Jordi Abante Llenas

Universitat de Barcelona

Department of Biomedical Sciences

Department of Mathematics and Computer Science

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RESEARCH INTERESTS	Machine Learning, Computational Genomics, Epigenetics.
LANGUAGES	Catalan (native), Spanish (native), English (proficient), French (basic).
PROGRAMMING	julia, python, R, bash, perl, C++, Matlab, LaTeX.

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.

- Computational biology
- 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.

- Computational biology
- 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

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* (R&R).

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.

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

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, 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, 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	*In vivo reprogramming to rescue alterations in Huntington's disease.* PIs: J. M. Canals Coll, P. I. Radeva. Funding agency: "la Caixa" Foundation (9/19-8/23).

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	**Course Assistant & Guest Lecturer**	Fall 2018, 2019, 2020

TEACHING

Course Assistant & Guest Lecturer   Fall 2018, 2019, 2020
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

Teaching Assistant & Guest Lecturer   Spring 2015
ENGR-112 Foundations of Engineering II
Texas A&M University, College Station, TX, U.S.
- Tutored students and managed a team of grading assistants

MENTORING

Stanford University, Stanford, CA, U.S.
- Aasavari Kakne, MS - Stanford ICME   Fall 2021
- Angelika Hirsch, Ph.D - Stanford Biophysics   Fall 2021
- Ayushi Tandel, MS - Stanford Computer Science   Fall 2021
- Nathaniel Chien, MS - Stanford Computer Science   Fall 2021

Johns Hopkins University, Baltimore, MD, U.S.
- Sandeep Kambhampati, BS - Johns Hopkins BME   2020-2021

AWARDS
& HONORS

Best Thesis Award   5/2015
Polytechnic University of Catalonia Barcelona, Catalonia, Spain

Golden Key Honor Society   5/2016
Texas A&M University, College Station, Texas, U.S.

Phi Kappa Phi   4/2016
Texas A&M University, College Station, Texas, U.S.

IEEE-Eta Kappa Nu Honor Society   1/2016
Texas A&M University, College Station, Texas, U.S.

REVIEWER	Intelligent Systems in Molecular Biology (ISMB) 2022	2/2022

INDUSTRY EXPERIENCE

R&D Engineer   5/2016 - 8/2016
Sensory Value
Sant Cugat del Vallès, Catalonia, Spain
• Machine learning applied to market research

R&D Engineer   3/2013 - 5/2014
Cinergia, Control Intel·ligent de l'Energia
Barcelona, Catalonia, Spain
• Power electronics R&D for EV applications

UNIVERSITY SERVICE

Biomedical Data Science JEDI committee   2021-2022
Department of Biomedical Data Science
Stanford University, Stanford, CA, U.S.
• Member of justice, equity, diversity, and inclusion (JEDI) committee

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

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 International Society for Computational Biology (ISCB).
AFFILIATIONS