

John Anthony Capra

- CONTACT INFORMATION Gladstone Institutes *e-mail:* tony.capra-at-gladstone.ucsf.edu
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- RESEARCH INTERESTS
- Applying computational methods to problems in evolution, molecular biology, 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.
- EDUCATION AND TRAINING
- Gladstone Institutes, University of California, San Francisco, CA USA**
Postdoctoral Fellow, October 2009 – Present
- 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
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| Society for Molecular Biology and Evolution (SMBE) Travel Award | 2012 |
| Gladstone Institutes Leadership Award | 2012 |
| PhRMA Foundation Postdoctoral Fellowship in Informatics | 2011 – 2013 |
| NIH Quantitative and Computational Biology Program Training Fellowship | 2004 – 2009 |
| Princeton University Wu Graduate Fellowship | 2004 – 2008 |
| Columbia University Oxford Scholar | 2002 – 2003 |
- PUBLICATIONS
- Wamstad JA, Alexander JM, Truty RM, Shrikumar A, Li F, Eilertson KE, Ding H, 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*. Under Revision in **Cell**.
- Capra JA**, Williams AG, and Pollard KS. *ProteinHistorian: Tools for Comparative Analysis of Eukaryote Protein Origins*. **PLoS Computational Biology**. In Press.
- 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 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.

RESEARCH
EXPERIENCE

Postdoctoral Scholar, University of California, San Francisco October 2009 – Present

- Characterized patterns of GC-biased evolution across eukaryotes
- Examined population data from human genomes for signatures of recent non-adaptive evolution
- Predicted and tested the impact of lineage-specific non-coding substitutions in the human and mouse genomes

Graduate Student, Princeton University September 2004 – June 2009

- Developed methods for the prediction of functionally important sites in proteins using information theory and analysis of protein sequence and structure
- Used comparative genomics to explore the functional role G-quadruplex DNA structures in *S. cerevisiae*

	Research Assistant , Network Computing Lab, Columbia University	Summer 2003
	<ul style="list-style-type: none"> • Evaluated the performance of different compression methods in thin-client systems 	
	Research Assistant , University of Tennessee, Memphis	Summers 2001, 2002
	<ul style="list-style-type: none"> • Developed the iScope system for real-time, online research telemicroscopy 	
	Scientific Programmer , University of Tennessee, Memphis	Summers 1999, 2000
	<ul style="list-style-type: none"> • Developed computer tools for genetics research lab. Created online atlases of the mouse brain (www.mbl.org) 	
MENTORING EXPERIENCE	Mentor , University of California, San Francisco	
	Mentored two graduate students' rotation projects with our group.	
	<ul style="list-style-type: none"> • Liz Howe – <i>Predicting Accelerated Evolution in Ascomycota Fungi</i> • Trevor Sorrells – <i>Why are young genes shorter than old genes?</i> 	Fall 2010 Spring 2010
	Mentor , Princeton University	
	Mentored undergraduate students from underrepresented groups in the Summer Programming Experience and Research Experience for Undergraduates programs.	
	<ul style="list-style-type: none"> • Bettina Burgett – <i>Sequence-based Prediction of Protein-Protein Interaction Sites</i> • Elijah Lowe – <i>Online Tools for Predicting Evolutionary Conservation</i> 	Summer 2008 Summer 2007
TEACHING EXPERIENCE	Writing Center Fellow , Princeton University	Fall 2007 – Spring 2009
	Discussed papers—ranging from freshman essays to PhD theses—in weekly one-on-one conferences with students.	
	Assistant in Instruction , Princeton University	Spring 2006, Spring 2007
	COS 234 A Quantitative Integrated Introduction to the Natural Sciences: Taught weekly computer science recitation, held office hours, and developed and graded assignments for a class of ~25 students.	
SERVICE	Reviewer for: PLoS Computational Biology, Bioinformatics, Trends in Genetics, Molecular Biology and Evolution, Statistical Applications in Genetics and Molecular Biology, Nucleic Acids Research, International Journal of Biomedical Data Mining, Pattern Recognition Letters	2008 – 2011
	Princeton Computer Science Graduate Committee	2004 – 2009
SOFTWARE	I maintain several software packages and web servers to support my research and make algorithms I developed available to the community.	
	<ul style="list-style-type: none"> • ProteinHistorian (http://lighthouse.ucsf.edu/ProteinHistorian/) • ConCavity (http://compbio.cs.princeton.edu/concavity/) • GroupSim (http://compbio.cs.princeton.edu/specificity/) • Jensen-Shannon divergence (http://compbio.cs.princeton.edu/conservation/) 	2011 – Present 2009 – Present 2008 – Present 2007 – Present
SELECTED PRESENTATIONS	“Comparative Genomics of Humanness – What does our DNA tell us about what makes us human?” American Association of Physical Anthropologists Annual Meeting	April 2011
	“GC-biased substitution in fast evolving regions across the eukaryotes” (poster) UCSF Human Genetics 5th Anniversary Symposium	October 2010

“Evidence for the rapid integration of novel genes into cellular networks” (poster)
Cold Spring Harbor Biology of Genomes Meeting

May 2010

REFERENCES

Katherine Pollard (Postdoctoral Advisor)
Associate Professor, Gladstone Institutes
University of California, San Francisco
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(415) 734-2711

Mona Singh (Doctoral Advisor)
Associate Professor, Computer Science and Lewis-Sigler Institute for Integrative Genomics
Princeton University
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Thomas Funkhouser (Collaborator and PhD Committee member)
Professor, Computer Science
Princeton University
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Virginia Zakian (Collaborator)
Harry C. Wiess Professor, Molecular Biology
Princeton University
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