Curriculum Vitae
Nicholas Eriksson

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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 Grants 1R43HG006981-01 and 2R44HG006981-02, Development of a web-based database and research engine for genetic discovery
2012 – 2013	Principal Investigator, MJFF Research Grant, Using external research experts to mine the 23andMe Parkinson's database
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 (52 total, 18 as first/last/unordered author)

2020 52. Genome-wide association study identifies 48 common genetic variants associated with handedness. Gabriel Cuellar-Partida, Joyce Y. Tung, **N. Eriksson**, Eva Albrecht, Fazil Aliev, Ole A. Andreassen, Inês Barroso, Jacques S. Beckmann, Marco P. Boks, Dorret I. Boomsma, Heather A. Boyd, Monique M. B. Breteler, Harry Campbell, Daniel I. Chasman, Lynn F. Cherkas, Gail Davies, Eco J. C. de Geus, Ian J. Deary, Panos Deloukas, Danielle M. Dick, David L. Duffy, Johan G. Eriksson, Tõnu Esko, Bjarke Feenstra, Frank Geller, Christian Gieger, Ina Giegling, Scott D. Gordon, Jiali Han, Thomas F. Hansen, Annette M. Hartmann, Caroline Hayward, Kauko Heikkilä, Andrew A. Hicks, Joel N. Hirschhorn, Jouke-Jan Hottenga, Jennifer E. Huffman, Liang-Dar Hwang, M. Arfan Ikram, Jaakko Kaprio, John P. Kemp, Kay-Tee Khaw, Norman Klopp, Bettina Konte, Zoltan Kutalik, Jari Lahti, Xin Li, Ruth J. F. Loos, Michelle Luciano, Sigurdur H. Magnusson, Massimo Mangino, Pedro Marques-Vidal, Nicholas G. Martin, Wendy L. McArdle, Mark I. McCarthy, Carolina Medina-Gomez, Mads Melbye, Scott A. Melville, Andres Metspalu, Lili Milani, Vincent Mooser, Mari Nelis, Dale R. Nyholt, Kevin S. O'Connell, Roel A. Ophoff, Cameron Palmer, Aarno Palotie, Teemu Palviainen, Guillaume Pare, Lavinia Paternoster, Leena Peltonen, Brenda W. J. H. Penninx, Ozren Polasek, Peter P. Pramstaller, Inga Prokopenko, Katri Raikkonen, Samuli Ripatti, Fernando Rivadeneira, Igor Rudan, Dan Rujescu, Johannes H. Smit, George Davey Smith, Jordan W. Smoller, Nicole Soranzo, Tim D. Spector, Beate St Pourcain, John M. Starr, Hreinn Stefánsson, Stacy Steinberg, Maris Teder-Laving, Gudmar Thorleifsson, Kári Stefánsson, Nicholas J. Timpson, André G. Uitterlinden, Cornelia M. van Duijn, Frank J. A. van Rooij, Jaqueline M. Vink, Peter Vollenweider, Eero Vuoksimaa, Gérard Waeber, Nicholas J. Wareham, Nicole Warrington, Dawn Waterworth, Thomas Werge, H.-Erich Wichmann, Elisabeth Widen, Gonneke Willemsen, Alan F. Wright, Margaret J. Wright, Mousheng Xu, Jing Hua Zhao, Peter Kraft, David A. Hinds, Cecilia M. Lindgren, Reedik Mägi, Benjamin M. Neale, David M. Evans, and Sarah E. Medland . *Nature Human Behaviour* (2020)

2019 51. Inferring Multidimensional Rates of Aging from Cross-Sectional Data. E. Pierson, P.W. Koh, T. Hashimoto, D. Koller, J. Leskovec, **N. Eriksson**, and P. Liang. *Proc Mach Learn Res.* 2019 Apr; 89: 97–107.

2018 50. Self-report data as a tool for subtype identification in genetically-defined Parkinson's disease. A.R. Winslow, C.L. Hyde, J.B. Wilk, **N. Eriksson**, P. Cannon, M.R. Miller, W.D. Hirst. *Scientific Reports* volume 8, Article number: 12992 (2018)

49. Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Milly S Tedja, Robert Wojciechowski, Pirro G Hysi, **N. Eriksson**, Nicholas A Furlotte, Virginie JM Verhoeven, Adriana I Iglesias, Magda A Meester-Smoor, Stuart W Tompson, Qiao Fan, Anthony P Khawaja, Ching-Yu Cheng, René Höhn, Kenji Yamashiro, Adam Wenocur, Clare Grazal, Toomas Haller, Andres Metspalu, Juho Wedenoja, Jost B Jonas, Ya Xing Wang, Jing Xie, Paul Mitchell, Paul J Foster, Barbara EK Klein, Ronald Klein, Andrew D Paterson, S Mohsen Hosseini, Rupal L Shah, Cathy Williams, Yik Ying Teo, Yih Chung Tham, Preeti Gupta, Wanting Zhao, Yuan Shi, Woei-Yuh Saw, E-Shyong Tai, Xue Ling Sim, Jennifer E Huffman, Ozren Polašek, Caroline Hayward, Goran Bencic, Igor Rudan, James F Wilson, Peter K Joshi, Akitaka Tsujikawa, Fumihiko Matsuda, Kristina N Whisenhunt, Tanja Zeller, Peter J van der Spek, Roxanna Haak, Hanne Meijers-Heijboer, Elisabeth M van Leeuwen, Sudha K Iyengar, Jonathan H Lass, Albert Hofman, Fernando Rivadeneira, André G Uitterlinden, Johannes R Vingerling, Terho Lehtimäki, Olli T Raitakari, Ginevra Biino, Maria Pina Concas, Tae-Hwi Schwantes-An, Robert P Igo, Gabriel Cuellar-Partida, Nicholas G Martin,

Jamie E Craig, Puya Gharahkhani, Katie M Williams, Abhishek Nag, Jugnoo S Rahi, Phillippa M Cumberland, Cécile Delcourt, Céline Bellenguez, Janina S Ried, Arthur A Bergen, Thomas Meitinger, Christian Gieger, Tien Yin Wong, Alex W Hewitt, David A Mackey, Claire L Simpson, Norbert Pfeiffer, Olavi Pärssinen, Paul N Baird, Veronique Vitart, Najaf Amin, Cornelia M van Duijn, Joan E Bailey-Wilson, Terri L Young, Seang-Mei Saw, Dwight Stambolian, Stuart MacGregor, Jeremy A Guggenheim, Joyce Y Tung, Christopher J Hammond, Caroline CW Klaver. *Nat Genet.* 2018; 50, 834-–848

48. Analysis of shared heritability in common disorders of the brain. Verneri Anttila, Brendan Bulik-Sullivan, Hilary K Finucane, Raymond K Walters, Jose Bras, Laramie Duncan, Valentina Escott-Price, Guido J Falcone, Padhraig Gormley, Rainer Malik, Nikolaos A Patsopoulos, Stephan Ripke, Zhi Wei, Dongmei Yu, Phil H Lee, Patrick Turley, Benjamin Grenier-Boley, Vincent Chouraki, Yoichiro Kamatani, Claudine Berr, Luc Letenneur, Didier Hannequin, Philippe Amouyel, Anne Boland, Jean-François Deleuze, Emmanuelle Duron, Badri N Vardarajan, Christiane Reitz, Alison M Goate, Matthew J Huentelman, M Ilyas Kamboh, Eric B Larson, Ekaterina Rogaeva, Peter St George-Hyslop, Hakon Hakonarson, Walter A Kukull, Lindsay A Farrer, Lisa L Barnes, Thomas G Beach, F Yesim Demirci, Elizabeth Head, Christine M Hulette, Gregory A Jicha, John SK Kauwe, Jeffrey A Kaye, James B Leverenz, Allan I Levey, Andrew P Lieberman, Vernon S Pankratz, Wayne W Poon, Joseph F Quinn, Andrew J Saykin, Lon S Schneider, Amanda G Smith, Joshua A Sonnen, Robert A Stern, Vivianna M Van Deerlin, Linda J Van Eldik, Denise Harold, Giancarlo Russo, David C Rubinsztein, Anthony Bayer, Magda Tsolaki, Petra Proitsi, Nick C Fox, Harald Hampel, Michael J Owen, Simon Mead, Peter Passmore, Kevin Morgan, Markus M Nöthen, Jonathan M Schott, Martin Rossor, Michelle K Lupton, Per Hoffmann, Johannes Kornhuber, Brian Lawlor, Andrew Mcquillin, Ammar Al-Chalabi, Joshua C Bis, Agustin Ruiz, Mercè Boada, Sudha Seshadri, Alexa Beiser, Kenneth Rice, Sven J van der Lee, Philip L De Jager, Daniel H Geschwind, Matthias Riemenschneider, Steffi Riedel-Heller, Jerome I Rotter, Gerhard Ransmayr, Bradley T Hyman, Carlos Cruchaga, Montserrat Alegret, Bendik Winsvold, Priit Palta, Kai-How Farh, Ester Cuenca-Leon, Nicholas Furlotte, Tobias Kurth, Lannie Ligthart, Gisela M Terwindt, Tobias Freilinger, Caroline Ran, Scott D Gordon, Guntram Borck, Hieab HH Adams, Terho Lehtimäki, Juho Wedenoja, Julie E Buring, Markus Schürks, Maria Hrafnsdottir, Jouke-Jan Hottenga, Brenda Penninx, Ville Artto, Mari Kaunisto, Salli Vepsäläinen, Nicholas G Martin, Grant W Montgomery, Mitja I Kurki, Eija Hämäläinen, Hailiang Huang, Jie Huang, Cynthia Sandor, Caleb Webber, Bertram Muller-Myhsok, Stefan Schreiber, Veikko Salomaa, Elizabeth Loehrer, Hartmut Göbel, Alfons Macaya, Patricia Pozo-Rosich, Thomas Hansen, Thomas Werge, Jaakko Kaprio, Andres Metspalu, Christian Kubisch, Michel D Ferrari, Andrea C Belin, Arn MJM van den Maagdenberg, John-Anker Zwart, Dorret Boomsma, **N. Eriksson**, Jes Olesen, Daniel I Chasman, Dale R Nyholt, Richard Anney, Andreja Avbersek, Larry Baum. *Science* 22 Jun 2018: Vol. 360, Issue 6395, eaap8757

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.

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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.

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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.

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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
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

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