

~ Jade Yu Cheng ~

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Appointments	Current	AI/ML lead	The Walt Disney Company, USA.
	2018	Data scientist	Strong Analytics LLC, a DS consulting and ML development firm, USA.
	2017	Data scientist, Postdoc	Statistics and Genetics, University of California, Berkeley, USA
	2016	Data scientist, Postdoc	Natural History Museum of Denmark, University of Copenhagen, Denmark
	2013-2016	Ph.D. fellow	Department of CS & Bioinformatics, Aarhus University, Denmark
Education	2016	Ph.D.	Computer Science, Aarhus University, Denmark
	2011	M.S.	Information & Computer Science; University of Hawai'i at Mānoa, USA
		M.S. (dual)	Bioengineering; University of Hawai'i at Mānoa, USA
	2006	B.S.	Biotechnology; Nankai University, China
Work Experience	AI/ML lead · The Walt Disney Company		
	2019 — Current	Unite artificial intelligence and machine learning techniques with day-to-day operations to transform digital and travel operations. Support innovations and solution-oriented analytics via statistical modeling, numeric optimization, and predictive inference.	
	Data scientist · Strong Analytics LLC		
	2018	Design, implement, and deploy artificial intelligence and machine learning algorithms, construct data science pipelines to power smarter products and automated operations. Projects include NLP, DNN, anomaly detection, forecasting, classification, clusterization, etc.	
	Data scientist, Postdoc · University of California, Berkeley & Natural History Museum of Denmark		
	2015 — 2017	Under the supervision of Prof. Rasmus Nielsen, developed a suite of statistical methods and software to infer population structure, build evolutionary trees, detect selection outliers, etc. Techniques include mixture analysis, model-based classification, quadratic programming, etc.	
	Ph.D. fellow · Aarhus University · Computer Science · Bioinformatics Research Centre		
	2013 — 2016	Under the supervision of Prof. Thomas Mailund, investigated demographic inference with coalescent hidden Markov models, developed numerical optimizations, admixture modeling, etc. Techniques include model inference, hidden Markov model, heuristic-based optimization, etc.	
	Data scientist · 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. Technologies include 23andme API, Plink, Google visualization and maps API, OAuth, JSON, SVG, HTML, CSS, JavaScript, etc.	
	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.	
	Software developer and database administrator · Jab-Ex Corporation (Professional intern)		
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.		
Research Experience	M.S. research · University of Hawai'i at Mānoa · Department of Information and Computer Science		
	2009 — 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 include OLPC, Sugar, MAX232CPE, Lego NXT, NXT-G, LeJOS, Java, Bluetooth, etc.	
	M.S. research · University of Hawai'i at Mānoa · Department of Bioengineering		
2007 — 2008	Under the supervision of Prof. Marla Berry and Prof. Peter Hoffman, constructed and analyzed expression vectors and target proteins with mutations from selenocysteine to cystin.		
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	



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Selected Software	Evolutionary-optimization: a suite of black-box optimizers Nemetree : interactive visualization for phylogenetic trees Nemepos : interactive visualization for partially ordered sets ‘Ohana: a suite of software to infer population structure, admixture, and selection AdmixCoalHMM: coalescence hidden Markov modeling and optimizations	www.github.com/strongio/evolutionary-optimization www.jade-cheng.com/trees www.jade-cheng.com/graphs/nemepos www.jade-cheng.com/ohana www.github.com/jade-cheng/Jocx
Selected Publications	Google Scholar: https://scholar.google.com/citations?hl=en&user=CvOBf0sAAAAJ Cheng, Jade Yu, Stern, Aaron J, Racimo, Fernando, and Nielsen, Rasmus. “Detecting selection in multiple populations by modeling ancestral admixture components.” <i>Molecular Biology and Evolution</i> (2022). Alves, Joel M, Carneiro Miguel, Cheng, Jade Yu, ... Jiggins, Francis M. “Parallel adaptation of rabbit populations to myxoma virus.” <i>Science</i> (2019). Ilardo, Melissa A., Ida Moltke, Thorfinn S. Korneliussen, Jade Cheng, et al. "Physiological and Genetic Adaptations to Diving in Sea Nomads." <i>Cell</i> 173, no. 3 (2018). Cheng, Jade Yu, Mailund, Thomas, and Nielsen, Rasmus. “Fast admixture analysis and population tree estimation for SNP and NGS data.” <i>Bioinformatics</i> (2017). Athanasiadis, Georgios, Jade Yu. Cheng, Bjarni J. Vilhjálmsson, Frank G. Jørgensen, ... Thomas Espeseth et al. “Nationwide genomic study in Denmark reveals remarkable population homogeneity.” <i>Genetics</i> (2016). 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.” <i>Nature</i> (2016). Lan, Tianying, Jade Y. Cheng, Aakrosh Ratan, ... Thomas Mailund, and Charlotte Lindqvist. “Genome-wide evidence for a hybrid origin of modern polar bears.” <i>bioRxiv</i> (2016). Cheng, Jade Yu. “Learning with Admixture: Modeling, Optimization, and Applications in Population Genetics.” <i>forskningsdatabasen Denmark</i> (2016). 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). Cheng, Jade Yu. “Demographic Inference with Coalescent Hidden Markov Model and More.” <i>cs.au.dk</i> (2014).	
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, SQL, R, C++11, JavaScript, TypeScript, PHP, C, C#, LaTeX, x86 Assembly, BAT, BASH, make, LISP, Mathematica, NXT-G, HTML, CSS, XML, SVG, JSON Libraries Pandas, scikit-learn, LLM, RAG, PalmAPI, VertexAI, NLTK, spaCy, HF Transformers, BERT, Keras, TensorFlow, PyTorch, FBProphet, Statsmodels, ARIMA, pgmpy, PyMC3, Spark SQL, Spark ML, UDF, tesseraact, Flask, D3js, numpy, scipy, matplotlib, seaborn, Plotly, Dash, 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 PostgreSQL, Orator ORM, DataGrip, MySQL, MySQL Workbench, IBM DB2, MS SQL, UCSC Genome Browser, Server and Report Builder AI/ML topics numerical optimization, classification, clusterization, forecasting, outlier detection, supervised and unsupervised learning, NLP, OCR, deep Learning, regression, SVM, kernels, naive Bayes, decision tree and forest, kNN, Kmeans, GMM, PCA, hidden Markov model, search, etc. Other REST API, Docker, Amazon AWS, S3, EC2, Parquet, Tableau, HPC cluster, SLURM, Git, Linux, GNOME, PyCharm, Eclipse, Inkscape, Google Docs, Atom, Lint4J, Shell, Galaxy, Nachos, VirtualBox, UNIX Networking, Wireshark, Visual Studio 2005-2008, MPLAB, PIC16F873A, 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	Statistics & Genetics, UC Berkeley & U of Copenhagen CS & Bioinformatics, Aarhus University Information & CS, 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

