

Jordi Abante

Stanford University
Stanford School of Medicine
Department of Biomedical Data 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, L^AT_EX.

EDUCATION & TRAINING **Stanford University** 9/2021 - Present
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

- B.S., Industrial Engineering 9/2008 - 5/2014
- Major: Signal Processing

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”. *Nature* (under review).

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, A. Idrizi, R. Tryggvadottir, C. Callahan, C. Bonifant, K. Rabin, P.A. Brown, 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

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

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 Departmental Seminars, Johns Hopkins University, 10/2019.

POSTER
SESSIONS

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.

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 - 8/2017
“la Caixa” Foundation, Barcelona, Catalonia, Spain
• Funded my Ph.D. at Johns Hopkins University

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.	
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