David A. Knowles

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Nationality: British

Education

PHD Engineering (Machine Learning)

University of Cambridge

Thesis: Bayesian non-parametric models and inference for sparse and hierarchical latent structure

Advisor: Prof. Zoubin Ghahramani

2007-2008 MSc Bioinformatics and Systems Biology - Distinction

Imperial College London

Thesis: *Statistical tools for ulta-deep pyrosequencing of fast evolving viruses.*Thesis advisor: Prof. Susan Holmes, Statistics Department, Stanford University.

2003-2007 MENG Engineering - Distinction

Thesis: A non-parametric extension to Independent Components Analysis.

Thesis advisor: Prof. Zoubin Ghahramani. BA Natural Sciences (Physics) - First Class

University of Cambridge

Academic Positions

2014-ongoing Postdoctoral researcher (Genetics, Pathology)

Stanford University

Co-advisors: Prof. Jonathan Pritchard, Prof. Sylvia Plevritis

POSTDOCTORAL RESEARCHER (Computer Science)

Stanford University

Advisor: Prof. Daphne Koller

2008-2012 PHD Candidate, Roger Needham Scholar, Wolfson College, University of Cambridge

Machine Learning Group, Cambridge University Engineering Department

2006 Summer Undergraduate Research Fellow

California Institute of Technology

Honours & Awards

2017 Stanford Cancer Systems Biology Symposium — Poster Award

The International Society for Bayesian Statistics Travel Award for best invited Bayesian paper
The International Society for Bayesian Statistics Dennis V. Lindley Prize for innovative research in

Bayesian Statistics

2007 Charles Lamb University prize for first place in Information Engineering

Sir Joseph Larmor Silver Plate for undergraduates adjudged to be the most worthy for intellectual qualifications or moral conduct and practical activities

Three other college prizes (Cargill, Cunningham and College)

2005 Wright Prize for ranking 5/600 in Natural Sciences

Earle Year Prize for top 4 students across all subjects at St. John's College Hollinshead-Howles Prize for top Natural Scientist at St. John's College

BP Prize for Advanced Physics

Gaskell Year Prize for ranking 9/600 in Natural Sciences

Hollinshead-Howles Prize for Part IA

Top 50 nationally in Royal Society of Chemistry Olympiad

Top 50 nationally in Mathematics Olympiad

Fellowships

2008-2012 Roger Needham Scholarship, Wolfson College, University of Cambridge, funded by Microsoft Re-

search

Summer Undergraduate Research Fellow, *California Institute of Technology*

Industry Positions

2009-2012 Contract Software Engineer

Microsoft Research Cambridge

Extending Infer.NET.

2009 Research Intern

Microsoft Research Cambridge

Non-conjugate Variational Message Passing. Supervisor: Thomas P. Minka.

2005 Equity Research Intern

UBS Investment Bank, London

Developed a financial model of Belgacom Telecom. Declined offer.

Software Engineering Intern

Data Connection Limited, London

Developed an automatic build system using Unix shell scripts.

Teaching & Mentoring

²⁰¹⁷ CBIO 244: Lecture Series in Cancer Systems Biology

Statistical, Mathematical, and Computational Consulting (SMACC) hosted by Stanford ICME

Advising five groups of students for graduate machine learning (CS229) course projects

Advised undergraduate student for CURIS Undergraduate Research Internship

Stanford Statistics guest lecture on Bayesian nonparametrics

2009-2011 Statistics advisor, Cambridge University Statistics Clinic

Supervisor, Cambridge University Engineering Department, Digital Signal Processing

2009-2011 Demonstrator, Cambridge University Engineering Department, C++ programming

2007-2009 Private Mathematics tutor, Camtutors

Reviewing & Service

JOURNALS

Machine Learning, PLOS Genetics, PLOS Computational Biology, Bioinformatics, Genome Research, Journal of the American Statistical Association, Statistics and Computing (Springer), Bayesian Analysis, Journal of Mathematical Biology, Journal of Machine Learning Research, Journal of Computational and Graphical Statistics, Journal of the Royal Statistical Society: Series B, IEEE Transactions on Pattern Analysis and Machine Intelligence, Annals of Applied Statistics

Conferences

Pacific Biocomputing Symposium (PBS), International Conference on Artificial Intelligence and Statistics (AISTATS), International Joint Conferences on Artificial Intelligence (IJCAI), Advances in Neural Information Processing Systems (NIPS), International Conference on Machine Learning (ICML)

Workshops

PC member for NIPS Workshop on Computational Biology, PC member for NIPS Workshop on Optimization in Machine Learning

Professional affiliations

Early Stage Investigators in Cancer Systems Biology Steering Committee, International Society of Bayesian Analysis (ISBA) Chair of the Continuing Education Committee

Selected Talks

2011

2011

2017	Statistical and Computational Challenges in Large Scale Molecular Biology. Banff International
	Research Station for Mathematical Innovation and Discovery
2015	Highlights from Bayesian Analysis (Joint Statistical Meeting session), invited speaker
2015	Statistical and Computational Challenges In Bridging Functional Genomics, Epigenomics, Molec-
	ular QTLs, and Disease Genetics at the Banff International Research Station for Mathematical In-
	novation and Discovery
2015	The Biology of Genomes meeting at Cold Spring Harbor Laboratory
2014	NIPS Variational Inference Workshop (invited speaker)
2013	RECOMB/ISCB Conference on Regulatory & Systems Genomics
2012	Stanford Biostatistics Workshop
2012	BayLearn, the Bay Area Machine Learning Symposium
2012	Collegio Carlo Alberto Statistics Seminar
2011	Cambridge Statistics Initiative One Day Special Meeting
2011	27th Conference on Uncertainty in Artificial Intelligence (UAI)
2011	NIPS Workshop on Predictive Models in Personalized Medicine
2011	RAD Lab, University of California at Berkeley

28th International Conference on Machine Learning (ICML)

Eighth Workshop on Bayesian Nonparametrics; Veracruz, Mexico

Publications

JOURNAL ARTICLES

- David A. Knowles, Joe R. Davis, Hilary Edgington, Anil Raj, Marie-Julie Favé, Xiaowei Zhu, James B. Potash, Myrna M. Weissman, Jianxin Shi, Douglas F. Levinson, Philip Awadalla, Sara Mostafavi, Stephen B. Montgomery, Alexis Battle. Allele-specific expression reveals interactions between genetic variation and environment. *Nature Methods*.
- Lindsay A. Becker, Brenda Huang, Gregor Bieri, Rosanna Ma, **David A. Knowles**, Paymaan Jafar-Nejad, James Messing, Hong Joo Kim, Armand Soriano, Georg Auburger, Stefan M. Pulst, J. Paul Taylor, Frank Rigo, and Aaron D. Gitler. Therapeutic reduction of ataxin 2 extends lifespan and reduces pathology in TDP-43 mice. *Nature*.
- Po-Yuan Tung, John D Blischak, Chiaowen Joyce Hsiao, **David A Knowles**, Jonathan E Burnett, Jonathan K Pritchard, Yoav Gilad. Batch effects and the effective design of single-cell gene expression studies. *Nature Scientific Reports*.
- Emily K Tsang, Nathan S Abell, Xin Li, Vanessa Anaya, Konrad J Karczewski, **David A Knowles**, Raymond G Sierra, Kevin S Smith, Stephen B Montgomery. Small RNA Sequencing in Cells and Exosomes Identifies eQTLs and 14q32 as a Region of Active Export. *G3: Genes | Genomes | Genetics*.
- Yang I. Li, Bryce van de Geijn, Anil Raj, **David A. Knowles**, Allegra A. Petti, David Golan, Yoav Gilad, Jonathan K. Pritchard. RNA splicing is a primary link between genetic variation and disease. *Science*.
- Kimberly R. Kukurba, Princy Parsana, Kevin S. Smith, Zachary Zappala, David A. Knowles, Marie-Julie Fave, Xin Li, Xiaowei Zhu, James B. Potash, Myrna M. Weissman, Jianxin Shi, Anshul Kundaje, Douglas F. Levinson, Philip Awadalla, Sara Mostafavi, Alexis Battle, Stephen B. Montgomery. Impact of the X chromosome and sex on regulatory variation. Genome Research.
- Joe R. Davis, Laure Fresard, **David A. Knowles**, Mauro Pala, Carlos D. Bustamante, Alexis Battle, Stephen B. Montgomery. An Efficient Multiple-Testing Adjustment for eQTL Studies that Accounts for Linkage Disequilibrium between Variants. *American Journal of Human Genetics*.
- David A. Knowles and Zoubin Ghahramani. Pitman-Yor Diffusion Trees for Bayesian hierarchical clustering. *IEEE TPAMI Special Issue on Bayesian Nonparametrics*.
- Konstantina Palla, **David A. Knowles** and Zoubin Ghahramani. Relational learning and network modelling using infinite latent attribute models. *IEEE TPAMI Special Issue on Bayesian Nonparametrics*.
- Xin Li, Alexis Battle, Konrad J. Karczewski, Zach Zappala, David A. Knowles, Kevin S. Smith, Kim R. Kukurba, Eric Wu, Noah Simon, Stephen B. Montgomery. Transcriptome Sequencing of a Large Human Family Identifies the Impact of Rare Noncoding Variants. In American Journal of Human Genetics.
- Kimberly R. Kukurba, Rui Zhang, Xin Li, Kevin S. Smith, **David A. Knowles**, Meng How Tan, Robert Piskol, Monkol Lek, Michael Snyder, Daniel G. MacArthur, Jin Billy Li, Stephen B. Montgomery (2014). Allelic Expression of Deleterious Protein-Coding Variants across Human Tissues. *PLoS Genetics*.
- Tim Salimans, David A. Knowles. Fixed-Form Variational Posterior Approximation through Stochas-

tic Linear Regression. Bayesian Analysis 8(4) [Winner of the 2014 Lindley Prize].

Daniel Glass, Ana Vinuela, Mathew N Davies, Adaikalavan Ramasamy, Leopold Parts, **David A**. **Knowles**, Andrew A Brown, Asa K Hedman, Kerrin S Small, Alfonso Buil, Elin Grundberg, Alexandra C Nica, Paola Di Meglio, Frank O Nestle, Mina Ryten, The UK Brain Expression consortium, Muther Consortium, Richard Durbin, Mark I McCarthy, Panagiotis Deloukas, Emmanouil T Dermitzakis, Mike E Weale, Veronique Bataille & Tim D Spector. Gene expression changes with age in skin, adipose tissue, blood and brain. *Genome Biology*.

Elin Grundberg, Kerrin S Small, Åsa K Hedman, Alexandra C Nica, Alfonso Buil, Sarah Keildson, Jordana T Bell, Tsun-Po Yang, Eshwar Meduri, Amy Barrett, James Nisbett, Magdalena Sekowska, Alicja Wilk, So-Youn Shin, Daniel Glass, Mary Travers, Josine L Min, Sue Ring, Karen Ho, Gudmar Thorleifsson, Augustine Kong, Unnur Thorsteindottir, Chrysanthi Ainali, Antigone S Dimas, Neelam Hassanali, Catherine Ingle, **David A. Knowles**, Maria Krestyaninova, Christopher E Lowe, Paola Di Meglio, Stephen B Montgomery, Leopold Parts, Simon Potter, Gabriela Surdulescu, Loukia Tsaprouni, Sophia Tsoka, Veronique Bataille, Richard Durbin, Frank O Nestle, Stephen O'Rahilly, Nicole Soranzo, Cecilia M Lindgren, Krina T Zondervan, Kourosh R Ahmadi, Eric E Schadt, Kari Stefansson, George Davey Smith, Mark I McCarthy, Panos Deloukas, Emmanouil T Dermitzakis, Tim D Spector & The Multiple Tissue Human Expression Resource (MuTHER) Consortium. Mapping cis- and trans-regulatory effects across multiple tissues in twins. *Nature Genetics*.

Mehregan Movassagh, Mun-Kit Choy, **David A. Knowles**, Lina Cordeddu, Syed Haider, Thomas Down, Lee Siggens, Ana Vujic, Ilenia Simeoni, Chris Penkett, Martin Goddard, Pietro Lio, Martin Bennett, Roger Foo. Distinct epigenomic features in human cardiomyopathy. *Circulation, American Heart Association*.

Cornelia Schone, Anne Venner, **David A. Knowles**, Mahesh M Karnani, Denis Burdakov. Dichotomous cellular properties of mouse orexin/hypocretin neurons. In *The Journal of Physiology.*

David A. Knowles and Zoubin Ghahramani. Nonparametric Bayesian Sparse Factor Models with application to Gene Expression modelling. In *Annals of Applied Statistics*.

Daniel Glass, Leopold Parts, **David A. Knowles**, Abraham Aviv, and Tim D. Spector. No Correlation Between Childhood Maltreatment and Telomere Length. In *Biological Psychiatry*.

PEER—REVIEWED CONFERENCE PAPERS

2011

2011

2010

Konstantina Palla, **David A. Knowles** and Zoubin Ghahramani. A birth-death process for feature allocation. *Proceedings of the 34st International Conference on Machine Learning (ICML).*

Amar Shah, **David A. Knowles**, Zoubin Ghahramani. Stochastic Variational Inference Algorithms for the Beta Bernoulli Process. In *Proceedings of the 32nd International Conference on Machine Learning (ICML)*.

Kien Nguyen, **David A. Knowles**, Joerg Bredno. Nuclei classification in histology images: use of contextual information. *International Symposium on Biomedical Imaging (ISBI)*.

Konstantina Palla, **David A**. **Knowles** and Zoubin Ghahramani. A reversible infinite HMM using normalised random measures. In *Proceedings of the 31st International Conference on Machine Learning (ICML 2014).*

Creighton Heaukulani, **David A. Knowles** and Zoubin Ghahramani. Beta Diffusion Trees. In *Proceedings of the 31st International Conference on Machine Learning (ICML 2014)*.

Novi Quadrianto, Viktoriia Sharmanska, **David A. Knowles**, Zoubin Ghahramani. The Supervised IBP: Neighbourhood Preserving Infinite Latent Feature Models. In *Proceedings of the 29th Conference on Uncertainty in Artificial Intelligence (UAI 2013).*

- David A. Knowles*, Konstantina Palla* and Zoubin Ghahramani. A nonparametric variable clustering model. In *Advances in Neural Information Processing Systems 25 (NIPS 2012)*.
- Konstantina Palla, **David A. Knowles** and Zoubin Ghahramani. An Infinite Latent Attribute Model for Network Data. In *Proceedings of the 29th International Conference on Machine Learning (ICML 2012).*
- Andrew Wilson, **David A. Knowles** and Zoubin Ghahramani. Gaussian Process Regression Networks. In *Proceedings of the 29th International Conference on Machine Learning (ICML 2012).*
- David A. Knowles and Thomas P. Minka. Non-conjugate Variational Message Passing for Multinomial and Binary Regression. In *Advances in Neural Information Processing Systems 24 (NIPS 2011).*
- David A. Knowles and Zoubin Ghahramani. Pitman-Yor Diffusion Trees. In *Proceedings of the* 27th Conference on Uncertainty in Artificial Intelligence (UAI 2011).
- David A. Knowles, Jurgen Van Gael, and Zoubin Ghahramani. Message Passing Algorithms for the Dirichlet Diffusion Tree. In *Proceedings of the 28th International Conference on Machine Learning (ICML 2011)*.
- Finale Doshi*, **David A. Knowles***, Shakir Mohamed* and Zoubin Ghahramani. Large Scale Non-parametric Inference: Data Parallelisation in the Indian Buffet Process. In *Advances in Neural Information Processing Systems 22 (NIPS 2009)*.
- David A. Knowles and Zoubin Ghahramani. Infinite Sparse Factor Analysis and Infinite Independent Components Analysis. In *Proceedings of the 7th International Conference on Independent Component Analysis and Signal Separation (ICA 2007).*

WORKSHOP ABSTRACTS AND PAPERS

- David A. Knowles, Yang Li, Jonathan Pritchard. LeafCutter: Annotation-free quantification and prediction of RNA splicing. *American Society of Human Genetics 66th Annual Meeting*.
- Yang Li, Bryce van de Geijn, Allegra Petti, Anil Raj, **David A. Knowles**, John Blischak, Yoav Gilad, Jonathan Pritchard. The effects of human genetic variation on the gene regulatory cascade. *American Society of Human Genetics 65th Annual Meeting*.
- David A. Knowles, Joe R. Davis, Stephen B. Montgomery, Alexis Battle. Detecting gene-by-environment interactions using allele specific expression. *The Biology of Genomes Meeting (CSHL)*.
- Emily K. Tsang, Xin Li, Vanessa Anaya, Konrad J. Karczewski, **David A. Knowles**, Kevin S. Smith, Stephen B. Montgomery. Dissecting the genetic regulation of exosome RNA cargo in a large family. *American Society of Human Genetics 64th Annual Meeting*.
- Joe R. Davis, **David A. Knowles**, Stephen B. Montgomery, Alexis Battle. Rare variation and the genomic context of allele-specific expression. *American Society of Human Genetics 64th Annual Meeting*.
- David A. Knowles, Alexis Battle, Daphne Koller. Discovering latent cancer characteristics predictive of drug sensitivity. *RECOMB/ISCB Conference on Regulatory & Systems Genomics (selected for oral presentation).*
- Alexis Battle*, **David A. Knowles***, Sara Mostafavi, Xiaowei Zhu, James B. Potash, Myrna M. Weissman, Courtney McCormick, Christian D. Haudenschild, Kenneth B. Beckman, Jianxin Shi, Rui Mei, Alexander E. Urban, Douglas F. Levinson, Daphne Koller, Stephen B. Montgomery. The relationship between common environmental and genetic effects on human gene splicing and expression. *American Society of Human Genetics 63rd Annual Meeting*.

^{*}These authors contributed equally.

- David A. Knowles, Leopold Parts, Daniel Glass and John M. Winn. Inferring an individual's "physiological" age from multiple ageing-related phenotypes. *Cambridge Statistics Initiative Special One-Day Meeting*.
- David A. Knowles, Jurgen Van Gael and Zoubin Ghahramani. Message Passing Algorithms for the Dirichlet Diffusion Tree. *Eighth Workshop on Bayesian Nonparametrics*.
- David A. Knowles, Leopold Parts, Daniel Glass and John M. Winn. Modeling skin and ageing phenotypes using latent variable models in Infer.NET. NIPS Workshop on Predictive Models in Personalized Medicine.
- David A. Knowles and Susan Holmes. Statistical tools for ultra-deep pyrosequencing of fast evolving viruses. *NIPS Computational Biology Workshop*.

WORKING PAPERS/UNDER SUBMISSION

Diego Calderon, Anand Bhaskar, **David A. Knowles**, David Golan, Towfique Raj, Audrey Fu, Jonathan K. Pritchard. Inferring Relevant Cell Types For Complex Traits Using Single-Cell Gene Expression.

http://biorxiv.org/content/early/2017/05/10/136283.

D Leland Taylor, **David A Knowles**, Laura J Scott, Andrea H Ramirez, Francesco Paolo Casale, Brooke N Wolford, Li Guan, Arushi Varshney, Ricardo D'Oliveira Albanus, Stephen CJ Parker, Narisu Narisu, Peter S Chines, Michael R Erdos, Ryan P Welch, Leena Kinnunen, Jouko Saramies, Jouko Sundvall, Timo A Lakka, Markku Laakso, Jaakko Tuomilehto, Heikki A Koistinen, Oliver Stegle, Michael Boehnke, Ewan Birney, Francis S Collins. Interactions between genetic variation and cellular environment in skeletal muscle gene expression.

http://biorxiv.org/content/early/2017/02/03/105429.

Yang I Li*, **David A Knowles***, Jonathan K Pritchard. LeafCutter: Annotation-free quantification of RNA splicing.

http://biorxiv.org/content/early/2016/03/16/044107.

- David A. Knowles. Stochastic gradient variational Bayes for gamma approximating distributions. http://arxiv.org/abs/1509.01631
- Tim Salimans, **David A. Knowles**. On Using Control Variates with Stochastic Approximation for Variational Bayes and its Connection to Stochastic Linear Regression. http://arxiv.org/abs/1401.1022 [stat.ML]
- David A. Knowles*, Konstantina Palla* and Zoubin Ghahramani. A dependent partition-valued process for multitask clustering and time evolving network modelling. http://arxiv.org/abs/1303.3265 [stat.ML]

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