CURRICULUM VITAE

Name: Kathryn Roeder, UPMC Professor of Statistics and Life Sciences
E-mail: roeder@andrew.cmu.edu.
www: `http://www.stat.cmu.edu/~roeder`
Address: Department of Statistics and Data Science
Carnegie Mellon University
Pittsburgh, PA 15213

EDUCATION: Ph.D. (Statistics), 1988, Pennsylvania State University
B.S. (Wildlife Resources, summa cum laude), 1982, University of Idaho

POSITIONS: **Carnegie Mellon University**, Pittsburgh, PA
Vice Provost for Faculty; 2015-2019
Departments of Statistics and Data Science & Computational Biology
1998-present, Professor; 1994-1997, Associate Professor
Yale University, New Haven, CT
1991-1994, Associate Professor; 1988-1991, Assistant Professor

SELECTED PROFESSIONAL ACTIVITIES & AWARDS:

COPSS Distinguished Achievement Award and Lectureship, 2020
University Professorship, 2020
National Academy of Sciences, 2019
Web of Science, Clarivate Analytics Cross-Fields Highly Cited Researcher, 2018, 2020
UPMC Professor of Statistics and Life Sciences, 2017
Penn State Eberly College of Science Outstanding Alumni Award, 2014
Janet L Norwood Award, outstanding achievement by a woman in Statistical Sciences, 2013
Medallion Lecture, 1999
Presidents' Award, COPSS 1997
COPSS Snedecor Award, for best biometrical paper, 1995-1997
NSF Young Investigator Award, 1992-1997
Distinguished Lecturer
Michael Woodroofe Lecture, UMich Statistics, 2024
Krishnaiah Lecture, Pennsylvania State University, 2023
CC Li Lecture 2021
Selected JASA-App Paper for JSM 2020-JASA section
INSAR Keynote Speaker 2019
Norman Breslow Lecture, 2019
Myra Samuels Lecture, 2017
Graybill Conference, Keynote Speaker, 2017
Seaver Lecturer Mount Sinai School of Medicine, 2014
Donna J. Brogan Lecture, Emory University, 2014
Myrto Lefkopoulou Lecture, Harvard School of Public Health, 1998
Kansas State University, 1997

Goucher College, 1995
Purdue University's School of Science, 1994

Institute of Mathematical Statistics
Elected Fellow, 1997
Executive Secretary, 1996-1999
Program Chair, Spring Meetings, 1994

American Statistical Association
Elected Fellow, 1996
Associate Editor, Journal of the American Statistical Association, T&M 1994-1999, 2001-2005
Associate Editor, Journal of the American Statistical Association, CS&A 1999-2008

American Association for the Advancement of Science (AAAS)
Statistics Section chair 2017
Elected fellow 2020

International Statistical Institute
Elected member, 1995

International Biometrics Society
Associate Editor, Biometrics, 1997-
Best Abstract Award, 1992

Genetics Society
Associate Editor 2014 -2015

Fellow Asia-Pacific Artificial Intelligence Association (AAIA) 2024

Ph.D. Advisees:

Jinhong Du, Maya Shen, Catherine Wang,
Jinjin Tian (2023), Tim Barry (2023), Yue Li (2022),
Ron Yurko (2022), Minshi Peng (2021), Kevin Lin (2020), Fuchen Liu (2019),
Li Liu (2014), Corneliu Bodea (2015), Cong Lu (2016), Lingxue Zhu (2018),
Daniel Percival (2012), Drew Crossett (2012), Gaia Bellone (2012),
Diana Luca (2008), Hoa Nguyen (2005), Jung-Ying Tzeng (2003), Xiaohua Zhang (2002),
Bobby Jones (2001), Johnny Lam, Kevin Lynch (1997), and Chris Andrews (1997).

Advisory Boards:

Autism Sister Project, by Autism Science Foundation, 2015-
External Advisory Board, NIH Big Data, Purdue University, 2015-
FBI on DNA forensics, 1995
NRC/NAS on DNA forensics, 1994-95
Carnegie Commission Study on Early Childhood Development, 1994

Publications

Lindsay, B.G. and **Roeder, K.**, . A unified treatment of integer parameter models. *Journal of the American Statistical Association*, 82:758–764, 1987.

Roeder, K., , Dennis, B., and Garton, E.O. Estimating density from variable circular plot census. *Journal of Wildlife Management*, 51:224–230, 1987.

Devlin, B., **Roeder, K.**, , and Ellstrand, N.C. Fractional paternity assignment: Theoretical development and comparison to other methods. *Theoretical and Applied Genetics*, 76:369–380, 1988.

Roeder, K., , Devlin, B., and Lindsay, B.G. Application of maximum likelihood methods to population genetic data for the estimation of individual fertilities. *Biometrics*, 45:363–380, 1989.

Devlin, B., Risch, N., and **Roeder, K.**, . No excess of homozygosity at loci used for DNA fingerprinting. *Science*, 249:1416–1420, Sep 1990.

Roeder, K., . Density estimation with confidence sets exemplified by superclusters and voids in the galaxies. *Journal of the American Statistical Association*, 85:616–624, 1990.

Devlin, B., Risch, N., and **Roeder**, K. Response. *Science*, 253:1039–1041, Aug 1991.

Devlin, B., Risch, N., and **Roeder, K.**, . Estimation of allele frequencies for VNTR loci. *Am. J. Hum. Genet.*, 48:662–676, Apr 1991.

Lindsay, B.G. and **Roeder, K.**, . Residual diagnostics for mixture models. *Journal of the American Statistical Association*, 87:785–794, 1992.

Roeder, K. Discussion of 'Statistical issues concerning quasar absorption systems, by D. Tytler. In Feigelson, E.D. and Babu, G.J., editors, *Statistical Challenges in Astronomy*. Springer Verlag, New York, 1992.

Roeder, K., . Semiparametric estimation of normal mixture densities. *Annals of Statistics*, 20:929–943, 1992.

Cox, D.R., Gleser, L., **Roeder**, K., and Reid, N. Report on double blind refereeing. *Statistical Science*, 8:310–317, 1993.

Devlin, B., Risch, N., and **Roeder, K.**, . Forensic inference from DNA fingerprints. *Journal of the American Statistical Association*, 87:337–350, 1993.

Devlin, B., Risch, N., and **Roeder, K.**, . NRC report on DNA typing. *Science*, 260:1057–1059, May 1993.

Devlin, B., Risch, N., and **Roeder, K.**, . Statistical evaluation of DNA fingerprinting: a critique of the NRC's report. *Science*, 259:748–749, Feb 1993.

Devlin, B., Risch, N., and **Roeder, K.**, . Comments on the statistical aspects of the NRC's report on DNA typing. *J. Forensic Sci.*, 39:28–40, Jan 1994.

Roeder, K. DNA fingerprinting: A review of the controversy (with discussion). *Statistical Science*, 9:222–278, 1994.

Roeder, K., . A graphical technique for detecting the number of components in a normal mixture. *Journal of the American Statistical Association*, 89:487–495, 1994.

Devlin, B., Fienberg, S., Resnick, D., and **Roeder**, K. Galton redux: Eugenics, intelligence, race, and society. *Journal of the American Statistical Association*, 90:1483–1488, 1995.

Devlin, B., Fienberg, S., Resnick, D., and **Roeder**, K. Wringing *The Bell Curve*: A cautionary tale about the realtionships among race, genes and IQ. *Chance*, 3:27–36, 1995.

Devlin, B. and **Roeder**, K. DNA profiling: Statistics and population genetics. In Faigman, D., Daye, D., Saks, M., and Sanders, J., editors, *Scientific Evidence Reference Manual*, 1995.

Lambert, D. and **Roeder**, K. Overdispersion diagnostics for generalized linear models. *Journal of the American Statistical Association*, 90:1225–1236, 1995.

Roeder, K. Discussion of accurate restoration of DNA sequences, by G. Churchill. In Gatsonis, C., Hodges, J.S., Kass, R.E., and Singpurwalla, N.D., editors, *Case Studies in Bayesian Statistics*, Springer Lecture Notes in Statistics. Springer, New York, 1995.

Devlin, B., Risch, N., and **Roeder, K.**, . Disequilibrium mapping: composite likelihood for pairwise disequilibrium. *Genomics*, 36:1–16, Aug 1996.

Roeder, K., , Carroll, R.J., and Lindsay, B.G. A nonparametric maximum likelihood approach to case-control studies with errors in covariables. *Journal of the American Statistical Association*, 91:722–732, 1996.

Andrews, C., Devlin, B., Perlin, M., and **Roeder, K.**, . Binning clones by hybridization with complex probes: statistical refinement of an inner product mapping method. *Genomics*, 41:141–154, Apr 1997.

Crowley, E. M., **Roeder, K.**, , and Bina, M. A statistical model for locating regulatory regions in genomic DNA. *J. Mol. Biol.*, 268:8–14, Apr 1997.

Daniels, M., Devlin, B., and **Roeder**, K. Of genes and IQ. In Devlin, B., Fienberg, S.E., Resnick, D., and **Roeder**, K., editors, *Intelligene, Genes and Success: Scientists Respond to The Bell Curve*. Springer-Verlag, New York, 1997.

Devlin, B., Daniels, M., and **Roeder, K.**, . The heritability of IQ. *Nature*, 388:468–471, Jul 1997.

Devlin, B., Fienberg, S.E., Resnick, D., and **R**oeder, K. editors. *Intelligence, Genes and Success: Scientists Respond to The Bell Curve*. Springer-Verlag, 1997.

Devlin, B., Kadane, J.B., and **Roeder**, K. Discussion of 'Bayesian analysis of DNA profiling data in forensic identification applications,' by L.A. Foreman et al. *Journal of the Royal Statistical Society B*, 160:429–69, 1997.

Lindsay, B.G. and **Roeder, K.**, . Moment-based oscillation properties of mixture models. *Annals of Statistics*, 25:378–386, 1997.

Mueller, P. and **Roeder, K.**, . A Bayesian semiparametric model for case-control studies with errors in variables. *Biometrika*, 84:523–538, 1997.

Roeder, K. DNA fingerprinting. In *Statistical Encyclopedia*, pages 200–206. Wiley, New York, update volume edition, 1997.

Roeder, K., and Wasserman, L. Discussion of 'On Bayesian analysis of mixtures with unknown number of components,' by S. Richardson and P.J. Green. *Journal of the Royal Statistical Society A*, 59:782, 1997.

Roeder, K., and Wasserman, L. Practical Bayesian density estimation using mixtures of normals. *Journal of the American Statistical Association*, 92:894–902, 1997.

Roeder, K., , Escobar, M., Kadane, J., and Balazs, I. Measuring heterogeneity in forensic databases using hierarchical Bayes models. *Biometrika*, 85(269-287), 1998.

Carroll, R. J., **Roeder, K.**, , and Wasserman, L. Flexible parametric measurement error models. *Biometrics*, 55:44–54, Mar 1999.

Devlin, B. and **Roeder, K.**, . Genomic control for association studies. *Biometrics*, 55:997–1004, Dec 1999.

Roeder, K., , Lynch, K., and Nagin, D. Modeling uncertainty in latent classs membership: A case study in criminology. *Journal of the American Statistical Association*, 94:766–776, 1999.

Bacanu, S. A., Devlin, B., and **Roeder, K.**, . The power of genomic control. *Am. J. Hum. Genet.*, 66:1933–1944, Jun 2000.

Devlin, B, Roeder, K, and Wasserman, L. Genomic control for association studies: a semiparametric test to detect excess-haplotype sharing. *Biostatistics*, 1(4):369–87, Dec 2000.

Lam, J. C., **Roeder, K.**, , and Devlin, B. Haplotype fine mapping by evolutionary trees. *Am. J. Hum. Genet.*, 66:659–673, Feb 2000.

Devlin, B., Fienberg, S.E., Resnick, D.P., and **Roeder**, K. Intelligence and success: Is it all in the genes? In Fish, J.M., editor, *Race and Intelligence: Separating Science from Myth.* Lawrence Erlbaum Associates, Mahwah, New Jersey, 2001.

Devlin, B., **Roeder, K.**, , and Bacanu, S. A. Unbiased methods for population-based association studies. *Genet. Epidemiol.*, 21:273–284, Dec 2001.

Devlin, B., **Roeder, K.**, , Otto, C., Tiobech, S., and Byerley, W. Genome-wide distribution of linkage disequilibrium in the population of Palau and its implications for gene flow in Remote Oceania. *Hum. Genet.*, 108:521–528, Jun 2001.

Devlin, B., **Roeder, K.**, , and Wasserman, L. Genomic control, a new approach to genetic-based association studies. *Theor Popul Biol*, 60:155–166, Nov 2001.

Jones, B., Nagin, D., and **Roeder, K.**, . A SAS procedure based on mixture model for estimating developmental trajectories. *Sociological Methods and Research*, 29(3):374–393, 2001.

Lockwood, J. R., **Roeder, K.**, , and Devlin, B. A Bayesian hierarchical model for allele frequencies. *Genet. Epidemiol.*, 20:17–33, Jan 2001.

Seltman, H., **Roeder, K.**, , and Devlin, B. Transmission/disequilibrium test meets measured haplotype analysis: family-based association analysis guided by evolution of haplotypes. *Am. J. Hum. Genet.*, 68:1250–1263, May 2001.

Bacanu, S. A., Devlin, B., and **Roeder, K.**, . Association studies for quantitative traits in structured populations. *Genet. Epidemiol.*, 22:78–93, Jan 2002.

Devlin, B., Bacanu, S. A., **Roeder, K.**, , Reimherr, F., Wender, P., Galke, B., Novasad, D., Chu, A., TCuenco, K., Tiobek, S., Otto, C., and Byerley, W. Genome-wide multipoint linkage analyses of multiplex schizophrenia pedigrees from the oceanic nation of Palau. *Mol. Psychiatry*, 7:689–694, 2002.

Devlin, B., Jones, B. L., Bacanu, S. A., and **Roeder, K.**, . Mixture models for linkage analysis of affected sibling pairs and covariates. *Genet. Epidemiol.*, 22:52–65, Jan 2002.

Devlin, B., Jones, B.L., Bacanu, S-A., and **Roeder, K.**, . Mixture and linear models for linkage analysis with covariates. *Genetic Epidemiology*, 23:449–455, 2002.

Devlin, B., Jones, B.L., Bacanu, S-A., and **Roeder, K.**, . Reply to olson: Mixture models for linkage analysis of affected sibling pairs and covariates. *Genetic Epidemiology*, 23:449–455, 2002.

Devlin, B., **Roeder**, K., and Bacanu, S-A. Unbiased methods for population-based association studies. *Genet Epidemiology*, 21:273–284, 2002.

Devlin, B, **Roeder**, K, and Wasserman, L. Statistical genetics: False discovery or missed discovery? *Heredity*, 91(6):537–538, December 2003.

Devlin, B., **Roeder, K.**, , and Wasserman, L. Analysis of multilocus models of association. *Genet. Epidemiol.*, 25:36–47, Jul 2003.

Seltman, H., **Roeder, K.**, , and Devlin, B. Evolutionary-based association analysis using haplotype data. *Genet. Epidemiol.*, 25:48–58, Jul 2003.

Tzeng, J-Y., Byerley, W., Devlin, B., **Roeder, K.**, , and Wasserman, L. Outlier detection and false discovery rates for whole-genome DNA matching. *Journal of the American Statistical Association*, 98:236–247, 2003.

Tzeng, J. Y., Devlin, B., Wasserman, L., and **Roeder, K.**, . On the identification of disease mutations by the analysis of haplotype similarity and goodness of fit. *Am. J. Hum. Genet.*, 72:891–902, Apr 2003.

Wang, G. Q., DiPietro, M., **Roeder, K.**, , Heng, C. K., Bunker, C. H., Hamman, R. F., and Kamboh, M. I. Cladistic analysis of human apolipoprotein a4 polymorphisms in relation to quantitative plasma lipid risk factors of coronary heart disease. *Ann. Hum. Genet.*, 67:107–124, Mar 2003.

Zhang, X., **Roeder, K.**, , Wallstrom, G., and Devlin, B. Integration of association statistics over genomic regions using Bayesian adaptive regression splines. *Hum. Genomics*, 1:20–29, Nov 2003.

Devlin, B., Bacanu, S. A., and **Roeder, K.**, . Genomic Control to the extreme. *Nat. Genet.*, 36:1129–1130, Nov 2004.

Devlin, B and **Roeder**, K. Avoiding stratification in association studies. In *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics*. Wiley, New York, 2005.

Klei, L., Bacanu, S. A., Myles-Worsley, M., Galke, B., Xie, W., Tiobech, J., Otto, C., **Roeder, K.**, , Devlin, B., and Byerley, W. Linkage analysis of a completely ascertained sample of familial schizophrenics and bipolars from Palau, Micronesia. *Hum. Genet.*, 117:349–356, Aug 2005.

Rinaldo, A., Bacanu, S. A., Devlin, B., Sonpar, V., Wasserman, L., and **Roeder, K.**, . Characterization of multilocus linkage disequilibrium. *Genet. Epidemiol.*, 28:193–206, Apr 2005.

Roeder, K., , Bacanu, S. A., Sonpar, V., Zhang, X., and Devlin, B. Analysis of single-locus tests to detect gene/disease associations. *Genet. Epidemiol.*, 28:207–219, Apr 2005.

Genovese, C., **Roeder, K.**, , and Wasserman, L. False discovery control with p-value weighting. *Biometrika*, 93:509–524, 2006.

Steffens, M., Lamina, C., Illig, T., Bettecken, T., Vogler, R., Entz, P., Suk, E. K., Toliat, M. R., Klopp, N., Caliebe, A., Konig, I. R., Kohler, K., Ludemann, J., Diaz Lacava, A., Fimmers, R., Lichtner, P., Ziegler, A., Wolf, A., Krawczak, M., N?rnberg, P., Hampe, J., Schreiber, S., Meitinger, T., Wichmann, H. E., **Roeder, K.**, , Wienker, T. F., and Baur, M. P. SNP-based analysis of genetic substructure in the German population. *Hum. Hered.*, 62:20–29, 2006.

Roeder, K., , Bacanu, S. A., Wasserman, L., and Devlin, B. Using linkage genome scans to improve power of association in genome scans. *Am. J. Hum. Genet.*, 78:243–252, Feb 2006.

Devlin, B., Klei, L., Myles-Worsley, M., Tiobech, J., Otto, C., Byerley, W., and **Roeder, K.**, . Genetic liability to schizophrenia in Oceanic Palau: a search in the affected and maternal generation. *Hum. Genet.*, 121:675–684, Jul 2007.

Klei, L. and **Roeder, K.**, . Testing for association based on excess allele sharing in a sample of related cases and controls. *Hum. Genet.*, 121:549–557, Jun 2007.

Roeder, K., , Devlin, B., and Wasserman, L. Improving power in genome-wide association studies: weights tip the scale. *Genet. Epidemiol.*, 31:741–747, Nov 2007.

Klei, L., Luca, D., Devlin, B., and **Roeder, K.**, . Pleiotropy and principal components of heritability combine to increase power for association analysis. *Genet. Epidemiol.*, 32:9–19, Jan 2008.

Luca, D., Ringquist, S., Klei, L., Lee, A. B., Gieger, C., Wichmann, H. E., Schreiber, S., Krawczak, M., Lu, Y., Styche, A., Devlin, B., **Roeder, K.**, , and Trucco, M. On the use of general control samples for genome-wide association studies: genetic matching highlights causal variants. *Am. J. Hum. Genet.*, 82:453–463, Feb 2008.

Silverberg, Mark S, Cho, Judy H, Rioux, John D, McGovern, Dermot P B, Wu, Jing, Annese, Vito, Achkar, Jean-Paul, Goyette, Philippe, Scott, Regan, Xu, Wei, Barmada, M Michael, Klei, Lambertus, Daly, Mark J, Abraham, Clara, Bayless, Theodore M, Bossa, Fabrizio, Griffiths, Anne M, Ippoliti, Andrew F, Lahaie, Raymond G, Latiano, Anna, Paré, Pierre, Proctor, Deborah D, Regueiro, Miguel D, Steinhart, A Hillary, Targan, Stephan R, Schumm, L Philip,

Kistner, Emily O, Lee, Annette T, Gregersen, Peter K, Rotter, Jerome I, Brant, Steven R, Taylor, Kent D, **Roeder**, Kathryn, and Duerr, Richard H. Ulcerative colitis-risk loci on chromosomes 1p36 and 12q15 found by genome-wide association study. *Nat Genet*, 41(2):216–20, Feb 2009.

Roeder, K. and Luca, D. Searching for disease susceptibility variants in structured populations. *Genomics*, 93:1–4, Jan 2009.

Roeder, Kathryn and Wasserman, Larry. Genome-wide significance levels and weighted hypothesis testing. *Stat Sci*, 24(4):398–413, Nov 2009.

Wasserman, L. and **Roeder, K.**, . High dimensional variable selection. *Ann Stat*, 37:2178–2201, Jan 2009.

Yerges, L. M., Klei, L., Cauley, J. A., **Roeder, K.**, , Kammerer, C. M., Moffett, S. P., Ensrud, K. E., Nestlerode, C. S., Marshall, L. M., Hoffman, A. R., Lewis, C., Lang, T. F., Barrett-Connor, E., Ferrell, R. E., Orwoll, E. S., and Zmuda, J. M. High-density association study of 383 candidate genes for volumetric BMD at the femoral neck and lumbar spine among older men. *J. Bone Miner. Res.*, 24:2039–2049, Dec 2009.

Anney, R., Klei, L., Pinto, D., Regan, R., Conroy, J., Magalhaes, T. R., Correia, C., Abrahams, B. S., Sykes, N., Pagnamenta, A. T., Almeida, J., Bacchelli, E., Bailey, A. J., Baird, G., Battaglia, A., Berney, T., Bolshakova, N., Bolte, S., Bolton, P. F., Bourgeron, T., Brennan, S., Brian, J., Carson, A. R., Casallo, G., Casey, J., Chu, S. H., Cochrane, L., Corsello, C., Crawford, E. L., Crossett, A., Dawson, G., Jonge, M., Delorme, R., Drmic, I., Duketis, E., Duque, F., Estes, A., Farrar, P., Fernandez, B. A., Folstein, S. E., Fombonne, E., Freitag, C. M., Gilbert, J., Gillberg, C., Glessner, J. T., Goldberg, J., Green, J., Guter, S. J., Hakonarson, H., Heron, E. A., Hill, M., Holt, R., Howe, J. L., Hughes, G., Hus, V., Igliozzi, R., Kim, C., Klauck, S. M., Kolevzon, A., Korvatska, O., Kustanovich, V., Lajonchere, C. M., Lamb, J. A., Laskawiec, M., Leboyer, M., Le Couteur, A., Leventhal, B. L., Lionel, A. C., Liu, X. Q., Lord, C., Lotspeich, L., Lund, S. C., Maestrini, E., Mahoney, W., Mantoulan, C., Marshall, C. R., McConachie, H., McDougle, C. J., McGrath, J., McMahon, W. M., Melhem, N. M., Merikangas, A., Migita, O., Minshew, N. J., Mirza, G. K., Munson, J., Nelson, S. F., Noakes, C., Noor, A., Nygren, G., Oliveira, G., Papanikolaou, K., Parr, J. R., Parrini, B., Paton, T., Pickles, A., Piven, J., Posey, D. J., Poustka, A., Poustka, F., Prasad, A., Ragoussis, J., Renshaw, K., Rickaby, J., Roberts, W., **Roeder, K.**, , Roge, B., Rutter, M. L., Bierut, L. J., Rice, J. P., Salt, J., Sansom, K., Sato, D., Segurado, R., Senman, L., Shah, N., Sheffield, V. C., Soorya, L., Sousa, I., Stoppioni, V., Strawbridge, C., Tancredi, R., Tansey, K., Thiruvahindrapduram, B., Thompson, A. P., Thomson, S., Tryfon, A., Tsiantis, J., Van Engeland, H., Vincent, J. B., Volkmar, F., Wallace, S., Wang, K., Wang, Z., Wassink, T. H., Wing, K., Wittemeyer, K., Wood, S., Yaspan, B. L., Zurawiecki, D., Zwaigenbaum, L., Betancur, C., Buxbaum, J. D., Cantor, R. M., Cook, E. H., Coon, H., Cuccaro, M. L., Gallagher, L., Geschwind, D. H., Gill, M., Haines, J. L., Miller, J., Monaco, A. P., Nurnberger, J. I., Paterson, A. D., Pericak-Vance, M. A., Schellenberg, G. D., Scherer, S. W., Sutcliffe, J. S., Szatmari, P., Vicente, A. M., Vieland, V. J., Wijsman, E. M., Devlin, B., Ennis, S., and Hallmayer, J. A genome-wide scan for common alleles affecting risk for autism. *Hum. Mol. Genet.*, 19:4072–4082, Oct 2010.

Crossett, A., Kent, B. P., Klei, L., Ringquist, S., Trucco, M., **Roeder, K.**, , and Devlin, B. Using ancestry matching to combine family-based and unrelated samples for genome-wide association studies. *Stat Med*, 29:2932–2945, Dec 2010.

Lee, A. B., Luca, D., Klei, L., Devlin, B., and **Roeder, K.**, . Discovering genetic ancestry using spectral graph theory. *Genet. Epidemiol.*, 34:51–59, Jan 2010.

Lee, A. B., Luca, D., and **Roeder, K.**, . A spectral graph approach to discovering genetic ancestry. *Ann Appl Stat*, 4:179–202, 2010.

Liu, Han, **Roeder**, Kathryn, and Wasserman, Larry. Stability approach to regularization selection (stars) for high dimensional graphical models. In Lafferty, J.D., Williams, C.K.I., Shawe-Taylor, J., Zemel, R.S., and Culotta, A., editors, *Advances in Neural Information Processing Systems 23*, pages 1432–1440. Curran Associates, Inc., 2010.

McGovern, D. P., Gardet, A., Torkvist, L., Goyette, P., Essers, J., Taylor, K. D., Neale, B. M., Ong, R. T., Lagace, C., Li, C., Green, T., Stevens, C. R., Beauchamp, C., Fleshner, P. R., Carlson, M., D'Amato, M., Halfvarson, J., Hibberd, M. L., Lordal, M., Padyukov, L., Andriulli, A., Colombo, E., Latiano, A., Palmieri, O., Bernard, E. J., Deslandres, C., Hommes, D. W., Jong, D. J., Stokkers, P. C., Weersma, R. K., Sharma, Y., Silverberg, M. S., Cho, J. H., Wu, J., **Roeder, K.**, , Brant, S. R., Schumm, L. P., Duerr, R. H., Dubinsky, M. C., Glazer, N. L., Haritunians, T., Ippoliti, A., Melmed, G. Y., Siscovick, D. S., Vasiliauskas, E. A., Targan, S. R., Annese, V., Wijmenga, C., Pettersson, S., Rotter, J. I., Xavier, R. J., Daly, M. J., Rioux, J. D., and Seielstad, M. Genome-wide association identifies multiple ulcerative colitis susceptibility loci. *Nat. Genet.*, 42:332–337, Apr 2010.

Pinto, Dalila, Pagnamenta, Alistair T, Klei, Lambertus, Anney, Richard, Merico, Daniele, Regan, Regina, Conroy, Judith, Magalhaes, Tiago R, Correia, Catarina, Abrahams, Brett S, Almeida, Joana, Bacchelli, Elena, Bader, Gary D, Bailey, Anthony J, Baird, Gillian, Battaglia, Agatino, Berney, Tom, Bolshakova, Nadia, Bölte, Sven, Bolton, Patrick F, Bourgeron, Thomas, Brennan, Sean, Brian, Jessica, Bryson, Susan E, Carson, Andrew R, Casallo, Guillermo, Casey, Jillian, Chung, Brian H Y, Cochrane, Lynne, Corsello, Christina, Crawford, Emily L, Crossett, Andrew, Cytrynbaum, Cheryl, Dawson, Geraldine, Jonge, Maretha, Delorme, Richard, Drmic, Irene, Duketis, Eftichia, Duque, Frederico, Estes, Annette, Farrar, Penny, Fernandez, Bridget A, Folstein, Susan E, Fombonne, Eric, Freitag, Christine M, Gilbert, John, Gillberg, Christopher, Glessner, Joseph T, Goldberg, Jeremy, Green, Andrew, Green, Jonathan, Guter, Stephen J, Hakonarson, Hakon, Heron, Elizabeth A, Hill, Matthew, Holt, Richard, Howe, Jennifer L, Hughes, Gillian, Hus, Vanessa, Igliozzi, Roberta, Kim, Cecilia, Klauck, Sabine M, Kolevzon, Alexander, Korvatska, Olena, Kustanovich, Vlad, Lajonchere, Clara M, Lamb, Janine A, Laskawiec, Magdalena, Leboyer, Marion, Le Couteur, Ann, Leventhal, Bennett L, Lionel, Anath C, Liu, Xiao-Qing, Lord, Catherine, Lotspeich, Linda, Lund, Sabata C, Maestrini, Elena, Mahoney, William, Mantoulan, Carine, Marshall, Christian R, McConachie, Helen, McDougle, Christopher J, McGrath, Jane, McMahon, William M, Merikangas, Alison, Migita, Ohsuke, Minshew, Nancy J, Mirza, Ghazala K, Munson, Jeff, Nelson, Stanley F, Noakes, Carolyn, Noor, Abdul, Nygren, Gudrun, Oliveira, Guiomar, Papanikolaou, Katerina, Parr, Jeremy R, Parrini, Barbara, Paton, Tara, Pickles, Andrew, Pilorge, Marion, Piven, Joseph, Ponting, Chris P, Posey, David J, Poustka, Annemarie, Poustka, Fritz, Prasad, Aparna,

Ragoussis, Jiannis, Renshaw, Katy, Rickaby, Jessica, Roberts, Wendy, **Roeder**, Kathryn, Roge, Bernadette, Rutter, Michael L, Bierut, Laura J, Rice, John P, Salt, Jeff, Sansom, Katherine, Sato, Daisuke, Segurado, Ricardo, Sequeira, Ana F, Senman, Lili, Shah, Naisha, Sheffield, Val C, Soorya, Latha, Sousa, Inês, Stein, Olaf, Sykes, Nuala, Stoppioni, Vera, Strawbridge, Christina, Tancredi, Raffaella, Tansey, Katherine, Thiruvahindrapduram, Bhooma, Thompson, Ann P, Thomson, Susanne, Tryfon, Ana, Tsiantis, John, Van Engeland, Herman, Vincent, John B, Volkmar, Fred, Wallace, Simon, Wang, Kai, Wang, Zhouzhi, Wassink, Thomas H, Webber, Caleb, Weksberg, Rosanna, Wing, Kirsty, Wittemeyer, Kerstin, Wood, Shawn, Wu, Jing, Yaspan, Brian L, Zurawiecki, Danielle, Zwaigenbaum, Lonnie, Buxbaum, Joseph D, Cantor, Rita M, Cook, Edwin H, Coon, Hilary, Cuccaro, Michael L, Devlin, Bernie, Ennis, Sean, Gallagher, Louise, Geschwind, Daniel H, Gill, Michael, Haines, Jonathan L, Hallmayer, Joachim, Miller, Judith, Monaco, Anthony P, Nurnberger, John I, Paterson, Andrew D, Pericak-Vance, Margaret A, Schellenberg, Gerard D, Szatmari, Peter, Vicente, Astrid M, Vieland, Veronica J, Wijsman, Ellen M, Scherer, Stephen W, Sutcliffe, James S, and Betancur, Catalina. Functional impact of global rare copy number variation in autism spectrum disorders. *Nature*, 466(7304):368–72, Jul 2010.

Wu, J., Devlin, B., Ringquist, S., Trucco, M., and **Roeder**, K. Screen and clean: a tool for identifying interactions in genome-wide association studies. *Genet. Epidemiol.*, 34:275–285, Apr 2010.

Yerges, L. M., Klei, L., Cauley, J. A., **Roeder, K.**, , Kammerer, C. M., Ensrud, K. E., Nestlerode, C. S., Lewis, C., Lang, T. F., Barrett-Connor, E., Moffett, S. P., Hoffman, A. R., Ferrell, R. E., Orwoll, E. S., and Zmuda, J. M. Candidate gene analysis of femoral neck trabecular and cortical volumetric bone mineral density in older men. *J. Bone Miner. Res.*, 25:330–338, Feb 2010.

Chu, S. H., **Roeder, K.**, , Ferrell, R. E., Devlin, B., DeMichele-Sweet, M. A., Kamboh, M. I., Lopez, O. L., and Sweet, R. A. TOMM40 poly-T repeat lengths, age of onset and psychosis risk in Alzheimer disease. *Neurobiol. Aging*, 32:1–9, Dec 2011.

Devlin, B., Melhem, N., and **Roeder, K.**, . Do common variants play a role in risk for autism? Evidence and theoretical musings. *Brain Res.*, 1380:78–84, Mar 2011.

Melhem, Nadine, Middleton, Frank, McFadden, Kathryn, Klei, Lambertus, Faraone, Stephen V, Vinogradov, Sophia, Tiobech, Josepha, Yano, Victor, Kuartei, Stevenson, **Roeder**, Kathryn, Byerley, William, Devlin, Bernie, and Myles-Worsley, Marina. Copy number variants for schizophrenia and related psychotic disorders in oceanic palau: risk and transmission in extended pedigrees. *Biol Psychiatry*, 70(12):1115–21, Dec 2011.

Neale, B. M., Rivas, M. A., Voight, B. F., Altshuler, D., Devlin, B., Orho-Melander, M., Kathiresan, S., Purcell, S. M., **Roeder, K.**, , and Daly, M. J. Testing for an unusual distribution of rare variants. *PLoS Genet.*, 7:e1001322, Mar 2011.

Percival, D., **Roeder, K.**, , Rosenfeld, R., and Wasserman, L. Structured, sparse regression with application to HIV drug resistance. *Ann Appl Stat*, 5:628–644, Jun 2011.

Sanders, S. J., Ercan-Sencicek, A. G., Hus, V., Luo, R., Murtha, M. T., Moreno-De-Luca, D., Chu, S. H., Moreau, M. P., Gupta, A. R., Thomson, S. A., Mason, C. E., Bilguvar, K.,

Celestino-Soper, P. B., Choi, M., Crawford, E. L., Davis, L., Wright, N. R., Dhodapkar, R. M., DiCola, M., DiLullo, N. M., Fernandez, T. V., Fielding-Singh, V., Fishman, D. O., Frahm, S., Garagaloyan, R., Goh, G. S., Kammela, S., Klei, L., Lowe, J. K., Lund, S. C., McGrew, A. D., Meyer, K. A., Moffat, W. J., Murdoch, J. D., O'Roak, B. J., Ober, G. T., Pottenger, R. S., Raubeson, M. J., Song, Y., Wang, Q., Yaspan, B. L., Yu, T. W., Yurkiewicz, I. R., Beaudet, A. L., Cantor, R. M., Curland, M., Grice, D. E., Gunel, M., Lifton, R. P., Mane, S. M., Martin, D. M., Shaw, C. A., Sheldon, M., Tischfield, J. A., Walsh, C. A., Morrow, E. M., Ledbetter, D. H., Fombonne, E., Lord, C., Martin, C. L., Brooks, A. I., Sutcliffe, J. S., Cook, E. H., Geschwind, D., **Roeder**, K., Devlin, B., and State, M. W. Multiple recurrent de novo CNVs, including duplications of the 7q11.23 Williams syndrome region, are strongly associated with autism. *Neuron*, 70:863–885, Jun 2011.

Zmuda, J. M., Yerges-Armstrong, L. M., Moffett, S. P., Klei, L., Kammerer, C. M., **Roeder**, K., Cauley, J. A., Kuipers, A., Ensrud, K. E., Nestlerode, C. S., Hoffman, A. R., Lewis, C. E., Lang, T. F., Barrett-Connor, E., Ferrell, R. E., and Orwoll, E. S. Genetic analysis of vertebral trabecular bone density and cross-sectional area in older men. *Osteoporos Int*, 22:1079–1090, Apr 2011.

Achkar, J-P, Klei, L, Bakker, P I W, Bellone, G, Rebert, N, Scott, R, Lu, Y, Regueiro, M, Brzezinski, A, Kamboh, M I, Fiocchi, C, Devlin, B, Trucco, M, Ringquist, S, **Roeder**, K, and Duerr, R H. Amino acid position 11 of hla-drbeta1 is a major determinant of chromosome 6p association with ulcerative colitis. *Genes Immun*, 13(3):245–52, Apr 2012.

Anney, Richard, Klei, Lambertus, Pinto, Dalila, Almeida, Joana, Bacchelli, Elena, Baird, Gillian, Bolshakova, Nadia, Bölte, Sven, Bolton, Patrick F, Bourgeron, Thomas, Brennan, Sean, Brian, Jessica, Casey, Jillian, Conroy, Judith, Correia, Catarina, Corsello, Christina, Crawford, Emily L, Jonge, Maretha, Delorme, Richard, Duketis, Eftichia, Duque, Frederico, Estes, Annette, Farrar, Penny, Fernandez, Bridget A, Folstein, Susan E, Fombonne, Eric, Gilbert, John, Gillberg, Christopher, Glessner, Joseph T, Green, Andrew, Green, Jonathan, Guter, Stephen J, Heron, Elizabeth A, Holt, Richard, Howe, Jennifer L, Hughes, Gillian, Hus, Vanessa, Igliozzi, Roberta, Jacob, Suma, Kenny, Graham P, Kim, Cecilia, Kolevzon, Alexander, Kustanovich, Vlad, Lajonchere, Clara M, Lamb, Janine A, Law-Smith, Miriam, Leboyer, Marion, Le Couteur, Ann, Leventhal, Bennett L, Liu, Xiao-Qing, Lombard, Frances, Lord, Catherine, Lotspeich, Linda, Lund, Sabata C, Magalhaes, Tiago R, Mantoulan, Carine, McDougle, Christopher J, Melhem, Nadine M, Merikangas, Alison, Minshew, Nancy J, Mirza, Ghazala K, Munson, Jeff, Noakes, Carolyn, Nygren, Gudrun, Papanikolaou, Katerina, Pagnamenta, Alistair T, Parrini, Barbara, Paton, Tara, Pickles, Andrew, Posey, David J, Poustka, Fritz, Ragoussis, Jiannis, Regan, Regina, Roberts, Wendy, **Roeder**, Kathryn, Roge, Bernadette, Rutter, Michael L, Schlitt, Sabine, Shah, Naisha, Sheffield, Val C, Soorya, Latha, Sousa, Inês, Stoppioni, Vera, Sykes, Nuala, Tancredi, Raffaella, Thompson, Ann P, Thomson, Susanne, Tryfon, Ana, Tsiantis, John, Van Engeland, Herman, Vincent, John B, Volkmar, Fred, Vorstman, J A S, Wallace, Simon, Wing, Kirsty, Wittemeyer, Kerstin, Wood, Shawn, Zurawiecki, Danielle, Zwaigenbaum, Lonnie, Bailey, Anthony J, Battaglia, Agatino, Cantor, Rita M, Coon, Hilary, Cuccaro, Michael L, Dawson, Geraldine, Ennis, Sean, Freitag, Christine M, Geschwind, Daniel H, Haines, Jonathan L, Klauck, Sabine M, McMahon, William M, Maestrini, Elena, Miller, Judith, Monaco, Anthony P, Nelson, Stanley F, Nurnberger, John I, Oliveira, Guiomar, Parr, Jeremy R, Pericak-Vance, Margaret A, Piven, Joseph, Schellenberg, Gerard D, Scherer,

Stephen W, Vicente, Astrid M, Wassink, Thomas H, Wijsman, Ellen M, Betancur, Catalina, Buxbaum, Joseph D, Cook, Edwin H, Gallagher, Louise, Gill, Michael, Hallmayer, Joachim, Paterson, Andrew D, Sutcliffe, James S, Szatmari, Peter, Vieland, Veronica J, Hakonarson, Hakon, and Devlin, Bernie. Individual common variants exert weak effects on the risk for autism spectrum disorderspi. *Hum Mol Genet*, 21(21):4781–92, Nov 2012.

Brehm, John M, Acosta-Pérez, Edna, Klei, Lambertus, **Roeder**, Kathryn, Barmada, Michael, Boutaoui, Nadia, Forno, Erick, Kelly, Roxanne, Paul, Kathryn, Sylvia, Jody, Litonjua, Augusto A, Cabana, Michael, Alvarez, María, Colón-Semidey, Angel, Canino, Glorisa, and Celedón, Juan C. Vitamin d insufficiency and severe asthma exacerbations in puerto rican children. *Am J Respir Crit Care Med*, 186(2):140–6, Jul 2012.

Brehm, John M, Acosta-Pérez, Edna, Klei, Lambertus, **Roeder**, Kathryn, Barmada, Michael M, Boutaoui, Nadia, Forno, Erick, Cloutier, Michelle M, Datta, Soma, Kelly, Roxanne, Paul, Kathryn, Sylvia, Jody, Calvert, Deanna, Thornton-Thompson, Sherell, Wakefield, Dorothy, Litonjua, Augusto A, Alvarez, María, Colón-Semidey, Angel, Canino, Glorisa, and Celedón, Juan C. African ancestry and lung function in puerto rican children. *J Allergy Clin Immunol*, 129(6):1484–90.e6, Jun 2012.

Buxbaum, Joseph D, Daly, Mark J, Devlin, Bernie, Lehner, Thomas, **Roeder**, Kathryn, State, Matthew W, and Autism Sequencing Consortium, . The autism sequencing consortium: large-scale, high-throughput sequencing in autism spectrum disorders. *Neuron*, 76(6):1052–6, Dec 2012.

Ionita-Laza, Iuliana, Makarov, Vlad, ARRA Autism Sequencing Consortium, , and Buxbaum, Joseph D. Scan-statistic approach identifies clusters of rare disease variants in lrp2, a gene linked and associated with autism spectrum disorders, in three datasets. *Am J Hum Genet*, 90(6):1002–13, Jun 2012.

Klei, Lambertus, Sanders, Stephan J, Murtha, Michael T, Hus, Vanessa, Lowe, Jennifer K, Willsey, A Jeremy, Moreno-De-Luca, Daniel, Yu, Timothy W, Fombonne, Eric, Geschwind, Daniel, Grice, Dorothy E, Ledbetter, David H, Lord, Catherine, Mane, Shrikant M, Lese Martin, Christa, Martin, Donna M, Morrow, Eric M, Walsh, Christopher A, Melhem, Nadine M, Chaste, Pauline, Sutcliffe, James S, State, Matthew W, Cook, Edwin H, **Roeder**, Kathryn, and Devlin, Bernie. Common genetic variants, acting additively, are a major source of risk for autism. *Mol Autism*, 3(1):9, Oct 2012.

Mechanic, Leah E, Chen, Huann-Sheng, Amos, Christopher I, Chatterjee, Nilanjan, Cox, Nancy J, Divi, Rao L, Fan, Ruzong, Harris, Emily L, Jacobs, Kevin, Kraft, Peter, Leal, Suzanne M, McAllister, Kimberly, Moore, Jason H, Paltoo, Dina N, Province, Michael A, Ramos, Erin M, Ritchie, Marylyn D, **Roeder**, Kathryn, Schaid, Daniel J, Stephens, Matthew, Thomas, Duncan C, Weinberg, Clarice R, Witte, John S, Zhang, Shunpu, Zöllner, Sebastian, Feuer, Eric J, and Gillanders, Elizabeth M. Next generation analytic tools for large scale genetic epidemiology studies of complex diseases. *Genet Epidemiol*, 36(1):22–35, Jan 2012.

Neale, Benjamin M, Kou, Yan, Liu, Li, Ma'ayan, Avi, Samocha, Kaitlin E, Sabo, Aniko, Lin, Chiao-Feng, Stevens, Christine, Wang, Li-San, Makarov, Vladimir, Polak, Paz, Yoon, Seungtai, Maguire, Jared, Crawford, Emily L, Campbell, Nicholas G, Geller, Evan T, Valladares, Otto,

Schafer, Chad, Liu, Han, Zhao, Tuo, Cai, Guiqing, Lihm, Jayon, Dannenfelser, Ruth, Jabado, Omar, Peralta, Zuleyma, Nagaswamy, Uma, Muzny, Donna, Reid, Jeffrey G, Newsham, Irene, Wu, Yuanqing, Lewis, Lora, Han, Yi, Voight, Benjamin F, Lim, Elaine, Rossin, Elizabeth, Kirby, Andrew, Flannick, Jason, Fromer, Menachem, Shakir, Khalid, Fennell, Tim, Garimella, Kiran, Banks, Eric, Poplin, Ryan, Gabriel, Stacey, DePristo, Mark, Wimbish, Jack R, Boone, Braden E, Levy, Shawn E, Betancur, Catalina, Sunyaev, Shamil, Boerwinkle, Eric, Buxbaum, Joseph D, Cook, Edwin H, Devlin, Bernie, Gibbs, Richard A, **Roeder**, Kathryn, Schellenberg, Gerard D, Sutcliffe, James S, and Daly, Mark J. Patterns and rates of exonic de novo mutations in autism spectrum disorders. *Nature*, 485(7397):242–5, May 2012.

Sanders, Stephan J, Murtha, Michael T, Gupta, Abha R, Murdoch, John D, Raubeson, Melanie J, Willsey, A Jeremy, Ercan-Sencicek, A Gulhan, DiLullo, Nicholas M, Parikshak, Neelroop N, Stein, Jason L, Walker, Michael F, Ober, Gordon T, Teran, Nicole A, Song, Youeun, El-Fishawy, Paul, Murtha, Ryan C, Choi, Murim, Overton, John D, Bjornson, Robert D, Carriero, Nicholas J, Meyer, Kyle A, Bilguvar, Kaya, Mane, Shrikant M, Sestan, Nenad, Lifton, Richard P, Günel, Murat, **Roeder**, Kathryn, Geschwind, Daniel H, Devlin, Bernie, and State, Matthew W. De novo mutations revealed by whole-exome sequencing are strongly associated with autism. *Nature*, 485(7397):237–41, May 2012.

Whitcomb, David C, Larusch, Jessica, Krasinskas, Alyssa M, Klei, Lambertus, Smith, Jill P, Brand, Randall E, Neoptolemos, John P, Lerch, Markus M, Tector, Matt, Sandhu, Bimaljit S, Guda, Nalini M, Orlichenko, Lidiya, Alzheimer's Disease Genetics Consortium, , Albert, Marilyn S, Albin, Roger L, Apostolova, Liana G, Arnold, Steven E, Baldwin, Clinton T, Barber, Robert, Barnes, Lisa L, Beach, Thomas G, Beecham, Gary W, Beekly, Duane, Bennett, David A, Bigio, Eileen H, Bird, Thomas D, Blacker, Deborah, Boxer, Adam, Burke, James R, Buxbaum, Joseph D, Cairns, Nigel J, Cantwell, Laura B, Cao, Chuanhai, Carney, Regina M, Carroll, Steven L, Chui, Helena C, Clark, David G, Cribbs, David H, Crocco, Elizabeth A, Cruchaga, Carlos, Decarli, Charles, Demirci, F Yesim, Dick, Malcolm, Dickson, Dennis W, Duara, Ranjan, Ertekin-Taner, Nilufer, Faber, Kelley M, Fallon, Kenneth B, Farlow, Martin R, Ferris, Steven, Foroud, Tatiana M, Frosch, Matthew P, Galasko, Douglas R, Ganguli, Mary, Gearing, Marla, Geschwind, Daniel H, Ghetti, Bernardino, Gilbert, John R, Gilman, Sid, Glass, Jonathan D, Goate, Alison M, Graff-Radford, Neill R, Green, Robert C, Growdon, John H, Hakonarson, Hakon, Hamilton-Nelson, Kara L, Hamilton, Ronald L, Harrell, Lindy E, Head, Elizabeth, Honig, Lawrence S, Hulette, Christine M, Hyman, Bradley T, Jicha, Gregory A, Jin, Lee-Way, Jun, Gyungah, Kamboh, M Ilyas, Karydas, Anna, Kaye, Jeffrey A, Kim, Ronald, Koo, Edward H, Kowall, Neil W, Kramer, Joel H, Kramer, Patricia, Kukull, Walter A, Laferla, Frank M, Lah, James J, Leverenz, James B, Levey, Allan I, Li, Ge, Lin, Chiao-Feng, Lieberman, Andrew P, Lopez, Oscar L, Lunetta, Kathryn L, Lyketsos, Constantine G, Mack, Wendy J, Marson, Daniel C, Martin, Eden R, Martiniuk, Frank, Mash, Deborah C, Masliah, Eliezer, McKee, Ann C, Mesulam, Marsel, Miller, Bruce L, Miller, Carol A, Miller, Joshua W, Montine, Thomas J, Morris, John C, Murrell, Jill R, Naj, Adam C, Olichney, John M, Parisi, Joseph E, Peskind, Elaine, Petersen, Ronald C, Pierce, Aimee, Poon, Wayne W, Potter, Huntington, Quinn, Joseph F, Raj, Ashok, Raskind, Murray, Reiman, Eric M, Reisberg, Barry, Reitz, Christiane, Ringman, John M, Roberson, Erik D, Rosen, Howard J, Rosenberg, Roger N, Sano, Mary, Saykin, Andrew J, Schneider, Julie A, Schneider, Lon S, Seeley, William W, Smith, Amanda G, Sonnen, Joshua A, Spina, Salvatore, Stern, Robert A, Tanzi, Rudolph E, Trojanowski, John Q,

Troncoso, Juan C, Tsuang, Debby W, Valladares, Otto, Van Deerlin, Vivianna M, Van Eldik, Linda J, Vardarajan, Badri N, Vinters, Harry V, Vonsattel, Jean Paul, Wang, Li-San, Weintraub, Sandra, Welsh-Bohmer, Kathleen A, Williamson, Jennifer, Woltjer, Randall L, Wright, Clinton B, Younkin, Steven G, Yu, Chang-En, Yu, Lei, Alkaade, Samer, Amann, Stephen T, Anderson, Michelle A, Baillie, John, Banks, Peter A, Conwell, Darwin, Coté, Gregory A, Cotton, Peter B, Disario, James, Farrer, Lindsay A, Forsmark, Chris E, Johnstone, Marianne, Gardner, Timothy B, Gelrud, Andres, Greenhalf, William, Haines, Jonathan L, Hartman, Douglas J, Hawes, Robert A, Lawrence, Christopher, Lewis, Michele, Mayerle, Julia, Mayeux, Richard, Melhem, Nadine M, Money, Mary E, Muniraj, Thiruvengadam, Papachristou, Georgios I, Pericak-Vance, Margaret A, Romagnuolo, Joseph, Schellenberg, Gerard D, Sherman, Stuart, Simon, Peter, Singh, Vijay P, Slivka, Adam, Stolz, Donna, Sutton, Robert, Weiss, Frank Ulrich, Wilcox, C Mel, Zarnescu, Narcis Octavian, Wisniewski, Stephen R, O'Connell, Michael R, Kienholz, Michelle L, **Roeder**, Kathryn, Barmada, M Michael, Yadav, Dhiraj, and Devlin, Bernie. Common genetic variants in the cldn2 and prss1-prss2 loci alter risk for alcohol-related and sporadic pancreatitis. *Nat Genet*, 44(12):1349–54, Nov 2012.

Zhao, Tuo, Liu, Han, **Roeder**, Kathryn, Lafferty, John, and Wasserman, Larry. Huge: High dimensional undirected graph estimation. *JMLR*, 13:1059–1062, Apr 2012.

Zhao, Tuo, **Roeder**, Kathryn, and Liu, Han. Smooth-projected neighborhood pursuit for high-dimensional nonparanormal graph estimation. In Bartlett, P., Pereira, F.C.N., Burges, C.J.C., Bottou, L., and Weinberger, K.Q., editors, *Advances in Neural Information Processing Systems 25*, pages 162–170. 2012.

Cross-Disorder Group of the Psychiatric Genomics Consortium, , Lee, S Hong, Ripke, Stephan, Neale, Benjamin M, Faraone, Stephen V, Purcell, Shaun M, Perlis, Roy H, Mowry, Bryan J, Thapar, Anita, Goddard, Michael E, Witte, John S, Absher, Devin, Agartz, Ingrid, Akil, Huda, Amin, Farooq, Andreassen, Ole A, Anjorin, Adebayo, Anney, Richard, Anttila, Verneri, Arking, Dan E, Asherson, Philip, Azevedo, Maria H, Backlund, Lena, Badner, Judith A, Bailey, Anthony J, Banaschewski, Tobias, Barchas, Jack D, Barnes, Michael R, Barrett, Thomas B, Bass, Nicholas, Battaglia, Agatino, Bauer, Michael, Bayés, Mònica, Bellivier, Frank, Bergen, Sarah E, Berrettini, Wade, Betancur, Catalina, Bettecken, Thomas, Biederman, Joseph, Binder, Elisabeth B, Black, Donald W, Blackwood, Douglas H R, Bloss, Cinnamon S, Boehnke, Michael, Boomsma, Dorret I, Breen, Gerome, Breuer, René, Bruggeman, Richard, Cormican, Paul, Buccola, Nancy G, Buitelaar, Jan K, Bunney, William E, Buxbaum, Joseph D, Byerley, William F, Byrne, Enda M, Caesar, Sian, Cahn, Wiepke, Cantor, Rita M, Casas, Miguel, Chakravarti, Aravinda, Chambert, Kimberly, Choudhury, Khalid, Cichon, Sven, Cloninger, C Robert, Collier, David A, Cook, Edwin H, Coon, Hilary, Cormand, Bru, Corvin, Aiden, Coryell, William H, Craig, David W, Craig, Ian W, Crosbie, Jennifer, Cuccaro, Michael L, Curtis, David, Czamara, Darina, Datta, Susmita, Dawson, Geraldine, Day, Richard, De Geus, Eco J, Degenhardt, Franziska, Djurovic, Srdjan, Donohoe, Gary J, Doyle, Alysa E, Duan, Jubao, Dudbridge, Frank, Duketis, Eftichia, Ebstein, Richard P, Edenberg, Howard J, Elia, Josephine, Ennis, Sean, Etain, Bruno, Fanous, Ayman, Farmer, Anne E, Ferrier, I Nicol, Flickinger, Matthew, Fombonne, Eric, Foroud, Tatiana, Frank, Josef, Franke, Barbara, Fraser, Christine, Freedman, Robert, Freimer, Nelson B, Freitag, Christine M, Friedl, Marion, Frisén, Louise, Gallagher, Louise, Gejman, Pablo V, Georgieva, Lyudmila, Gershon, Elliot S, Geschwind, Daniel H, Giegling, Ina, Gill, Michael, Gordon, Scott D, Gordon-Smith, Katherine, Green, Elaine K, Greenwood,

Tiffany A, Grice, Dorothy E, Gross, Magdalena, Grozeva, Detelina, Guan, Weihua, Gurling, Hugh, De Haan, Lieuwe, Haines, Jonathan L, Hakonarson, Hakon, Hallmayer, Joachim, Hamilton, Steven P, Hamshere, Marian L, Hansen, Thomas F, Hartmann, Annette M, Hautzinger, Martin, Heath, Andrew C, Henders, Anjali K, Herms, Stefan, Hickie, Ian B, Hipolito, Maria, Hoefels, Susanne, Holmans, Peter A, Holsboer, Florian, Hoogendijk, Witte J, Hottenga, Jouke-Jan, Hultman, Christina M, Hus, Vanessa, Ingason, Andrés, Ising, Marcus, Jamain, Stéphane, Jones, Edward G, Jones, Ian, Jones, Lisa, Tzeng, Jung-Ying, Kähler, Anna K, Kahn, René S, Kandaswamy, Radhika, Keller, Matthew C, Kennedy, James L, Kenny, Elaine, Kent, Lindsey, Kim, Yunjung, Kirov, George K, Klauck, Sabine M, Klei, Lambertus, Knowles, James A, Kohli, Martin A, Koller, Daniel L, Konte, Bettina, Korszun, Ania, Krabbendam, Lydia, Krasucki, Robert, Kuntsi, Jonna, Kwan, Phoenix, Landén, Mikael, Långström, Niklas, Lathrop, Mark, Lawrence, Jacob, Lawson, William B, Leboyer, Marion, Ledbetter, David H, Lee, Phil H, Lencz, Todd, Lesch, Klaus-Peter, Levinson, Douglas F, Lewis, Cathryn M, Li, Jun, Lichtenstein, Paul, Lieberman, Jeffrey A, Lin, Dan-Yu, Linszen, Don H, Liu, Chunyu, Lohoff, Falk W, Loo, Sandra K, Lord, Catherine, Lowe, Jennifer K, Lucae, Susanne, MacIntyre, Donald J, Madden, Pamela A F, Maestrini, Elena, Magnusson, Patrik K E, Mahon, Pamela B, Maier, Wolfgang, Malhotra, Anil K, Mane, Shrikant M, Martin, Christa L, Martin, Nicholas G, Mattheisen, Manuel, Matthews, Keith, Mattingsdal, Morten, McCarroll, Steven A, McGhee, Kevin A, McGough, James J, McGrath, Patrick J, McGuffin, Peter, McInnis, Melvin G, McIntosh, Andrew, McKinney, Rebecca, McLean, Alan W, McMahon, Francis J, McMahon, William M, McQuillin, Andrew, Medeiros, Helena, Medland, Sarah E, Meier, Sandra, Melle, Ingrid, Meng, Fan, Meyer, Jobst, Middeldorp, Christel M, Middleton, Lefkos, Milanova, Vihra, Miranda, Ana, Monaco, Anthony P, Montgomery, Grant W, Moran, Jennifer L, Moreno-De-Luca, Daniel, Morken, Gunnar, Morris, Derek W, Morrow, Eric M, Moskvina, Valentina, Muglia, Pierandrea, Mühleisen, Thomas W, Muir, Walter J, Müller-Myhsok, Bertram, Murtha, Michael, Myers, Richard M, Myin-Germeys, Inez, Neale, Michael C, Nelson, Stan F, Nievergelt, Caroline M, Nikolov, Ivan, Nimgaonkar, Vishwajit, Nolen, Willem A, Nöthen, Markus M, Nurnberger, John I, Nwulia, Evaristus A, Nyholt, Dale R, O'Dushlaine, Colm, Oades, Robert D, Olincy, Ann, Oliveira, Guiomar, Olsen, Line, Ophoff, Roel A, Osby, Urban, Owen, Michael J, Palotie, Aarno, Parr, Jeremy R, Paterson, Andrew D, Pato, Carlos N, Pato, Michele T, Penninx, Brenda W, Pergadia, Michele L, Pericak-Vance, Margaret A, Pickard, Benjamin S, Pimm, Jonathan, Piven, Joseph, Posthuma, Danielle, Potash, James B, Poustka, Fritz, Propping, Peter, Puri, Vinay, Quested, Digby J, Quinn, Emma M, Ramos-Quiroga, Josep Antoni, Rasmussen, Henrik B, Raychaudhuri, Soumya, Rehnström, Karola, Reif, Andreas, Ribasés, Marta, Rice, John P, Rietschel, Marcella, **Roeder**, Kathryn, Roeyers, Herbert, Rossin, Lizzy, Rothenberger, Aribert, Rouleau, Guy, Ruderfer, Douglas, Rujescu, Dan, Sanders, Alan R, Sanders, Stephan J, Santangelo, Susan L, Sergeant, Joseph A, Schachar, Russell, Schalling, Martin, Schatzberg, Alan F, Scheftner, William A, Schellenberg, Gerard D, Scherer, Stephen W, Schork, Nicholas J, Schulze, Thomas G, Schumacher, Johannes, Schwarz, Markus, Scolnick, Edward, Scott, Laura J, Shi, Jianxin, Shilling, Paul D, Shyn, Stanley I, Silverman, Jeremy M, Slager, Susan L, Smalley, Susan L, Smit, Johannes H, Smith, Erin N, Sonuga-Barke, Edmund J S, St Clair, David, State, Matthew, Steffens, Michael, Steinhausen, Hans-Christoph, Strauss, John S, Strohmaier, Jana, Stroup, T Scott, Sutcliffe, James S, Szatmari, Peter, Szelinger, Szabocls, Thirumalai, Srinivasa, Thompson, Robert C, Todorov, Alexandre A, Tozzi, Federica, Treutlein, Jens, Uhr, Manfred, Oord, Edwin J C G, Van Grootheest, Gerard, Van Os, Jim, Vicente, Astrid M,

Vieland, Veronica J, Vincent, John B, Visscher, Peter M, Walsh, Christopher A, Wassink, Thomas H, Watson, Stanley J, Weissman, Myrna M, Werge, Thomas, Wienker, Thomas F, Wijsman, Ellen M, Willemsen, Gonneke, Williams, Nigel, Willsey, A Jeremy, Witt, Stephanie H, Xu, Wei, Young, Allan H, Yu, Timothy W, Zammit, Stanley, Zandi, Peter P, Zhang, Peng, Zitman, Frans G, Zöllner, Sebastian, International Inflammatory Bowel Disease Genetics Consortium (IIBDGC), , Devlin, Bernie, Kelsoe, John R, Sklar, Pamela, Daly, Mark J, O'Donovan, Michael C, Craddock, Nicholas, Sullivan, Patrick F, Smoller, Jordan W, Kendler, Kenneth S, and Wray, Naomi R. Genetic relationship between five psychiatric disorders estimated from genome-wide snps. *Nat Genet*, 45(9):984–94, Sep 2013.

Crossett, A., A.B., Lee, L., Klei, B., Devlin, and Roeder, K. Refining genetically inferred relationships using treelet covariance smoothing. *Annals of Applied Statistics*, 7:669–690, 2013.

Hamilton, P J, Campbell, N G, Sharma, S, Erreger, K, Herborg Hansen, F, Saunders, C, Belovich, A N, NIH ARRA Autism Sequencing Consortium, , Sahai, M A, Cook, E H, Gether, U, McHaourab, H S, Matthies, H J G, Sutcliffe, J S, and Galli, A. De novo mutation in the dopamine transporter gene associates dopamine dysfunction with autism spectrum disorder. *Mol Psychiatry*, 18(12):1315–23, Dec 2013.

He, Xin, Sanders, Stephan J, Liu, Li, De Rubeis, Silvia, Lim, Elaine T, Sutcliffe, James S, Schellenberg, Gerard D, Gibbs, Richard A, Daly, Mark J, Buxbaum, Joseph D, State, Matthew W, Devlin, Bernie, and **Roeder**, Kathryn. Integrated model of de novo and inherited genetic variants yields greater power to identify risk genes. *PLoS Genet*, 9(8):e1003671, 2013.

Lim, Elaine T, Raychaudhuri, Soumya, Sanders, Stephan J, Stevens, Christine, Sabo, Aniko, MacArthur, Daniel G, Neale, Benjamin M, Kirby, Andrew, Ruderfer, Douglas M, Fromer, Menachem, Lek, Monkol, Liu, Li, Flannick, Jason, Ripke, Stephan, Nagaswamy, Uma, Muzny, Donna, Reid, Jeffrey G, Hawes, Alicia, Newsham, Irene, Wu, Yuanqing, Lewis, Lora, Dinh, Huyen, Gross, Shannon, Wang, Li-San, Lin, Chiao-Feng, Valladares, Otto, Gabriel, Stacey B, dePristo, Mark, Altshuler, David M, Purcell, Shaun M, NHLBI Exome Sequencing Project, , State, Matthew W, Boerwinkle, Eric, Buxbaum, Joseph D, Cook, Edwin H, Gibbs, Richard A, Schellenberg, Gerard D, Sutcliffe, James S, Devlin, Bernie, **Roeder**, Kathryn, and Daly, Mark J. Rare complete knockouts in humans: population distribution and significant role in autism spectrum disorders. *Neuron*, 77(2):235–42, Jan 2013.

Liu, Li, Sabo, Aniko, Neale, Benjamin M, Nagaswamy, Uma, Stevens, Christine, Lim, Elaine, Bodea, Corneliu A, Muzny, Donna, Reid, Jeffrey G, Banks, Eric, Coon, Hillary, Depristo, Mark, Dinh, Huyen, Fennel, Tim, Flannick, Jason, Gabriel, Stacey, Garimella, Kiran, Gross, Shannon, Hawes, Alicia, Lewis, Lora, Makarov, Vladimir, Maguire, Jared, Newsham, Irene, Poplin, Ryan, Ripke, Stephan, Shakir, Khalid, Samocha, Kaitlin E, Wu, Yuanqing, Boerwinkle, Eric, Buxbaum, Joseph D, Cook, Edwin H, Devlin, Bernie, Schellenberg, Gerard D, Sutcliffe, James S, Daly, Mark J, Gibbs, Richard A, and **Roeder**, Kathryn. Analysis of rare, exonic variation amongst subjects with autism spectrum disorders and population controls. *PLoS Genet*, 9(4):e1003443, Apr 2013.

Ringquist, Steven, Bellone, Gaia, Lu, Ying, **Roeder**, Kathryn, and Trucco, Massimo. Clustering and alignment of polymorphic sequences for hla-drb1 genotyping. *PLoS One*, 8(3):e59835, 2013.

Schafer, Chad M, Campbell, Nicholas G, Cai, Guiqing, Yu, Fei, Makarov, Vladimir, Yoon, Seungtai, Daly, Mark J, Gibbs, Richard A, Schellenberg, Gerard D, Devlin, Bernie, Sutcliffe, James S, Buxbaum, Joseph D, and **Roeder**, Kathryn. Whole exome sequencing reveals minimal differences between cell line and whole blood derived dna. *Genomics*, Jun 2013.

Willsey, A Jeremy, Sanders, Stephan J, Li, Mingfeng, Dong, Shan, Tebbenkamp, Andrew T, Muhle, Rebecca A, Reilly, Steven K, Lin, Leon, Fertuzinhos, Sofia, Miller, Jeremy A, Murtha, Michael T, Bichsel, Candace, Niu, Wei, Cotney, Justin, Ercan-Sencicek, A Gulhan, Gockley, Jake, Gupta, Abha R, Han, Wenqi, He, Xin, Hoffman, Ellen J, Klei, Lambertus, Lei, Jing, Liu, Wenzhong, Liu, Li, Lu, Cong, Xu, Xuming, Zhu, Ying, Mane, Shrikant M, Lein, Ed S, Wei, Liping, Noonan, James P, **Roeder**, Kathryn, Devlin, Bernie, Sestan, Nenad, and State, Matthew W. Coexpression networks implicate human midfetal deep cortical projection neurons in the pathogenesis of autism. *Cell*, 155(5):997–1007, Nov 2013.

Zhao, Tuo, **Roeder**, Kathryn, and Liu, Han. Positive semidefinite rank-based correlation matrix estimation with application to semiparametric graph estimation. *Journal of Computational and Graphical Statistics*, (DOI: 10.1080/10618600.2013.858633), 2013.

Blumenthal, Ian, Ragavendran, Ashok, Erdin, Serkan, Klei, Lambertus, Sugathan, Aarathi, Guide, Jolene R, Manavalan, Poornima, Zhou, Julian Q, Wheeler, Vanessa C, Levin, Joshua Z, Ernst, Carl, **Roeder**, Kathryn, Devlin, Bernie, Gusella, James F, and Talkowski, Michael E. Transcriptional consequences of 16p11.2 deletion and duplication in mouse cortex and multiplex autism families. *Am J Hum Genet*, 94(6):870–83, Jun 2014.

Cicek, A Ercument, **Roeder**, Kathryn, and Ozsoyoglu, Gultekin. Mira: mutual information-based reporter algorithm for metabolic networks. *Bioinformatics*, 30(12):i175–84, Jun 2014.

De Rubeis, Silvia, He, Xin, Goldberg, Arthur P, Poultney, Christopher S, Samocha, Kaitlin, Ercument Cicek, A, Kou, Yan, Liu, Li, Fromer, Menachem, Walker, Susan, Singh, Tarjinder, Klei, Lambertus, Kosmicki, Jack, Fu, Shih-Chen, Aleksic, Branko, Biscaldi, Monica, Bolton, Patrick F, Brownfeld, Jessica M, Cai, Jinlu, Campbell, Nicholas G, Carracedo, Angel, Chahrour, Maria H, Chiocchetti, Andreas G, Coon, Hilary, Crawford, Emily L, Crooks, Lucy, Curran, Sarah R, Dawson, Geraldine, Duketis, Eftichia, Fernandez, Bridget A, Gallagher, Louise, Geller, Evan, Guter, Stephen J, Sean Hill, R, Ionita-Laza, Iuliana, Jimenez Gonzalez, Patricia, Kilpinen, Helena, Klauck, Sabine M, Kolevzon, Alexander, Lee, Irene, Lei, Jing, Lehtimäki, Terho, Lin, Chiao-Feng, Ma'ayan, Avi, Marshall, Christian R, McInnes, Alison L, Neale, Benjamin, Owen, Michael J, Ozaki, Norio, Parellada, Mara, Parr, Jeremy R, Purcell, Shaun, Puura, Kaija, Rajagopalan, Deepthi, Rehnström, Karola, Reichenberg, Abraham, Sabo, Aniko, Sachse, Michael, Sanders, Stephan J, Schafer, Chad, Schulte-Rüther, Martin, Skuse, David, Stevens, Christine, Szatmari, Peter, Tammimies, Kristiina, Valladares, Otto, Voran, Annette, Wang, Li-San, Weiss, Lauren A, Jeremy Willsey, A, Yu, Timothy W, Yuen, Ryan K C, The DDD Study, , Homozygosity Mapping Collaborative for Autism, , UK10K Consortium, , The Autism Sequencing Consortium, , Cook, Edwin H, Freitag, Christine M, Gill, Michael, Hultman, Christina M, Lehner, Thomas, Palotie, Aarno, Schellenberg, Gerard D, Sklar, Pamela, State, Matthew W, Sutcliffe, James S, Walsh, Christopher A, Scherer, Stephen W, Zwick, Michael E, Barrett, Jeffrey C, Cutler, David J, **Roeder**, Kathryn, Devlin, Bernie, Daly, Mark J, and Buxbaum, Joseph D. Synaptic, transcriptional and chromatin genes disrupted in autism. *Nature*, 515(7526):209–215, Nov 2014.

Dong, Shan, Walker, Michael F, Carriero, Nicholas J, DiCola, Michael, Willsey, A Jeremy, Ye, Adam Y, Waqar, Zainulabedin, Gonzalez, Luis E, Overton, John D, Frahm, Stephanie, Keaney, John F, Teran, Nicole A, Dea, Jeanselle, Mandell, Jeffrey D, Hus Bal, Vanessa, Sullivan, Catherine A, DiLullo, Nicholas M, Khalil, Rehab O, Gockley, Jake, Yuksel, Zafer, Sertel, Sinem M, Ercan-Sencicek, A Gulhan, Gupta, Abha R, Mane, Shrikant M, Sheldon, Michael, Brooks, Andrew I, **Roeder**, Kathryn, Devlin, Bernie, State, Matthew W, Wei, Liping, and Sanders, Stephan J. De novo insertions and deletions of predominantly paternal origin are associated with autism spectrum disorder. *Cell Rep*, 9(1):16–23, Oct 2014.

Gaugler, Trent, Klei, Lambertus, Sanders, Stephan J, Bodea, Corneliu A, Goldberg, Arthur P, Lee, Ann B, Mahajan, Milind, Manaa, Dina, Pawitan, Yudi, Reichert, Jennifer, Ripke, Stephan, Sandin, Sven, Sklar, Pamela, Svantesson, Oscar, Reichenberg, Abraham, Hultman, Christina M, Devlin, Bernie, **Roeder**, Kathryn, and Buxbaum, Joseph D. Most genetic risk for autism resides with common variation. *Nat Genet*, 46(8):881–5, Aug 2014.

Liu, Li, Lei, Jing, Sanders, Stephan J, Willsey, Arthur Jeremy, Kou, Yan, Cicek, Abdullah Ercument, Klei, Lambertus, Lu, Cong, He, Xin, Li, Mingfeng, Muhle, Rebecca A, Ma'ayan, Avi, Noonan, James P, Sestan, Nenad, McFadden, Kathryn A, State, Matthew W, Buxbaum, Joseph D, Devlin, Bernie, and **Roeder**, Kathryn. Dawn: a framework to identify autism genes and subnetworks using gene expression and genetics. *Mol Autism*, 5(1):22, 2014.

Melhem, Nadine M, Lu, Cong, Dresbold, Cara, Middleton, Frank A, Klei, Lambertus, Wood, Shawn, Faraone, Stephen V, Vinogradov, Sophia, Tiobech, Josepha, Yano, Victor, **Roeder**, Kathryn, Byerley, William, Myles-Worsley, Marina, and Devlin, Bernie. Characterizing runs of homozygosity and their impact on risk for psychosis in a population isolate. *Am J Med Genet B Neuropsychiatr Genet*, 165B(6):521–30, Sep 2014.

Samocha, Kaitlin E, Robinson, Elise B, Sanders, Stephan J, Stevens, Christine, Sabo, Aniko, McGrath, Lauren M, Kosmicki, Jack A, Rehnström, Karola, Mallick, Swapan, Kirby, Andrew, Wall, Dennis P, MacArthur, Daniel G, Gabriel, Stacey B, DePristo, Mark, Purcell, Shaun M, Palotie, Aarno, Boerwinkle, Eric, Buxbaum, Joseph D, Cook, Edwin H, Gibbs, Richard A, Schellenberg, Gerard D, Sutcliffe, James S, Devlin, Bernie, **Roeder**, Kathryn, Neale, Benjamin M, and Daly, Mark J. A framework for the interpretation of de novo mutation in human disease. *Nat Genet*, 46(9):944–50, Sep 2014.

Cicek, A Ercument, **Roeder**, Kathryn, and Ozsoyoglu, Gultekin. Mira: mutual information-based reporter algorithm for metabolic networks. *Bioinformatics*, 31(7):1160, Apr 2015.

Cotney, Justin, Muhle, Rebecca A, Sanders, Stephan J, Liu, Li, Willsey, A Jeremy, Niu, Wei, Liu, Wenzhong, Klei, Lambertus, Lei, Jing, Yin, Jun, Reilly, Steven K, Tebbenkamp, Andrew T, Bichsel, Candace, Pletikos, Mihovil, Sestan, Nenad, **Roeder**, Kathryn, State, Matthew W, Devlin, Bernie, and Noonan, James P. The autism-associated chromatin modifier chd8 regulates other autism risk genes during human neurodevelopment. *Nat Commun*, 6:6404, 2015.

Liu, Li, Lei, Jing, and **Roeder**, Kathryn. Network assisted analysis to reveal the genetic basis of autism. *Ann Appl Stat*, 9(3):1571–1600, 2015.

Bodea, Corneliu A, Neale, Benjamin M, Ripke, Stephan, International IBD Genetics Consortium, , Daly, Mark J, Devlin, Bernie, and **Roeder**, Kathryn. A method to exploit the structure of genetic ancestry space to enhance case-control studies. *Am J Hum Genet*, 98(5):857–68, May 2016.

Fromer, Menachem, Roussos, Panos, Sieberts, Solveig K, Johnson, Jessica S, Kavanagh, David H, Perumal, Thanneer M, Ruderfer, Douglas M, Oh, Edwin C, Topol, Aaron, Shah, Hardik R, Klei, Lambertus L, Kramer, Robin, Pinto, Dalila, Gümüş, Zeynep H, Cicek, A Ercument, Dang, Kristen K, Browne, Andrew, Lu, Cong, Xie, Lu, Readhead, Ben, Stahl, Eli A, Xiao, Jianqiu, Parvizi, Mahsa, Hamamsy, Tymor, Fullard, John F, Wang, Ying-Chih, Mahajan, Milind C, Derry, Jonathan M J, Dudley, Joel T, Hemby, Scott E, Logsdon, Benjamin A, Talbot, Konrad, Raj, Towfique, Bennett, David A, De Jager, Philip L, Zhu, Jun, Zhang, Bin, Sullivan, Patrick F, Chess, Andrew, Purcell, Shaun M, Shinobu, Leslie A, Mangravite, Lara M, Toyoshiba, Hiroyoshi, Gur, Raquel E, Hahn, Chang-Gyu, Lewis, David A, Haroutunian, Vahram, Peters, Mette A, Lipska, Barbara K, Buxbaum, Joseph D, Schadt, Eric E, Hirai, Keisuke, **Roeder**, Kathryn, Brennand, Kristen J, Katsanis, Nicholas, Domenici, Enrico, Devlin, Bernie, and Sklar, Pamela. Gene expression elucidates functional impact of polygenic risk for schizophrenia. *Nat Neurosci*, 19(11):1442–1453, Nov 2016.

Autism Spectrum Disorders Working Group of The Psychiatric Genomics Consortium, . Meta-analysis of gwas of over 16,000 individuals with autism spectrum disorder highlights a novel locus at 10q24.32 and a significant overlap with schizophrenia. *Mol Autism*, 8:21, 2017.

Bodea, Corneliu A, Middleton, Frank A, Melhem, Nadine M, Klei, Lambertus, Song, Youeun, Tiobech, Josepha, Marumoto, Pearl, Yano, Victor, Faraone, Stephen V, **Roeder**, Kathryn, Myles-Worsley, Marina, Devlin, Bernie, and Byerley, William. Analysis of shared haplotypes amongst palauans maps loci for psychotic disorders to 4q28 and 5q23-q31. *Mol Neuropsychiatry*, 2(4):173–184, Feb 2017.

Chaste, Pauline, **Roeder**, Kathryn, and Devlin, Bernie. The yin and yang of autism genetics: How rare de novo and common variations affect liability. *Annu Rev Genomics Hum Genet*, 18:167–187, Aug 2017.

De Rubeis, Silvia, **Roeder**, Kathryn, and Bernie, Devlin. Neurodevelopmental mechanisms of pediatric psychiatric disorders: Animal and human studies. 2017.

Kosmicki, Jack A, Samocha, Kaitlin E, Howrigan, Daniel P, Sanders, Stephan J, Slowikowski, Kamil, Lek, Monkol, Karczewski, Konrad J, Cutler, David J, Devlin, Bernie, **Roeder**, Kathryn, Buxbaum, Joseph D, Neale, Benjamin M, MacArthur, Daniel G, Wall, Dennis P, Robinson, Elise B, and Daly, Mark J. Refining the role of de novo protein-truncating variants in neurodevelopmental disorders by using population reference samples. *Nat Genet*, Feb 2017.

Zhu, Lingxue, Lei, Jing, Devlin, Bernie, and **Roeder**, Kathryn. Testing high-dimensional covariance matrices, with application to detecting schizophrenia risk genes. *Ann Appl Stat*, 11(3):1810–1831, Sep 2017.

An, Joon-Yong, Lin, Kevin, Zhu, Lingxue, Werling, Donna M, Dong, Shan, Brand, Harrison, Wang, Harold Z, Zhao, Xuefang, Schwartz, Grace B, Collins, Ryan L, Currall, Benjamin B,

Dastmalchi, Claudia, Dea, Jeanselle, Duhn, Clif, Gilson, Michael C, Klei, Lambertus, Liang, Lindsay, Markenscoff-Papadimitriou, Eirene, Pochareddy, Sirisha, Ahituv, Nadav, Buxbaum, Joseph D, Coon, Hilary, Daly, Mark J, Kim, Young Shin, Marth, Gabor T, Neale, Benjamin M, Quinlan, Aaron R, Rubenstein, John L, Sestan, Nenad, State, Matthew W, Willsey, A Jeremy, Talkowski, Michael E, Devlin, Bernie, **Roeder**, Kathryn, and Sanders, Stephan J. Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. *Science*, 362(6420), 12 2018.

Chen, Siwei, Fragoza, Robert, Klei, Lambertus, Liu, Yuan, Wang, Jiebiao, **Roeder**, Kathryn, Devlin, Bernie, and Yu, Haiyuan. An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. *Nat Genet*, Jun 2018.

Dobbyn, Amanda, Huckins, Laura M, Boocock, James, Sloofman, Laura G, Glicksberg, Benjamin S, Giambartolomei, Claudia, Hoffman, Gabriel E, Perumal, Thanneer M, Girdhar, Kiran, Jiang, Yan, Raj, Towfique, Ruderfer, Douglas M, Kramer, Robin S, Pinto, Dalila, CommonMind Consortium, , Akbarian, Schahram, Roussos, Panos, Domenici, Enrico, Devlin, Bernie, Sklar, Pamela, Stahl, Eli A, and Sieberts, Solveig K. Landscape of conditional eqtl in dorsolateral prefrontal cortex and co-localization with schizophrenia gwas. *Am J Hum Genet*, 102(6):1169–1184, 06 2018.

Hauberg, Mads E, Fullard, John F, Zhu, Lingxue, Cohain, Ariella T, Giambartolomei, Claudia, Misir, Ruth, Reach, Sarah, Johnson, Jessica S, Wang, Minghui, Mattheisen, Manuel, Børglum, Anders Dupont, Zhang, Bin, Sieberts, Solveig K, Peters, Mette A, Domenici, Enrico, Schadt, Eric E, Devlin, Bernie, Sklar, Pamela, **Roeder**, Kathryn, Roussos, Panos, and CommonMind Consortium, . Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. *Mol Psychiatry*, May 2018.

Liu, Fuchen, Choi, David, Xie, Lu, and **Roeder**, Kathryn. Global spectral clustering in dynamic networks. *Proc Natl Acad Sci U S A*, 115(5):927–932, Jan 2018.

Werling, Donna M, Brand, Harrison, An, Joon-Yong, Stone, Matthew R, Zhu, Lingxue, Glessner, Joseph T, Collins, Ryan L, Dong, Shan, Layer, Ryan M, Markenscoff-Papadimitriou, Eirene, Farrell, Andrew, Schwartz, Grace B, Wang, Harold Z, Currall, Benjamin B, Zhao, Xuefang, Dea, Jeanselle, Duhn, Clif, Erdman, Carolyn A, Gilson, Michael C, Yadav, Rachita, Handsaker, Robert E, Kashin, Seva, Klei, Lambertus, Mandell, Jeffrey D, Nowakowski, Tomasz J, Liu, Yuwen, Pochareddy, Sirisha, Smith, Louw, Walker, Michael F, Waterman, Matthew J, He, Xin, Kriegstein, Arnold R, Rubenstein, John L, Sestan, Nenad, McCarroll, Steven A, Neale, Benjamin M, Coon, Hilary, Willsey, A Jeremy, Buxbaum, Joseph D, Daly, Mark J, State, Matthew W, Quinlan, Aaron R, Marth, Gabor T, **Roeder**, Kathryn, Devlin, Bernie, Talkowski, Michael E, and Sanders, Stephan J. An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. *Nat Genet*, 50(5):727–736, May 2018.

Yip, Benjamin Hon Kei, Bai, Dan, Mahjani, Behrang, Klei, Lambertus, Pawitan, Yudi, Hultman, Christina M, Grice, Dorothy E, **Roeder**, Kathryn, Buxbaum, Joseph D, Devlin, Bernie, Reichenberg, Abraham, and Sandin, Sven. Heritable variation, with little or no maternal effect, accounts for recurrence risk to autism spectrum disorder in sweden. *Biol Psychiatry*, 83(7):589–597, Apr 2018.

Zhu, Lingxue, Lei, Jing, Devlin, Bernie, and **Roeder**, Kathryn. A unified statistical framework for single cell and bulk rna sequencing data. *Ann Appl Stat*, 12(1):609–632, Mar 2018.

Grove, Jakob, Ripke, Stephan, Als, Thomas D, Mattheisen, Manuel, Walters, Raymond K, Won, Hyejung, Pallesen, Jonatan, Agerbo, Esben, Andreassen, Ole A, Anney, Richard, Awashti, Swapnil, Belliveau, Rich, Bettella, Francesco, Buxbaum, Joseph D, Bybjerg-Grauholm, Jonas, Bækvad-Hansen, Marie, Cerrato, Felecia, Chambert, Kimberly, Christensen, Jane H, Churchhouse, Claire, Dellenvall, Karin, Demontis, Ditte, De Rubeis, Silvia, Devlin, Bernie, Djurovic, Srdjan, Dumont, Ashley L, Goldstein, Jacqueline I, Hansen, Christine S, Hauberg, Mads Engel, Hollegaard, Mads V, Hope, Sigrun, Howrigan, Daniel P, Huang, Hailiang, Hultman, Christina M, Klei, Lambertus, Maller, Julian, Martin, Joanna, Martin, Alicia R, Moran, Jennifer L, Nyegaard, Mette, Nærland, Terje, Palmer, Duncan S, Palotie, Aarno, Pedersen, Carsten Bøcker, Pedersen, Marianne Giørtz, dPoterba, Timothy, Poulsen, Jesper Buchhave, Pourcain, Beate St, Qvist, Per, Rehnström, Karola, Reichenberg, Abraham, Reichert, Jennifer, Robinson, Elise B, **Roeder**, Kathryn, Roussos, Panos, Saemundsen, Evald, Sandin, Sven, Satterstrom, F Kyle, Davey Smith, George, Stefansson, Hreinn, Steinberg, Stacy, Stevens, Christine R, Sullivan, Patrick F, Turley, Patrick, Walters, G Bragi, Xu, Xinyi, Autism Spectrum Disorder Working Group of the Psychiatric Genomics Consortium, , BUPGEN, , Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium, , 23andMe Research Team, , Stefansson, Kari, Geschwind, Daniel H, Nordentoft, Merete, Hougaard, David M, Werge, Thomas, Mors, Ole, Mortensen, Preben Bo, Neale, Benjamin M, Daly, Mark J, and Børglum, Anders D. Identification of common genetic risk variants for autism spectrum disorder. *Nat Genet*, 51(3):431–444, 03 2019.

Wang, Jiebiao, Devlin, Bernie, and **Roeder**, Kathryn. Using multiple measurements of tissue to estimate subject- and cell-type-specific gene expression. *Bioinformatics*, Aug 2019.

Werling, Donna M., Pochareddy, Sirisha, Choi, Jinmyung, An, Joon-Yong, Sheppard, Brooke, Peng, Minshi, Li, Zhen, Dastmalchi, Claudia, Santpere, Gabriel, Sousa, Andre M. M., Tebbenkamp, Andrew T. N., Kaur, Navjot, Gulden, Forrest O., Breen, Michael S., Liang, Lindsay, Gilson, Michael C., Zhao, Xuefang, Dong, Shan, Klei, Lambertus, Cicek, A. Ercument, Buxbaum, Joseph D., Adle-Biassette, Homa, Thomas, Jean-Leon, Aldinger, Kimberly A., O'Day, Diana R., Glass, Ian A., Zaitlen, Noah A., Talkowski, Michael E., **Roeder**, Kathryn, State, Matthew W., Devlin, Bernie, Sanders, Stephan J., and Sestan, Nenad. Whole-genome and rna sequencing reveal variation and transcriptomic coordination in the developing human prefrontal cortex. *bioRxiv*, 2019.

Zhu, Lingxue, Lei, Jing, Klei, Lambertus, Devlin, Bernie, and **Roeder**, Kathryn. Semisoft clustering of single-cell data. *Proc Natl Acad Sci U S A*, 116(2):466–471, 01 2019.

Buxbaum, Joseph D, Cutler, David J, Daly, Mark J, Devlin, Bernie, **Roeder**, Kathryn, Sanders, Stephan J, and Autism Sequencing Consortium, . Not all autism genes are created equal: A response to myers et al. *Am J Hum Genet*, 107(5):1000–1003, Nov 2020.

Chen, Siwei, Wang, Jiebiao, Cicek, Ercument, **Roeder**, Kathryn, Yu, Haiyuan, and Devlin, Bernie. De novo missense variants disrupting protein-protein interactions affect risk for autism through gene co-expression and protein networks in neuronal cell types. *Mol Autism*, 11(1):76, Oct 2020.

Jalbrzikowski, Maria, Liu, Fuchen, Foran, William, Klei, Lambertus, Calabro, Finnegan J, **Roeder**, Kathryn, Devlin, Bernie, and Luna, Beatriz. Functional connectome fingerprinting accuracy in youths and adults is similar when examined on the same day and 1.5-years apart. *Hum Brain Mapp*, Jul 2020.

Jalbrzikowski, Maria, Liu, Fuchen, Foran, William, **Roeder**, Kathryn, Devlin, Bernie, and Luna, Beatriz. Resting-state functional network organization is stable across adolescent development for typical and psychosis spectrum youth. *Schizophr Bull*, 46(2):395–407, 02 2020.

Lin, K.Z., Liu, H., and **Roeder**, K. Covariance-based sample selection for heterogeneous data: Applications to gene expression and autism risk gene detection. *Journal of the American Statistical Association*, 0(0):1–14, 2020.

Nguyen, Aivi T, Wang, Kui, Hu, Gang, Wang, Xuran, Miao, Zhen, Azevedo, Joshua A, Suh, EunRan, Van Deerlin, Vivianna M, Choi, David, **Roeder**, Kathryn, Li, Mingyao, and Lee, Edward B. Apoe and trem2 regulate amyloid-responsive microglia in alzheimer's disease. *Acta Neuropathol*, Aug 2020.

Satterstrom, F Kyle, Kosmicki, Jack A, Wang, Jiebiao, Breen, Michael S, De Rubeis, Silvia, An, Joon-Yong, Peng, Minshi, Collins, Ryan, Grove, Jakob, Klei, Lambertus, Stevens, Christine, Reichert, Jennifer, Mulhern, Maureen S, Artomov, Mykyta, Gerges, Sherif, Sheppard, Brooke, Xu, Xinyi, Bhaduri, Aparna, Norman, Utku, Brand, Harrison, Schwartz, Grace, Nguyen, Rachel, Guerrero, Elizabeth E, Dias, Caroline, Autism Sequencing Consortium, , iPSYCH-Broad Consortium, , Betancur, Catalina, Cook, Edwin H, Gallagher, Louise, Gill, Michael, Sutcliffe, James S, Thurm, Audrey, Zwick, Michael E, Børglum, Anders D, State, Matthew W, Cicek, A Ercument, Talkowski, Michael E, Cutler, David J, Devlin, Bernie, Sanders, Stephan J, **Roeder**, Kathryn, Daly, Mark J, and Buxbaum, Joseph D. Large-scale exome sequencing study implicates both developmental and functional changes in the neurobiology of autism. *Cell*, 180(3):568–584.e23, 02 2020.

Yurko, Ronald, G'Sell, Max, **Roeder**, Kathryn, and Devlin, Bernie. A selective inference approach for false discovery rate control using multiomics covariates yields insights into disease risk. *Proc Natl Acad Sci U S A*, 117(26):15028–15035, 06 2020.

Yurko, Ronald, **Roeder**, Kathryn, Devlin, Bernie, and G'Sell, Max. H-magma, inheriting a shaky statistical foundation, yields excess false positives. *Ann Hum Genet*, Dec 2020.

Barry, Timothy, Wang, Xuran, Morris, John A., **Roeder**, Kathryn, and Katsevich, Eugene. Conditional resampling improves calibration and sensitivity in single-cell crispr screen analysis. *Genome Biology*, 2021.

Klei, Lambertus, McClain, Lora Lee, Mahjani, Behrang, Panayidou, Klea, De Rubeis, Silvia, Grahnat, Anna-Carin Säll, Karlsson, Gun, Lu, Yangyi, Melhem, Nadine, Xu, Xinyi, Reichenberg, Abraham, Sandin, Sven, Hultman, Christina M, Buxbaum, Joseph D, **Roeder**, Kathryn, and Devlin, Bernie. How rare and common risk variation jointly affect liability for autism spectrum disorder. *Mol Autism*, 12(1):66, 10 2021.

Lin, Kevin Z, Lei, Jing, and **Roeder**, Kathryn. Exponential-family embedding with application to cell developmental trajectories for single-cell rna-seq data. *J Am Stat Assoc*, 116(534):457–470, 2021.

Lin, Kevin Z, Liu, Han, and **Roeder**, Kathryn. Covariance-based sample selection for heterogeneous data: Applications to gene expression and autism risk gene detection. *J Am Stat Assoc*, 116(533):54–67, 2021.

Mahjani, Behrang, De Rubeis, Silvia, Gustavsson Mahjani, Christina, Mulhern, Maureen, Xu, Xinyi, Klei, Lambertus, Satterstrom, F Kyle, Fu, Jack, Talkowski, Michael E, Reichenberg, Abraham, Sandin, Sven, Hultman, Christina M, Grice, Dorothy E, **Roeder**, Kathryn, Devlin, Bernie, and Buxbaum, Joseph D. Prevalence and phenotypic impact of rare potentially damaging variants in autism spectrum disorder. *Mol Autism*, 12(1):65, 10 2021.

Peng, Minshi, Li, Yue, Wamsley, Brie, Wei, Yuting, and **Roeder**, Kathryn. Integration and transfer learning of single-cell transcriptomes via cfit. *Proc Natl Acad Sci U S A*, 118(10), 03 2021.

Peng, Minshi, Wamsley, Brie, Elkins, Andrew G, Geschwind, Daniel H, Wei, Yuting, and **Roeder**, Kathryn. Cell type hierarchy reconstruction via reconciliation of multi-resolution cluster tree. *Nucleic Acids Res*, 49(16):e91, 09 2021.

Qiu, Yixuan, Wang, Jiebiao, Lei, Jing, and **Roeder**, Kathryn. Identification of cell-type-specific marker genes from co-expression patterns in tissue samples. *Bioinformatics*, Apr 2021.

Tian, Jinjin, Wang, Jiebiao, and **Roeder**, Kathryn. Esco: single cell expression simulation incorporating gene co-expression. *Bioinformatics*, Feb 2021.

Wang, Jiebiao, **Roeder**, Kathryn, and Devlin, Bernie. Bayesian estimation of cell type-specific gene expression with prior derived from single-cell data. *Genome Res*, Apr 2021.

Wang, Xuran, Choi, David, and **Roeder**, Kathryn. Constructing local cell-specific networks from single-cell data. *Proc Natl Acad Sci U S A*, 118(51), 12 2021.

Yurko, Ronald, **Roeder**, Kathryn, Devlin, Bernie, and G'Sell, Max. An approach to gene-based testing accounting for dependence of tests among nearby genes. *Brief Bioinform*, 22(6), Nov 2021.

Cai, Zhanrui, Lei, Jing, and **Roeder**, Kathryn. Model-free prediction test with application to genomics data. *Proc Natl Acad Sci U S A*, 119(34):e2205518119, Aug 2022.

Chen, Danfeng, Tashman, Katherine, Palmer, Duncan S, Neale, Benjamin, **Roeder**, Kathryn, Bloemendal, Alex, Churchhouse, Claire, and Ke, Zheng Tracy. A data harmonization pipeline to leverage external controls and boost power in gwas. *Hum Mol Genet*, 31(3):481–489, 02 2022.

Cuddleston, Winston H, Fan, Xuanjia, Sloofman, Laura, Liang, Lindsay, Mossotto, Enrico, Moore, Kendall, Zipkowitz, Sarah, Wang, Minghui, Zhang, Bin, Wang, Jiebiao, Sestan, Nenad, Devlin, Bernie, **Roeder**, Kathryn, Sanders, Stephan J, Buxbaum, Joseph D, and Breen, Michael S. Spatiotemporal and genetic regulation of a-to-i editing throughout human brain development. *Cell Rep*, 41(5):111585, Nov 2022.

Du, Jin-Hong, Cai, Zhanrui, and **Roeder**, Kathryn. Robust probabilistic modeling for single-cell multimodal mosaic integration and imputation via scvaeit. *Proc Natl Acad Sci U S A*, 119(49):e2214414119, Dec 2022.

Fu, Jack M, Satterstrom, F Kyle, Peng, Minshi, Brand, Harrison, Collins, Ryan L, Dong, Shan, Wamsley, Brie, Klei, Lambertus, Wang, Lily, Hao, Stephanie P, Stevens, Christine R, Cusick, Caroline, Babadi, Mehrtash, Banks, Eric, Collins, Brett, Dodge, Sheila, Gabriel, Stacey B, Gauthier, Laura, Lee, Samuel K, Liang, Lindsay, Ljungdahl, Alicia, Mahjani, Behrang, Sloofman, Laura, Smirnov, Andrey N, Barbosa, Mafalda, Betancur, Catalina, Brusco, Alfredo, Chung, Brian H Y, Cook, Edwin H, Cuccaro, Michael L, Domenici, Enrico, Ferrero, Giovanni Battista, Gargus, J Jay, Herman, Gail E, Hertz-Picciotto, Irva, Maciel, Patricia, Manoach, Dara S, Passos-Bueno, Maria Rita, Persico, Antonio M, Renieri, Alessandra, Sutcliffe, James S, Tassone, Flora, Trabetti, Elisabetta, Campos, Gabriele, Cardaropoli, Simona, Carli, Diana, Chan, Marcus C Y, Fallerini, Chiara, Giorgio, Elisa, Girardi, Ana Cristina, Hansen-Kiss, Emily, Lee, So Lun, Lintas, Carla, Ludena, Yunin, Nguyen, Rachel, Pavinato, Lisa, Pericak-Vance, Margaret, Pessah, Isaac N, Schmidt, Rebecca J, Smith, Moyra, Costa, Claudia I S, Trajkova, Slavica, Wang, Jaqueline Y T, Yu, Mullin H C, Autism Sequencing Consortium (ASC), , Broad Institute Center for Common Disease Genomics (Broad-CCDG), , iPSYCH-BROAD Consortium, , Cutler, David J, De Rubeis, Silvia, Buxbaum, Joseph D, Daly, Mark J, Devlin, Bernie, **Roeder**, Kathryn, Sanders, Stephan J, and Talkowski, Michael E. Rare coding variation provides insight into the genetic architecture and phenotypic context of autism. *Nat Genet*, 54(9):1320–1331, Sep 2022.

Mahjani, Behrang, Klei, Lambertus, Mattheisen, Manuel, Halvorsen, Matthew W, Reichenberg, Abraham, **Roeder**, Kathryn, Pedersen, Nancy L, Boberg, Julia, Schipper, Elles, Bulik, Cynthia M, Landén, Mikael, Fundín, Bengt, Mataix-Cols, David, Sandin, Sven, Hultman, Christina M, Crowley, James J, Buxbaum, Joseph D, Rück, Christian, Devlin, Bernie, and Grice, Dorothy E. The genetic architecture of obsessive-compulsive disorder: Contribution of liability to ocd from alleles across the frequency spectrum. *Am J Psychiatry*, 179(3):216–225, Mar 2022.

Cai, Zhanrui, Lei, Jing, and **Roeder**, Kathryn. Asymptotic distribution-free independence test for high dimension data. *Journal of the American Statistical Association*, 0(ja):1–20, 2023.

Du, Jin-Hong, Wasserman, Larry, and Roeder, Kathryn. Simultaneous inference for generalized linear models with unmeasured confounders. *ArXiv*, Sep 2023.

Jin-Hong Du, Kathryn **Roeder** and Kuchibhotla, Arun Kumar. Extrapolated cross-validation for randomized ensembles. *Journal of Computational and Graphical Statistics*, 0(0):1–12, 2023.

Morris, John A, Caragine, Christina, Daniloski, Zharko, Domingo, Júlia, Barry, Timothy, Lu, Lu, Davis, Kyrie, Ziosi, Marcello, Glinos, Dafni A, Hao, Stephanie, Mimitou, Eleni P, Smibert, Peter, **Roeder**, Kathryn, Katsevich, Eugene, Lappalainen, Tuuli, and Sanjana, Neville E. Discovery of target genes and pathways at gwas loci by pooled single-cell crispr screens. *Science*, page eadh7699, May 2023.

Qiu, Yixuan, Lei, Jing, and **Roeder**, Kathryn. Gradient-based sparse principal component analysis with extensions to online learning. *Biometrika*, 110(2):339–360, Jun 2023.

Tian, Jinjin, Lei, Jing, and **Roeder**, Kathryn. From local to global gene co-expression estimation using single-cell rna-seq data. *Biometrics (in press)*, 2023.

Wang, Catherine, Hayes, Rebecca, **Roeder**, Kathryn, and Jalbrzikowski, Maria. Neurobiological clusters are associated with trajectories of overall psychopathology in youth. *Biol Psychiatry Cogn Neurosci Neuroimaging*, Apr 2023.

Wen, Cindy, Margolis, Michael, Dai, Rujia, Zhang, Pan, Przytycki, Pawel F., Vo, Daniel D., Bhattacharya, Arjun, Matoba, Nana, Jiao, Chuan, Kim, Minsoo, Tsai, Ellen, Hoh, Celine, Aygün, Nil, Walker, Rebecca L., Chatzinakos, Christos, Clarke, Declan, Pratt, Henry, Consortium, PsychENCODE, Peters, Mette A., Gerstein, Mark, Daskalakis, Nikolaos P., Weng, Zhiping, Jaffe, Andrew E., Kleinman, Joel E., Hyde, Thomas M., Weinberger, Daniel R., Bray, Nicholas J., Sestan, Nenad, Geschwind, Daniel H., **Roeder**, Kathryn, Gusev, Alexander, Pasaniuc, Bogdan, Stein, Jason L., Love, Michael I., Pollard, Katherine S., Liu, Chunyu, and Gandal, Michael J. Cross-ancestry, cell-type-informed atlas of gene, isoform, and splicing regulation in the developing human brain. *Science (in 2nd review)*, 2023.

Barry, Timothy, Mason, Kaishu, **Roeder**, Kathryn, and Katsevich, Eugene. Robust differential expression testing for single-cell crispr screens at low multiplicity of infection. *Genome Biol*, 25(1):124, May 2024.

Barry, Timothy, **Roeder**, Kathryn, and Katsevich, Eugene. Exponential family measurement error models for single-cell crispr screens. *Biostatistics*, Apr 2024.

Du, Jin-Hong, Wasserman, Larry, and **Roeder**, Kathryn. Simultaneous inference for generalized linear models with unmeasured confounders, 2024.

Du, Jin-Hong, Zeng, Zhenghao, Kennedy, Edward H., Wasserman, Larry, and **Roeder**, Kathryn. Causal inference for genomic data with multiple heterogeneous outcomes, 2024.

Lin, Kevin Z, Qiu, Yixuan, and **Roeder**, Kathryn. esvd-de: cohort-wide differential expression in single-cell rna-seq data using exponential-family embeddings. *BMC Bioinformatics*, 25(1):113, Mar 2024.

Moon, Haeun, Du, Jin-Hong, Lei, Jing, and **Roeder**, Kathryn. Augmented doubly robust post-imputation inference for proteomic data. *bioRxiv*, 2024.

Zhang, Tianyu, Lei, Jing, and **Roeder**, Kathryn. Debiased projected two-sample comparisonscfor single-cell expression data, 2024.

Zhang, Tianyu, Zhou, Geyu, Klei, Lambertus, Liu, Peng, Chouldechova, Alexandra, Zhao, Hongyu, **Roeder**, Kathryn, G'Sell, Max, and Devlin, Bernie. Evaluating and improving health equity and fairness of polygenic scores. *HGG Adv*, 5(2):100280, Apr 2024.

Invited Presentations at Meetings:

1991 WNAR Meetings
1991 IMS Statistical Challenges in Astronomy meetings
1992 IBC Meetings
1992 ENAR Meetings
1992 ASA meetings

1992 IMS Likelihood meetings
1993 Bayesian Statistics in Science and Technology
1993 Hierarchical Bayes Conference
1994 IMS Meetings
1994 NRC/NAS Committee on DNA Fingerprinting.
1995 IMS Meetings
1995 Human Genetics Meetings
1996 Genome Mapping and Sequencing
1996 ASA, New Jersey Chapter meetings
1996 ASA, Joint statistical meetings
1996 Social Science and Statistics: in honor of Clifford Clogg.
1997 Canadian statistical meetings
1997 Human Genetics Meetings
1998 ENAR Meetings
1998 Ohio State, Cleveland Clinic & Case Western Reserve Minisymposium (featured speaker)
1998 ASA Meetings
1999 ENAR Meetings, IMS SIP
1999 JSM Meetings
2000 IMS/Bernoulli Society Meetings
2000 Association Analysis for Neurobehavioral Genetics
2000 Speaker for Atlanta Chapter of American Statistical Association
2001 Pennsylvania State University, Alumni Society Meetings.
2002 SNP2000 Consortium (international conference on genomics)
2002 DIMACS Conference on Haplotypes
2003 Genomics Bonn — Genetics of Complex Disease.
2003 UAB Short Course in Statistical Genetics
2004 Keil Workshop, Germany
2004 RECOMB Workshop
2004 UAB Short Course in Statistical Genetics
2004 Pymatuning Short Course in Statistical Genetics
2004 Biological Language Conference, CMU
2005 Joint Statistics Meetings
2005 Canadian Statistical Society Meetings, Presidential Invited Address
2005 UAB Short Course in Statistical Genetics
2005 American Society Human Genetics Meetings, Plenary Session
2005 American Society Human Genetics Meetings, Special Invited Session
2005 National Academy of Sciences, Session on Forensic Inference
2006 National Academy of Sciences invited speaker for the national meetings
2006 American Society Human Genetics Meetings, Special Invited Session
2007 Emerging Design and Analysis Issues in Genomic Studies in Population Sciences.
2007 Computational Biology Genomic Conferences at CMU.
2008 American Society Human Genetics Meetings, Special Invited Session
2008 GENEVA meeting on Genome-wide Association analysis. Featured Speaker
2008 Statistics in Biology, special conference, University of Iowa.
2009 JSM Special Invited Session.

2009 Gordon Conference on Genetics and Genomics.
2010 JSM Special Invited Session.
2010 NCI special invited speaker for the division
2010 NIH conference "Next Generation Tools for Genetic Studies of Complex Diseases"
2011 4th Paris Workshop on Genomics, invited speaker
2011 Special conference in honor of Brad Efron, Washington DC
2011 IPAM invited speaker, UCLA
2012 PQG Conference Sequencing and Complex Traits: beyond 1000 Genomes.
2013 COPSS Junior Researcher Panel: Building a Research Career.
2013 COPSS 50'th Anniversary Session: Reflections on Statistical Science.
2013 JSM invited speaker.
2013 Speaker at Janet L. Norwood Award Ceremony.
2014 Donna J Brogan Lecturer, Emery University.
2014 International Indian Statistical Association Plenary Speaker
2014 Seaver Distinguished Lecturer, Mount Sinai School of Medicine
2015 SFARI invited Webinar speaker for autism research
2015 JSM Invited speaker
2016 ENAR Invited speaker
2016 JSM Invited speaker
2016 Nature conference on Genetics of Common Disease, invited speaker
2016 Molecular Psychiatry Meetings, invited speaker
2016 Women in Statistics Conference
2017 ENAR Invited speaker
2017 Graybill conference, Keynote speaker
2017 JSM Invited speaker
2017 Nature Neuro Genetics conference, invited speaker
2018 Women in Data Science Invited speaker
2018 Pamela Sklar Symposium, Invited speaker
2018 New Aspects on Statistics, Financial Econometrics, and Data Science, invited speaker
2018 NCI SeqSPACE Webinar, Invited speaker
2019 BIRS workshop, Invited speaker
2019 ENAR, Invited speaker
2019 SFARI, Invited speaker
2019 INSAR, Keynote speaker
2019 Stanley Center symposium, Invited speaker
2020 JASA-App Paper for JSM 2020-JASA section
2020 Keynote speaker Pamela Sklar Psychiatric Genetics and Neuroscience conference
2020 COPSS Distinguished Achievement Award and Lectureship
2021 Keynote speaker for ACM-BCB workshop on single-cell genomics
2021 Keynote speaker for Machine Learning Frontiers in Precision Medicine (Europe)
2021 CC Li Distinguished Lecture
2021 JSM invited speaker
2022 ENAR invited speaker
2022 ASA banquet speaker
2022 Allen Brain Institute invited speaker

2023 Cold Spring Harbor, Probabilistic Modeling in Genomics, Keynote speaker
2023 ICSA Applied Statistics Symposium, Keynote speaker
2023 WNAR Invited speaker
2023 JSM Invited speaker
2023 Krishnaiah Lecture, Pennsylvania State University
2024 ENAR Invited speaker
2024 Michael Woodroofe Lecture, UMich Statistics
2024 Qunxian Distinguished University-Level Lecture
2024 Keynote speaker ASA SSGG Conference
2024 Hsu Distinguished Lecture Series, Tsinghua University
2024 Keynote speaker Joint Conference of Statistics and Data Science (China)

Invited Presentations at Departments:

U. of Connecticut (1989)
Carnegie Mellon (1989,1992)
Rutgers (1991)
Harvard Biostatistics (1991)
U. of Chicago (1991, 1995)
U. of Indiana (1991)
U. of Georgia (1992)
North Carolina State (1992)
Stanford University (1993)
Bellcore (1993)
Harvard (1994)
Johns Hopkins, Biostat & Stat (1994)
U. Michigan, Biostat (1995)
Rice University (1996)
CMU Dept of Biology (2000)
Center of Disease Control (2000)
Pennsylvania State University (2001)
UCLA Genetics and Biostatistics (2003)
University of Chicago (2007)
Texas A&M University (2012)
Pennsylvania State University (2014),
University of Chicago (2015),
Purdue University (2017)
University of North Carolina (2018),
University of Michigan (2019),
University of Washington (2019),
Mount Sinai school of Medicine (2020),
Stanford (2021),
Novartis (2022) ,
Columbia Comp Bio (2023),
Michigan Statistics (2024),
Ray Carroll's 75th Birthday Conference (2024)

AT&T Bell Labs. (1990,1992,1996)
Yale Math (1991)
Johns Hopkins, Biostat (1991)
U. of Chicago, School of Business (1991)
Northwestern (1991)
Purdue (1991,1994)
UCLA (1992)
U. of Pittsburgh (1992)
U. Victoria (1993)
Yale Law School (1994)
Duke (1994)
NIST (1995)
Univ of Texas (1996)
Kansas State University (1998)
Univ of Pittsburgh, Biostat (2000)
Cleveland Clinic (2001)
Harvard Statistics (2002)
N Carolina State Univ. (2005)
University of Toronto (2010)
Carnegie Mellon University, Lane Center (2013)
Stanford (2015),
Emery University (2017)
UC Berkeley (2017)
Johns Hopkins (2018)
University of Pittsburgh (2019)
University of Toronto (2020)
Duke University (2020
Harvard (2021)
Chicago (2022)
Columbia Biostatistics (2024)
Xiamen University, China (2024)