CURRICULUM VITAE

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Address: Department of Statistics and Data Science
Carnegie Mellon University
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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:

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
- 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:

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.** Estimation of allele frequencies for VNTR loci. *Am. J. Hum. Genet.*, 48:662–676, Apr 1991.

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

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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 editors, **R**oeder, K. *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.

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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.

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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.

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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.

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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.

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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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Barbosa, Mafalda, Bishop, Somer, Brusco, Alfredo, Bybjerg-Grauholm, Jonas, Carracedo, Angel, Chan, Marcus C.Y., Chiocchetti, Andreas G., Chung, Brian H. Y., Coon, Hilary, Cuccaro, Michael L., Currò, Aurora, Bernardina, Bernardo Dalla, Doan, Ryan, Domenici, Enrico, Dong, Shan, Fallerini, Chiara, Fernández-Prieto, Montserrat, Ferrero, Giovanni Battista, Freitag, Christine M., Fromer, Menachem, Gargus, J. Jay, Geschwind, Daniel, Giorgio, Elisa, González-Peñas, Javier, Guter, Stephen, Halpern, Danielle, Hansen-Kiss, Emily, He, Xin, Herman, Gail E., Hertz-Picciotto, Irva, Hougaard, David M., Hultman, Christina M., Ionita-Laza, Iuliana, Jacob, Suma, Jamison, Jesslyn, Jugessur, Astanand, Kaartinen, Miia, Knudsen, Gun Peggy, Kolevzon, Alexander, Kushima, Itaru, Lee, So Lun, Lehtimäki, Terho, Lim, Elaine T., Lintas, Carla, Lipkin, W. Ian, Lopergolo, Diego, Lopes, Fátima, Ludena, 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, Parellada, 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, Zachi, 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.

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.

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fect, 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.

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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.

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)