

# ~ Jade Yu Cheng ~

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- Appointments** 2017 (current) Postdoc, Data Scientist. Genetics and Statistics, University of California, Berkeley, USA  
2016 - 2017 Postdoc, Data Scientist. 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**
- | <b>Teaching Assistant · Aarhus University</b>         |                                       | <b>Teaching Assistant · University of Hawai'i at Mānoa</b> |   |
|---|---------------------------------------|--|---|
| 2016  | Q4 Introduction to Data Science       | 2011   | Spring Algorithms                                 |
| 2015  | Q1 Introduction to Bioinformatics (R) | 2010   | Spring Introduction to Computer Science II (Java) |
| 2014  | Q1 Databases (SQL)                    | 2010   | Fall Algorithms                                   |
| 2013  | Q4 Algorithms and Data Structures II  | 2009   | Fall Discrete Mathematics for Computer Science II |
| 2013  | Q3 Algorithms and Data Structures I   | 2009   | Fall Machine-Level and Systems Programming        |
| 2013  | Q2 Applied Programming (Python)       | 2009   | Spring Algorithms                                 |
| <b>Adjunct Professor · Hawai'i Pacific University</b> |                                       | 2009   | Spring Programming Language Theory (Assembly)     |
| 2012  | Spring Computer Science II (Java)     | 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 to infer population structure, estimate component covariances, build evolutionary trees, and detect selection outliers from called genotypes and genotype likelihoods.  
*Keywords:* mixture analysis, model-based classification, numerical optimization, quadratic programming, sequential QP, constraint optimization, Nelder-Mead, admixture, simulation
- 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.  
*Keywords:* 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.  
*Technologies:* 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.  
*Technologies:* 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.



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- Publications**
- Cheng, Jade Yu**, Mailund, Thomas, and Nielsen, Rasmus. "Fast admixture analysis and population tree estimation for SNP and NGS data." *Bioinformatics* (2017), p.btx098.
- Cheng, Jade Yu**, and Mailund, Thomas. "Ancestral population genomics using coalescence hidden Markov models and heuristic optimisation algorithms." *Computational biology and chemistry* 57 (2015): 80-92.
- Cheng, Jade Yu**, and Nielsen, Rasmus. "Ohana: detecting selection in multiple populations by modelling ancestral admixture components." 2017 In preparation
- Cheng, Jade Yu**, and Mailund, Thomas. "A coalescent hidden Markov model for inferring admixture relationships." 2017 In preparation
- Alves, Joel M, Carneiro Miguel, **Cheng, Jade Yu**, ... Jiggins, Francis M. "Parallel adaptation of rabbit populations to myxoma virus." 2017 In preparation
- 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
- 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." *Genetics* (2016): genetics-116.
- Malaspinas, Anna, 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." *Nature* (2016).
- 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." *bioRxiv* (2016): 047498.
- 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." *PLoS One* 11, no. 8 (2016): e0161822.
- 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." *Genome Biology* 17, no. 1 (2016): 251.
- 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)
- Cheng, Jade Yu**. "Learning with Admixture: Modeling, Optimization, and Applications in Population Genetics." *forskningsdatabasen Danmark* (2016).
- Cheng, Jade Yu**. "Demographic Inference with Coalescent Hidden Markov Model and More." *cs.au.dk* (2014).
- Software**
- 'Ohana: a suite of software to infer population structure, admixture, and selection [www.jade-cheng.com/ohana](http://www.jade-cheng.com/ohana)
- nemetree : interactive visualization for phylogenetic trees [www.jade-cheng.com/trees](http://www.jade-cheng.com/trees)
- nemepos : interactive visualization for partially ordered sets [www.jade-cheng.com/graphs/nemepos](http://www.jade-cheng.com/graphs/nemepos)
- AdmxCoalHMM: coalescence hidden Markov modeling and optimizations [www.github.com/jade-cheng/jocx](http://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 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
- Libraries numpy, scipy, matplotlib, nltk, scikit-learn, 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
- Database MySQL, MySQL Workbench, IBM DB2, MS SQL, UCSC Genome Browser, Server and Report
- Other 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 Genetics and Statistics, UC Berkeley & U of Copenhagen [rasmus\\_nielsen@berkeley.edu](mailto:rasmus_nielsen@berkeley.edu)
- Thomas Mailund CS and Bioinformatics, Aarhus University [mailund@birc.au.dk](mailto:mailund@birc.au.dk)
- Edoardo Biagioni ICS, University of Hawai'i at Mānoa [esb@ics.hawaii.edu](mailto:esb@ics.hawaii.edu)
- Ralph Freese Math, University of Hawai'i at Mānoa [ralph@hawaii.edu](mailto:ralph@hawaii.edu)

