C U R R I C U L U M V I T A E

Danny Antaki

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https://dantaki.github.io

EDUCATION

University of California San Diego — La Jolla, CA
PhD, Biomedical Sciences Graduate Program — 2013-2018

Dissertation: *Disparity between Maternal and Paternal Contributions to Inherited Risk for Autism*
Advisor: Jonathan Sebat

Purdue University — West Lafayette, IN
BS, General Biology — 2009-2013

GPA: 3.86, Dean's List and Honors Biology.

APPOINTMENTS

Postdoctoral Scholar — October 2018-Present
Joseph Gleeson Laboratory for Pediatric Brain Disease
Rady Children's Institute for Genomic Medicine; *University of California, San Diego* — La Jolla, CA

I aim to better characterize the link between genotype and phenotype, focusing on neurodevelopmental disorders. Projects include mapping genetic modifiers of early neural development using an outbred mouse cohort, characterizing somatic mosaicism in a healthy human brain to better understand brain development through lineage tracing, and developing a somatic structural variation deep learning model for deeply sequenced genomes.

RESEARCH EXPERIENCE

PhD Thesis Research — 2014-September 2018
Jonathan Sebat Lab, University of California, San Diego — La Jolla, CA

I discovered novel genetic risk associations in Autism, specifically implicating a strong paternal-origin effect of deletions in functionally constrained cis-regulatory elements. Pivotal to this finding was the development of a structural variant genotyping machine learning algorithm I devised that was applied to over 10,000 whole genomes.

Undergraduate Honors Thesis 2009-2013
John Anderson Lab, Purdue University West Lafayette, IN

I leveraged publicly available data to investigate structural similarity of envelope proteins among pathogens of tropical diseases using computational approaches.

Howard Hughes Medical Institute Summer Internship June 2012-August 2012
Daisuke Kihara Lab, Purdue University West Lafayette, IN

I sought to characterize functional similarity for the proteome of *E.coli* by applying an algorithm that determines pairwise similarity according to Gene Ontology terms.

PUBLICATIONS

1. Martin W. Breuss, **Danny Antaki**, Renee D. George, Morgan Kleiber, Kiely N. James, Laurel L. Ball, Oanh Hong, Ileena Mitra, Sara A. Wirth, Jing Gu, Camila A. B. Garcia, Madhusudan Gujral, William M. Brandler, Damir Musaev, An Nguyen, Jennifer McEvoy-Venneri, Renatta Knox, Evan Sticca, Martha Cristina Cancino Botello, Javiera Uribe Fenner, Maria Cárcel Pérez, Maria Arranz, Andrea B. Moffitt, Michael Wigler, Amaia Hervás, Orrin Devinsky, Melissa Gymrek, Jonathan Sebat, Joseph G. Gleeson. (2019) *The Genetic Landscape of Sperm Mosaicism and its Implications for Human Disease.* Nature Medicine *in press.*

2. Kymberleigh A. Pagel, **Danny Antaki**, AoJie Lian, Matthew Mort, David N. Cooper, Jonathan Sebat, Lilia M. Iakoucheva, Sean D. Mooney, Predrag Radivojac. (2019) *Pathogenicity and Functional Impact of Non-Frameshifting Insertion/Deletion Variation in the Human Genome.* PLoS Computational Biology 15(6): e1007112

3. William M. Brandler*, **Danny Antaki***, Madhusudan Gujral*, Morgan L. Kleiber, Joe Whitney, Michelle S. Maile, Oanh Hong, Timothy R. Chapman, Shirley Tan, Prateek Tandon, Timothy Pang, Shih C. Tang, Keith K. Vaux, Yan Yang, Eoghan Harrington, Sissel Juul, Daniel J. Turner, Bhooma Thiruvahindrapuram, Gaganjot Kaur, Zhuozhi Wang, Stephen F. Kingsmore, Joseph G. Gleeson, Denis Bisson, Boyko Kakaradov, Amalio Telenti, J. Craig Venter, Roser Corominas, Claudio Toma, Bru Cormand, Isabel Rueda, Silvina Guijarro, Karen S. Messer, Caroline M. Nievergelt, Maria J. Arranz, Eric Courchesne, Karen Pierce, Alysson R. Muotri, Lilia M. Iakoucheva, Amaia Hervas, Stephen W. Scherer, Christina Corsello, Jonathan Sebat. (2018) *Paternally Inherited Cis-Regulatory Structural Variants are Associated with Autism.* Science 360.6386: 327-331. *****, authors contributed equally to this work

4. **Danny Antaki**, William M Brandler, Jonathan Sebat. (2017) *SV^2: Accurate Structural Variation Genotyping and De Novo Mutation Detection from Whole Genomes.* Bioinformatics, 34(10), 1774-1777.

5. William M. Brandler*, **Danny Antaki*,** Madhusudan Gujral*, Amina Noor, Gabriel Rosanio, Timothy R. Chapman, Daniel J. Barrera, Guan Ning Lin, Dheeraj Malhotra, Amanda C. Watts, Lawrence C. Wong, Jasper A. Estabillo, Therese E. Gadomski, Oanh Hong, Karin V. Fuentes Fajardo, Abhishek Bhandari, Renius Owen, Michael Baughn, Jeffrey Yuan, Terry Solomon,

Alexandra G. Moyzis, Michelle S. Maile, Stephan J. Sanders, Gail E. Reiner, Keith K. Vaux, Charles M. Strom, Kang Zhang, Alysson R. Muotri, Natacha Akshoomoff, Suzanne M. Leal, Karen Pierce, Eric Courchesne, Lilia M. Iakoucheva, Christina Corsello, Jonathan Sebat. (2016) *Frequency and Complexity of De Novo Structural Mutation in Autism.* American Journal of Human Genetics 98:4, 2016, 667-679. *****, authors contributed equally to this work

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CONSORTIA PUBLICATIONS

1. Mark J.P. Chaisson, Ashley D. Sanders, Xuefang Zhao, Ankit Malhotra, David Porubsky, Tobias Rausch, Eugene J. Gardner, Oscar Rodriguez, Li Guo, Ryan L. Collins, Xian Fan, Jia Wen, Robert E. Handsaker, Susan Fairley, Zev N. Kronenberg, Xiangmeng Kong, Fereydoun Hormozdiari, Dillon Lee, Aaron M. Wenger, Alex Hastie, **Danny Antaki**, Peter Audano, Harrison Brand, Stuart Cantsilieris, Han Cao, Eliza Cerveira, Chong Chen, Xintong Chen, Chen-Shan Chin, Zechen Chong, Nelson T. Chuang, Christine C. Lambert, Deanna M. Church, Laura Clarke, Andrew Farrell, Joey Flores, Timur Galeev, David Gorkin, Madhusudan Gujral, Victor Guryev, William Haynes Heaton, Jonas Korlach, Sushant Kumar, Jee Young Kwon, Jong Eun Lee, Joyce Lee, Wan-Ping Lee, Sau Peng Lee, Shantao Li, Patrick Marks, Karine Viaud-Martinez, Sascha Meiers, Katherine M. Munson, Fabio Navarro, Bradley J. Nelson, Conor Nodzak, Amina Noor, Sofia Kyriazopoulou-Panagiotopoulou, Andy Pang, Yunjiang Qiu, Gabriel Rosanio, Mallory Ryan, Adrian Stutz, Diana C.J. Spierings, Alistair Ward, AnneMarie E. Welch, Ming Xiao, Wei Xu, Chengsheng Zhang, Qihui Zhu, Xiangqun Zheng-Bradley, Ernesto Lowy, Sergei Yakneen, Steven McCarroll, Goo Jun, Li Ding, Chong Lek Koh, Bing Ren, Paul Flicek, Ken Chen, Mark B. Gerstein, Pui-Yan Kwok, Peter M. Lansdorp, Gabor Marth, Jonathan Sebat, Xinghua Shi, Ali Bashir, Kai Ye, Scott E. Devine, Michael Talkowski, Ryan E. Mills, Tobias Marschall, Jan O. Korbel, Evan E. Eichler, Charles Lee. *Multi-Platform Discovery of Haplotype-Resolved Structural Variation in Human Genomes.* (2019) Nature Communications 10(1), 1784

   I participated as a project analysis member as a part of the Human Genome Structural Variation Consortium, a subset of the 1000 Genomes Project. There I supplied alignments and structural variant calls from TruSeq synthetic single molecule libraries. Additionally, I provided SNPs and INDELs calls using GATK HaplotypeCaller from deep Illumina paired-end sequencing libraries. I also aided in filtering tandem duplications called in Illumina paired-end genomes.

2. Christian R. Marshall*, Daniel P. Howrigan*, Daniele Merico*, Bhooma Thiruvahindrapuram, Wenting Wu, Douglas S. Greer, **Danny Antaki**, Aniket Shetty, Peter A. Holmans, Dalila Pinto, Madhusudan Gujral, William M. Brandler, Dheeraj Malhotra, Zhouzhi Wang, Karin V. Fuentes Fajarado, Michelle S. Maile, Stephan Ripke, Ingrid Agartz, Margot Albus, Madeline Alexander, Farooq Amin, Joshua Atkins, Silviu A. Bacanu, Richard A. Belliveau Jr, Sarah E. Bergen, Marcelo Bertalan, Elizabeth Bevilacqua, Tim B. Bigdeli, Donald W. Black, Richard Bruggeman, Nancy G. Buccola, Randy L. Buckner, Brendan Bulik-Sullivan, William Byerley, Wiepke Cahn, Guiqing Cai, Murray J. Cairns, Dominique Campion, Rita M. Cantor, Vaughan J. Carr, Noa Carrera, Stanley V. Catts, Kimberley D. Chambert, Wei Cheng, C. Robert Cloninger, David Cohen, Paul Cormican, Nick Craddock, Benedicto Crespo-Facorro, James J. Crowley, David Curtis, Michael Davidson, Kenneth L. Davis, Franziska Degenhardt, Jurgen Del Favero, Lynn E. DeLisi, Dimitris Dikeos, Timothy Dinan, Srdjan Djurovic, Gary Donohoe, Elodie Drapeau,

Jubao Duan, Frank Dudbridge, Peter Eichhammer, Johan Eriksson, Valentina Escott-Price, Laurent Essioux, Ayman H. Fanous, Kai-How Farh, Martilias S. Farrell, Josef Frank, Lude Franke, Robert Freedman, Nelson B. Freimer, Joseph I. Friedman, Andreas J. Forstner, Menachem Fromer, Giulio Genovese, Lyudmila Georgieva, Elliot S. Gershon, Ina Giegling, Paola Giusti-Rodríguez, Stephanie Godard, Jacqueline I. Goldstein, Jacob Gratten, Lieuwe de Haan, Marian L. Hamshere, Mark Hansen, Thomas Hansen, Vahram Haroutunian, Annette M. Hartmann, Frans A. Henskens, Stefan Herms, Joel N. Hirschhorn, Per Hoffmann, Andrea Hofman, Hailiang Huang, Masashi Ikeda, Inge Joa, Anna K. Kähler, René S. Kahn, Luba Kalaydjieva, Juha Karjalainen, David Kavanagh, Matthew C. Keller, Brian J Kelly, James L. Kennedy, Yunjung Kim, James A. Knowles, Bettina Konte, Claudine Laurent, Phil Lee, S. Hong Lee, Sophie E. Legge, Bernard Lerer, Deborah L. Levy, Kung-Yee Liang, Jeffrey Lieberman, Jouko Lönnqvist, Carmel M. Loughland, Patrik K. E. Magnusson, Brion S. Maher, Wolfgang Maier, Jacques Mallet, Manuel Mattheisen, Morten Mattingsdal, Robert W. McCarley, Colm McDonald, Andrew M. McIntosh, Sandra Meier, Carin J. Meijer, Ingrid Melle, Raquelle I. Mesholam-Gately, Andres Metspalu, Patricia T. Michie, Lili Milani, Vihra Milanova, Younes Mokrab, Derek W. Morris, Bertram Müller-Myhsok, Kieran C. Murphy, Robin M. Murray, Inez Myin-Germeys, Igor Nenadic, Deborah A. Nertney, Gerald Nestadt, Kristin K. Nicodemus, Laura Nisenbaum, Annelie Nordin, Eadbhard O'Callaghan, Colm O'Dushlaine, Sang-Yun Oh, Ann Olincy, Line Olsen, F. Anthony O'Neill, Jim Van Os, Christos Pantelis, George N. Papadimitriou, Elena Parkhomenko, Michele T. Pato, Tiina Paunio, Psychosis Endophenotypes International Consortium, Diana O. Perkins, Tune H. Pers, Olli Pietiläinen, Jonathan Pimm, Andrew J. Pocklington, John Powell, Alkes Price, Ann E. Pulver, Shaun M. Purcell, Digby Quested, Henrik B. Rasmussen, Abraham Reichenberg, Mark A. Reimers, Alexander L. Richards, Joshua L. Roffman, Panos Roussos, Douglas M. Ruderfer, Veikko Salomaa, Alan R. Sanders, Adam Savitz, Ulrich Schall, Thomas G. Schulze, Sibylle G. Schwab, Edward M. Scolnick, Rodney J. Scott, Larry J. Seidman, Jianxin Shi, Jeremy M. Silverman, Jordan W. Smoller, Erik Söderman, Chris C. A. Spencer, Eli A. Stahl, Eric Strengman, Jana Strohmaier, T. Scott Stroup, Jaana Suvisaari, Dragan M. Svrakic, Jin P. Szatkiewicz, Srinivas Thirumalai, Paul A. Tooney, Juha Veijola, Peter M. Visscher, John Waddington, Dermot Walsh, Bradley T. Webb, Mark Weiser, Dieter B. Wildenauer, Nigel M. Williams, Stephanie Williams, Stephanie H. Witt, Aaron R. Wolen, Brandon K. Wormley, Naomi R. Wray, Jing Qin Wu, Clement C. Zai, Rolf Adolfsson, Ole A. Andreassen, Douglas H. R. Blackwood, Elvira Bramon, Joseph D. Buxbaum, Sven Cichon, David A. Collier, Aiden Corvin, Mark J. Daly, Ariel Darvasi, Enrico Domenici, Tõnu Esko, Pablo V. Gejman, Michael Gill, Hugh Gurling, Christina M. Hultman, Nakao Iwata, Assen V. Jablensky, Erik G. Jönsson, Kenneth S. Kendler, George Kirov, Jo Knight, Douglas F. Levinson, Qingqin S. Li, Steven A. McCarroll, Andrew McQuillin, Jennifer L. Moran, Bryan J. Mowry, Markus M. Nöthen, Roel A. Ophoff, Michael J. Owen, Aarno Palotie, Carlos N. Pato, Tracey L. Petryshen, Danielle Posthuma, Marcella Rietschel, Brien P. Riley, Dan Rujescu, Pamela Sklar, David St Clair, James T. R. Walters, Thomas Werge, Patrick F. Sullivan, Michael C. O'Donovan, Stephen W. Scherer, Benjamin M. Neale, Jonathan Sebat* & CNV and Schizophrenia Working Groups of the Psychiatric Genomics. *Contribution of Copy Number Variants to Schizophrenia from a Genome-Wide Study of 41,321 Subjects.* (2016) Nature Genetics 49, 27–35. *, authors contributed equally to this work

In collaboration with the CNV and Schizophrenia Working Group of the Psychiatric Genomics Consortium, I performed an *in-silico* validation of CNV calls from many different microarray platforms in over 40,000 individuals. This critical analysis provided *in silico* validation of novel genetic associations reported in the work. Additionally, I designed and

carried out the analysis that showed that schizophrenia risk alleles are enriched for non-allelic homologous recombination events.

3. Peter H. Sudmant, Tobias Rausch, Eugene J. Gardner, Robert E. Handsaker, Alexej Abyzov, John Huddleston, Yan Zhang, Kai Ye, Goo Jun, Markus Hsi-Yang Fritz, Miriam K. Konkel, Ankit Malhotra, Adrian M. Stütz, Xinghua Shi, Francesco Paolo Casale, Jieming Chen, Fereydoun Hormozdiari, Gargi Dayama, Ken Chen, Maika Malig, Mark J.P. Chaisson, Klaudia Walter, Sascha Meiers, Seva Kashin, Erik Garrison, Adam Auton, Hugo Y.K. Lam, Xinmeng Jasmine Mu, Can Alkan, **Danny Antaki**, Taejeong Bae, Eliza Cerveira, Peter Chines, Zechen Chong, Laura Clarke, Elif Dal, Li Ding, Sarah Emery, Xian Fan, Madhusudan Gujral, Fatma Kahveci, Jeffrey M. Kidd, Yu Kong, Eric-Wubbo Lameijer, Shane McCarthy, Paul Flicek, Richard A. Gibbs, Gabor Marth, Christopher E. Mason, Androniki Menelaou, Donna M. Muzny, Bradley J. Nelson, Amina Noor, Nicholas F. Parrish, Matthew Pendleton, Andrew Quitadamo, Benjamin Raeder, Eric E. Schadt, Mallory Romanovitch, Andreas Schlattl, Robert Sebra, Andrey A. Shabalin, Andreas Untergasser, Jerilyn A. Walker, Min Wang, Fuli Yu, Chengsheng Zhang, Jing Zhang, Xiangqun Zheng-Bradley, Wanding Zhou, Thomas Zichner, Jonathan Sebat, Mark A. Batzer, Steven A. McCarroll, Ryan E. Mills, Mark B. Gerstein, Ali Bashir, Oliver Stegle, Scott E. Devine, Charles Lee, Evan E. Eichler, Jan O. Korbel, 1000 Genomes Project Consortium. (2015) *An integrated map of structural variation in 2,504 human genomes* Nature 526 (7571), 75-81.

   In collaboration with the 1000 Genomes Project, I designed and performed the analysis to validate complex structural rearrangements in the individual NA12878 using TruSeq (at the time, dubbed Moleculo) synthetic long reads.

BOOK CHAPTERS

1. Mattia Mori, Lesia Kovalenko, Sébastien Lyonnais, **Danny Antaki**, Bruce E. Torbett, Maurizio Botta, Gilles Mirambeau, Yves Mély. (2015) *Nucleocapsid Protein: A Desirable Target for Future Therapies Against HIV-1*. The Future of HIV-1 Therapeutics. Current Topics in Microbiology and Immunology, vol 389.

PATENTS and PATENT APPLICATIONS

1. Jonathan Sebat, Joseph G. Gleeson, Morgan Kleiber, Danny Antaki, William M. Brandler. *Methods for Inferring Disease Risk in Offspring by Detection of Somatic mosaic Variants in Parental Sperm or Somatic Tissues*, US Provisional Application No. 62/512,368, March 30, 2017

INVITED PRESENTATIONS

Danny Antaki, William M. Brandler, Madhusudan Gujral, and Jonathan Sebat. (2018) Paternally inherited cis-regulatory structural variants are associated with autism. Genetics Training Program 11th Annual Retreat, *University of California, San Diego*

Danny Antaki, William M. Brandler, Madhusudan Gujral, and Jonathan Sebat. (2018) Paternally inherited cis-regulatory structural variants are associated with autism. Biomedical Sciences Recruitment, *University of California, San Diego*

Danny Antaki, William M. Brandler and Jonathan Sebat. (2017) SV^2: Accurate Structural Variation Genotyping and De Novo Mutation Detection for Whole Genomes. Medical and Population Genetics Seminar, *University of California, San Diego*

Danny Antaki, William M. Brandler, Madhusudan Gujral, and Jonathan Sebat. (2015) Whole Genome Sequencing Identifies Complex and Balanced De Novo Structural Variation in Autism. Cellular and Molecular Medicine Symposium, *University of California, San Diego*

POSTERS

Danny Antaki, Lu Wang, Selcan Aydin, Devin Porter, Ted Choi, Steven Munger, and Joseph Gleeson (2019) Mapping Genetic Modifiers of Early Neural Development with the Diversity Outbred Stock. Complex Traits Consortium 17th Annual Meeting, San Diego, CA

Danny Antaki, William M. Brandler, Madhusudan Gujral, Prateek Tandon, and Jonathan Sebat (2018) Differences in the Maternal and Paternal Contribution to Inherited Risk for Autism. American Society of Human Genetics, San Diego, CA

Danny Antaki, William M. Brandler and Jonathan Sebat. (2017) SV^2: Accurate Structural Variation Genotyping and De Novo Mutation Detection for Whole Genomes. American Society of Human Genetics, Orlando FL

Danny Antaki, William M. Brandler, Madhusudan Gujral, and Jonathan Sebat. (2015) Whole Genome Sequencing Identifies Complex and Balanced De Novo Structural Variation in Autism. World Congress of Psychiatric Genetics, Toronto Canada

Danny Antaki, William M. Brandler, Madhusudan Gujral, and Jonathan Sebat. (2015) Whole Genome Sequencing Identifies Complex and Balanced De Novo Structural Variation in Autism. American Society of Human Genetics, Baltimore MD

Danny Antaki, Madhusudan Gujral, William M. Brandler, Jaccob J. Michaelson, Dheeraj Malhotra, Jasper A. Estabillo, Christina Corsello, Jonathan Sebat. (2014) Discovery, validation and genotyping of CNVs by analysis of genome sequence and microarray. American Society of Human Genetics, San Diego CA

TEACHING

Guest Lecturer, BIOM 201 Seminars in Biomedical Research — Fall 2019
University of California, San Diego
Introduction to Michael Talkowski's Research on Structural Variation and Psychiatric Disease

Guest Lecturer, BICD 100 Genetics — Summer 2017 & 2018
University of California, San Diego
Structural Variation: Accelerator of Evolution

Guest Lecturer, Advanced Statistics Summer Course — Summer 2017
University of California, San Diego
Genotyping Structural Variation with Machine Learning

Teaching Assistant, BIPN 150 Diseases of the Nervous System — Winter 2016
University of California, San Diego

ACADEMIC HONORS

Honors Biology Student, Purdue University — 2010-2013
Dean's List, Purdue University — 2010-2013

GRANTS AND AWARDS

Amazon Web Services Academic Research Grant for $25,000 — 2017
Funded ongoing study of rare structural variants in Autism

Amazon Web Services Academic Research Grant for $15,000 — 2015
Funded development of SV^2 by analyzing 2,504 low coverage genomes

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TRAINING PROGRAMS

Genetics Training Program — 2014-2017
University of California, San Diego
NIH predoctoral training grant T32 GM008666

OUTREACH AND COMMITTEES

Panelist, Introduction to Graduate Studies in the Division of Biological Sciences — 2019
University of California, San Diego

Poster Judge, Student Research Showcase 2019
University of California, San Diego

Poster Judge, BILD 4: Intro to Biology Lab 2019
University of California, San Diego

Coordinator, Genetics Training Program 11th Annual Retreat 2018
University of California, San Diego

Co-coordinator, Genetics, Bioinformatics, and Systems Biology Colloquium 2017-2018
University of California, San Diego

Co-coordinator, Annual Biomedical Sciences Student Invited Speaker Seminar 2015
University of California, San Diego

PROGRAMMING LANGUAGES

Python (excellent)
- Machine learning/Deep learning (`scikit-learn, keras, TensorFlow`)
- `htslib` integration (`pysam`)
- Data analysis (`numpy`, `pandas`)
- Performance/C-integration (`cython`)
- Visualization (`matplotlib, seaborn`)
- Genetic analysis

Perl (excellent)

R (good)

C/C++ (good)
- `htslib` integration (`htslib`/`Bamtools`)

Bash (very good)

SELECTED SOFTWARE PROJECTS

SV^2 (Support-Vector Structural-Variant genotyper) https://github.com/dantaki/SV2

SV^2 is a machine learning algorithm for genotyping deletions and duplications from paired-end whole genome sequencing data. SV^2 can rapidly integrate variant calls from multiple SV discovery algorithms into a unified callset with high genotyping accuracy and detection of *de novo* mutations. SV^2 is open source and written in Python/Cython.

TRAINEES MENTORED

Dan Averbuj: Visiting masters student, San Diego State University	2019-
Beibei Cao: Undergraduate University of California, San Diego	2019-
Prathik Korategere Vijay Kumar: Bioinformatics analyst	2016
Aojie Lian, Visiting PhD student, Central South University, Changsha, China	2018-2019
An Nguyen: Undergraduate summer fellow, University of California, San Diego	2019-
Kevin Ramos: Undergraduate, University of California, San Diego	2019-
Aniket Shetty: Bioinformatics analyst	2015-2016
Zijing Angela Wang: Undergraduate, University of California, San Diego	2019-