

# Jordi Abante

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The Johns Hopkins University

Whitaker Biomedical Engineering Institute (CIS)

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## RESEARCH INTERESTS

Machine Learning, Genomics, Transcriptomics, Epigenetics.

## LANGUAGES

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

## SKILLS

julia, python, R, bash, perl, C++, Matlab,  $\text{\LaTeX}$ .

## EDUCATION & TRAINING

### **Stanford University**

8/2021 - Present

Palo Alto, California, U.S.

- Postdoctoral research fellow at the Salzman lab
- Center for Computational, Evolutionary & Human Genomics
- Biomedical Data Science Department & Biochemistry Department
- Computational & experimental methods for spatial transcriptomics

### **The Johns Hopkins University**

Baltimore, Maryland, U.S.

- Ph.D., Electrical and Computer Engineering 8/2016 - 8/2021<sup>1</sup>
- 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

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<sup>1</sup>Successfully defended dissertation on May 10, 2021.

RESEARCH  
EXPERIENCE

**Research Assistant**

9/2016 - 6/2021

Whitaker Biomedical Engineering Institute (CIS)  
The 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 Leader & 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**, S. Kambhampati, A.P. Feinberg, J. Goutsias. “Estimating DNA methylation potential energy landscapes from nanopore sequencing data”. *Nature Methods* (under review).

M. 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). **Featured in Nature Communications 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, The 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*, 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.

TEACHING &  
MENTORING

**Undergraduate Student Mentor** Fall 2020 - Spring 2021

Whiting School of Engineering

The Johns Hopkins University, Baltimore, MD, U.S.

- Mentored Sandeep Kambhampati, senior in Biomedical Engineering
- Johns Hopkins University PURA grant awarded to Sandeep

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

EN.520.622. Principles of Complex Networked Systems

Whiting School of Engineering

The Johns Hopkins University, Baltimore, MD, U.S.

- Guest lecturer (Fall 2020)
- 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

Dwight Look College of Engineering

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

- Guest lecturer
- Responsible of grading by managing a team of grading assistants
- Provided students with one-on-one tutoring and out of class assistance

FELLOWSHIPS

**Stanford CEHG Postdoctoral Fellowship** 10/2021 - 9/2022

Center for Computational, Evolutionary and Human Genomics (CEHG)

Stanford University, Palo Alto, California, U.S.

- Provided funds to launch my first year of postdoctoral research

	<b>“la Caixa” Fellowship</b> 8/2016 - 8/2017 “la Caixa” Foundation, Barcelona, Catalonia, Spain • Provided funds for my first two years in my Ph.D. program
INDUSTRY EXPERIENCE	<b>R&amp;D Engineer</b> 5/2016 - 8/2016 Sensory Value Sant Cugat del Vallès, Catalonia, Spain • Machine learning applied to market research
	<b>R&amp;D Engineer</b> 3/2013 - 5/2014 Cinergia, Control Intel·ligent de l'Energia Barcelona, Catalonia, Spain • Power electronics R&D for EV applications
AWARDS & HONORS	<b>Best Thesis Award</b> 5/2015 Polytechnic University of Catalonia Barcelona, Catalonia, Spain
	<b>Golden Key Honor Society</b> 5/2016 Texas A&M University, College Station, Texas, U.S.
	<b>Phi Kappa Phi</b> 4/2016 Texas A&M University, College Station, Texas, U.S.
	<b>IEEE-Eta Kappa Nu Honor Society</b> 1/2016 Texas A&M University, College Station, Texas, U.S.
UNIVERSITY SERVICE	<b>ECE Department Head Search</b> Spring 2021 Johns Hopkins University Baltimore, Maryland, U.S. • Collaborated in the hiring process of 8 candidates
COMMUNITY SERVICE	<b>Voluntariat per la llengua</b> Fall 2020, Spring 2021 Baltimore, Maryland, U.S. • Language partner for people interested in learning Catalan
	<b>Our Daily Bread Volunteer</b> 2020 Baltimore, Maryland, U.S. • Cooked food for families in need during COVID 19 pandemic

**Barclay Hopkins STEM Partnership** 2017

The 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.