

~ Jade Yu Cheng ~

8500 Waterwillow Pl · Orlando, FL 32827, USA

US Mobile: +1-808-206-5059 · Denmark Mobile: +45-9398-1013 · Email: jade.cheng@cs.au.dk · Website: www.jade-cheng.com

Appointments	2017 (current)	Postdoc. Genetics and Statistics, University of California, Berkeley, USA
	2016 - 2017	Postdoc. Natural History Museum of Denmark, University of Copenhagen, Denmark
Education	August 2016	Ph.D. Computer Science, Bioinformatics; Aarhus University, Denmark
	May 2011	M.S. Information & Computer Science; University of Hawai'i at Mānoa, USA
	December 2008	M.S. Molecular Biosciences and Bioengineering; University of Hawai'i at Mānoa, USA
	July 2006	B.S. Biotechnology; Nankai University, China
Teaching Experience	Teaching Assistant · Aarhus University	
	2016 Q4	Introduction to Data Science
	2015 Q1	Introduction to Bioinformatics (R)
	2014 Q1	Databases (SQL)
	2013 Q4	Algorithms and Data Structures II
	2013 Q3	Algorithms and Data Structures I
	2013 Q2	Applied Programming (Python)
	Adjunct Professor · Hawai'i Pacific University	
	2012 Spring	Computer Science II (Java)
	Teaching Assistant · University of Hawai'i at Mānoa	
	2011 Spring	Algorithms
	2010 Spring	Introduction to Computer Science II (Java)
	2010 Fall	Algorithms
2009 Fall	Discrete Mathematics for Computer Science II	
2009 Fall	Machine-Level and Systems Programming	
2009 Spring	Algorithms	
2009 Spring	Programming Language Theory (Assembly)	
2008 Fall	Introduction to Computer Science II (Java)	
Research Experience	Directed Research · University of California, Berkeley · Center for Theoretical Evolutionary Genomics	
	Jan 2015 – present	Under the supervision of Prof. Rasmus Nielsen, developed a suite of statistical methods and software tools used to infer population structure, estimate component covariances, build evolutionary trees, and detect selection outliers from called genotypes and genotype likelihoods. <i>Keywords:</i> statistical modeling, simulation, model-based classification, numerical optimization, quadratic programming, sequential QP, constraint optimization, Nelder-Mead, admixture
	Directed Research · Aarhus University · Computer Science · Bioinformatics Research Centre	
	2013 – 2016	Under the supervision of Prof. Thomas Mailund, investigated demographic inference with coalescent hidden Markov models, extended an inference framework with complex model construction, heuristic-based optimizations, and the modeling of admixture events. <i>Keywords:</i> parametric model inference, sequential Markov coalescence, coalescent hidden Markov models, numerical optimization, heuristic-based optimization, simulation
	Directed Research · Aarhus University · Centre for Biocultural History	
	2013 – 2014	Contributed as a core member of the Hvorkommerdufra project, a large-scale study of the Danish population's genetic history through the participation of approximately 800 students from 36 Danish high schools. <i>Technologies:</i> 23andme API, principle component analysis, Plink, Google visualization and maps API, OAuth authorization, C# with LINQ, PHP, JavaScript, HTML, CSS, Python, JSON, SVG
	Directed Research · University of Hawai'i at Mānoa · Department of Information and Computer Science	
2010 – 2011	Under the supervision of Prof. Edoardo Biagioni, investigated the OLPC Acoustic tape measure algorithm on the Lego NXT; implementation allowed two peers to measure physical distance using only audio pulses and stock components. <i>Technologies:</i> OLPC, Sugar, MAX232CPE, Lego NXT, NXT-G Toolkit, Java, LeJOS, Eclipse, Bluetooth, JWPlayer, Dewplayer	
Work Experience	Software Developer, Database Administrator · Jab-Ex Corporation (Volunteer)	
	2011 – 2014	Designed, developed, and maintained web applications and databases; created a content management system for a professional musician.
	Software Developer · Texas Health, Arlington Memorial Hospital, Cardiac Rehabilitation (Volunteer)	
2011 – 2012	Designed and developed an experimental audio system that allows RNs to control and monitor educational audio tracks that patients hear as they exercise.	
Software Developer · Hawai'i Water Resources Research Center		
2011 – 2012	Created a content management database and a web application that allow authors, editors, and administrators to submit, edit, and revise conference abstracts and manuscripts.	



~ Jade Yu Cheng ~

8500 Waterwillow Pl · Orlando, FL 32827, USA

US Mobile: +1-808-206-5059 · Denmark Mobile: +45-9398-1013 · Email: jade.cheng@cs.au.dk · Website: www.jade-cheng.com

Publications	<p>Cheng, Jade Yu, Mailund, Thomas, and Nielsen, Rasmus. "Fast admixture analysis and population tree estimation for SNP and NGS data." <i>Bioinformatics</i> (2017), p.btx098.</p> <p>Cheng, Jade Yu, and Mailund, Thomas. "Ancestral population genomics using coalescence hidden Markov models and heuristic optimisation algorithms." <i>Computational biology and chemistry</i> 57 (2015): 80-92.</p> <p>Cheng, Jade Yu, and Nielsen, Rasmus. "Ohana: detecting selection in multiple populations by modelling ancestral admixture components." 2017 In preparation</p> <p>Cheng, Jade Yu, and Mailund, Thomas. "A coalescent hidden Markov model for inferring admixture relationships." 2017 In preparation</p> <p>Ilardo, Melissa, Moltke, Ida, Korneliussen, Thorfinn, Cheng, Jade Yu, ... Nielsen, Rasmus, and Willerslev, Eske. "Physiological and genetic adaptations to diving in Sea Nomads." 2017 Submitted</p> <p>Athanasiadis, Georgios, Jade Y. Cheng, Bjarni J. Vilhjálmsson, Frank G. Jørgensen, Thomas D. Als, Stephanie Le Hellard, Thomas Espeseth et al. "Nationwide genomic study in Denmark reveals remarkable population homogeneity." <i>Genetics</i> (2016): genetics-116.</p> <p>Malaspinas, Anna-Sapfo, Michael C. Westaway, Craig Muller, Vitor C. Sousa, Oscar Lao, Isabel Alves, Anders Bergström Georgios Athanasiadis, Jade Y Cheng, et al. "A genomic history of Aboriginal Australia." <i>Nature</i> (2016).</p> <p>Lan, Tianying, Jade Y. Cheng, Aakrosh Ratan, Webb Miller, Stephan Schuster, Sean Farley, Richard Shideler, Thomas Mailund, and Charlotte Lindqvist. "Genome-wide evidence for a hybrid origin of modern polar bears." <i>bioRxiv</i> (2016): 047498.</p> <p>Athanasiadis, Georgios, Frank G. Jørgensen, Jade Y. Cheng, Peter C. Kjærgaard, Mikkel H. Schierup, and Thomas Mailund. "Spitting for science: Danish high school students commit to a large-scale self-reported genetic study." <i>PLoS One</i> 11, no. 8 (2016): e0161822.</p> <p>Abascal, Federico, André Corvelo, Fernando Cruz, José L. Villanueva-Cañas, Anna Vlasova, Marina Marcet-Houben, Begoña Martínez-Cruz, Jade Y Cheng, et al. "Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx." <i>Genome Biology</i> 17, no. 1 (2016): 251.</p> <p>Luseadra McKerracher, Jade Y. Cheng, Mark Collard, Peter C Kjærgaard. "Lucy turns 40: four decades of trends in research interest about Australopithecus afarensis map onto and even anticipate four decades of trends in broader research interest in human evolution" Submitted (2015)</p> <p>Cheng, Jade Yu. "Learning with Admixture: Modeling, Optimization, and Applications in Population Genetics." <i>forskningsdatabasen Denmark</i> (2016).</p> <p>Cheng, Jade Yu. "Demographic Inference with Coalescent Hidden Markov Model and More." <i>cs.au.dk</i> (2014).</p>		
Software	'Ohana: a suite of software to infer population structure, admixture, and selection nemetree : interactive visualization for phylogenetic trees nemepos : interactive visualization for partially ordered sets AdmxCoalHMM: coalescence hidden Markov modeling and optimizations	www.jade-cheng.com/ohana www.jade-cheng.com/trees www.jade-cheng.com/graphs/nemepos www.github.com/jade-cheng/jocx	
Dissemination	2017 Invited, School of Mathematics and Statistics, Victoria University of Wellington, New Zealand 2017 Society for Molecular Biology & Evolution, Austin, USA 2015 Probabilistic Modeling in Genomics, Cold Spring Harbor Laboratory New York, USA 2015 Visiting, Center for Theoretical Evolutionary Genomics, UC Berkeley, USA 2015 Asia Pacific Bioinformatics, HsinChu Taiwan 2014 Society for Bioinformatics in Northern Europe, Oslo, Norway 2014 Big Data, MADALGO, Aarhus, Denmark		
Technologies	Languages Libraries Database Other	Python, Java, C++11, JavaScript, TypeScript, PHP, SQL, C, C#, LaTeX, R, x86 Assembly, BAT, BASH, make, LISP, Mathematica, NXT-G, HTML, CSS, XML, SVG, JSON numpy, scipy, matplotlib, pyVCF, ape, JRE, JDBC, Swing, BLAS, LAPACK, jQuery, jQuery UI, phpMyAdmin, GD, 23andme API, Google maps and visualization API, OAuth 2.0, Java Applets, Highcharts JS, LeJOS, XStream, POSIX, BSD Sockets, Pthreads, Mono, .NET 4.0 MySQL, MySQL Workbench, IBM DB2, MS SQL, UCSC Genome Browser, Server and Report Builder HPC cluster, SLURM, Amazon EC2, PyCharm, Git, Linux, GNOME, Eclipse, Inkscape, Google Docs, Atom, Lint4J, Shell, Galaxy, Nachos, VirtualBox, UNIX Networking, Wireshark, Visual Studio 2005-2008, PIC16F873A, MPLAB, Click Modular Router, NetBeans, OLPC, Lego NXT	
Personal	From: Chengdu, China	Languages: Mandarin Chinese and English	Citizenship: USA
References	Rasmus Nielsen Thomas Mailund Edoardo Biagioni Ralph Freese	Genetics and Statistics, UC Berkeley & U of Copenhagen CS and Bioinformatics, Aarhus University ICS, University of Hawai'i at Mānoa Math, University of Hawai'i at Mānoa	rasmus_nielsen@berkeley.edu mailund@birc.au.dk esb@ics.hawaii.edu ralph@hawaii.edu

