkeley University, 11/2020

@ Gerstein Lab, Yale University, 11/2020

@ Knowles Lab, Columbia University, 10/2020

@ Marks Lab, Harvard University, 10/2020

Statistical modeling and analysis of allele-specific DNA methylation at the haplotype level @ Electrical & Computer Engineering Department, Johns Hopkins University, 10/2019.

POSTER SESSIONS

J. Abante, C. Vila, I. Castañeda, O. Varea, P.I. Radeva, J.M. Canals. “In silico sex deconvolution in single-cell RNA-seq data”. *Sociedad Española de Terapia Génica y Celular 2023*, Pamplona, Spain, June 2023.

O. Varea, C. Vila, C. Gomis, **J. Abante**, I. Castañeda, S. Palma, S.V. Rowlands, Z. Kokaia, P.I. Radeva, A.E. Rosser, J.M. Canals. “Characterization of striatal progenitors for the search of a cell-therapy based strategy for Huntington’s disease”. *Sociedad Española de Terapia Génica y Celular 2023*, Pamplona, Spain, June 2023.

J. Abante, P. Wang, J. Salzman. “DIVE: a reference free statistical approach to diversity-generating & mobile genetic element discovery”. *European Conference on Computational Biology 2022*, Sitges, Barcelona, Spain, September 2022.

J. Abante, S. Kambhampati, A.F. Feinberg, J. Goutsias. “On the estimation of epigenetic energy landscapes from nanopore sequencing data”. *Machine Learning in Computational and Systems Biology, Intelligent Systems for Molecular Biology and European Conference on Computational Biology 2021*, July 2021.

J. Abante, N. Ghaffari, C.D. Johnson, A. Datta. “Using hidden Markov models to analyze next-generation sequencing data”. *ENG-LIFE 2016: At the Interface of Engineering and Life Sciences*, College Station, TX, U.S., 2016.

RESEARCH PROJECTS

Alternative in vitro human methods for studying neurodegenerative diseases.
PIs: J. M. Canals Coll, J.L. Labandeira, J.A. del Río, P.I. Radeva, J. Samitier, J. Soriano, G. Vidal.
Funding agency: Ministerio de Ciencia e Innovación – NextGenerationEU (01/2023-01/2026) .

In vivo reprogramming to rescue alterations in Huntington’s disease.
PIs: J. M. Canals Coll, P. I. Radeva.
Funding agency: “la Caixa” Foundation (9/19-9/24).

A Mesoscopic Bottom-up Approach for Understanding and Modulating the Physical Epigenome.
PIs: A. P. Feinberg, M. D. Fallin, J. Goutsias, K. D. Hansen, J. Rashelle, S. Szalay, and W. Timp.
Funding agency: National Science Foundation (9/19-8/23).

Integration of Genomics and the Environment.
PIs: A. P. Feinberg, Goutsias, T. Ha, and S. D. Taverna.
Funding agency: National Institutes of Health (9/16-8/21).

FELLOWSHIPS

Stanford CEHG Postdoctoral Fellowship 10/2021 - 9/2022
Center for Computational, Evolutionary and Human Genomics (CEHG)
Stanford University, Stanford, California, U.S.
• Provided funds to launch my first year of postdoctoral research

“la Caixa” Fellowship 8/2016 - 8/2018
“la Caixa” Foundation, Barcelona, Catalonia, Spain
• Funded my Ph.D. at Johns Hopkins University

TEACHING

Lecturer Fall 2023
Bayesian Statistics
Universitat de Barcelona, Barcelona, Catalonia, Spain
• Took care of the entire course.

	Lecturer (lab) Statistics Universitat de Barcelona, Barcelona, Catalonia, Spain • Took care of lab sessions.	Fall 2023
	Summer School Guest Lecturer Multi-omics data integration for personalized nutrition FoodPhyt summer school 2023 at Max-Rubner Institute, Karlsruhe, Germany • Lectured about genomics during 1st day of summer school.	Fall 2024
	Guest Lecturer Tissue Engineering and Regenerative Medicine Universitat de Barcelona, Barcelona, Catalonia, Spain • Lectured about genomics.	Spring 2024
	Course Assistant & Guest Lecturer EN.520.622. Principles of Complex Networked Systems Johns Hopkins University, Baltimore, MD, U.S. • Graded assignments and exams • Provided students with one-on-one tutoring and out of class assistance	Fall 2018, 2019, 2020
	Teaching Assistant & Guest Lecturer ENGR-112 Foundations of Engineering II Texas A&M University, College Station, TX, U.S. • Tutored students and managed a team of grading assistants	Spring 2015
THESIS SUPERVISION	Universitat de Barcelona , Barcelona, Catalonia, Spain • J. Rosell, MS - UB Biomedical Engineering • R. Smeriglio, MS - UB Biomedical Engineering • A. Melendez, BS - UPC Data Science	Spring 2023 Spring 2023 Spring 2023
MENTORING	Stanford University , Stanford, CA, U.S. • A. Kakne, MS - Stanford ICME • A. Hirsch, PhD - Stanford Biophysics • A. Tandel, MS - Stanford Computer Science • N. Chien, MS - Stanford Computer Science	Fall 2021 Fall 2021 Fall 2021 Fall 2021

	Johns Hopkins University , Baltimore, MD, U.S. • S. Kambhampati, BS - Johns Hopkins BME	2020-2021
AWARDS & HONORS	Best Thesis Award Polytechnic University of Catalonia Barcelona, Catalonia, Spain	5/2015
	Golden Key Honor Society Texas A&M University, College Station, Texas, U.S.	5/2016
	Phi Kappa Phi Texas A&M University, College Station, Texas, U.S.	4/2016
	IEEE-Eta Kappa Nu Honor Society Texas A&M University, College Station, Texas, U.S.	1/2016
REVIEWER	Review Editor @ Frontiers in Molecular Biosciences	07/2023 - now
	Reviewer @ Intelligent Systems in Molecular Biology (ISMB) 2022	2/2022
INDUSTRY EXPERIENCE	R&D Engineer Sensory Value Sant Cugat del Vallès, Catalonia, Spain • Machine learning applied to market research	5/2016 - 8/2016
	R&D Engineer Cinergia, Control Intel·ligent de l'Energia Barcelona, Catalonia, Spain • Power electronics R&D for EV applications	3/2013 - 5/2014
UNIVERSITY SERVICE	Biomedical Data Science JEDI committee Department of Biomedical Data Science Stanford University, Stanford, CA, U.S. • Member of justice, equity, diversity, and inclusion (JEDI) committee	2021-2022

	ECE Department Head Search Spring 2021 Department of Electrical & Computer Engineering (ECE) Johns Hopkins University, Baltimore, Maryland, U.S. • Collaborated in the hiring process of department head
COMMUNITY SERVICE	Jornades Tècniques sobre la malaltia de Huntington Spring 2023 Barcelona, Catalonia, Spain • Event organized by Associació Catalana de Malalts de Huntington • Outreach activity to engage with Huntington’s disease patients and families UniStem Day 2023 Spring 2023 Barcelona, Catalonia, Spain • Outreach activity to engage high school students in science Voluntariat per la llengua Fall 2020, Spring 2021 Baltimore, Maryland, U.S. • Language partner for people interested in learning Catalan Our Daily Bread Volunteer 2020 Baltimore, Maryland, U.S. • Cooked food for families in need during COVID 19 pandemic Barclay Hopkins STEM Partnership 2017 Johns Hopkins University, Baltimore, Maryland, U.S. • Worked with elementary school students to engage them in STEM The Big Event 2015-2016 Texas A&M University, College Station, Texas, U.S. • Provided yard work and window washing for elderly residents Grup de voluntariat ANTAR 2006-2008 Àgora International School, Sant Cugat del Vallès, Catalonia, Spain • Organized fundraising activities and food drives for people in need
REFERENCES	Available upon request.
PROFESSIONAL AFFILIATIONS	International Society for Computational Biology (ISCB).