

## CURRICULUM VITAE

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**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  
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  
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  
International Statistical Institute  
Elected member, 1995  
International Biometrics Society  
Associate Editor, Biometrics, 1997-  
Best Abstract Award, 1992  
Genetics Society  
Associate Editor 2014 -2015

#### Ph.D. Advisees:

Jinjin Liu, Tim Barron, Yue Li,  
Ron Yurko, Minshi Peng, Kevin Lin, Fuchen Liu,  
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 relationships 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, *Intelligence, 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.

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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 class 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.

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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.

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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.

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Yunin, Maciel, Patricia, Magnus, Per, Mahjani, Behrang, Maltman, Nell, Manoach, Dara S., Meiri, Gal, Menashe, Idan, Miller, Judith, Minshew, Nancy, Souza, Eduarda Montenegro M., Moreira, Danielle, Morrow, Eric M., Mors, Ole, Mortensen, Preben Bo, Mosconi, Matthew, Muglia, Pierandrea, Neale, Benjamin, Nordentoft, Merete, Ozaki, Norio, Palotie, Aarno, Parcellada, Mara, Passos-Bueno, Maria Rita, Pericak-Vance, Margaret, Persico, Antonio, Pessah, Isaac, Puura, Kaija, Reichenberg, Abraham, Renieri, Alessandra, Riberi, Evelise, Robinson, Elise B., Samocha, Kaitlin E., Sandin, Sven, Santangelo, Susan L., Schellenberg, Gerry, Scherer, Stephen W., Schlitt, Sabine, Schmidt, Rebecca, Schmitt, Lauren, Silva, Isabela Maya W., Singh, Tarjinder, Siper, Paige M., Smith, Moyra, Soares, Gabriela, Stoltenberg, Camilla, Suren, Pål, Susser, Ezra, Sweeney, John, Szatmari, Peter, Tang, Lara, Tassone, Flora, Teufel, Karoline, Trabetti, Elisabetta, Pilar Trelles, Maria del, Walsh, Christopher, Weiss, Lauren A., Werge, Thomas, Werling, Donna, Wigdor, Emilie M., Wilkinson, Emma, Willsey, Jeremy A., Yu, Tim, Yu, Mullin H.C., Yuen, Ryan, Zach, Elaine, Betancur, Catalina, Cook, Edwin H., Gallagher, Louise, Gill, Michael, Lehner, Thomas, Senthil, Geetha, 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, Buxbaum, Joseph D., and Daly, Mark J. Novel genes for autism implicate both excitatory and inhibitory cell lineages in risk. *bioRxiv*, 2018.

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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.

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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.

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.

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Katsevich, Eugene and **Roeder**, Kathryn. Conditional resampling improves sensitivity and specificity of single cell crispr regulatory screens. *bioRxiv*, 2020.

Lin, Kevin Z., Lei, Jing, and **Roeder**, Kathryn. Exponential-family embedding with application to cell developmental trajectories for single-cell rna-seq data. *bioRxiv*, 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, Viviana 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.

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Wang, Jiebiao, Kathryn, , and Devlin, Bernie. Bayesian estimation of cell-type-specific gene expression per bulk sample with prior derived from single-cell data. *bioRxiv*, 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.

### 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

### 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)

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)