Curriculum Vitae

Nicholas Eriksson

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Date of Birth:	1978 (Montana, USA)	Date of CV:	February 2014

Education/Employment

2009 –		Principal Scientist, Statistical Genetics, **23andMe, Inc.**, Mountain View, CA
2008 – 2009		Scientist, Statistical Genetics, **23andMe, Inc.**, Mountain View, CA
2007 – 2008		Visiting Assistant Professor, **Department of Statistics, University of Chicago**, Chicago, IL
2006 – 2007		NSF Postdoctoral Research Fellow, **Department of Statistics, Stanford University**, Stanford, CA
2006 – 2007		Postdoctoral Fellow, **Mathematical Sciences Research Institute**, Berkeley, CA
2006	Ph.D.	Mathematics, **University of California, Berkeley** (advisor: Bernd Sturmfels)
2006		Designated Emphasis in Computational and Genomic Biology, **University of California, Berkeley**
2001	S.B.	Mathematics, **Massachusetts Institute of Technology**, Cambridge, MA

Scientific/Academic honors and grants

2012 – 2013	Principal Investigator, NIH Grant 1R43HG006981-01, Development of a web-based database and research engine for genetic discovery ($232,602)
2012 – 2013	Principal Investigator, MJFF Research Grant, Using external research experts to mine the 23andMe Parkinson's database ($26,400)
2006 – 2008	National Science Foundation Postdoctoral Research Fellowship in the Mathematical Sciences
2006	Bernard Friedman Prize, University of California, Berkeley, top thesis in applied mathematics
2001 – 2004	National Defense Science and Engineering Graduate Fellowship
2001	National Science Foundation Graduate Research Fellowship (Declined)
1997	Third place, Westinghouse Science Talent Search, q-series, elliptic curves, and odd values of the partition function.

Research interests

- Statistics, machine learning and discrete mathematics
- Genetic architecture and risk prediction of complex traits
- Integrating sequencing data into genome-wide association studies
- Cancer tumor progression and HIV population evolution

Publications

Peer-reviewed and submitted articles (32 total, 18 as first/last/unordered author)

submitted 32. Genetic variants associated with motion sickness point to roles for inner ear development, neurological processes, and glucose homeostasis. B. S. Hromatka, J. Y. Tung, A. K. Kiefer, C. B. Do, D. A. Hinds, **N. Eriksson**. *Submitted*, 2014.

31. Reducing pervasive false positive identical-by-descent segments detected by large-scale pedigree analysis. E. Y. Durand, **N. Eriksson**, C. Y. McLean. *Submitted*, 2014.

2013 30. Genome-wide association analysis identifies 11 risk variants associated with the asthma with hay fever phenotype. M. A. R. Ferreira, M. C. Matheson, C. S. Tang, R. Granell, W. Ang, J. Hui, A. K. Kiefer, D. L. Duffy, S. Baltic, P. Danoy, M. Bui, L. Price, P. D. Sly, **N. Eriksson**, P. A. Madden, M. J. Abramson, P. G. Holt, A. C. Heath, M. Hunter, B. Musk, C. F. Robertson, P. Le Souef, W. Montgomery, A.J. Henderson, J. Y. Tung, S. C. Dharmage, M. A. Brown, A. James, P. J. Thompson, C. Pennell, N. G. Martin, D. M. Evans, D. A. Hinds, J. L. Hopper. *Journal of Allergy and Clinical Immunology*, 31 December 2013

29. Gradiant Boosting as a SNP filter: an evaluation using simulated and hair morphology data. G. H. Lubke, C. Laurin, R. Walters, **N. Eriksson**, P. Hysi, T. D. Spector, G. W. Montgomery, D. I. Boomsma, N. G. Martin, and S. E. Medland. *Journal of Data Mining in Genomics & Proteomics*, 2013, 4:4

28. Serum iron levels and the risk of Parkinson's disease: a Mendelian randomization study. I. Pichler, F. Del Greco M., M. Gogele, C. M. Lill, L. Bertram, C. B. Do, **N. Eriksson**, T. Foroud, R. H. Myers, M. Nalls, M. F. Keller, B. Benyamin, J. B. Whitfield, P. P. Pramstaller, A. A. Hicks, J. Thompson, and C. Minelli. *PLOS Med.* 10(6): e1001462.

27. A genome-wide association meta-analysis of self-reported allergy identifies shared and allergy-specific susceptibility loci. D. A. Hinds, G. McMahon, A. K. Kiefer, C. B. Do, **N. Eriksson**, D. M. Evans, B. St Pourcain, S. M. Ring, J. L. Mountain, U. Francke, G. Davey-Smith, N. J. Timpson, and J. Y. Tung. *Nat Genet*, 2013 June 30.

26. Variants near elastic microfibril genes are associated with non-syndromic striae distensae. J. Y. Tung, A.K. Kiefer, M. Mullins, U. Francke, and **N. Eriksson**. *J Invest Dermatol*, 2013 Apr 30

25. Genome-wide analysis points to roles for extracellular matrix remodeling, the visual cycle, and neuronal development in myopia. A. K. Kiefer, J. Y. Tung, C. B. Do, D. A. Hinds, J. L. Mountain, U. Francke, and **N. Eriksson**. *PLoS Genet.*, 9(2): e1003299.

24. Dealing with the unexpected: Consumer responses to direct-access *BRCA* mutation testing. U. Francke, C. Dijamco, A. K. Kiefer, **N. Eriksson**, B. R. Moiseff, J. Y. Tung, and J. L. Mountain. *PeerJ*, 1:e8.

23. Androgenetic alopecia: identification of four new genetic risk loci and evidence for the contribution of WNT-signaling to its etiology. S. Heilmann, A. K. Kiefer, N. Fricker, D. Drichel, A. M. Hillmer, C. Herold, J. Y. Tung, **N. Eriksson**, S. Redler, R. C. Betz, R. Li, A. Karason, D. R. Nyholt, K. Song, S. H. Vermeulen, S. Kanoni, G. Dedoussis, N. G. Martin, L. A. Kiemeney, V. Mooser, K. Stefansson, J. B. Richards, T. Becker, F. F. Brockschmidt, D. A. Hinds, and M. M. Nothen. *J Invest Dermatol*, 2013 Jan 28.

2012 22. A genetic variant near olfactory receptor genes influences cilantro preference. **N. Eriksson**, S. Wu, C. B. Do, A. K. Kiefer, J. Y. Tung, J. L. Mountain, D. A. Hinds, and U. Francke. *Flavour*, 1:22, Dec 2012.

21. Comparison of Family History and SNPs for Predicting Risk of Complex Disease. C. B. Do, D. A. Hinds, U. Francke, and **N. Eriksson**. *PLoS Genet.*, 8(10): e1002973, October 2012.

20. Genetic variants associated with breast size also influence breast cancer risk. **N. Eriksson**, G. M. Benton, C. B. Do, A. K. Kiefer, J. L. Mountain, D. A. Hinds, U. Francke, and J. Y. Tung. *BMC Med Genet*, 13(1):53, Jun 2012

19. Six novel susceptibility Loci for early-onset androgenetic alopecia and their unexpected association with common diseases. R. Li, F. F. Brockschmidt, A. K. Kiefer, H. Stefansson, D. R. Nyholt, K. Song, S. H. Vermeulen, S. Kanoni, D. Glass, S. E. Medland, M. Dimitriou, D. Waterworth, J. Y. Tung, F. Geller, S. Heilmann, A. M. Hillmer, V. Bataille, S. Eigelshoven, S. Hanneken, S. Moebus, C. Herold, M. den Heijer, G. W. Montgomery, P. Deloukas, **N. Eriksson**,

A. C. Heath, T. Becker, P. Sulem, M. Mangino, P. Vollenweider, T. D. Spector, G. Dedoussis, N. G. Martin, L. A. Kiemeney, V. Mooser, K. Stefansson, D. A. Hinds, M. M. Nothen, and J. B. Richards. *PLoS Genet.*, 8(5):e1002746, May 2012.

18. Cryptic distant relatives are common in both isolated and cosmopolitan genetic samples. B. M. Henn, L. Hon, J. M. Macpherson, **N. Eriksson**, S. Saxonov, I. Pe'er, and J. L. Mountain. *PLoS ONE*, 7(4):e34267, 2012.

17. Novel associations for hypothyroidism include known autoimmune risk loci. **N. Eriksson**, J. Y. Tung, A. K. Kiefer, D. A. Hinds, U. Francke, J. L. Mountain, and C. B. Do. *PLoS ONE*, 7(4):e34442, 2012.

16. Comprehensive research synopsis and systematic meta-analyses in Parkinson's disease genetics: The PDGene database. C. M. Lill, J. T. Roehr, M. B. McQueen, F. K. Kavvoura, S. Bagade, B. M. Schjeide, L. M. Schjeide, E. Meissner, U. Zauft, N. C. Allen, T. Liu, M. Schilling, K. J. Anderson, G. Beecham, D. Berg, J. M. Biernacka, A. Brice, A. L. DeStefano, C. B. Do, **N. Eriksson**, S. A. Factor, M. J. Farrer, T. Foroud, T. Gasser, T. Hamza, J. A. Hardy, P. Heutink, E. M. Hill-Burns, C. Klein, J. C. Latourelle, D. M. Maraganore, E. R. Martin, M. Martinez, R. H. Myers, M. A. Nalls, N. Pankratz, H. Payami, W. Satake, W. K. Scott, M. Sharma, A. B. Singleton, K. Stefansson, T. Toda, J. Y. Tung, J. Vance, N. W. Wood, C. P. Zabetian, P. Young, R. E. Tanzi, M. J. Khoury, F. Zipp, H. Lehrach, J. P. Ioannidis, and L. Bertram. *PLoS Genet.*, 8(3):e1002548, 2012.

2011 15. The temporal order of genetic and pathway alterations in tumorigenesis. M. Gerstung, **N. Eriksson**, J. Lin, B. Vogelstein, and N. Beerenwinkel. *PLoS ONE*, 6(11):e27136, 2011.

14. Efficient replication of over 180 genetic associations with self-reported medical data. J. Y. Tung, C. B. Do, D. A. Hinds, A. K. Kiefer, J. M. Macpherson, A. B. Chowdry, U. Francke, B. T. Naughton, J. L. Mountain, A. Wojcicki, and **N. Eriksson**. *PLoS ONE*, 6(8):e23473, 2011.

13. Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease. C. B. Do, J. Y. Tung, E. Dorfman, A. K. Kiefer, E. M. Drabant, U. Francke, J. L. Mountain, S. M. Goldman, C. M. Tanner, J. W. Langston, A. Wojcicki, and **N. Eriksson**. *PLoS Genet.*, 7(6):e1002141, Jun 2011.

12. ShoRAH: estimating the genetic diversity of a mixed sample from next-generation sequencing data. O. Zagordi, A. Bhattacharya, **N. Eriksson**, and N. Beerenwinkel. *BMC Bioinformatics*, 12:119, Apr 2011.

11. Parametric analysis of alignment and phylogenetic uncertainty. A. S. Malaspinas, **N. Eriksson**, and P. Huggins. *Bull. Math. Biol.*, 73:795–810, Apr 2011.

2010 10. Web-based, participant-driven studies yield novel genetic associations for common traits. **N. Eriksson**, J. M. Macpherson, J. Y. Tung, L. S. Hon, B. Naughton, S. Saxonov, L. Avey, A. Wojcicki, I. Pe'er, and J. Mountain. *PLoS Genet.*, 6:e1000993, Jun 2010.

2008 9. Viral population estimation using pyrosequencing. **N. Eriksson**, L. Pachter, Y. Mitsuya, S. Y. Rhee, C. Wang, B. Gharizadeh, M. Ronaghi, R. W. Shafer, and N. Beerenwinkel. *PLoS Comput. Biol.*, 4:e1000074, Apr 2008.

8. Sequence editing by Apolipoprotein B RNA-editing catalytic component and epidemiological surveillance of transmitted HIV-1 drug resistance. R. J. Gifford, S. Y. Rhee, **N. Eriksson**, T. F. Liu, M. Kiuchi, A. K. Das, and R. W. Shafer. *AIDS*, 22:717–725, Mar 2008.

2007 7. Conjuctive Bayesian networks. N. Beerenwinkel, N. Eriksson, and B. Sturmfels. *Bernoulli*, 13(4):893–909, 2007.

6. Apollonian Circle Packings: Number Theory II. Spherical and Hyperbolic Packings. N. Eriksson and J. C. Lagarias. *Ramanujan Journal*, 14(3):437–469, 2007.

2006 5. Polyhedral conditions for the nonexistence of the MLE for hierarchical log-linear models. N. Eriksson, S. E. Fienberg, A. Rinaldo, and S. Sullivant. *J. Symbolic Comput.*, 41(2):222–233, 2006.

4. Markov bases for noncommutative Fourier analysis of ranked data. P. Diaconis and N. Eriksson. *J. Symbolic Comput.*, 41(2):182–195, 2006.

3. Evolution on distributive lattices. N. Beerenwinkel, N. Eriksson, and B. Sturmfels. *J Theor Biol*, 242(2):409–420, Sep 2006.

2004 2. Toric ideals of homogeneous phylogenetic models. N. Eriksson. In the proceedings of *ISSAC 2004*, pages 149–154. ACM, New York, 2004.

1999 1. q-series, elliptic curves, and odd values of the partition function. N. Eriksson. *International Journal of Mathematics and Mathematical Sciences*, 22(1):55–66, 1999

Theses and book chapters

2009 6. Using invariants for phylogenetic tree construction. N. Eriksson. In *Emerging Applications of Algebraic Geometry*, pages 89–108. Springer, New York, 2009.

2007 5. Metric learning for phylogenetic invariants. N. Eriksson and Y. Yao. *ArXiv preprint*, 2007.

2006 4. Algebraic combinatorics for computational biology. N. Eriksson. PhD thesis, University of California, Berkeley, 2006.

2005 3. Ultra-Conserved Elements in Vertebrate and Fly Genomes. M. Drton, N. Eriksson, and G. Leung. In L. Pachter and B. Sturmfels, editors, *Algebraic Statistics for Computational Biology*, chapter 22, pages 387–402. Cambridge University Press, Cambridge, UK, 2005.

2. Tree Construction using Singular Value Decompsition. N. Eriksson. In L. Pachter and B. Sturmfels, editors, *Algebraic Statistics for Computational Biology*, chapter 19, pages 347–358. Cambridge University Press, Cambridge, UK, 2005.

1. Phylogenetic algebraic geometry. N. Eriksson, K. Ranestad, B. Sturmfels, and S. Sullivant. In C. Ciliberto, A. Geramita, B. Harbourne, R-M. Roig, and K. Ranestad, editors, *Projective varieties with unexpected properties*, pages 237–255. Walter de Gruyter GmbH & Co. KG, Berlin, 2005.

Invited and Conference talks

2014 May Association for Psychological Science Annual Convention, San Francisco, CA
—— Feb. Computation-Intensive Probabilistic and Statistical Methods for Large-Scale Population Genomics, Berkeley, CA
—— Feb. Genomics in Medicine, San Francisco, CA
2013 Oct. American Society of Human Genetics Annual Meeting, Boston, MA
—— May Advanced Topics in Genomics and Cell Biology, UNICAMP, Campinas, Brazil
—— Mar. Broad Institute, Medical and Population Genetics Program Seminar
—— Jan. Monell Chemical Senses Center, Philadelphia, PA
—— Jan. Genomic Medicine Symposium, Berkeley, CA
2012 Nov. American Society of Human Genetics Annual Meeting, San Francisco, CA
—— Oct. EMBL PhD Symposium, Heidelberg, Germany
—— Oct. Colloquium, IST Vienna
—— Jun. IEEE New Frontiers in Computing, Stanford University
—— Apr. NHGRI Seminar, Bethesda, MD
—— Mar. Bay Area Discrete Mathematics Day, UC Berkeley
—— Feb. MJFF LRRK2 and Parkinson's meeting, Tel Aviv
2011 Oct. UC San Diego Institute for Genomic Medicine Annual Symposium

—— Sep. IBM Almaden Research, Seminar
—— Sep. Human Genomic Variation Conference, Berkeley, CA
2010 Nov. Broad Institute, Seminar
—— Apr. Network Biology 2.0 conference, Broad Institute
—— Apr. Friends of the National Library of Science, NIH
2009 Dec. Partnering for Cures Meeting, New York
—— Dec. Cure Parkinsons Trust Genetics Conference, Royal Society of Medicine, London
—— Oct. American Society of Human Genetics Annual Meeting, Honolulu, HI
—— Oct. Society for Industrial and Applied Mathematics Annual Meeting, San Francisco, CA
—— Sep. UC San Francisco Biostatistics Seminar
—— May International Symposium on Bioinformatics Research and Applications (keynote)
—— May Oxford University, Wellcome Trust Centre for Human Genetics
2008 Mar. Brown University, CCMB Seminar
—— Feb. University of Miami, Mathematics Seminar
—— Feb. Virginia Bioinformatics Institute
—— Jan. Columbia University, Statistics seminar
—— Jan. Viral Paradigms: Molecules, Populations, Ecosystems and Infectious Disease; Georgia Tech
—— Jan. Duke University, Mathematics seminar
—— Dec. University of Basel, Switzerland, Bioinformatics seminar
—— Oct. AMS Central Section Annual Meeting, Chicago, IL
—— Jul. Second Argentine School of Mathematics and Biology, La Falda, Argentina
—— Jun. UC Irvine, 2007 WNAR/IMS annual meeting
2007 May Stanford University, Workshop in Biostatistics
—— Apr. UC San Diego, Computational biology seminar
—— Apr. UCLA, Statistics seminar
—— Mar. University of Minnesota, Combinatorics seminar
—— Feb. Bay area biosystematists meeting
—— Feb. Duke University, Mathematics seminar
—— Jan. Stanford University, BioMathematical Methodology Seminar
2006 Nov. University of Chicago / Toyota Technological Institute Seminar
—— Nov. University of Chicago, Statistics seminar
—— Sep. UC Davis, Berkeley-Davis Mathematical Genomics Meeting
—— Jun. MSRI Summer Graduate Workshop: Mathematical aspects of computational biology
—— Mar. University of Miami, Mathematics colloquium
—— Mar. University of Miami, Combinatorics seminar
—— Feb. Massachusetts Institute of Technology, Special applied mathematics seminar
—— Jan. Carnegie Mellon University, Statistics seminar
—— Jan. Joint AMS/MAA Meeting, Special Session on Algebraic Statistics: Theory and Practice
2005 Dec. First Argentine School of Mathematics and Biology, La Cumbre, Argentina
2004 Jul. University of Barcelona, Seminari D'àlgebra commutativa, combinatòria, i computacional
—— Jul. University of Cantabria, Santander, Spain, International Symposium on Symbolic and Algebraic Computation

Referee and review activities

PLoS Genetics
Genome Medicine
Human Molecular Genetics
Journal of Medical Genetics
Journal of Symbolic Computation
RECOMB
Annals of Combinatorics
Statistical Applications in Genetics and Molecular Biology
Statistica Sinica
BMC Bioinformatics
JAMA

Teaching activities

2008	Spring	Statistics 234 (Statistical Models/Methods), University of Chicago
2008	Winter	Reading course on metagenomics and population genetics, University of Chicago
2007	Fall	Statistics 234 (Statistical Models/Methods), University of Chicago
2007	July	Second Argentine School of Mathematics and Biology, short course on Drug resistance in HIV
2005	Dec	First Argentine School of Mathematics and Biology, short course on Algebraic statistics for computational biology
2004	Fall	Calculus 1A, UC Berkeley, Graduate Student Instructor