Curriculum Vitae
Nicholas Eriksson

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Date of Birth:	1978 (Montana, USA)	Date of CV:	May 2018

Education/Employment

2018 –		Senior Scientist, Health R&D **23andMe, Inc.**, Mountain View, CA
2016 – 2018		Principal Data Scientist, **Calico Labs**, South San Francisco, CA
2014 – 2016		Data Scientist, **Coursera**, Mountain View, CA
2009 – 2014		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

2013 – 2014	Principal Investigator, NIH Grant 2R44HG006981-02, Development of a web-based database and research engine for genetic discovery ($805,975)
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 and skills

- Statistics, machine learning and discrete mathematics
- Genomics and human complex trait genetics
- Cancer tumor progression and HIV population evolution
- Skills: R, python, and SQL (fluent). C++, javascript, scala (basic).

Publications

Peer-reviewed and submitted articles (47 total, 18 as first/last/unordered author)

2018 47. Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. N.R. Wray, S. Ripke, M. Mattheisen, M. Trzaskowski, E.M. Byrne, A. Abdellaoui, M.J. Adams, E. Agerbo, T.M. Air, T.MF Andlauer, S-A. Bacanu, M. Bækvad-Hansen, A.FT Beekman, T.B. Bigdeli, E.B. Binder, D.RH Blackwood, J. Bryois, H.N Buttenschøn, J. Bybjerg-Grauholm, N. Cai, E. Castelao, J.H. Christensen, T-K Clarke, J.IR Coleman, L. Colodro-Conde, B. Couvy-Duchesne, N. Craddock, G.E. Crawford, C.A. Crowley, H.S. Dashti, G. Davies, I.J. Deary, F. Degenhardt, E.M. Derks, N. Direk, C.V. Dolan, E.C. Dunn, T.C. Eley, **N. Eriksson**, V. Escott-Price, F.H. Farhadi Kiadeh, H.K. Finucane, A.J Forstner, J. Frank, H.A. Gaspar, M. Gill, P. Giusti-Rodríguez, F.S. Goes, S.D. Gordon, J. Grove, L.S. Hall, E. Hannon, C.S. Hansen, T.F. Hansen, S. Herms, I.B. Hickie, P. Hoffmann, G. Homuth, C. Horn, J-J Hottenga, D.M. Hougaard, M. Hu, C.L. Hyde, M. Ising, R. Jansen, F. Jin, E. Jorgenson, J.A. Knowles, I.S. Kohane, J. Kraft, W.W. Kretzschmar, J. Krogh, Z. Kutalik, J.M. Lane, Y. Li, Y. Li, P.A. Lind, X. Liu, L. Lu, D.J. MacIntyre, D.F. MacKinnon, R.M. Maier, W. Maier, J. Marchini, H. Mbarek, P. McGrath, P. McGuffin, S.E. Medland, D. Mehta, C.M. Middeldorp, E. Mihailov, Y. Milaneschi, L. Milani, J. Mill, F.M. Mondimore, G.W. Montgomery, S. Mostafavi, N. Mullins, M. Nauck, B. Ng, M.G. Nivard, D.R. Nyholt, P.F. O'Reilly, H. Oskarsson, M.J. Owen, J.N. Painter, C.B. Pedersen, M.G. Pedersen, R.E. Peterson, E. Pettersson, W.J. Peyrot, G. Pistis, D. Posthuma, S.M. Purcell, J.A. Quiroz, P. Qvist, J.P. Rice, B.P. Riley, M. Rivera, S.S. Mirza, R. Saxena, R. Schoevers, E.C. Schulte, L. Shen, J. Shi, S.I. Shyn, E. Sigurdsson, G.BC Sinnamon, J.H. Smit, D.J. Smith, H. Stefansson, S. Steinberg, C.A. Stockmeier, F. Streit, J. Strohmaier, K.E. Tansey, H. Teismann, A. Teumer, W. Thompson, P.A. Thomson, T.E. Thorgeirsson, C. Tian, M. Traylor, J. Treutlein, V. Trubetskoy, A.G. Uitterlinden, D. Umbricht, S. Van der Auwera, A.M. van Hemert, A. Viktorin. *Nat Genet.* 2018; 50, 668–681

2017 46. Genome-wide association and HLA region fine-mapping studies identify susceptibility loci for multiple common infections. C. Tian, B.S. Hromatka, A.K. Kiefer, **N. Eriksson**, S. Noble, J.Y. Tung, D.A. Hinds. *Nat Commun.* 2017; 8; 599

45. A genetic investigation of sex bias in the prevalence of attention deficit hyperactivity disorder. J. Martin, R.K. Walters, D. Demontis, M. Mattheisen, S.H. Lee, E. Robinson, I. Brikell, L. Ghirardi, H. Larsson, P. Lichtenstein, **N. Eriksson**, 23andMe Research Team, Psychiatric Genomics Consortium: ADHD Subgroup, iPSYCH-Broad ADHD Workgroup, T. Werge, P.B. Mortensen, M.G. Pedersen, O. Mors, M. Nordentoft, D.M. Hougaard, J. Bybjerg-Grauholm, N. Wray, B. Franke, S.V. Faraone, M.C. O'Donovan, A. Thapar, A.D. Børglum, B.M. Neale. *bioRxiv* (2017)

44. Discovery Of The First Genome-Wide Significant Risk Loci For ADHD. D. Demontis, R.K. Walters, J. Martin, M. Mattheisen, T.D. Als, E. Agerbo, R. Belliveau, J. Bybjerg-Grauholm, M. Bækved-Hansen, F. Cerrato, K. Chambert, C. Churchhouse, A. Dumont, **N. Eriksson**, M. Gandal, J. Goldstein, J. Grove, C.S. Hansen, M. Hauberg, M. Hollegaard, D.P. Howrigan, H. Huang, J. Maller, A.R. Martin, J. Moran, J. Pallesen, D.S. Palmer, C.B. Pedersen, M.G. Pedersen, T. Poterba, J.B. Poulsen, S. Ripke, E.B. Robinson, F.K. Satterstrom, C. Stevens, P. Turley, H. Won, ADHD Working Group of the Psychiatric Genomics Con, Early Lifecourse and Genetic Epidemiology (EAGLE), 23andMe Research Team, O.A. Andreassen, C. Burton, D. Boomsma, B. Cormand, S. Dalsgaard, B. Franke, J. Gelernter, D. Geschwind, H. Hakonarson, J. Haavik, H. Kranzler, J. Kuntsi, K. Langley, K-P. Lesch, C. Middeldorp, A. Reif, L.A. Rohde, P. Roussos, R. Schachar, P. Sklar, E. Sonuga-Barke, P.F. Sullivan, A. Thapar, J.Y. Tung, I. Waldman, M. Nordentoft, D.M. Hougaard, T. Werge, O. Mors, P.B. Mortensen, M.J. Daly, S.V. Faraone, A.D. Børglum, B.M. Neale. *bioRxiv* (2017)

43. Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. L.C. Tsoi, P.E. Stuart, C. Tian, J.E. Gudjonsson, S. Das, M. Zawistowski, E. Ellinghaus, J.N. Barker, V. Chandran, N. Dand, K.C. Duffin, C. Enerbäck, T. Esko, A. Franke, D.D. Gladman, P. Hoffmann, K. Kingo, S. Kõks, G. G. Krueger, H.W. Lim, A. Metspalu, U. Mrowietz, S. Mucha, P. Rahman, A. Reis, T. Tejasvi, R. Trembath, J.J. Voorhees, S. Weidinger, M. Weichenthal, X. Wen, **N. Eriksson**, H.M. Kang, D.A. Hinds, R.P. Nair, G.R. Abecasis, J.T. Eldera. *Nat Commun.* 2017; 8: 15382

2016 42. Genome-wide analysis identifies 12 loci influencing human reproductive behavior. N. Barban, R. Jansen, R. de Vlaming, A. Vaez, J.J. Mandemakers, F.C. Tropf, X. Shen, J.F. Wilson, D.I. Chasman, I.M. Nolte, V. Tragante, S.W. van der Laan, JRB Perry, A. Kong, T. S Ahluwalia, E. Albrecht, L. Yerges-Armstrong, G. Atzmon, K. Auro, K. Ayers, A. Bakshi, D. Ben-Avraham, K. Berger, A. Bergman, L. Bertram, L.F. Bielak, G. Bjornsdottir, M. Jan Bonder, L. Broer, M. Bui, C. Barbieri, A. Cavadino, J.E. Chavarro, C. Turman, M. Pina Concas, H.J. Cordell, G. Davies, P. Eibich, **N. Eriksson**, T. Esko, J. Eriksson, F. Falahi, J.F. Felix, M.A. Fontana, L. Franke, I. Gandin, A.J. Gaskins, C. Gieger, E. P Gunderson, X. Guo, C. Hayward, C. He, E. Hofer, H. Huang, P.K. Joshi, S. Kanoni, R. Karlsson, S. Kiechl, A. Kifley, A. Kluttig, P. Kraft, V. Lagou, C. Lecoeur, J. Lahti, R. Li-Gao, P. A Lind, T. Liu, E. Makalic, C. Mamasoula, L. Matteson, H. Mbarek, P.F. McArdle, G. McMahon, SFW Meddens, E. Mihailov, M. Miller, S.A. Missmer, C. Monnereau, P.J. van der Most, R. Myhre, M.A Nalls, T. Nutile, I. Panagiota Kalafati, E. Porcu, I. Prokopenko, K.B. Rajan, J. Rich-Edwards, C.A. Rietveld, A. Robino, L.M. Rose, R. Rueedi, K.A. Ryan, Y. Saba, D. Schmidt, J.A. Smith, L. Stolk, E. Streeten, A. Tönjes, G. Thorleifsson, S. Ulivi, J. Wedenoja, J. Wellmann, P. Willeit, J. Yao, L. Yengo, J. Hua Zhao, W. Zhao, D.V. Zhernakova, N. Amin, H. Andrews, B. Balkau, N. Barzilai, S. Bergmann, G. Biino, H. Bisgaard, K. Bønnelykke, D. I Boomsma, J.E. Buring, H. Campbell, S. Cappellani, M. Ciullo, S.R. Cox, F. Cucca, D. Toniolo, G. Davey-Smith, I.J. Deary, G. Dedoussis, P. Deloukas, C.M. van Duijn, EJC de Geus, J.G. Eriksson, D.A. Evans, J.D. Faul, C. Felicita Sala, P. Froguel, P. Gasparini, G. Girotto, H-J Grabe, K. Halina Greiser, PJF Groenen, H.G. de Haan, J. Haerting, T.B. Harris, A.C. Heath, K. Heikkilä, A. Hofman, G. Homuth, E.G. Holliday, J. Hopper, E. Hyppönen. *Nature Genetics* 48, 1462–1472 (2016)

41. Germline variants predispose to both JAK2 V617F clonal hematopoiesis and myeloproliferative neoplasms. D.A. Hinds, K.E. Barnholt, R.A. Mesa, A.K. Kiefer, C.B. Do, **N. Eriksson**, J.L. Mountain, U. Francke, J.Y. Tung, H.M. Nguyen, H. Zhang, L. Gojenola, J.L. Zehnder, J. Gotlib. *Blood* (2016) doi:10.1182/blood-2015-06-652941

40. Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. P. Gormley, V. Anttila, B.S. Winsvold, P. Palta, T. Esko, T.H. Pers, K-H. Farh, E. Cuenca-Leon, M. Muona, N.A. Furlotte, T. Kurth, A. Ingason, G. McMahon, L. Ligthart, G.M. Terwindt, M. Kallela, T.M. Freilinger, C. Ran, S.G. Gordon, A.H. Stam, S. Steinberg, G. Borck, M. Koiranen, L. Quaye, H.H.H. Adams, T. Lehtimäki, A-P. Sarin, J. Wedenoja, D.A. Hinds, J.E. Buring, M. Schürks, P.M. Ridker, M.G. Hrafnsdottir, H. Stefansson, S.M. Ring, J-J. Hottenga, B.W.J.H. Penninx, M. Färkkilä, V. Artto, M. Kaunisto, S. Vepsäläinen, R. Malik, A.C. Heath, P.A.F. Madden, N.G. Martin, G.W. Montgomery, M.I. Kurki, M. Kals, R. Mägi, K. Pärn, E. Hämäläinen, H. Huang, A.E. Byrnes, L. Franke, J. Huang, E. Stergiakouli, P.H. Lee, C. Sandor, C. Webber, Z. Cader, B. Muller-Myhsok, S. Schreiber, T. Meitinger, J.G. Eriksson, V. Salomaa, K. Heikkilä, E. Loehrer, A.G. Uitterlinden, A. Hofman, C.M. van Duijn, L. Cherkas, L.M. Pedersen, A. Stubhaug, C.S. Nielsen, M. Männikkö, E. Mihailov, L. Milani, H. Göbel, A-L. Esserlind, A.F. Christensen, T.F. Hansen, T. Werge, V. Anttila, V. Artto, A.C. Belin, D.I. Boomsma, S. Børte, L. Cherkas, A.F. Christensen, B. Cormand, E. Cuenca-Leon, G.D. Smith, M. Dichgans, C. van Duijn, E. Eising, T. Esko, A-L. Esserlind, M. Ferrari, R.R Frants, T. M Freilinger, L.

Griffiths, E. Hamalainen, T.F. Hansen, M. Hiekkala, M.A. Ikram, A. Ingason, M-R. Järvelin, R. Kajanne, M. Kallela, J. Kaprio, M. Kaunisto, C. Kubisch, M. Kurki, T. Kurth, L. Launer, T. Lehtimaki, D. Lessel, L. Ligthart, N. Litterman, A.M.J.M.van den Maagdenberg, A. Macaya, R. Malik, M. Mangino, G. McMahon, B. Muller-Myhsok, C. Northover, J. Olesen, L.M. Pedersen, N. Pedersen, D. Posthuma, P. Pozo-Rosich, A. Pressman, L. Quaye, O. Raitakari, M. Schürks, C. Sintas, H. Stefansson, S. Steinberg, D. Strachan, G.M. Terwindt, M. Vila-Pueyo, M. Wessman, B.S. Winsvold, W. Wrenthal, H. Zhao, J-A. Zwart, J. Kaprio, A.J. Aromaa, O. Raitakari, M.A. Ikram, T. Spector, M-R. Järvelin, A. Metspalu, C. Kubisch, D.P. Strachan, M.D. Ferrari, A.C. Belin, M. Dichgans, M. Wessman, A.M.J.M. van den Maagdenberg, J-A. Zwart, D.I. Boomsma, G.D. Smith, K. Stefansson, **N. Eriksson**, M.J. Daly, B.M. Neale, J. Olesen, D.I. Chasman, D.R. Nyholt, A. Palotie. *Nature Genetics* (2016) doi:10.1038/ng.3598

39. GWAS of 89,283 individuals identifies genetic variants associated with self-reporting of being a morning person. Y. Hu, A. Shmygelska, D. Tran, **N. Eriksson**, J.Y. Tung, D.A. Hinds. *Nature Communications* 7, Article number: 10448, Feb 2016.

2015 38. Virtual research visits and direct-to-consumer genetic testing in Parkinson's disease. E.R. Dorsey, K.C. Darwin, S. Mohammed, S. Donohue, A. Tethal, M.A. Achey, S. Ward, E. Caughey, E.D. Conley, **N. Eriksson**, B. Ravina. *Digital Health*, Jun 2015.

37. Assessment of the Genetic Basis of Rosacea by Genome-Wide Association Study. A. L. S. Chang, I. Raber, J. Xu, R. Li, R. Spitale, J. Chen, A. K. Kiefer, C. Tian, **N. Eriksson**, D. A. Hinds, J. Y. Tung. *Journal of Investigative Dermatology*, March 2015.

36. 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**. *Human Molecular Genetics*, 2015.

35. Escape from crossover interference increases with maternal age. C. L. Campbell, N. A. Furlotte, **N. Eriksson**, D. A. Hinds, A. Auton. *Nature Communications*, 6, Feb 2015.

2014 34. Replicability and Robustness of Genome-Wide-Association Studies for Behavioral Traits. C. A. Rietveld, D. Conley, **N. Eriksson**, T. Esko, S. E. Medland, A. A. E. Vinkhuyzen, J. Yang, J. D. Boardman, C. F. Chabris, C. T. Dawes, B. W. Domingue, D. A. Hinds, M. Johannesson, A. K. Kiefer, D. Laibson, P. K. E. Magnusson, J. L. Mountain, S. Oskarsson, O. Rostapshova, A. Teumer, J. Y. Tung, P. M. Visscher, D. J. Benjamin, D. Cesarini, P. D. Koellinger. *Psychological Science,* Nov 2014, vol. 25, no. 11, 1975-1986.

33. NeuroX, a Fast and Efficient Genotyping Platform for Investigation of Neurodegenerative Diseases. M. A. Nalls, J. Bras, D. G. Hernandez, M. F. Keller, E. Majounie, A. E. Renton, M. Saad, I. Jansen, R. Guerreiro, S. Lubbe, V. Plagnol, J. R. Gibbs, C. Schulte, N. Pankratz, M. Sutherland, L. Bertram, C. M. Lill, A. L. DeStefano, T. Faroud, **N. Eriksson**, J. Y. Tung, C. Edsall, N. Nichols, J. Brooks, S. Arepalli, H. Pliner, C. Letson, P. Heutink, M. Martinez, T. Gasser, B. J. Traynor, N. Wood, J. Hardy, A. B. Singleton. *Neurobiology of Aging,* 4 Aug 2014.

32. Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. M. A. Nalls, N. Pankratz, C. M. Lill, C. B. Do, D. G. Hernandez, M. Saad, A. L. DeStefano, E. Kara, J. Bras, M. Sharma, C. Schulte, M. F. Keller, S. Arepalli, C. Letson, C. Edsall, H. Stefansson, X. Liu, H. Pliner, J. H. Lee, R. Cheng, International Parkinson's Disease Genomics Consortium (IPDGC), Parkinson's Study Group (PSG) Parkinson's Research: The Organized GENetics Initiative (PROGENI), 23andMe, GenePD, NeuroGenetics Research Consortium (NGRC), Hussman Institute of Human Genomics (HIHG), The Ashkenazi Jewish Dataset Investigator, Cohorts for Health and Aging Research in Genetic Epidemiology (CHARGE), North American Brain Expression Consortium (NABEC), United Kingdom Brain Expression Consortium (UKBEC), Greek Parkinson's Disease Consortium, Alzheimer Genetic

Analysis Group, M. A. Ikram, J. P. A. Ioannidis, G. M Hadjigeorgiou, J. C. Bis, M. Martinez, J. S. Perlmutter, A. Goate, K. Marder, B. Fiske, M. Sutherland, G. Xiromerisiou, R. H. Myers, L. N. Clark, K. Stefansson, J. A. Hardy, P. Heutink, H. Chen, N. W. Wood, H. Houlden, H. Payami, A. Brice, W. K. Scott, T. Gasser, L. Bertram, **N. Eriksson**, T. Foroud, A. B. Singleton. *Nature Genetics* (2014) doi:10.1038/ng.3043

31. Reducing pervasive false positive identical-by-descent segments detected by large-scale pedigree analysis. E. Y. Durand, **N. Eriksson**, C. Y. McLean. *Mol Biol Evol*, 30 April 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. Genome-Wide Association Analysis Implicates Elastic Microfibrils in the Development of 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.
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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.
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11. Parametric analysis of alignment and phylogenetic uncertainty. A. S. Malaspinas, **N. Eriksson**, and P. Huggins. *Bull. Math. Biol.*, 73:795–810, Apr 2011.

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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*

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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.

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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

2015 7. Who's Benefiting from MOOCs, and Why. C. Zhenghao, B. Alcorn, G. Christensen, **N. Eriksson**, D. Koller, E.J. Emanuel. *Harvard Business Review*, September 22, 2015.

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

2015 Mar. Coursera Partners Conference, Irvine, CA

2014 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. Columbia University Computer Science Seminar, New York, NY
—— 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	Annals of Combinatorics
Genome Medicine	Statistical Applications in Genetics and Molecular Biology
Human Molecular Genetics	Statistica Sinica
Journal of Medical Genetics	BMC Bioinformatics
Journal of Symbolic Computation	JAMA
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Teaching

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