

John Anthony Capra

CONTACT INFORMATION	2215 Garland Avenue 519A Light Hall Vanderbilt University Nashville, TN 37212	<i>e-mail:</i> tony.capra-at-vanderbilt.edu <i>www:</i> http://www.capralab.org/ <i>phone:</i> (615) 343-3671
RESEARCH INTERESTS	<ul style="list-style-type: none">• Applying computational methods to problems in genetics, evolution, and biomedicine.• Analyzing genome-scale data to understand the functional effects of non-coding genetic differences between individuals and species.• Modeling evolutionary processes that drive the creation of lineage-specific traits and diseases.	
ACADEMIC EMPLOYMENT	Vanderbilt University , Nashville, Tennessee USA Assistant Professor , Department of Biomedical Informatics Investigator , Center for Human Genetics Research	February 2013 – Present
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	Gladstone Institutes Award for Excellence in Scientific Leadership Society for Molecular Biology and Evolution (SMBE) Travel Award PhRMA Foundation Postdoctoral Fellowship in Informatics Princeton University Wu Graduate Fellowship Columbia University Oxford Scholar	2012 2012 2011 – 2013 2004 – 2008 2002 – 2003
PUBLICATIONS	Erwin GD, Truty RM, Kostka D, Pollard KS*, Capra JA* . <i>Integrating Diverse Datasets Improves Developmental Enhancer Prediction</i> . Under Review , 2013. * co-senior 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. <i>Acetylation of K7 Residues Marks Paused RNA Polymerase II in Mammalian Cells</i> . Under Revision , 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**, In press, 2013.

Capra JA, Stolzer M, Durand D, Pollard KS. *How old is my gene?*. **Trends in Genetics**, In press, 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 Daily.

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.

ACADEMIC
MENTORING

Advisor, Vanderbilt University

- Mike Sivley (Biomedical Informatics) Summer 2013 – Present
- Corinne Simonti (Human Genetics) Summer 2013 – Present

Mentor, University of California, San Francisco

Mentored UCSF graduate students' rotation projects with my postdoctoral group.

- Tara Friedrich – *Sex-specific Recombination and GC-biased Evolution* Spring 2012
- Liz Howe – *Predicting Accelerated Evolution in Ascomycota Fungi* Fall 2010
- Trevor Sorrells – *Why are young genes shorter than old genes?* Summer 2010

Mentor, Princeton University

Mentored undergraduate students from underrepresented groups in the Summer Programming Experience and Research Experience for Undergraduates programs.

- Bettina Burgett – *Sequence-based Prediction of Protein-Protein Interaction Sites* Summer 2008
- Elijah Lowe – *Online Tools for Predicting Evolutionary Conservation* Summer 2007

SOFTWARE

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

- **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

SELECTED
PRESENTATIONS

“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

“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

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

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

“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

“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