CURRICULUM VITAE

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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-
Departments of Statistics & 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:

Penn State Eberly College of Science Outstanding Alumni Award, 2014
Janet L Norwood Award, outstanding achievement by a woman in Statistical Sciences, 2013
Presidents' Award, Committee of Presidents of Statistical Societies 1997
Snedecor Award, for best biometrical paper, 1995-1997
NSF Young Investigator Award, 1992-1997
Distinguished Lecturer
- Myra Samuels Lecturer, 2017
- Seaver Lecturer, Mount Sinai School of Medicine, 2014
- Donna J. Brogan Lecturer, Emory University, 2014
- Myrto Lefkopoulou Lecturer, Harvard School of Public Health, 1998
- Kansas State University, 1997
- Goucher College, 1995
- Purdue University's School of Science, 1994

Institute of Mathematical Statistics
- Medallian Lecture, 1999
- 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
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
American Association for the Advancement of Science (AAAS)
Statistics Section Chair 2017 -2018
Regular BMRD Panelist for NIH, 2006-2009
Advisor to:
FBI on DNA forensics, 1995
NRC/NAS on DNA forensics, 1994-95
Carnegie Commission Study on Early Childhood Development, 1994

Ph.D. Advisees:

Lingxue Zhu (in progress), Kevin Lin (in progress), Fuchen Liu (in progress),
Li Liu (2014), Corneliu Bodea (2015), Cong Lu (2016),
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-

1 Books, Reviews, Comments and Other Publications:

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

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.

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

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.

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.

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., 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.

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.

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

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.

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

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.

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

Devlin, B., Daniels, M., and Roeder, K. The heritability of IQ. *Nature*, 388:468–471, Jul 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. and Wasserman, L. Practical Bayesian density estiation 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., 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.

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

Devlin, B., Roeder, K., and Wasserman, L. False discovery or missed discovery? *Heredity (Edinb)*, 91:537–538, Dec 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.

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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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.

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.

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.

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.

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.

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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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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
216 Women in Statistics Conference
2017 ENAR Invited speaker
2017 Graybill conference, Keynote speaker
2017 JSM Invited speaker
2017 Nature Neuroscience conference, invited speaker
2018 Pamela Sklar Symposium, Invited speaker
2018 New Aspects on Statistics, Financial Econometrics, and Data Science, 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)

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)
University of North Carolina (2018)