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CURRICULUM VITAE

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PERSONAL:

Date of birth: February 4, 1963. Married, Two children
Citizenship: United States

EDUCATION:

1983 B.S., East China Normal University, Shanghai, China
1986 M.S., Biostatistics, University of Michigan, Ann Arbor, Michigan
1989 Ph.D., Biostatistics, University of Michigan, Ann Arbor, Michigan

PROFESSIONAL EXPERIENCE:

1987-1988 Research Associate, Department of Biostatistics, University of Michigan
1988-1989 Research Intern, Biostatistics Center, University of Wisconsin
1989-1990 Research Fellow, Department of Biostatistics, Harvard University
1990-1991 Research Assistant Professor, Department of Biostatistics, University of Washington
1991-1994 Assistant Professor, Department of Biostatistics, University of Washington
1992-1994 Assistant Member, Division of Public Health Sciences, Fred Hutchinson Cancer Research Center
1994-1998 Associate Professor, Department of Biostatistics, University of Washington
1994-1998 Associate Member, Division of Public Health Sciences, Fred Hutchinson Cancer Research Center
1997-1998 Genentech Distinguished Professor in Biostatistics, University of Washington
1998-2000 Professor, Department of Biostatistics, University of Washington
1998-2000 Member, Division of Public Health Sciences, Fred Hutchinson Cancer Research Center
1998-present Special Government Employee (Consultant), Food and Drug Administration, U.S. Department of Health and Human Services
2001-2007 Affiliate Professor, Department of Biostatistics, University of Washington
2001-present Dennis Gillings Distinguished Professor, Department of Biostatistics, University of North Carolina
2002-present Member, Center for AIDS Research, University of North Carolina
2003-present Member, Lineberger Comprehensive Cancer Center, University of North Carolina

AWARDS AND HONORS:

1988-1989 Rackham Predoctoral Fellowship, University of Michigan
1989-1990 Fogarty Fellowship, National Institutes of Health
1992-1997 First Independent Research Award, National Institutes of Health
1999 Fellow, Institute of Mathematical Statistics
1999 Mortimer Spiegelman Award, American Public Health Association
2000 Fellow, American Statistical Association

2000	<i>Journal of the American Statistical Association – Theory and Methods</i> Discussion Paper
2002	Myrto Lefkopoulou Distinguished Lecturer, Harvard University
2003	Odoroff Memorial Lecturer, University of Rochester
2003	Highly Cited Researcher in Mathematics, Thomson ISI
2005-2015	National Institutes of Health MERIT Award
2006	<i>Journal of the American Statistical Association – Theory and Methods</i> Discussion Paper
2007	<i>Journal of the Royal Statistical Society, Series B</i> Discussion Paper
2011	Keynote address, ICSA (International Chinese Statistical Association) Applied Statistics Symposium
2015	COPSS (Committee of Presidents of Statistical Societies) George W. Snedecor Award
2015	ICSA (International Chinese Statistical Association) Distinguished Achievement Award
2019	Keynote address, The Second Conference on Lifetime Data Science, Pittsburgh, PA

PROFESSIONAL MEMBERSHIPS:

American Statistical Association
International Biometric Society
Institute of Mathematical Statistics
International Chinese Statistical Association
American Society of Human Genetics
International Genetic Epidemiology Society

EDITORIAL SERVICE:

1997-2000	Associate Editor, <i>Biometrics</i>
1998-2001	Associate Editor, <i>Probability and Statistics Letters</i>
1999-2009	Associate Editor, <i>Statistica Sinica</i>
1999-present	Associate Editor, <i>Biometrika</i>
2006-2009	Associate Editor, <i>Scandinavian Journal of Statistics</i>
2012-2018	Associate Editor, <i>Journal of the American Statistical Association – Applications and Case Studies</i>
2014-present	Associate Editor, <i>Genetic Epidemiology</i>
2014-present	Associate Editor, <i>Journal of the American Statistical Association – Theory and Methods</i>
2017-present	Editor, <i>Statistical Theory and Related Fields</i>
2019-present	Associate Editor, <i>Journal of the American Statistical Association – Reviews</i>

ADVISORY BOARDS AND COMMITTEES:

1994-1995	Organizing Committee (Chair), First Seattle Symposium in Biostatistics: Survival Analysis
1997	Biostatistics Study Section, National Institutes of Health
1998	Program Committee, The Fourth ICSA Statistical Conference
1999	IMS Program Committee, Joint Statistical Meetings
1999	AIDS & Related Research Review Group, National Institutes of Health
1999-2000	Organizing Committee (Chair), Second Seattle Symposium in Biostatistics: Analysis of Correlated Data
2000-2010	Visiting Lecturer Program in Statistical Science, Committee of Presidents of the Statistical Societies (COPSS)
2000-2002	Mortimer Spiegelman Award Committee (Chair, 2002), American Public Health Association
2001-2003	Social Sciences, Nursing, Epidemiology and Methods (SNEM-5) Study Section, National Institutes of Health
2002	Site Visit Team, Biostatistics Branch, National Cancer Institute
2002	Review Panel for SNEM-5 Member Applications, National Institutes of Health
2003-2004	Program Committee, The International Biometric Society ENAR 2004 Spring Meetings
2004-2006	Review Panel for BMRD Member Applications, National Institutes of Health

2004-2013	National Heart, Lung and Blood Institute's Protocol Review and DSMB Committees for the Cardiovascular Outcomes in Renal Atherosclerotic Lesions Trial
2004	Independent Expert Panel on Statistical Methods for the Analysis of Organ Transplantation Data, Health Resources and Services Administration, U.S. Department of Health and Human Services
2006	National Cancer Institute P01 Cluster Review
2006-2007	Program Committee (Chair) and Organizing Committee (Co-Chair), ICSA 16 th Applied Statistics Symposium
2007	External Advisory Committee, Public Health Sciences Division, Fred Hutchinson Cancer Research Center
2004, -08, -10	Tenure Review Committees, Harvard University
2015-2019	Data Monitoring Committee, Celgene ACE-536-B-THAL-001 Study
2018-present	Data Monitoring Committee, Celgene ACE-536-B-THAL-002 Study
2019-present	Data Monitoring Committee, Celgene ACE-536-B-THAL-004 Study
2017-present	Statistical Science Advisory Board on Biosimilars, AMGEN
2019	Special Emphasis Panel for Member Conflict: Epidemiology and Genetic Epidemiology, National Institutes of Health

PEER-REVIEWED ARTICLES

Google Scholar: <https://scholar.google.com/citations?user=SG22hu0AAAAJ&hl=en>

Citations: 30,000

h-index: 83

1. Wei LJ, **Lin DY**, Weissfeld L: Regression analysis of multivariate incomplete failure time data by modeling marginal distributions. *Journal of the American Statistical Association* 84: 1065-1073, 1989.
2. **Lin DY**, Wei LJ: The robust inference for the Cox proportional hazards model. *Journal of the American Statistical Association* 84: 1074-1078, 1989.
3. Wei LJ, Smythe RT, **Lin DY**, Park TS: Statistical inference with data-dependent treatment allocation rules. *Journal of the American Statistical Association* 85: 156-162, 1990.
4. **Lin DY**: MULCOX: A computer program for the Cox regression analysis of multiple failure time variables. *Computer Methods and Programs in Biomedicine* 32: 125-135, 1990.
5. Wei LJ, Ying Z, **Lin DY**: Linear regression analysis of censored survival data based on rank tests. *Biometrika* 77: 845-851, 1990.
6. **Lin DY**, Wei LJ: Global goodness-of-fit tests for the general Cox regression model. *Statistica Sinica* 1: 1-17, 1991.
7. **Lin DY**: Nonparametric sequential testing in clinical trials with incomplete multivariate observations. *Biometrika* 78: 123-131, 1991.
8. **Lin DY**, Wei LJ: Repeated confidence intervals for a scale change in a sequential survival study. *Biometrics* 47: 289-294, 1991.
9. **Lin DY**: Goodness-of-fit analysis for the Cox regression model based on a class of parameter estimators. *Journal of the American Statistical Association* 86: 725-728, 1991.
10. **Lin DY**, Wei LJ, DeMets DL: Exact statistical inference for group sequential trials. *Biometrics* 47: 1399-1408, 1991.
11. **Lin DY**, Liu PY: Nonparametric sequential tests against ordered alternatives in multiple-armed clinical trials. *Biometrika* 79: 420-425, 1992.
12. **Lin DY**, Geyer CJ: Computational methods for semiparametric linear regression with censored data. *Journal of Computational and Graphical Statistics* 1: 77-90, 1992.
13. **Lin DY**: Sequential log rank tests adjusting for covariates with the accelerated life model. *Biometrika* 79: 523-529, 1992.
14. **Lin DY**: GOF-COX: A computer program for the goodness-of-fit analysis of the Cox proportional hazards model. *Computer Methods and Programs in Biomedicine* 38: 101-105, 1992.
15. **Lin DY**, Fischl MJA, Schoenfeld DA: Evaluating the role of CD4-lymphocyte counts as surrogate endpoints in human immunodeficiency virus clinical trials. *Statistics in Medicine* 12:835-842, 1993.

16. **Lin DY**: MULCOX2: A general computer program for the Cox regression analysis of multivariate failure time data. *Computer Methods and Programs in Biomedicine* 40:279-293, 1993.
17. Koenig JQ, Larson TV, Hanley QS, Rebolledo V, Dumler K, Checkoway H, Wang SZ, **Lin DY**, Pierson WE: Pulmonary function changes in children associated with fine particulate matter. *Environmental Research* 63:26-38, 1993.
18. **Lin DY**, Wei LJ, Ying Z: Checking the Cox model with cumulative sums of martingale-based residuals. *Biometrika* 80:557-572, 1993.
19. **Lin DY**, Ying Z: A simple nonparametric estimator of the bivariate survival function under univariate censoring. *Biometrika* 80:573-581, 1993.
20. **Lin DY**, Ying Z: Cox regression with incomplete covariate measurements. *Journal of the American Statistical Association* 88:1341-1349, 1993.
21. **Lin DY**, Ying Z: Semiparametric analysis of the additive risk model. *Biometrika* 81:61-71, 1994.
22. **Lin DY**, Fleming TR, Wei LJ: Confidence bands for survival curves under the proportional hazards model. *Biometrika* 81:73-81, 1994.
23. Guo SW, **Lin DY**: Regression analysis of multivariate grouped survival data. *Biometrics* 50:632-639, 1994.
24. **Lin DY**: Cox regression analysis of multivariate failure time data: The marginal approach. *Statistics in Medicine* 13:2233-2247, 1994.
25. **Lin DY**, Ying Z: Semiparametric inference for the accelerated life model with time-dependent covariates. *Journal of Statistical Planning and Inference* 44:47-63, 1995.
26. Crawford SW, Pepe M, **Lin DY**, Benedetti F, Deeg HJ: Abnormalities of pulmonary function tests after marrow transplantation predict non-relapse mortality. *American Journal of Respiratory and Critical Care Medicine* 152:690-695, 1995.
27. Combes B, Carithers RL, Maddrey WC, **Lin DY et al.**: A randomized, double-blind, placebo-controlled trial of ursodeoxycholic acid in primary biliary cirrhosis. *Hepatology* 22:759-766, 1995.
28. **Lin DY**, Ying Z: Semiparametric analysis of general additive-multiplicative hazard models for counting processes. *The Annals of Statistics* 23:1712-1734, 1995.
29. Psaty BW, Siscovick DS, Weiss NS, Koepsell TD, Rosendaal FR, **Lin DY**, Hekbert SR, Wagner EM, Furberg CD: Hypertension and outcomes research: from clinical trials to clinical epidemiology. *American Journal of Hypertension* 9:178-183, 1996.
30. **Lin DY**, Spiekerman CF: Model checking techniques for parametric regression with censored data. *Scandinavian Journal of Statistics* 23:157-177, 1996.
31. Yip PSF, Huggins RM, **Lin DY**: Inference for capture-recapture experiments in continuous time with variable capture rates. *Biometrika* 83:477-483, 1996.
32. **Lin DY**, Robins JM, Wei LJ: Comparing two failure time distributions in the presence of dependent censoring. *Biometrika* 83:381-393, 1996.
33. Spiekerman CF, **Lin DY**: Checking the marginal Cox model for correlated failure time data. *Biometrika* 83:143-156, 1996.
34. **Lin DY**, Shen L, Ying Z, Breslow NE: Group sequential designs for monitoring survival probabilities. *Biometrics* 52:1033-1041, 1996.
35. DeGruttola V, Fleming TR, **Lin DY**, Coombs R: Validating surrogate markers: Are we being naive? *Journal of Infectious Diseases* 175:237-246, 1997.
36. **Lin DY**: Nonparametric inference for cumulative incidence functions in competing-risks studies. *Statistics in Medicine* 16:901-910, 1997.
37. **Lin DY**, Feuer EJ, Etzioni R, Wax Y: Estimating medical costs from incomplete follow-up data. *Biometrics* 53:419-434, 1997.
38. **Lin DY**, Fleming TR, DeGruttola V: Estimating the proportion of treatment effect explained by a surrogate marker. *Statistics in Medicine* 16:1515-1527, 1997.
39. Deeg HJ, **Lin DY**, Leisenring W, Boeckh M, Anasetti C, Appelbaum FR, Chauncey TR, Doney K, Flowers M, Martin P, Nash R, Schoch G, Sullivan KM, Whitherspoon RP, Storb R: Cyclosporine or cyclosporine plus methylprednisolone for prophylaxis of graft-versus-host disease: a prospective randomized trial. *Blood* 89:3880-3887, 1997.

40. Heckbert SR, Weiss NS, Koepsell TD, Lemaitre RN, Smith NL, Siscovick DS, **Lin DY**, Psaty BM: Duration of estrogen replacement therapy in relation to the risk of incident myocardial infarction in postmenopausal women. *Archives of Internal Medicine* 157:1330-1336, 1997.
41. Schwartz SM, Siscovick DS, Longstreth WT, Psaty BM, Beverly RK, Raghunathan TE, **Lin DY**, Koepsell TD: Use of low-dose oral contraceptives and stroke in young women. *Annals of Internal Medicine* 127:596-603, 1997.
42. **Lin DY**, Oakes D, Ying Z: Additive hazards regression with current status data. *Biometrika* 85:289-298, 1998.
43. **Lin DY**, Psaty BM, Kronmal RA: Assessing the sensitivity of regression results to unmeasured confounders in observational studies. *Biometrics* 54:948-963, 1998.
44. **Lin DY**, Wei LJ, Ying Z: Accelerated failure time models for counting processes. *Biometrika* 85:605-618, 1998.
45. Spiekerman CF, **Lin DY**: Marginal regression models for multivariate failure time data. *Journal of the American Statistical Association* 93:1164-1175, 1998.
46. Albert JM, Ioannidis JPA, Reichelderfer P, Conway B, Coombs RW, Crane L, DeMasi R, Dixon DO, Flandre P, Hughes MD, Kalish L, Larntz K, **Lin DY**, et al: Statistical issues for HIV surrogate endpoints: Point/counterpoint. *Statistics in Medicine* 17:2435-2462, 1998.
47. **Lin DY**, Arbogast P, Siscovick DS, Lemaitre RN: Poisson regression with missing durations of exposure. *Biometrics* 55:252-257, 1999.
48. **Lin DY**, Yip PSF: Parametric regression models for continuous-time removal and recapture studies. *Journal of the Royal Statistical Society, Series B* 61:401-411, 1999.
49. **Lin DY**, Sun W, Ying Z: Nonparametric estimation of the gap time distributions for serial events with censored data. *Biometrika* 86:59-70, 1999.
50. Fisher LD, **Lin DY**: Time-dependent covariates in the Cox proportional hazards regression model. *Annual Review of Public Health* 20:145-157, 1999.
51. Diehr P, Yanez D, Ash A, Hombrook M, **Lin DY**: Methods for analyzing health care utilization and costs. *Annual Review of Public Health* 20:125-144, 1999.
52. Psaty BM, Koepsell TD, **Lin DY**, Weiss NS, Siscovick DS, Rosendaal FR, Pahor M, Furberg CD: Assessment and control for confounding by indication in observational studies. *Journal of the American Geriatrics Society* 47:749-754, 1999.
53. Lemaitre RN, Siscovick DS, Raghunathan TE, Weinmann S, Arbogast P, **Lin DY**: Leisure-time physical activity and the risk of primary cardiac arrest. *Archives of Internal Medicine* 159:686-690, 1999.
54. **Lin DY**, Yao Q, Ying Z: A general theory on stochastic curtailment for censored survival data. *Journal of the American Statistical Association* 94:510-521, 1999.
55. Psaty BM, Weiss NS, Furberg CD, Koepsell TD, Siscovich DS, Rosendaal FR, Smith NL, Heckbert SR, Kaplan RC, **Lin DY**, Fleming TR, Wagner EH: Surrogate endpoints, health outcomes, and the drug-approval process for the treatment of risk factors for cardiovascular diseases. *Journal of the American Medical Association* 282:786-790, 1999.
56. Etzioni RD, Feuer EJ, Sullivan SD, **Lin DY**, Hu C, Ramsey SD: On the use of survival analysis techniques to estimate medical care costs. *Journal of Health Economics* 18:365-380, 1999.
57. Yip PSF, Zhou Y, **Lin DY**, Fang XZ: Estimation of population size based on additive hazards models for continuous-time recapture experiments. *Biometrics* 55:904-908, 1999.
58. Kulich M, **Lin DY**: Additive hazards regression with covariate measurement error. *Journal of the American Statistical Association* 95: 238-248, 2000.
59. **Lin DY**: Linear regression analysis of censored medical costs. *Biostatistics* 1:35-47, 2000.
60. **Lin DY**: On fitting Cox's proportional hazards models to survey data. *Biometrika* 87:37-47, 2000.
61. Kulich M, **Lin DY**: Additive hazards regression for case-cohort studies. *Biometrika* 87:73-87, 2000.
62. Ghosh D, **Lin DY**: Nonparametric analysis of recurrent events and death. *Biometrics* 56:554-562, 2000.
63. **Lin DY**: Proportional means regression for censored medical costs. *Biometrics* 56:775-778, 2000.
64. **Lin DY**, Wei LJ, Yang I, Ying Z: Semiparametric regression for the mean and rate functions of recurrent events. *Journal of the Royal Statistical Society, Series B* 62:711-730, 2000.
65. Fleming TR, **Lin DY**: Survival analysis in clinical trials: past developments and future directions. *Biometrics* 56:971-983, 2000 (Editors' Invited Paper).

66. Siscovick DS, Raghunathan TE, **Lin DY**, Weinmann S, Arbogast P, Lemaitre RV, Psaty BM, Alexander R, Cobb L: Influenza vaccination and the risk of primary cardiac arrest. *American Journal of Epidemiology* 152:674-677, 2000.
67. **Lin DY**, Ying Z: Semiparametric and nonparametric regression analysis of longitudinal data (with discussion). *Journal of the American Statistical Association* 96:103-126, 2001 (Editor's Invited Paper for the 2000 Joint Statistical Meetings).
68. **Lin DY**, Ying Z: Nonparametric tests for the gap time distributions of serial events based on censored data. *Biometrics* 57:369-375, 2001.
69. **Lin DY**, Wei LJ, Ying Z: Semiparametric transformation models for point processes. *Journal of the American Statistical Association* 96:620-628, 2001.
70. Willan AR, **Lin DY**: Incremental net benefit in randomized clinical trials. *Statistics in Medicine* 20:1563-1574, 2001.
71. Whitsel EA, Raghunathan TE, Pearce RM, **Lin DY**, Rautaharju PM, Lemaitre R, Siscovick DS: RR interval variation, the QT interval index and risk of primary cardiac arrest among patients without clinically recognized heart disease. *European Heart Journal* 22:165-173, 2001.
72. Heckbert SR, Kaplan RC, Weiss NS, Psaty BM, **Lin DY**, Furberg CD, Starr JR, Anderson GD, LaCroix AZ: Risk of recurrent coronary events in relation to use and recent initiation of postmenopausal hormone therapy. *Archives of Internal Medicine* 161:1709-1713, 2001.
73. Rea TD, Heckbert SR, Kaplan RC, Psaty BM, Smith NL, Lemaitre RN, **Lin DY**: Body mass index and the risk of recurrent coronary events following acute myocardial infarction. *American Journal of Cardiology* 88:467-472, 2001.
74. **Lin DY**, Wei LJ, Ying Z: Model-checking techniques based on cumulative residuals. *Biometrics* 58:1-12, 2002.
75. Arbogast PG, **Lin DY**, Siscovick DS, Schwartz SM: Estimating incidence rates from population-based case-control studies in the presence of nonrespondents. *Biometric Journal* 44:227-239, 2002.
76. Ghosh D, **Lin DY**: Marginal regression models for recurrent and terminal events. *Statistica Sinica* 12: 663-688, 2002.
77. Hu C, **Lin DY**: Cox regression with covariate measurement error. *Scandinavian Journal of Statistics* 29: 637-655, 2002.
78. Willan AR, **Lin DY**, Cook RJ, Chen EB: Using inverse-weighting in cost-effectiveness analysis with censored data. *Statistical Methods in Medical Research* 11: 539-551, 2002.
79. Lemaitre RN, Siscovick DS, Psaty BM, Pearce RM, Raghunathan TE, Whitsel EA, Weinmann SA, Anderson GD, **Lin DY**: Inhaled Beta-2 adrenergic receptor agonists and primary cardiac arrest. *American Journal of Medicine* 113: 711-716, 2002.
80. Willan AR, Chen EB, Cook RJ, **Lin DY**: Incremental net benefit in randomized clinical trials with quality-adjusted survival. *Statistics in Medicine* 22: 353-363, 2003.
81. **Lin DY**: Regression analysis of incomplete medical cost data. *Statistics in Medicine* 22: 1181-1200, 2003.
82. **Lin DY**, Ying Z: Semiparametric regression analysis of longitudinal data with informative drop-outs. *Biostatistics* 4: 385-398, 2003.
83. Jin Z, **Lin DY**, Wei LJ, Ying Z: Rank-based inference for the accelerated failure time model. *Biometrika* 90: 341-353, 2003.
84. Ghosh D, **Lin DY**: Semiparametric analysis of recurrent events data in the presence of dependent censoring. *Biometrics* 59: 877-885, 2003.
85. Rea TD, Siscovick DS, Psaty BM, Pearce RM, Raghunathan TE, Whitsel EA, Cobb LA, Weinmann S, Anderson GD, Arbogast P, **Lin DY**: Digoxin therapy and the risk of primary cardiac arrest in patients with congestive heart failure: Effect of mild-moderate renal impairment. *Journal of Clinical Epidemiology* 56: 646-650, 2003.
86. Combes B, Luketic VA, Peters MG, Zetterman RK, Garcia-Tsao G, Munoz SJ, **Lin DY**, Flye N, Carithers RL: Prolonged follow-up of patients in the U.S. multicenter trial of ursodeoxycholic acid for primary biliary cirrhosis. *American Journal of Gastroenterology* 99: 264-268, 2004.
87. **Lin DY**: Haplotype-based association analysis in cohort studies of unrelated individuals. *Genetic Epidemiology* 26: 255-264, 2004.

88. Hu C, **Lin DY**: Semiparametric failure time regression with replicates of mismeasured covariates. *Journal of the American Statistical Association* 99: 105-118, 2004.
89. Kulich M, **Lin DY**: Improving the efficiency of relative-risk estimation in case-cohort studies. *Journal of the American Statistical Association* 99: 832-844, 2004.
90. **Lin DY**, Zou F: Assessing genomewide statistical significance in linkage studies. *Genetic Epidemiology* 27: 202-214, 2004.
91. Diao G, **Lin DY**, Zou F: Mapping quantitative trait loci with censored observations. *Genetics* 168: 1689-1698, 2004. PMID: PMC1448809.
92. Zou F, Fine JP, Hu J, **Lin DY**: An efficient resampling method for assessing genomewide statistical significance in mapping quantitative trait loci. *Genetics* 168: 2307-2316, 2004. PMID: PMC1448705.
93. Arbogast PG, **Lin DY**: Goodness-of-fit methods for matched case-control studies. *Canadian Journal of Statistics* 32: 373-386, 2004.
94. Arbogast PG, **Lin DY**: Model-checking techniques for stratified case-control studies. *Statistics in Medicine* 24: 229-247, 2005.
95. Zeng D, **Lin DY**: Estimating haplotype-disease associations with pooled genotype data. *Genetic Epidemiology* 28: 70-82, 2005.
96. Willan AR, **Lin DY**, Manca A: Regression methods for cost-effectiveness analysis with censored data. *Statistics in Medicine* 24: 131-145, 2005.
97. Diao G, **Lin DY**: A powerful and robust method for mapping quantitative trait loci in general pedigrees. *American Journal of Human Genetics* 77: 97-111, 2005.
98. Zeng D, **Lin DY**, Yin G: Maximum likelihood estimation for the proportional odds model with random effects. *Journal of the American Statistical Association* 100: 470-483, 2005.
99. **Lin DY**: An efficient Monte Carlo approach to assessing statistical significance in genomic studies. *Bioinformatics* 21: 781-787, 2005.
100. Whitsel EA, Boyko EJ, Rautaharju PM, Raghunathan TE, **Lin DY**, Pearce RM, Weinmann SA, Siscovick DS: Electrocardiographic QT interval prolongation and risk of primary cardiac arrest in diabetic patients. *Diabetes Care* 28: 2045-2047, 2005.
101. **Lin DY**: On rapid simulation of p-values in association studies. *American Journal of Human Genetics* 77: 513-514, 2005. PMID: PMC1226216.
102. Diao G, **Lin DY**: Semiparametric methods for mapping quantitative trait loci with censored data. *Biometrics* 61: 789-798, 2005.
103. Pan Z, **Lin DY**: Goodness-of-fit methods for generalized linear mixed models. *Biometrics* 61: 1000-1009, 2005.
104. **Lin DY**, Zeng D, Millikan R: Maximum likelihood estimation of haplotype effects and haplotype-environment interactions in association studies. *Genetic Epidemiology* 29: 299-312, 2005.
105. Jin Z, **Lin DY**, Ying Z: Rank regression analysis of multivariate failure time data based on marginal linear models. *Scandinavian Journal of Statistics* 33: 1-23, 2006.
106. **Lin DY**: Evaluating statistical significance in two-stage genomewide association studies. *American Journal of Human Genetics* 78: 505-509, 2006. PMID: PMC1380293.
107. Diao G, **Lin DY**: Improving the power of association tests for quantitative traits in family studies. *Genetic Epidemiology* 30: 301-313, 2006.
108. Jin Z, **Lin DY**, Ying Z: On least-squares regression with censored data. *Biometrika* 93: 147-161, 2006.
109. **Lin DY**, Zeng D: Likelihood-based inference on haplotype effects in genetic association studies (with discussion). *Journal of the American Statistical Association* 101: 89-118, 2006.
110. Zeng D, **Lin DY**: Efficient estimation of semiparametric transformation models for counting processes. *Biometrika* 93: 627-640, 2006.
111. Zeng D, **Lin DY**, Avery CL, North KE, Bray MS: Efficient semiparametric estimation of haplotype-disease associations in case-cohort and nested case-control studies. *Biostatistics* 7: 486-502, 2006.
112. Diao G, **Lin DY**: Semiparametric variance-component models for linkage and association analyses of censored trait data. *Genetic Epidemiology* 30: 570-581, 2006.
113. Lange LA, Carlson CS, Hindorff LA, Lange EM, Walston J, Durda JP, Cushman M, Bis JC, Zeng D, **Lin DY**, Kuller LH, Nickerson DA, Psaty BM, Tracy RP, Reiner AP: Association of polymorphisms in the

- CRP gene with circulating c-reactive protein levels and cardiovascular events. *Journal of the American Medical Association* 296: 2703-2711, 2006.
114. **Lin DY**, Huang BE: The use of inferred haplotypes in downstream analyses. *American Journal of Human Genetics* 80: 577-579, 2007. PMID: PMC1821109.
 115. Huang BE, **Lin DY**: Efficient association mapping of quantitative trait loci with selective genotyping. *American Journal of Human Genetics* 80: 567-576, 2007. PMID: PMC1821103.
 116. Zeng D, **Lin DY**: Semiparametric transformation models with random effects for recurrent events. *Journal of the American Statistical Association* 102: 167-180, 2007.
 117. Zeng D, **Lin DY**: Maximum likelihood estimation in semiparametric regression models with censored data (with discussion). *Journal of the Royal Statistical Society, Series B* 69: 507-564, 2007.
 118. **Lin DY**: On the Breslow estimator. *Lifetime Data Analysis* 13: 471-480, 2007.
 119. Huang BE, Amos CI, **Lin DY**: Detecting haplotype effects in genomewide association studies. *Genetic Epidemiology* 31: 803-812, 2007.
 120. Zeng D, **Lin DY**: Efficient estimation for the accelerated failure time model. *Journal of the American Statistical Association* 102:1387-1396, 2007.
 121. Zeng D, **Lin DY**, Lin X: Semiparametric transformation models with random effects for clustered failure time data. *Statistica Sinica* 18: 355-377, 2008. PMID: PMC2756664.
 122. **Lin DY**, Hu Y, Huang BE: Simple and efficient analysis of disease association with missing genotype data. *American Journal Human Genetics* 82: 444-452, 2008. PMID: PMC2427170.
 123. Johnson BA, **Lin DY**, Zeng Z: Penalized estimating functions and variable selection in semiparametric regression models. *Journal of the American Statistical Association* 103: 672-680, 2008. PMID: PMC2850080.
 124. Zeng D, **Lin DY**: Efficient resampling methods for non-smooth estimating functions. *Biostatistics* 9: 355-363, 2008. PMID: PMC2673016.
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 205. Wojcik GL*, Graff M*, Nishimura KK*, Tao R*, Haessler J*, Gignoux CR*, Highland HM*, Patel YM*, Sorokin EP, Avery CL, Belbin GM, Bien SA, Cheng I, Cullina S, Hodonsky CJ, Hu Y, Huckins LM, Jeff J, Justice AE, Kocarnik JM, Lim U, Lin BM, Lu Y, Nelson SC, Park SSL, Poisner H, Preuss MH, Richard MA, Schurmann C, Setiawan VW, Sockell A, Vahi K, Verbanck M, Vishnu A, Walker RW, Young KL, Zubair N, Acuna-Alonso V, Ambite JL, Barnes KC, Boerwinkle E, Bottinger E, Bustamante CD, Caberto C, Canizales-Quintero S, Conomos MP, Deelman E, Do R, Doheny K, Fernandez-Rhodes L, Fornage M, Hailu B, Heiss G, Henn B, Hindorff LA, Jackson RD, Laurie CA, Laurie CC, Li Y, **Lin**

- DY**, Moreno-Estrada A, Nadkarni G, Norman PJ, Pooler LC, Reiner AP, Romm J, Sabati C, Sandoval K, Sheng X, Stahl EA, Stram DO, Thornton TA, Wassel CL, Wilkens LR, Winkler CA, Yoneyama S, Buyske S, Haiman CA, Kooperberg C, Le Marchand L, Loos RJF, Matise TC, North KE, Peters U, Kenny EE, Carlson CS: Genetic analyses of diverse populations improves discovery for complex traits. *Nature* 570: 514-518, 2019. *shared first authorship (Dr. Tao is Dr. Lin's Ph.D. student.). NIHMS1036898.
206. Raulerson CK, Ko A, Kidd JC, Currin KW, Brotman SM, Cannon ME, Wu Y, Spracklen CN, Jackson AU, Stringham HM, Welch RP, Fuchsberger C, Locke AE, Narisu N, Lusi AJ, Civelek M, Furey TS, Kuusisto J, Collins FS, Boehnke M, Scott LJ, **Lin DY**, Love MI, Laakso M, Pajukanta P, Mohlke KL: Adipose tissue gene expression associations reveal hundreds of candidate genes for cardiometabolic traits. *American Journal of Human Genetics* 105: 773-787, 2019.
207. Gao F, Zeng D, Couper D, **Lin DY**: Semiparametric regression analysis of multiple right- and interval-censored events. *Journal of the American Statistical Association* 114: 1232-1240, 2019. PMID: PMC6777710.
208. Deng Q, Bai X, Liu D, Roy D, Ying Z, **Lin DY**: Power and sample size for dose-finding studies with survival endpoints under model uncertainty. *Biometrics* 75: 308-314, 2019. PMID: PMC6411454.
209. Palace J, **Lin DY**, Zeng D, Majed M, Elson L, Hamid S, Messina S, Misu T, Sagen J, Whittam D, Yoshiki T, Leite MI, Weinshenker B, Cabre P, Jacob A, Nakashima I, Fujihara K, Pittock SJ: Outcome prediction models in AQP4-IgG positive neuromyelitis optica spectrum disorders. *Brain* 142: 1310-1323, 2019. PMID: PMC6487334
210. Little PL, **Lin DY**, Sun W: Associating somatic mutations to clinical outcomes: a pan-cancer study of survival time. *Genome Medicine* 11: 37, 2019. PMID: PMC6540540.

IN-PRESS ARTICLES

211. Wong KY, Zeng D, **Lin DY**: Robust score tests with missing data in genomics studies. *Journal of the American Statistical Association* doi: 10.1080/01621459.2018.1514304. NIHMS995801.
212. McCabe SD, **Lin DY**, Love ML: Consistency and overfitting of multi-omics methods on experimental data. *Briefings in Bioinformatics* doi: 10.1093/bib/bbz070. PMC Journal – In Process.
213. Tao R, Zeng D, **Lin DY**: Optimal designs of two-phase studies. *Journal of the American Statistical Association*.
214. Zeng D, Pan Z, **Lin DY**: Design and analysis of bridging studies with prior probabilities on the null and alternative hypotheses. *Biometrics*.

SUBMITTED MANUSCRIPTS

215. Zeng D, Kosorok MR, **Lin DY**: Nonparametric maximum likelihood estimation in linear regression with unknown transformation.
216. Wang J, Zeng D, **Lin DY**: Semiparametric single-index models for optimal treatment regimens with censored outcomes.
217. **Lin DY**, Zeng D, Couper D: A general framework for integrative analysis of incomplete multi-omics data.
218. Wong KY, Zeng D, **Lin DY**: Variable selection for multiple types of high-dimensional features with missing data.
219. Wang R, **Lin DY**, Jiang Y: SCOPE: a normalization and copy number estimation method for single-cell DNA sequencing.

BOOKS

220. **Lin DY**, Fleming TR: *Proceedings of the First Seattle Symposium in Biostatistics: Survival Analysis*. Springer-Verlag, 1997.
221. **Lin DY**, Heagerty P: *Proceedings of the Second Seattle Symposium in Biostatistics: Analysis of Correlated Data*. Springer-Verlag, 2004.

OTHER PUBLICATIONS (PROCEEDINGS, DISCUSSIONS, BOOK CHAPTERS)

222. Brown MB, **Lin DY**, Normolle DP, Herzog AR: Models for and the effect of nonresponse in a survey of

- the noninstitutionalized elderly. In *The 1988 Proceedings of the Section on Survey Research Methods of the American Statistical Association*, 1988, pp. 615-620.
223. **Lin DY**, Wei LJ: Discussion of C Jennison and BW Turnbull, “Interim analyses: the repeated confidence interval approach.” *Journal of the Royal Statistical Society, Series B* 51:347-348, 1989.
224. **Lin DY**, Wei LJ: Discussion of JH Ware, “Investigating therapies of potentially great benefit: ECMO.” *Statistical Science* 4:324-325, 1989.
225. **Lin DY**, Wei LJ: Discussion of A Agresti, “A survey of exact inference for contingency tables.” *Statistical Science* 7:166-167, 1992.
226. **Lin DY**: Multivariate failure time data. In *Recent Advances in the Designs and Analysis of Clinical Trials*. P. Thall, ed., pp. 73-93, 1995. Kluwer Academic Publishers.
227. **Lin DY**: Marginal models for multivariate survival data. In *Encyclopedia of Biostatistics*. P. Armitage, T. Colton, eds., pp. 2407-2412, 1998. John Wiley & Sons.
228. **Lin DY**, Ying Z: Additive hazards regression models for survival data. In *Proceedings of the First Seattle Symposium in Biostatistics: Survival Analysis*. D.Y. Lin, T.R. Fleming, eds., pp. 185-198, 1997. Springer-Verlag.
229. **Lin DY**, Kronmal RA, Psaty BM: Reply to the letter to the editor. *Biometrics* 55: 990, 1999.
230. **Lin DY**: Survival analysis. In *Advanced Medical Statistics*. Y. Lu, J. Q. Fan, eds., pp. 815-835, 2003. World Scientific Publishing Co.
231. **Lin DY**: A note on permutation tests in multistage association scans – Reply to Dudbridge. *American Journal of Human Genetics* 78: 1096, 2006.
232. Elston RC, **Lin DY**, Zheng G: Multi-stage sampling for genetic studies. *Annual Review of Genomics and Human Genetics* 8: 327-342, 2007.
233. Zeng D, **Lin DY**: Discussion of P. Diggle, D. Farewell and R. Henderson, “Analysis of longitudinal data with drop-out: objectives, assumptions and a proposal.” *Journal of the Royal Statistical Society, Series C* 56: 544-545, 2007.
234. **Lin DY**, Huang BE: The use of inferred haplotypes in downstream analysis – Reply to P. Kraft and D.O. Stram. *American Journal of Human Genetics* 81: 865-866, 2007.
235. Gijbels I, **Lin DY**, Ying Z: Non- and semi-parametric analysis of failure time data with missing failure indicators. In *Complex Datasets and Inverse Problems*. R. Liu, W. Strawderman, C.H. Zhang, eds., pp. 203-223, 2007, IMS Lecture Notes – Monograph Series, Ohio.
236. Marchenko YV, Carroll RJ, **Lin DY**, Amos CI: Semiparametric analysis of case-control genetic data in the presence of environmental factors. *STATA Journal* 8: 305-333, 2008.
237. **Lin DY**, Hu Y: Reply to Marchini and Howie. *American Journal of Human Genetics* 83: 539-540, 2008. PMID: PMC2561930.
238. **Lin DY**: Genetic association analysis. In *Encyclopedia of Clinical Trials*. R. D’Agostino, L. Sullivan, J. Massaro, eds., 2008. John Wiley & Sons.
239. **Lin DY**: Transformation models. In *Handbook of Survival Analysis*. J. P. Klein, H. C. van Houwelingen, J. G. Ibrahim, T. H. Scheike, eds., 2014. Chapman and Hall.
240. **Lin DY**: Discussion of the paper by R. L. Prentice and Y. Huang: Optimal designs and efficient inference for biomarker studies. *Statistical Theory and Related Fields* 2: 21-22, 2018.
241. Zeng D, **Lin DY**: Maximum likelihood estimation for case-cohort and nested case-control studies. In *Handbook of Statistical Methods for Case-Control Studies*. Ø. Borgan, N. Breslow, N. Chatterjee, M. H. Gail, A. Scott, C. J. Wild, eds., pp. 391-404, 2018. Chapman and Hall/CRC.
242. Diao G, Zeng D, **Lin DY**: Analysis of secondary phenotype data under case-control designs. In *Handbook of Statistical Methods for Case-Control Studies*. Ø. Borgan, N. Breslow, N. Chatterjee, M. H. Gail, A. Scott, C. J. Wild, eds., pp. 515-528, 2018. Chapman and Hall/CRC.
243. **Lin DY**: Review of the book “*The Statistical Analysis of Multivariate Failure Time Data: A Marginal Modeling Approach*” by R. L. Prentice and S. Zhao. *Biometrics* 75: 1416-1417, 2019.

INVITED PRESENTATIONS IN CONFERENCES

1. “Sequential log rank tests adjusting for covariates with the accelerated life model.” The International Biometric Society ENAR Spring Meeting, Houston, TX, 1991.

2. "Evaluating the role of CD4 change as a surrogate endpoint in AIDS clinical trials." The International Biometric Society WNAR Meeting, Santa Barbara, CA, 1991.
3. "Analysis of the accelerated failure time model." (Short Course) The 46th Annual Conference on Applied Statistics, Atlantic City, NJ, 1990.
4. "Regression analysis of multivariate failure time data." (Short Course) The 49th Annual Conference on Applied Statistics, Atlantic City, NJ, 1993.
5. "Cox regression analysis with incomplete covariate measurements." Joint Statistical Meetings, San Francisco, CA, 1993.
6. "Semiparametric analysis of general hazard-based survival models." The International Biometric Society ENAR Spring Meeting, Cleveland, OH, 1994.
7. "Checking the marginal Cox model for correlated failure time data." International Research Conference on Lifetime Data Models in Reliability and Survival Analysis, Boston, MA, 1994.
8. "Monitoring medical studies with survival endpoints." Third World Congress of the Bernoulli Society and 57th Annual Meeting of the Institute of Mathematical Statistics, Chapel Hill, NC, 1994.
9. "Analysis of multivariate failure time data: Marginal modeling approaches." XVIIth International Biometric Conference, Hamilton, Canada, 1994.
10. "On modeling the marginal distributions of multivariate failure times." The International Biometric Society ENAR Spring Meeting, Birmingham, AL, 1995.
11. "On the analysis of competing risks data." Harvard School of Public Health/Schering-Plough Workshop on Biostatistical Perspectives in Clinical and Pharmaceutical Research. Boston, MA, 1995.
12. "Analysis of multiple events data." (Short Course) ICSA 1997 Applied Statistics Symposium, Rutgers University, NJ, 1997.
13. "Estimating the proportion of treatment effect explained by a surrogate marker." Joint Statistical Meetings, Anaheim, CA, 1997.
14. "Checking the adequacy of semiparametric regression models for current status data." The International Biometric Society ENAR Spring Meeting, Pittsburgh, PA, 1998.
15. "An update on semiparametric additive hazards regression." and "Nonparametric inferences for the gap time distributions of serial events." Workshop on Event History Analysis. Montreal, Canada, 1998.
16. "Additive hazards regression for censored data." IVth Taipei International Statistical Symposium, Taipei, Taiwan, 1998.
17. "Regression analysis of censored medical costs." The International Biometric Society ENAR Spring Meeting, Chicago, IL, 2000.
18. "Semiparametric failure-time regression with mismeasured or missing covariates." The International Biometric Society ENAR Spring Meeting, Charlotte, NC 2001.
19. "Regression analysis of incomplete medical cost data." 22nd Annual Conference of the International Society for Clinical Biostatisticians, Stockholm, Sweden, 2001.
20. "Censoring and cost-effectiveness analysis." The International Biometric Society ENAR Spring Meeting, Arlington, VA, 2002.
21. "Analysis of multivariate failure time data." INSERM Workshop, La Londe-Les-Maures, France, 2004.
22. "Checking the Cox proportional hazards model with cumulative sums of martingale residuals." INSERM workshop, La Londe-Les-Maures, France, 2004.
23. "Maximum likelihood estimation in transformation models for counting processes." Joint Statistical Meetings, Toronto, Canada, 2004.
24. "Analysis of multivariate failure time data." (short course) FDA/Industry Workshop, Washington, D.C., 2004.
25. "Efficient semiparametric estimation of haplotype-disease association in cohort studies." Joint Statistical Meetings, Minneapolis, MN, 2005.
26. "Maximum likelihood estimation in semiparametric models with censored data." Workshop on Statistical Analysis of Complex Event History Data, Oslo, Norway, 2005.
27. "Statistical analysis of haplotype-disease association." Joint Statistical Meetings, Seattle, WA, 2006.
28. "Semiparametric transformation models with random effects for highly stratified survival data." Joint Statistical Meetings, Seattle, WA, 2006.
29. "Analysis of multivariate failure time data." (short course) Joint Statistical Meetings, Seattle, WA, 2006.

30. "Maximum likelihood estimation in semiparametric regression models with censored data." 12th Army Conference on Applied Statistics, RTP, NC, 2006.
31. "Maximum likelihood estimation in semiparametric regression models with censored data." Ordinary Meeting, Royal Statistical Society, London, Great Britain, 2007.
32. "Likelihood-based inference on haplotype-disease association." The International Biometric Society ENAR Spring Meeting, Atlanta, 2007.
33. "Statistical analysis of haplotype-disease associations using HAPSTAT." (tutorial) The International Biometric Society ENAR Spring Meeting, Atlanta, 2007.
34. "Analysis of multivariate failure time data." (short course) ICSA 2007 Applied Statistics Symposium, Raleigh, NC.
35. "Analysis of censored data." (short course) Joint Statistical Meetings, Salt Lake City, 2007.
36. "HAPSTAT: Statistical analysis of haplotype-disease association." Interface 2008, Durham, North Carolina, 2008.
37. "Analysis of multivariate failure time data." (short course) Joint Statistical Meetings, Denver, Colorado, 2008.
38. "Estimating genetic effects and gene-environment interactions with missing data." The International Biometric Society ENAR Spring Meeting, San Antonio, 2009.
39. "Survival analysis in clinical trials." ASA LearnSTAT course, Teaneck, NJ, 2009.
40. "Meta-analysis: Summary statistics vs. original data." Biostatistics 50/60 Anniversary Conference, University of Michigan, 2009.
41. "Statistical issues in genomewide association studies." Biostatistics 60th Anniversary Conference, UNC, 2009.
42. "Maximum likelihood estimation in semiparametric regression models with censored data." International Biostatistics Conference, Hefei, China, 2009.
43. "Estimating genetic effects and gene-environment interactions with missing data." Joint Statistical Meetings, Vancouver, Canada, 2010.
44. "Predictive accuracy of covariates for event times." The International Biometric Society ENAR Spring Meeting, Miami, FL, 2011.
45. "Survival analysis with incomplete genetic data." Workshop on Analysis of Survival and Event History Data, Montreal, Canada, 2011.
46. "Statistical analysis of recurrent event data." ICSA 2011 Applied Statistics Symposium, NYC, 2011.
47. "Statistical issues in the analysis of disease association with next-generation sequence data", Joint Statistical Meetings, Miami Beach, FL, 2011.
48. "Ross Prentice's contributions to statistical science." Prentice Symposium, Seattle, WA, 2011.
49. "A general framework for detecting disease associations with rare variants in sequencing studies." Annual Meeting of International Genetic Epidemiology Society, Heidelberg, Germany, 2011 (platform presentation).
50. "Quantitative trait analysis in the NHLBI Exome Sequencing Project." Annual Meeting of the American Society of Human Genetics, Montreal, Canada, 2011 (platform presentation).
51. "A general framework for detecting disease associations with rare variants in sequencing studies," RTP Statistical Genetics Conference, 2011.
52. "Quantitative trait analysis under trait-dependent sampling," The International Biometric Society ENAR Spring Meeting, Washington, DC, 2012.
53. "Variable selection in meta-analysis of high-dimensional genetic data," Joint Statistical Meetings, San Diego, CA, 2012.
54. "Designs and analysis of sequencing studies with trait-dependent sampling," The International Biometric Society ENAR Spring Meeting, Orlando, FL, 2013.
55. "Survival analysis in clinical trials," (short course). The International Biometric Society ENAR Spring Meeting, Orlando, FL, 2013.
56. "Designs and analysis of sequencing studies with trait-dependent sampling," The Second Taihu International Statistics Forum, Wuxi, China, 2013.
57. "Nonparametric maximum likelihood estimation of semiparametric regression models with censored data," IMS-SWUFE International Conference on Statistics and Probability, Chengdu, China, 2013.

58. "Proportional means/rates models for the composite endpoint of recurrent and terminal events," Joint Statistical Meetings, Montreal, Canada, 2013.
59. "Statistical methods in genetic association studies," (short course) Joint Statistical Meetings, Montreal, Canada, 2013.
60. "Survival analysis in clinical trials," (short course) Food and Drug Administration, 2013.
61. "Analysis of recurrent event data in the presence of a terminal event," Paths to Precision Medicine, Harvard University, Boston, 2014.
62. "Analysis of recurrent event data," FDA/Advanced Statistics Workshop, Washington, DC, 2014.
63. "The magic of score statistics," The International Biometric Society ENAR Spring Meeting, Baltimore, MD, 2014.
64. "Efficient estimation of two-phase cohort studies," Joint Statistical Meetings, Boston, 2014.
65. "Meta-analysis: Is there an efficiency gain by using original data?" International Biostatistics Conference, Changchun, China, 2014.
66. "Some recent theoretical developments in meta-analysis," The 10th International Conference on Frontiers of Statistics, Beijing, China, 2015.
67. "Biomarker discovery and two-stage studies," The Fourth International Symposium on Biopharmaceutical Statistics, Beijing, China, 2015.
68. "Simultaneous inference on treatment effects in survival studies with factorial designs," ICSA China Statistics Conference, Shanghai, China, 2015.
69. "Genetic association analysis under complex survey sampling," Joint Statistical Meetings, Seattle, 2015.
70. "Recent theoretical developments in meta-analysis," The International Biometric Society ENAR Spring Meeting, Austin, TX, 2016.
71. "Maximum likelihood estimation for semiparametric regression models with interval-censored data," Joint Statistical Meetings, Chicago, IL, 2016.
72. "Maximum likelihood estimation for semiparametric regression models with interval-censored data," Duke-Industry Statistics Symposium, Durham, NC, 2016.
73. "Integrative association analysis of multiple genomics platforms," Joint Statistical Meetings, Baltimore, 2017.
74. "Designs and analysis of sequencing studies," Joint Statistical Meetings, Vancouver, Canada, 2018.
75. "Integrative analysis of incomplete multi-omics data," The International Biometric Society ENAR Spring Meeting, Philadelphia, PA, 2019.
76. "Semiparametric single-index models for optimal treatment regimens with censored outcomes," Duke-Industry Statistics Symposium, Durham, NC, 2019.
77. "Semiparametric regression analysis of interval-censored data," The Second Conference on Lifetime Data Science, Pittsburgh, PA, 2019.

SEMINARS (SINCE 2002)

1. "Assessment and selection of regression models," Harvard University, 2002.
2. "Assessment and selection of regression models," Columbia University, 2002.
3. "Assessment and selection of regression models," Memorial Sloan Kettering Cancer Center, 2002.
4. "Selection and assessment of regression models," University of Pittsburgh, 2003.
5. "Selection and assessment of regression models," University of Rochester, 2003.
6. "Likelihood-based inference on haplotype effects in genetic association studies," North Carolina State University, 2004.
7. "Maximum likelihood estimation of haplotype effects and haplotype-environment interactions in genetic association studies," George Washington University, 2005.
8. "A general theory for the maximum likelihood estimation in semiparametric models with censored data," University of Oslo, 2005.
9. "Maximum likelihood estimation of haplotype effects and haplotype-environment interactions in genetic association studies," John Hopkins University, 2005.
10. "Likelihood-based inference on haplotype effects in genetic association studies," Washington University in St. Louis, 2005.

11. "Maximum likelihood estimation of haplotype effects and haplotype-environment interactions in genetic association studies," National Institute of Environmental Sciences, 2006.
12. "Likelihood-based inference on haplotype effects in genetic association studies," Duke University, 2006.
13. "Likelihood-based inference on haplotype effects in genetic association studies," University of Washington, 2006.
14. "Analysis of haplotype-disease association," Albert Einstein College of Medicine, 2007.
15. "A general framework for estimating genetic effects and gene-environment interactions with missing data," University of Michigan, 2008.
16. "A general framework for estimating genetic effects and gene-environment interactions with missing data," Columbia University, 2009.
17. "Accounting for unknown population substructure in the statistical analysis of genome-wide association studies," Fred Hutchinson Cancer Research Center, 2010.
18. "Accounting for unknown population substructure in the statistical analysis of genome-wide association studies," Stanford University, 2010.
19. "Meta-analysis with summary statistics vs. individual level data, with applications to genome-wide association studies," University of Pennsylvania, 2010.
20. "Meta-analysis with summary statistics vs. individual level data, with applications to genome-wide association studies," Harvard University, 2011.
21. "Statistical methods for detecting disease associations with rare variants in sequencing studies," Case Western Reserve University, 2011.
22. "Statistical methods for detecting disease associations with rare variants in sequencing studies," Yale University, 2011.
23. "Quantitative trait analysis in sequencing studies under trait-dependent sampling," Emory University, 2012.
24. "Quantitative trait analysis in sequencing studies under trait-dependent sampling," Duke University, 2013.
25. "Public health, genetics, and statistics," East China Normal University, 2013.
26. "On random-effects meta-analysis," Harvard University, 2014.
27. "Meta-analysis: Is there an efficiency gain by using original data?" Peking University, 2014.
28. "Nonparametric maximum likelihood estimation of semiparametric regression models with censored data," Tsinghua University, 2014.
29. "Nonparametric maximum likelihood estimation of semiparametric regression models with censored data," Chinese Academy of Sciences, 2014.
30. "Nonparametric maximum likelihood estimation of semiparametric regression models with censored data," East China Normal University, 2014.
31. "Meta-analysis: Is there an efficiency gain by using original data?" University of Pennsylvania, 2015.
32. "Maximum likelihood estimation for semiparametric regression models with interval-censored data," Fred Hutchinson Cancer Research Center, 2016.
33. "Biostatistics: Research and training," Peking University, 2018.
34. "Biostatistics: Research and training," Tsinghua University, 2018.
35. "Design and analysis of two-phase studies, with applications to genetic association studies," Washington University in St Louis, 2018.

PH.D. DISSERTATION ADVISEES

Past:

Name	Year Completed	Institution of Employment
Charles Spiekerman	1995	University of Washington
Michal Kulich	1997	Charles University
Debashis Ghosh	2000	University of Colorado
Patrick Arbogast	2000	Vanderbilt University
Chengcheng Hu	2001	University of Arizona
Zhiying Pan	2005	Amgen
Guoqing Diao	2006	George Mason University

Emma Huang	2007	Janssen R&D
Li Chen	2009	University of Kentucky
Yijuan Hu	2011	Emory University
Q. Chad He	2012	Fred Hutchinson Cancer Research Center
Zhengzheng Tang	2014	University of Wisconsin
Lu Mao	2016	University of Wisconsin
Ran Tao	2016	Vanderbilt University
Alex Wong	2017	The Hong Kong Polytechnic University
Fei Gao	2017	Fred Hutchinson Cancer Research Center
Paul Little	2019	Fred Hutchinson Cancer Research Center
Jin Wang	2019	Genentech

Current:

Chong Jin, Sean McCabe, Rujin Wang, Bridget Lin, John Kidd, Hannan Yang, Yu Gu

PH.D. DISSERTATION COMMITTEES

Past:

Marcia Ciol, Michael Kosorok, Li Hsu, Yu Shen, Ben Wang, Yihui Zhang, William Bradley McNeney, Monika Peckova, Ying Zhang, Antonio Eduardo Gomes, James Lovato, Daniela Gobinelli, Bin Nan, Zoe Moodie, Shuguang Song, Douglas E. Schaubel, Lan Kong, Guosheng Yin, Xiaoli Liu, Hana Lee, Andrew Sterrett, Sangwook Kang, Sarah Nyante, Se-Hee Kim, Alison Wise

Current:

Vasyl Zhabotynsky, Heejoon Jo

CLASSROOM TEACHING

University of Washington:

BIOST 514 Biostatistics I, 1991, 1992, 1993
 BIOST 576 Survival Analysis Methods, 1994, 1995, 1996, 1998, 1999, 2000
 BIOST 578 Special Topics in Advanced Biostatistics: Monitoring Clinical Trials, 1991
 BIOST 578 Special Topics in Advanced Biostatistics: Survival Analysis, 1998

University of North Carolina:

BIOS 280 Theory and Methods of Survival Analysis, 2002, 2004, 2005
 BIOS 780 Theory and Methods of Survival Analysis, 2007, 2009, 2010, 2013, 2015, 2017, 2019
 BIOS 740 Statistical Methods in Genetic Association Studies, 2012
 BIOS 782 Statistical Methods in Genetic Association Studies, 2014, 2016, 2018

SERVICE

Biostatistics Search Committee (Chair), 2001 – 2002
 Statistical Genetics Search Committee, 2001 – 2003
 Graduate Studies Committee, 2001 – present
 Seminar Committee, 2001 – present
 BIT Committee, 2005 – present
 Promotion and Tenure Committee, School of Public Health, 2002 – 2006
 Faculty Council, University of North Carolina, 2003 – 2008
 Research Council, School of Public Health, 2006 – present
 Search Committee (Cancer Center Biostatistics), 2006 – 2007
 Search Committee (Statistical Genetics), 2006 – 2007
 Biostatistics Self-Study Committee, 2007 – 2008
 Biostatistics Retreat Committee, 2007 – 2008
 Junior Faculty Mentoring committees: Fei Zou (Chair), Hongtu Zhu (Chair), Amy Herring, Anastasia Ivanova, Michael Wu, Ethan Lange (Genetics), Yun Li (Genetics), Sun Wei (Chair), Di Wu (Periodontology), Yuchao Jiang (Chair), Michael Love (Chair)

Search Committee (Clinical Trials), 2008 – 2009
Search Committee (Statistical Genetics), 2008 – 2009
Search Committee (Chair, Infectious Diseases), 2010 – 2011
Search Committee (Chair, Statistical Genetics), 2013 – 2014
Search Committee (Chair), 2014 – 2015
Search Committee (Statistical Genetics), 2016 – 2017
Search Committee for the Chair of the Genetics Department, 2016 – 2017
Search Committee for the Assistant Chair of Biostatistics, 2017

RESEARCH GRANTS

R01 GM047845 08/01/92 – 05/31/20
(MERIT Award 08/01/05 – 07/31/15)

National Institute of General Medical Sciences

Semiparametric Analysis of Censored Data in Current Medical Studies

Role: Principal Investigator

This research intends to tackle new challenges in the analysis of event time data from cutting-edge medical research, including genomics studies, personalized medicine, post-approval surveillance for drug safety, and disease networks.

R01 HG009974 03/01/18 – 01/31/23
(formerly R01 CA082659, 04/01/00 – 01/31/18)

National Human Genome Research Institute

Statistical Methods in Trans-Omics Chronic Disease Research

Role: Principal Investigator

The proposed research intends to develop novel and high-impact statistical methods for integrative analysis of trans-omics data from ongoing precision medicine studies of chronic diseases. The goal is to facilitate the creation of a new era of medicine in which each patient receives individualized care that matches their genetic code.

R01 AI029168 08/01/89 – 04/30/24
(MERIT Award 05/01/99 – 04/30/09)

National Institute of Allergy and Infectious Diseases

Statistical Issues in AIDS Research

Role: Principal Investigator for Subcontract

This project addresses important issues in the statistical analysis of data from trials of interventions for treatment or prevention of HIV infection, continuing current work on methods for clinical trials of AIDS therapeutics and extending the work scope to the exploration of design and analysis issues in field trials of vaccines for prevention of HIV infection.

P01 CA142538 4/1/15 – 3/31/20

National Cancer Institute

Statistical Methods for Cancer Clinical Trials – Project 3: Statistical/Computational Methods for Pharmacogenomics and Individualized Therapy

Role: Project Leader

This research intends to develop novel and high-impact statistical and computational tools for discovering genetic variants associated with interindividual differences in the efficacy and toxicity of cancer medications and for optimizing drug therapy on the basis of each patient's genetic constitution.

P01 CA142538 4/1/15 – 3/31/20

National Cancer Institute

Statistical Methods for Cancer Clinical Trials – Core A: Administrative Core

Role: Core contributor

The Administrative Core will provide essential administrative and scientific leadership, coordinating the

investigators across three institutions into an effective team and facilitating integration of project research, effective dissemination of research results, and management of resources and logistics.

P01 CA142538

4/1/15 – 3/31/20

National Cancer Institute

Statistical Methods for Cancer Clinical Trials – Core B: Computational Resources and Dissemination Core

Role: Core Director

To facilitate the acceptance and usage of new methods by the cancer research community, it is essential that the methods be evaluated rigorously and implemented in professional, robust, user-friendly software. Documentation and demonstrations of new software must be readily available to researchers and accessible to users with different backgrounds and experience levels. The Computational Resources and Dissemination Core (Core B) will be responsible for the critical functions required to achieve these objectives.

U01 DE025046

9/10/15 – 8/31/20

National Institute of Dental & Cranofacial Research

Genome-Wide Association Study of Early Childhood Caries

Role: Co-Investigator

This genome-wide association study of early childhood caries will enroll a multi-ethnic, community-based sample of 6,000 children ages 3 and 4 attending Head Start/Early Head Start programs in North Carolina. Dental caries data will be determined by study examiners using the International Caries Diagnosis System. DNA will be extracted from saliva samples and genotyped using high-density genotyping, imputation to 1000 Genomes Project reference panels and advanced statistical approaches to leverage differences in genetic structure between racial/ethnic groups.

R01 HL143885

4/1/19 – 3/31/23

National Heart, Lung and Blood Institute

Leveraging Multi-Omics Approaches to Examine Metabolic Challenges of Obesity in Relation to Cardiovascular Diseases

Role: Co-Investigator

We will develop and employ cutting-edge metabolomics and statistical methods to characterize known and unknown metabolite signals.