

John Anthony Capra, Ph.D.

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CONTACT INFORMATION	Vanderbilt University Dept. of Biological Sciences VU Station B, Box 35-1634 Nashville, TN 37235-1634	<i>e-mail:</i> tony.capra-at-vanderbilt.edu <i>www:</i> http://www.capralab.org/ <i>office:</i> U5221 BSB/MRB III <i>phone:</i> (615) 343-3671
ACADEMIC EMPLOYMENT	Vanderbilt University , Nashville, Tennessee USA Assistant Professor , Biological Sciences (primary); Vanderbilt Genetics Institute; Computer Science; Center for Structural Biology August 2014 – Present 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 <ul style="list-style-type: none">• Advisor: Katherine Pollard Princeton University , Princeton, New Jersey USA Ph.D. , Computer Science, June 2009 <ul style="list-style-type: none">• Advisor: Mona Singh• Thesis: <i>Algorithms for the Identification of Functional Sites in Proteins</i> 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 <ul style="list-style-type: none">• Subject: Mathematics	
HONORS AND AWARDS	Vanderbilt Chancellor's Award for Research Vanderbilt Center for Quantitative Sciences High Impact Research Award Gladstone Institutes Award for Excellence in Scientific Leadership Princeton University Wu Graduate Fellowship Columbia University Oxford Scholar	2017 2015, 2017 2012 2004 – 2008 2002 – 2003
PUBLICATIONS	Sivley RM, Dou X, Meiler J, Bush WS*, Capra JA* . <i>Comprehensive Analysis of Constraint on the Spatial Distribution of Missense Variants in Human Protein Structures</i> . American Journal of Human Genetics , In Press, 2018. * co-corresponding authors Sivley RM, Sheehan JH, Kropski JA, Cogan J, Blackwell TS, Phillips JA, Bush WS, Meiler J, Capra JA . <i>Three-dimensional spatial analysis of missense variants in RTEL1 identifies pathogenic variants in patients with Familial Interstitial Pneumonia</i> . BMC Bioinformatics , 19:18, 2018. Fish AE, Crawford DC, Capra JA* , Bush WS*. <i>Local Ancestry Transitions Modify SNP–Trait Associations</i> . Proceedings of the Pacific Symposium on Biocomputing , 23:424–435, 2018. *	

co-corresponding authors

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

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, Vernet B, Bastarache L, Bottinger E, Carrell DS, Chisholm RL, Crosslin DR, Hebring 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 Commu-**

nications, 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. *GENE STATION 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, Schder 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

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

SELECTED INVITED PRESENTATIONS	“My ancestor was a Neanderthal. Should I see a doctor?” Cole Lecture, Department of Biology, Wabash College	Nov. 6, 2017.
	“The Phenotypic Legacy of Neandertal Interbreeding on Modern Humans” Department of Biology, Georgia Tech	Feb. 8, 2017
	“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 Quantitative 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
“Comparative and Functional Genomics of Human-specific Gene Expression” Vanderbilt Center for Human Genetics Research Symposium	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” Vanderbilt Epidemiology and Biostatistics Ground Rounds	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

SELECTED
CONFERENCE
PRESENTATIONS

“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 at 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 at Society for Molecular Biology and Evolution Annual Meeting, Vienna July 2015

“How old is my gene?”
Symposium at Society for Molecular Biology and Evolution Annual Meeting, San Juan 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 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 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 AND
MENTORING

Teaching, Vanderbilt University

- Genome Science (BSCI 3272) Fall 2016, 2017
- Principles of Genetics (BSCI 2210) Spring 2016, 2017
- 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 have also lectured in several classes including Bioinformatics, Human Genetics I and II, Human Evolutionary Genetics, and Biological Anthropology.

Advisor, Vanderbilt University

Postdoctoral Scholars:

- Greg Sliwoski July 2016 – Present
- David Rinker December 2015 – Present

PhD Students:

- 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
- Tim O'Brien (Human Genetics, co-advised with Zhongming Zhao) Spring 2016 – Spring 2017
- Ling Chen (Biological Sciences) Summer 2015 – Present
- Alexandra Fish (Human Genetics, co-advised with Will Bush) Summer 2014 – Spring 2017
- Mike Sivley (Biomedical Informatics, co-advised with Will Bush) Fall 2013 – Fall 2017
- Corinne Simonti (Human Genetics) Summer 2013 – Spring 2017

Undergraduates/Interns:

- Maya Johnson (Vanderbilt School for Science and Mathematics) Spring 2018 – Present
- Chantay Young (Vanderbilt SyBBURE) Summer 2017 – Present
- Kevin Gomez (Vanderbilt School for Science and Mathematics) Spring 2017 – Fall 2018
- Shahrukh Malik (Vanderbilt International Scholars Program) Summer 2016
- Xiaoyi Dou (Vanderbilt Undergraduate) Spring 2016 – Spring 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