John Anthony Capra, Ph.D.

updated: August 8, 2019

Contact Information

Vanderbilt University
Dept. of Biological Sciences
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Nashville, TN 37235-1634

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Academic Employment

Vanderbilt University, Nashville, Tennessee USA

Associate Professor (with tenure), Biological Sciences (primary); Genetics Institute; Computer Science; Biomed. Informatics; Center for Structural Biology — August 2019 – Present

Assistant Professor, Biological Sciences (primary); Vanderbilt Genetics Institute; Computer Science; Biomedical Informatics; Center for Structural Biology — August 2014 – July 2019

Assistant Professor, Center for Human Genetics Research and Department of Biomedical Informatics — February 2013 – August 2014

Education And Training

Gladstone Institutes, University of California, San Francisco, CA USA

Postdoctoral Fellow, October 2009 – December 2012

- Advisor: Katherine Pollard

Princeton University, Princeton, New Jersey USA

Ph.D., Computer Science, June 2009

- Advisor: Mona Singh
- Thesis: *Algorithms for the Identification of Functional Sites in Proteins*

M.A., Computer Science, October 2006

Columbia College, Columbia University, New York, New York USA

B.A., Computer Science, May 2004
B.A., Mathematics, May 2004

Pembroke College, Oxford University, Oxford, UK

Columbia University Oxford Scholar, October 2002 – June 2003

- Subject: Mathematics

Honors and Awards

Vanderbilt Ellen Fanning Award for Mentorship in the Biological Sciences	2019
Gladstone Institutes Distinguished Alumni Seminar	2019
Vanderbilt Chancellor's Award for Research	2017
Vanderbilt Center for Quantitative Sciences High Impact Research Award	2015, 2017
Gladstone Institutes Award for Excellence in Scientific Leadership	2012
Princeton University Wu Graduate Fellowship	2004 – 2008
Columbia University Oxford Scholar	2002 – 2003

Manuscripts in Review

Tang ZZ*, Sliwoski GR, Chen G, Li B, and **Capra JA***. *Scan Tests Guided by Protein Structures Discover Rare-Variant Associations and Signal Regions.* 2018

Sliwoski G, Patel N, Sivley RM, Sanders CR, Meiler J, Bush WS, **Capra JA**. *Do available protein 3D structures reflect human genetic and functional diversity?.* **bioRxiv**, 637744, 2019.

Ely ZA, JM Moon JM, Sliwoski GR, Sangha AK, Shen XX, LaBella AL, Meiler J, **Capra JA**, Rokas A. *The impact of natural selection on the evolution and function of placentally expressed galectins.* **bioRxiv**, 505339, 2018.

Manuscripts in Revision

Rinker DC, Simonti CS, McArthur E, Shaw D, Hodges E, **Capra JA**. *Neanderthal introgression reintroduced functional alleles lost in the human out of Africa bottleneck.* **bioRxiv**, 533257, 2018.

Publications (Vanderbilt)

Colbran LL, Gamazon ER, Zhou D, Evans P, Cox NJ, **Capra JA**. *Imputing archaic hominin gene regulation reveals divergent regulation and phenotypic differences.* Accepted at **Nature Ecology and Evolution**, 2019.

Moon JM, **Capra JA**, Abbot A, Rokas A. *Signatures of recent positive selection in enhancers across 41 human tissues.* **G3**, 9(8): 2761–2774, 2019.

Smith SA, Phillips JB, Johnson ML, Abbot P, **Capra JA**, and Rokas A. *Genome wide association analysis uncovers variants for reproductive variation across dog breeds and links to domestication.* **Evol. Med. Public Health**, 2019(1): 93–103, 2019.

Benton ML, Talipineni SC, Kostka D*, **Capra JA***. *Genome-wide Enhancer Maps Differ Significantly in Genomic Distribution, Evolution, and Function.* **BMC Genomics**, 20: 511, 2019. * co-corresponding authors

Colbran LL, Chen L, **Capra JA**. *Sequence characteristics distinguish transcribed enhancers from promoters and predict their breadth of activity.* **Genetics**, 211(4): 1205–1217, 2019.

Kroncke BM, Mendenhall J, Smith DK, Sanders CR, **Capra JA**, George AL, Blume JD, Meiler J, Roden DM. *Protein structure aids predicting functional perturbation of missense variants in SCN5A and KCNQ1.* **Computational and Structural Biotechnology**, 17: 206–14, 2019.

Zhang J*, Simonti CN*, and **Capra JA**. *Genome-wide maps of distal gene regulatory regions active in the human placenta.* **PLOS One**, 13(12): e0209611, 2018.

Eidem, HR, Steenwyk JL, Wisecaver JH, **Capra JA**, Abbot P, and Rokas A. *integRATE: a desirability-based data integration framework for the prioritization of candidate genes across heterogeneous omics and its application to preterm birth.* **BMC Medical Genomics**, 11:107, 2018.

Chen L, Fish AE, **Capra JA**. *Prediction of gene regulatory enhancers across species reveals evolutionarily conserved sequence properties.* **PLOS Computational Biology**, 14(10): e1006484, 2018.

Moon JM, Aronoff DM, **Capra JA**, Abbot P, Rokas A. *Examination of Signatures of Recent Positive Selection on Genes Involved in Human Sialic Acid Biology.* **G3: Genes, Genomes, Genetics**, 8(4): 1315–1325, 2018.

Sivley RM, Dou X, Meiler J, Bush WS*, **Capra JA***. *Comprehensive Analysis of Constraint on the Spatial Distribution of Missense Variants in Human Protein Structures.* **American Journal of Human Genetics**, 102: 415–426, 2018. * co-corresponding authors

Sivley RM, Sheehan JH, Kropski JA, Cogan J, Blackwell TS, Phillips JA, Bush WS, Meiler J, **Capra JA**. *Three-dimensional spatial analysis of missense variants in RTEL1 identifies pathogenic variants in patients with Familial Interstitial Pneumonia.* **BMC Bioinformatics**, 19:18, 2018.

Fish AE, Crawford DC, **Capra JA***, Bush WS*. *Local Ancestry Transitions Modify SNP–Trait Associations.* **Proceedings of the Pacific Symposium on Biocomputing**, 23:424–435, 2018. * co-corresponding authors

Fish AE*, Chen L*, **Capra JA**. *Gene regulatory enhancers with evolutionarily conserved-activity are more pleiotropic than those with species-specific-activity.* **Genome Biology and Evolution**, evx194, 2017. * co-first authors

Abbot P and **Capra JA**. *What is a placental mammal anyway?.* **eLife**, 6:e30994, 2017.

Simonti CN, Pavlicev M, and **Capra JA**. *Transposable Element Exaptation into Regulatory Regions is Rare, Influenced by Evolutionary Age, and Subject to Pleiotropic Constraints.* **Molecular Biology and Evolution**, msx219, 2017.

Patel V and **Capra JA**. *Ancient human miRNAs are more likely to have broad functions and disease associations than young miRNAs.* **BMC Genomics**, 18: 672, 2017.

Colbran LL, Chen L, and **Capra JA**. *Short DNA sequence patterns accurately identify broadly active human enhancers.* **BMC Genomics**, 18: 536, 2017.

Eidem HR*, McGary KL*, **Capra JA**, Abbot P, and Rokas A. *The transformative potential of an integrative approach to pregnancy.* **Placenta**, 57: 204–215, 2017.

Wanzek K, Schwindt E, **Capra J**, Paeschke, K. *Mms1 binds to G-rich regions in Saccharomyces cerevisiae and influences replication and genome stability.* **Nucleic Acids Research**. gkx467, 2017.

Anderson KA, Huynh FK, Fisher-Wellman K, Stuart JD, Peterson BS, Douros JD, Wagner GR, Thompson JW, Madsen AS, Green MF, Sivley RM, Ilkayeva OR, Stevens RD, Backos DS, **Capra JA**, Olsen CA, Campbell JE, Muoio DM, Grimsrud PA, Hirschey MD. *SIRT4 Is a Lysine Deacylase that Controls Leucine Metabolism and Insulin Secretion.* **Cell Metabolism**, 25(4): 838–855, 2017.

Fish A, **Capra JA**, Bush WS. *Are Genetic Interactions Influencing Gene Expression Evidence for Biological Epistasis or Statistical Artifacts?* **American Journal of Human Genetics**. 99 (4): 817–830, 2016.

Samuels DC, Wang J, Ye F, He J, Levinson RT, Sheng Q, Zhao S, **Capra JA**, Shyr Y, Zheng W, Guo Y. *Heterozygosity Ratio, a Robust Global Genomic Measure of Autozygosity and Its Association with Height and Disease Risk.* **Genetics**, 204, 893–904. 2016.

McDonald KR, Guise AJ, Pourbozorgi-Langroudi P, Cristea IM, Zakian VA , **Capra JA***, and Sabouri N*. *Pfh1 is an accessory replicative helicase that interacts with the replisome to facilitate fork progression and preserve genome integrity.* **PLoS Genetics**, 12(9): e1006238, 2016. * co-corresponding authors

Sugitani N, Sivley RM, Perry KE, **Capra JA**, Chazin WJ. *XPA: A key scaffold for human nucleotide excision repair.* **DNA Repair**, 44: 123–135, 2016.

Simonti CN, Vernot B, Bastarache L, Bottinger E, Carrell DS, Chisholm RL, Crosslin DR, Hebbring SJ, Jarvik GP, Kullo IJ, Li R, Pathak J, Ritchie MD, Roden DM, Verma SS, Tromp G, Prato JD, Bush WS, Akey JM, Denny JC, and **Capra JA**. *The phenotypic legacy of admixture between modern humans and Neanderthals.* **Science**, 351 (6274):737–741, 2016.

Wang X, Pandey A, Mulligan M, Williams E, Mozhui K, Li Z, Jovaisaite V, Quarles D, Xiao Z, Huang J, **Capra JA**, Chen Z, Taylor W, Bastarache L, Niu X, Pollard K, Ciobanu D, Reznik

A, Tishkov A, Zhulin I, Peng J, Nelson SF, Denny J, Auwerx J, Lu L, and Williams R. *Joint mouse-human phenome-wide association to test gene function and disease risk.* **Nature Communications**, 7:10464, 2016.

Kim M, Cooper, BA, Venkat R, Phillips JB, Eidem HR, Hirbo J, Nutakki S, Williams SM, Muglia LJ, **Capra JA**, Petren K, Abbot P, Rokas A, and McGary KL. *GEneSTATION 1.0: a synthetic resource of diverse evolutionary and functional genomic data for studying the evolution of pregnancy-associated tissues and phenotypes.* **Nucleic Acids Research**, gkv1137, 2015.

Simonti CN and **Capra JA**. *The evolution of the human genome.* **Current Opinion in Genetics and Development**, 35:9–15, 2015.

Simonti CN, Pollard KS, Schroeder S, He D, Bruneau BG, Ott M, and **Capra JA**. *Evolution of lysine acetylation in the RNA polymerase II C-terminal domain.* **BMC Evolutionary Biology**, 15:35, 2015.

Capra JA. *Extrapolating histone marks across developmental stages, tissues, and species: an enhancer prediction case study.* **BMC Genomics**, 16:104, 2015.

Sabouri N*, **Capra JA***, and Zakian, VA. *The essential Schizosaccharomyces pombe Pfh1 DNA helicase promotes fork movement past G-quadruplex motifs to prevent DNA damage.* **BMC Biology**, 12:101, 2014. * equal contribution and corresponding authors

Yu YK, **Capra JA**, Stojmirovic A, Landsman D, and Altschul, SF. *Log-Odds Sequence Logos.* **Bioinformatics**, 31 (3): 324-331, 2015.

Capra JA* and Kostka D*. *Modeling DNA methylation dynamics with approaches from phylogenetics.* **Bioinformatics**, 30 (17): i408–i414, 2014. * co-corresponding authors

Erwin GD, Oksenberg N, Truty RM, Kostka D, Murphy KK, Ahituv N, Pollard KS*, **Capra JA***. *Integrating Diverse Datasets Improves Developmental Enhancer Prediction.* **PLoS Computational Biology**, 10(6): e1003677, 2014. * co-corresponding authors

Capra JA, Stolzer M, Durand D, Pollard KS. *How old is my gene?.* **Trends in Genetics**, 29(11): 659–668, 2013.

Publications (as trainee)

Schroeder S, Herker E, Itzen F, He D, Thomas S, Gilchrist, Kaehlcke K, Cho S, Pollard KS, **Capra JA**, Schnoelzer M, Cole PA, Geyer M, Bruneau B, Adelman K, and Ott M. *Acetylation of RNA Polymerase II Regulates Growth-Factor-Induced Gene Transcription in Mammalian Cells.* **Molecular Cell**, 52(3): 314–324, 2013.

Capra JA, Erwin GD, McKinsey G, Rubenstein JLR, Pollard KS. *Many Human Accelerated Regions are Developmental Enhancers.* **Philosophical Transactions of the Royal Society B**, 368: 20130025, 2013.

Capra, JA*, Hubisz, MJ*, Kostka D, Pollard KS, Siepel A. *A Model-Based Analysis of GC-Biased Gene Conversion in the Human and Chimpanzee Genomes.* **PLoS Genetics**, 9(8): e1003684, 2013. * co-first authors

Wamstad JA, Alexander JM, Truty RM, Shrikumar A, Li F, Eilertson KE, Ding H, Wylie JN, Pico AR, **Capra JA**, Erwin G, Kattman SJ, Keller GM, Srivastava D, Levine SS, Pollard KS, Holloway AK, Boyer LA, Bruneau BG. *Dynamic and Coordinated Epigenetic Regulation of Developmental Transitions in the Cardiac Lineage.* **Cell**, 151(1): 206–220, 2012.

Capra JA, Williams AG, and Pollard KS. *ProteinHistorian: Tools for Comparative Analysis of Eukaryote Protein Origins.* **PLoS Computational Biology**, 8(6): e1002567, 2012.

Katzman S*, **Capra JA***, Haussler D, and Pollard KS. *Ongoing GC-biased evolution is widespread in the human genome and enriched near recombination hotspots.* **Genome Biology and Evolution**, 3: 614–626, 2011. * co-first authors

Hirschey MD*, Shimazu T*, **Capra JA***, Pollard KS, and Verdin E. *SIRT1 and SIRT3 Deacetylate Homologous Substrates: AceCS1,2 and HMGCS1,2.* **Aging**, 3(6): 635–642, 2011. * co-first authors.

Capra JA and Pollard KS. *Substitution patterns are GC-biased in divergent sequences across the metazoans.* **Genome Biology and Evolution**, 3: 516–527, 2011.

Paeschke K, **Capra JA**, and Zakian VA. *DNA Replication through G-Quadruplex Motifs Is Promoted by the Saccharomyces cerevisiae Pif1 DNA Helicase.* **Cell**, 145(5): 678–691, 2011. Highlighted in Nature Reviews Molelcular Cellular Biology.

Capra JA, Pollard KS, and Singh M. *Novel genes exhibit distinct patterns of function acquisition and network integration.* **Genome Biology**. 11(12): R127, 2010. Highlighted on Genome Web.

Capra JA*, Paeschke K*, Singh M and Zakian VA. *G-quadruplex DNA sequences are evolutionarily conserved and associated with distinct genomic features in Saccharomyces cerevisiae.* **PLoS Computational Biology**. 6(7): e1000861, 2010. * co-first authors.

Capra JA, Carbone L, Riesenfeld SJ, and Wall JD. *Genomics through the lens of next-generation sequencing.* **Genome Biology**. 11(6): 306, 2010.

Capra JA, Laskowski RA, Thornton JM, Singh M and Funkhouser TA. *Predicting Protein Ligand Binding Sites by Combining Evolutionary Sequence Conservation and 3D Structure.* **PLoS Computational Biology**. 5(12): e1000585, 2009. Highlighted on Genome Web Daily.

Capra JA and Singh M. *Characterization and Prediction of Residues Determining Protein Functional Specificity.* **Bioinformatics**. 24(13): 1473–1480, 2008.

Capra JA and Singh M. *Prediction of Functionally Important Residues from Sequence Conservation.* **Bioinformatics**. 23(15):1875–82, 2007.

Rosen G, La Porte N, Diechtiareff B, Pung C, Nissanov J, Gustafson C, Bertrand L, Gefen S, Fan Y, Tretiak O, Manly K, Park M, Williams A, Connolly M, **Capra JA**, Williams R. *Informatics Center for Mouse Genomics: The Dissection of Complex Traits of the Nervous System.* **Neuroinformatics**. 1 (4): 327–342, 2003.

Rosen G, Williams A, **Capra JA**, Connolly M, Cruz B, Lu L, Airey D, Kulkarni A, Williams R. The Mouse Brain Library at www.mbl.org. *Int Mouse Genome Conference* 14: 166, 2000.

Research Grants

Currently Funded (as Principal Investigator):

The Evolution of Gene Regulation and Human Disease
NIH/NIGMS R35 GM127087
Role: Principal Investigator
04/01/2018 – 03/31/2023

Vanderbilt Center for Undiagnosed Diseases (VCUD)
NIH/NHGRI U01 HG007674

Role: Subcontract Principal Investigator
07/01/2018 – 06/30/2022

Integrating 'Omics and EHRs to Elucidate the Genetic Architecture of Preterm Birth
Burroughs Wellcome Fund
Role: Principal Investigator
06/01/2017 – 03/31/2021

Currently Funded (as Co-Investigator):

From Gene Discovery in Human Pregnancy to Mechanisms of Birth Timing
March of Dimes Prematurity Research Collaborative
Role: Section Lead (PI: Muglia/Rokas)
10/01/2018 – 04/30/2019

Analyses, Validation, and Resource Creation for Genome Sequencing of Complex Diseases
NIH/NHGRI U01 HG009086
Role: Co-Investigator (PI: Li/Cox)
05/08/2016 – 04/30/2020

Completed (as Principal Investigator):

Modeling the dynamics of genome-scale data on trees
NIH/NIGMS R01 GM115836
Role: Principal Investigator (with Dennis Kostka at Pitt)
08/01/2015 – 07/31/2018

Personalized Structural Biology to Guide Cancer Treatment
Vanderbilt Ingram Cancer Center – Ambassadors Discovery Program
Role: Principal Investigator
02/01/2017 – 01/31/2018

Evaluating the Influence of Neanderthal Interbreeding on the Human Visual System
Vanderbilt Center for Quantitative Sciences Pilot Project Award
Role: Principal Investigator
07/01/2015 – 06/30/2016

Elucidating the Gene Regulatory Landscape of Human Preterm Birth
March of Dimes – Innovation Catalyst Award
Role: Principal Investigator
01/01/2015 – 01/01/2017

Completed (as Co-Investigator):

Evolutionary Synthesis of Human Pregnancy
March of Dimes Prematurity Research Collaborative
Role: Co-Investigator
07/01/2013 – 06/01/2018

Selected Invited Presentations

"Diagnosing the Legacy of Neanderthal Interbreeding on Modern Humans"
Computational Biology and Bioinformatics Program, Duke University — November 18, 2019

"Integrating Genomic and Patient Data to Interpret Human and Neanderthal Genomes"
Genome Sciences, University of Washington — October 23, 2019

"Diagnosing the Legacy of Neanderthal Interbreeding on Modern Humans"
Institute for Computational Biology, Case Western Reserve University July 9, 2019

"Personalized Structural Biology Enables Variant Interpretation"
Vanderbilt Personalized Medicine Day June 4, 2019

"My ancestor was a Neanderthal. Should I see a doctor?"
Gladstone Institutes 40th Anniversary Distinguished Alumni Symposium April 30, 2019

"Using EHR-linked Biobanks to Explore the Complexity of Preterm Birth"
March of Dimes Prematurity Research Collaborative, Washington D.C. April 15, 2019

"Diagnosing the Legacy of Neanderthal Interbreeding on Modern Humans"
HudsonAlpha Institute for Biotechnology April 3, 2019

"Integrating Genomic and Patient Data to Interpret Human and Neanderthal Genomes"
UCSF Diabetes Center February 12, 2019

"Using evolution and machine learning to interpret human and Neanderthal genomes"
Cold Spring Harbor Simons Center for Quantitative Biology January 14, 2019

"Diagnosing the Legacy of Neanderthal Interbreeding on Modern Humans"
Human Medical Genetics and Genomics, University of Colorado, Denver Dec. 13, 2018

"The Immunological Consequences of Neanderthal Introgression"
ASM Microbe 2018, Atlanta, Georgia June 2018

"The legacy of Neanderthal Interbreeding on Human Skin"
EMBO: Perspectives on skin cancer prevention, Les Diablerets, Switzerland April 9, 2018

"My ancestor was a Neanderthal. Should I see a doctor?"
Cole Lecture, Deparment of Biology, Wabash College Nov. 6, 2017

"Diagnosing the Legacy of Neanderthal Interbreeding on Modern Humans"
Trevecca Nazarene University April 21, 2017

"The Phenotypic Legacy of Neandertal Interbreeding on Modern Humans"
Department of Biology, Georgia Tech Feb. 8, 2017

"Identification and evolutionary analysis of gene regulatory enhancers relevant to pregnancy"
March of Dimes Ohio Collaborative Retreat, Cincinnati, OH October 7, 2016

"The Phenotypic Legacy of Neandertal Interbreeding on Modern Humans"
Center for Academic Training and Research in Anthropogeny, UC San Diego April 29, 2016

"Identification and evolutionary analysis of pregnancy-relevant gene regulatory enhancers"
Cincinnati Children's Hospital Medical Center April 22, 2016

"The Phenotypic Legacy of Neandertal Interbreeding on Modern Humans"
AAAS Annual Meeting, Washington, DC February 11, 2016

"Genome-wide identification and evolutionary analysis of pregnancy-relevant gene regulatory enhancers"
March of Dimes Prematurity Research Center Nov. 4, 2015

"The clinical legacy of admixture between humans and Neanderthals"
Vanderbilt Molecular Biophysics/Center for Structural Biology Seminar Series Nov. 3, 2015

"The clinical legacy of admixture between humans and Neanderthals"
Vanderbilt Cancer Systems Biology Seminar Sept. 25, 2015

"Diagnosing the clinical legacy of admixture between humans and Neanderthals"
Fisk University Summer Science Cafe Seminar July 1, 2015

"Integrating Genome-scale Data to Predict the Effects of Human-specific Non-coding Mutations"
Duke University Department of Bioinformatics and Biostatistics February 2014

"Comparative and Functional Genomics of Human-specific Gene Expression"
University of Virginia Genome Sciences Seminar November 2013

"Comparative and Functional Genomics of Human-specific Gene Expression"
University of Kentucky Biology Ribble Seminar October 2013

"Integrating DNA Sequence Data, Evolutionary Models, and Functional Genomics to Identify Human-specific Gene Regulation"
Mathematics of Sequence Evolution Workshop, Université de Montréal September 2013

"Comparative and Functional Genomics of Human-specific Gene Regulation"
Department of Epidemiology and Biostatistics, Case Western Reserve University September 2013

"Comparative and Functional Genomics of Human-specific Gene Regulation"
Department of Biological Sciences, Vanderbilt University September 2013

"Comparative and Functional Genomics of Human-specific Gene Regulation"
Department of Pharmacology, University of TN, Memphis May 2013

"Integrating Genome-scale Data to Predict the Effects of Human specific Non Coding Mutations"
UT-ORNL-KBRIN Bioinformatics Summit March 2013

"Integrating Genome-scale Data to Predict the Effects of Human specific Non Coding Mutations"
Institute of Bioinformatics, University of Georgia September 2012

"Integrating Comparative and Functional Genomics to Predict the Effect of Human-specific Mutations"
Center for Human Genetics Research, Vanderbilt University April 2012

"Comparing genomes to understand the causes and effects of accelerated evolution in human"
UCSF Evolution Seminar Series February 2012

Conference Oral Presentations

"The Neanderthal Protein Structure Atlas: Comprehensive modeling of Neanderthal 3D structures"
Society for Molecular Biology and Evolution Annual Meeting, Manchester, UK July 2019

"Neanderthal introgression reintroduced thousands of ancestral alleles lost in the out of Africa bottleneck"
American Society for Human Genetics Annual Meeting, Orlando, FL October 2017

"The Evolution of Gene Expression" (Symposium)
Society for Molecular Biology and Evolution Annual Meeting, Austin, TX July 2017

"First depleted, then enriched: the evolution of transposable element regulatory function"
American Society for Human Genetics Annual Meeting, Vancouver, BC October 2016

"Probabilistic models for integrating genome-scale data with tree-like dependencies"
Cold Spring Harbor Probabilistic Modeling in Genomics 2015 Conference October 2015

"Exploring the consequences of ancient and contemporary gene flow" (Symposium)
Society for Molecular Biology and Evolution Annual Meeting, Vienna, Austria July 2015

"How old is my gene?" (Symposium)
Society for Molecular Biology and Evolution Annual Meeting, San Juan, PR July 2014

"A Model-Based Analysis of GC-Biased Gene Conversion in the Human and Chimpanzee Genomes"
Intelligent Systems in Molecular Biology (ISMB) Annual Meeting, Berlin July 2013

"ProteinHistorian: Tools for Comparative Analysis of Eukaryote Protein Origins"
Association for Computing Machinery International Conference on Bioinformatics, Computational Biology and Biomedicine, Orlando October 2012

"Predicting and Testing Human-specific Developmental Enhancers"
Society for Molecular Biology and Evolution Annual Meeting, Dublin, Ireland June 2012

"Modeling the contributions of GC-biased gene conversion and selection to fast-evolving regions of primate genomes"
Society for Molecular Biology and Evolution Annual Meeting, Dublin, Ireland June 2012

"Comparative Genomics of Humanness – What does our DNA tell us about what makes us human?"
American Association of Physical Anthropologists Annual Meeting, Minneapolis April 2011

Teaching

Teaching, Vanderbilt University

- Genome Science (BSCI 3272) Fall 2016, 2017, 2019
- Principles of Genetics (BSCI 2210) Spring 2016, 2017, 2018
- Evolution of the Human Genome (BSCI 3965) Fall 2015
- Biological Sciences Graduate Seminar (BSCI 6320) Spring 2014
- Tutorials in Human Genetics (HGEN 370) Fall 2014

I also guest lecture in several classes including Human Biology, Bioinformatics, Human Genetics I and II, Behavioral Genetics, Human Evolutionary Genetics, and Biological Anthropology.

Mentoring

Advisor, Vanderbilt University

Postdoctoral Scholars:

- Bian Li July 2019 – Present
- Greg Sliwoski July 2016 – May 2019
- David Rinker December 2015 – Present

Graduate Students:

- Evonne McArthur (Human Genetics/MSTP) Fall 2018 – Present
- Sarah Fong (Human Genetics) Summer 2018 – Present
- Keila Velázquez-Arcelay (Biological Sciences) Summer 2018 – Present
- Abin Abraham (Human Genetics/MSTP) Fall 2017 – Present
- Souhrid Mukherjee (Biological Sciences, co-advised with Jens Meiler) Summer 2017 – Present
- Mary Lauren Benton (Biomedical Informatics) Summer 2016 – Present
- Laura Colbran (Human Genetics) Summer 2016 – Present

- Ling Chen (Biological Sciences) Summer 2015 – Present

Completed PhDs Supervised:
- R. Michael Sivley (Biomedical Informatics, co-advised with Will Bush) Fall 2013 – Fall 2017
- Tim O'Brien (Human Genetics, local co-mentor) Spring 2016 – Spring 2017
- Alexandra Fish (Human Genetics, co-advised with Will Bush) Summer 2014 – Spring 2017
- Corinne Simonti (Human Genetics) Summer 2013 – Spring 2017

Undergraduates/Research Interns:
- Merian Gabra (TSU Undergraduate) Summer 2019
- Kevin Yang (Vanderbilt Undergraduate) Summer 2018 – Present
- Daniel Yan (Vanderbilt Undergraduate) Summer 2018
- Maya Johnson (Vanderbilt School for Science and Mathematics) Spring 2018 – Present
- Chantay Young (Vanderbilt SyBBURE) Summer 2017
- Kevin Gomez (Vanderbilt School for Science and Mathematics) Spring 2017 – Fall 2017
- Shahrukh Malik (Vanderbilt International Scholars Program) Summer 2016
- Xiaoyi Dou (Vanderbilt Undergraduate) Spring 2016 – Summer 2017
- Joanna Zhang (Vanderbilt Undergraduate) Summer 2015 – Spring 2017
- Zubia Shahid (University of the Sciences Masters Student) Summer 2015
- Laura Colbran (Carleton Undergraduate) Summer 2014
- Vir Patel (WKU Undergraduate) Summer 2014

PhD Committee Service, Vanderbilt University:
- Brittany Allison (Chemistry) PhD 2017
- Kerri-Ann Anderson (Biological Sciences, chair)
- Kelly Barnett (Biochemistry)
- Samantha Beik (Cancer Biology)
- Andrew Brooks (Human Genetics, chair) PhD 2019
- Haley Eidem (Biological Sciences) PhD 2018
- Jessica Finn (Microbiology and Immunology) PhD 2019
- Darwin Fu (Chemistry) PhD 2018
- Jake Hall (Human Genetics) PhD 2016
- Tyler Hansen (Biochemistry)
- Corey Hayford (Chemical and Physical Biology)
- Chuck Herring (Chemical and Physical Biology) PhD 2018
- Maria Luisa Jabbur (Biological Sciences)
- Nergis Kara (Biological Sciences) PhD 2018
- Mara Kim (Biological Sciences) PhD 2018
- Abigail Lind (Biomedical Informatics) PhD 2017
- Alyssa Lokits (Neurosciences) PhD 2017
- Robert Markowitz (Chemical and Physical Biology)
- Michelle Moon (Biological Sciences) PhD 2019
- Tim O'Brien (Human Genetics) PhD 2017
- Juan Felipe Ortiz (Biological Sciences) PhD 2019
- Cristina Robinson (Biological Sciences)
- Emily Ross (Human Genetics)
- Parker Rundstrom (Biological Sciences)
- Timothy Scott (Human Genetics)
- Abigail Searfoss (Chemical and Physical Biology, chair)
- Katherine Snyder (Biological Sciences)
- Jacob Steenwyk (Biological Sciences, chair)
- Alexander Thiemicke (Chemical and Physical Biology)
- Edward Van Opstal (Biological Sciences) PhD 2018
- Hope Woods (Chemical and Physical Biology, chair)

- Linhe Xu (Psychology)
- Yan Yan (Biological Sciences)

Service

Departmental Service:

Associate Director of Graduate Studies (Biological Sciences)	2019 – 2022
Biological Sciences Faculty Search Committee	2017 – 2018
Biological Sciences Graduate Admissions Committee	2016, 2017
Biological Sciences DGS Advisory Committee	2016, 2017
Biomedical Informatics Graduate Admissions Committee	2016 – Present
Vanderbilt Genetics Institute Search Committee (chair)	2016 – 2017
Biological Sciences Faculty Search Committee	2015 – 2016
Biological Sciences Faculty Search Committee	2014 – 2015

University Service:

BioVU Pre-review Committee	2014 – Present
BioVU MEGA Quality Control Task Force	2018 – Present

Professional Service:

Program Committee: ACM BCB 2013, ASHG 2014, RECOMB 2016, RECOMB/ISCB Regulatory and Systems Genomics 2018, RECOMB 2019, RECOMB/ISCB Regulatory and Systems Genomics 2019, RECOMB 2020
Session Moderator: ASHG 2015
Symposium Organizer: SMBE 2014, SMBE 2015, SMBE 2017

Reviewer for: Science, Cell, Nature Biotechnology, PNAS, eLife, Cell Reports, Genome Research, Genome Biology, Genetics in Medicine, PLoS Genetics, PLoS Computational Biology, Bioinformatics, Trends in Genetics, Molecular Biology and Evolution, Genome Biology and Evolution, American Journal of Human Genetics, Statistical Applications in Genetics and Molecular Biology, Nucleic Acids Research, BMC Evolutionary Biology, Evolution, Philosophical Transactions of the Royal Society B, International Journal of Biomedical Data Mining, Pattern Recognition Letters, Plant Physiology, Trends in Plant Sciences, Molecular Autism, PLoS One

Guest Editor: PLoS Genetics

I maintain several software packages and web servers to support my research and make algorithms I developed available to the community.

- **Neanderthal PheWAS Catalog** (https://phewas.mc.vanderbilt.edu/neanderthal)
  Enables exploration of phenotypes associated with Neanderthal admixture 2015 – Present
- **ProteinHistorian** (http://lighthouse.ucsf.edu/ProteinHistorian/)
  Performs comparative analysis of protein origins 2011 – Present
- **ConCavity** (http://compbio.cs.princeton.edu/concavity/)
  Predicts protein ligand binding sites 2009 – Present
- **GroupSim** (http://compbio.cs.princeton.edu/specificity/)
  Predicts specificity determining sites in proteins 2008 – Present
- **Jensen-Shannon divergence** (http://compbio.cs.princeton.edu/conservation/)
  Estimates evolutionary sequence conservation 2007 – Present

Outreach

I have been fortunate to have the opportunity to act as an ambassador of my field in the popular press. In 2017, I was profiled in the NY Times' "A Conversation With" series. I have been interviewed about my work by major print, radio, and television news outlets from around the world, including *The New York Times, The Wall St. Journal, The LA Times, The Guardian, The Atlantic*, PBS, the BBC, and many more. My work has also been featured multiple times in major science news outlets, such as *Science News, Nature News, The Scientist, Smithsonian*, and more. In 2018, I

was featured in a PBS/BBC documentary called "Neanderthals: Meet Your Ancestors." I was selected to participate with leaders in human genetics research in a two-day symposium organized by the Center for Academic Research and Training in Anthropogeny (CARTA) on "Ancient DNA and Human Evolution" in April 2016. Over the summer of 2017, I worked with curators at the London Science Museum to include results from my work in an interactive exhibit about the effects of interbreeding between humans and Neanderthals. Finally, I am commonly asked to comment on the latest work in human evolution.