CURRICULUM VITAE

Chun Li

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Contact Information

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Education

1992	B.A. in Mathematical Statistics, Nankai University, Tianjin, China
1998	M.S. in Statistics, Ohio State University, Columbus, Ohio
2002	Ph.D. in Biostatistics, University of Michigan, Ann Arbor, Michigan Dissertation: "Association Methods for Mapping Genes for Complex Diseases" Advisor: Michael Boehnke, Ph.D.

Award

2005-2006	Oswald T. Avery Teacher of the Year From Vanderbilt University Ph.D. Program in Human Genetics

Professional Experience

1996-1998	Teaching Assistant, Department of Statistics, Ohio State University
1998-2002	Research Assistant, Department of Biostatistics, University of Michigan
2002-2004	Assistant Professor, Department of Molecular Physiology and Biophysics, Vanderbilt University
2003-2005	Director, Genetic Data Analysis Core, Center for Human Genetics Research, Vanderbilt University
2004-2009	Assistant Professor, Department of Biostatistics, Vanderbilt University
2002-2014	Investigator, Center for Human Genetics Research, Vanderbilt University
2009-2014	Associate Professor (with tenure), Department of Biostatistics, Vanderbilt University
2009-Present	Visiting Professor, Shanghai Center for Bioinformation Technology
2014-Present	Associate Professor (with tenure), Department of Epidemiology and Biostatistics, Case Western Reserve University
2014-Present	Investigator, Institute for Computational Biology, Case Western Reserve University

Software

SampleSeq / SampleSeq2: Perl and R programs for enriching subject selection for targeted and whole-genome sequencing studies. http://biostat.mc.vanderbilt.edu/SampleSeq

ASAP (Advanced Sequence Automated Pipeline): Ruby programs for automated sequence data processing on computer clusters. http://biostat.mc.vanderbilt.edu/ASAP

SMUG (Somatic Mutation Gleaner): Java, Perl, and R programs for detecting tumor somatic mutations using next-generation sequencing data. http://biostat.mc.vanderbilt.edu/SMUG

GWAsimulator: A C++ program for simulating genotype data from SNP chips. It implements a rapid moving-window algorithm to simulate whole genome case-control or population samples. http://biostat.mc.vanderbilt.edu/GWAsimulator

GIST (Genotype-IBD Sharing Test): A C program for testing if marker genotype can account in part for the evidence of linkage in the marker region. http://biostat.mc.vanderbilt.edu/GIST

ATOM (Association Test via Optimally weighted Markers): An R program for a gene-based association test for case-control data. http://biostat.mc.vanderbilt.edu/ATOM

HWECC / HWETRIO: R programs for Hardy-Weinberg equilibrium tests using case-control or trio data. http://biostat.mc.vanderbilt.edu/HWECC and http://biostat.mc.vanderbilt.edu/HWETRIO

COBOT (Conditional Ordinal-By-Ordinal Test): R programs for testing for association between two ordinal variables while adjusting for covariates. http://biostat.mc.vanderbilt.edu/OrdinalRegression

Academic Activities

2003-2005	Member, Core Advisory Board, Vanderbilt Center for Human Genetics Research
2003-2008	Organizer, Statistical and Computational Genetics Journal Club
2004-2005	Secretary, Middle Tennessee Chapter, American Statistical Association
2005-2006	President, Middle Tennessee Chapter, American Statistical Association
June 13, 2004	Organizer, Mini-Symposium on Statistical Genetics, SIAM Conference on Discrete Mathematics, Nashville, Tennessee (http://www.siam.org/meetings/DM04/index.htm)
March 22, 2005	Chair, Session on Imaging of Brain Activity, IBS/ENAR meeting, Austin, Texas
2008-2009	Member, Statistical Genetics Faculty Search Committee, Center for Human Genetics Research, Vanderbilt University
July 7, 2012	Chair, Session 2, Tenth International Bioinformatics Workshop, Changchun, China
2012	Member, Advisory Committee for Genome Sciences Resource, Vanderbilt University
2004-Present	Member, Faculty Search Committee, Department of Biostatistics, Vanderbilt University
2011-2012	Member, BioVU Review Committee
2012-2013	Vice Chair, BioVU Review Committee
2013-2014	Chair, BioVU Review Committee (BioVU is Vanderbilt's DNA databank)

Guest Editor, *PLoS Genetics* (2014)

Manuscript review for

American Journal of Epidemiology
American Journal of Human Genetics
Am J of Respiratory and Critical Care Medicine
Annals of Human Genetics
Annals of Neurology
Bioinformatics
BMC Bioinformatics
Cancer Informatics
Circulation
Diabetes
European Journal of Human Genetics
Genetic Analysis Workshop (14, 15, 17)
Genetic Epidemiology
Genetics
Genome Research
Genomics
Herpesviridae
Human Heredity
Investigative Ophthalmology & Visual Science
Journal of Animal Breeding and Genetics
Journal of Multivariate Analysis
Journal of the American Statistical Association
Molecular Diagnosis & Therapy
Neuropsychiatric Genetics
Nuclear Acid Research
Obesity
Pacific Symposium on Biocomputing
PLoS Genetics
PLoS ONE
Science
Statistics in Medicine
Trend in Genetics

Grant review for

NIH/NICHD CHHD-C Developmental Biology Subcommittee (October 15-17, 2003)
American Diabetes Association (2004)
NIH/NHLBI Program Project Grant review panel (October 20, 2005)
Vanderbilt Kennedy Center for Research on Human Development (2006)
NIH/NHLBI Program Project Grant review panel (April 16, 2007)
NIH GCAT study section, Challenge grants (May, 2009)
NIH GCAT study section (June 7-8, 2012)
NIH/NIDDK Special Emphasis Panel ZDK1 GRB-7 (J2) (September 27, 2012)
Kuwait Foundation for the Advancement of Sciences (November, 2012)
NIH GCAT study section (February 20-21, 2013)
NIH/NIDDK Special Emphasis Panel 2013/10 ZDK1 GRB-6 (O2) (July 12, 2013)
NIH/CSR Special Emphasis Panel 2014/01 ZRG1 BST-F (02) (September 17, 2013)
NIH GHD study section (December 9-10, 2013)

Book proposal review for

Oxford University Press (2008)

Teaching Experience

Course Instructors:

Tutorials in Human Genetics (HGEN 371) (co-instructor: Marylyn Ritchie) Spring, 2005
(co-instructors: Marylyn Ritchie and Dana Crawford) Spring, 2007
(co-instructor: Dana Crawford) Spring, 2008-2009
(co-instructor: David Samuels) Spring, 2010-2014

We organize student presentation on key papers in statistical genetics and genetic epidemiology, and provide comments and feedback to students.

Advanced Statistical Inference (BIOS 362) Spring, 2013-2014
A second-year biostatistics PhD course on modern data analysis techniques.
Textbook: *The Elements of Statistical Learning: Data Mining, Inference, and Prediction* (2nd ed.)

Statistics for Biomedical Research (IGP 304) Spring, 2006
(co-instructor: Leena Choi) Spring, 2007
http://biostat.mc.vanderbilt.edu/IntroBiostatCourse2006
http://biostat.mc.vanderbilt.edu/IntroBiostatCourse2007
A course on introductory biostatistics for PhD students in the School of Medicine.
(I was awarded Teacher of the Year in 2006 by the PhD Program in Human Genetics for the course.)

Lectures:
Human Genetics (HGEN 341) Spring, 2005-2010
Five lectures each year on population genetics and quantitative trait locus analysis
Human Genetics (MPB 340) Spring, 2004
Lectures on population genetics and linkage analysis

Students

2004-2005	Advisor of Ms. Mame Diop (Initiative for Minority Student Development program)
2007-2008	Member, Ph.D. Dissertation Committee for Ryan Delahanty (advisor Sutcliffe)
2010-2012	Chair, Ph.D. Dissertation Committee for Zhuo Song (advisor Samuels)
2012-2013	Member, Ph.D. Dissertation Committee for Mary Ellen Koran (advisor Thornton-Wells)
2012-	Chair, Ph.D. Dissertation Committee for Joshua Hoffman (advisor Haines)

Grants

Current grant:
R01HG004517 (PIs Chun Li, Mingyao Li) 09/19/2008-07/31/2013 $1,250,000 direct
NIH/NHGRI
Developing Statistical Methods for Disease Gene Discovery
We propose to develop new statistical methods for copy number variation detection, multi-marker association, fine mapping using admixed populations, multiple comparison threshold determination, and other problems as the field of human genetics moves.

R01AI093234 (PIs Bryan Shepherd, Chun Li) 06/01/2011-04/30/2016 $1,250,000 direct
NIH/NIAID
Statistical Methods for Ordinal Variables in HIV/AIDS Studies
The major goal of this project is to develop statistical methods that account for the ordered nature of ordinal variables without making linearity assumptions and then applying these methods to HIV studies.

Past grants:
Vanderbilt Diabetes Center 04/01/2003-03/31/2005 $80,000 direct
New Statistical Methods for Diabetes Genetics Studies (PI Chun Li)

Professional Memberships

American Society of Human Genetics
American Statistical Association
Institute of Mathematical Statistics

Publications

Peer Reviewed

1. Ghosh S, Watanabe RM, Valle TT, Hauser ER, Magnuson VL, Langefeld CD, Ally DS, Mohlke KL, Silander K, Kohtamäki K, Chines P, Balow J, Birznieks G, Chang J, Eldridge W, Erdos MR, Karanjawala ZE, Knapp JI, Kudelko K, Martin C, Morales-Mena A, Musick A, Musick T, Pfahl C, Porter R, Rayman JB, Rha D, Segal L, Shapiro S, Sharaf R, Shurtleff B, So A, Tannenbaum J, Te C, Tovar J, Unni A, Welch C, Whiten R, Witt A, Blaschak-Harvan J, Douglas JA, Duren WL, Epstein MP, Fingerlin TE, Kaleta HS, Lange EM, **Li C**, McEachin RC, Stringham HM, Trager E, White PP, Eriksson J, Toivanen L, Vidgren G, Nylund SJ, Tuomilehto-Wolf E, Ross EH, Demirchyan E, Hagopian WA, Buchanan TA, Tuomilehto J, Bergman RN, Collins FS, Boehnke M (2000) The Finland-United States investigation of non-insulin-dependent diabetes mellitus genetics (FUSION) study. I. An autosomal genome scan for genes that predispose to type 2 diabetes. *American Journal of Human Genetics* 67:1174–1185 (PMID 11032783; PMC1288560)

2. Watanabe RM, Ghosh S, Langefeld CD, Valle TT, Hauser ER, Magnuson VL, Mohlke KL, Silander K, Ally DS, Chines P, Blaschak-Harvan J, Douglas JA, Duren WL, Epstein MP, Fingerlin TE, Kaleta HS, Lange EM, **Li C**, McEachin RC, Stringham HM, Trager E, White PP, Balow J, Birznieks G, Chang J, Eldridge W, Erdos MR, Karanjawala ZE, Knapp JI, Kudelko K, Martin C, Morales-Mena A, Musick A, Musick T, Pfahl C, Porter R, Rayman JB, Rha D, Segal L, Shapiro S, Sharaf R, Shurtleff B, So A, Tannenbaum J, Te C, Tovar J, Unni A, Welch C, Whiten R, Witt A, Kohtamäki K, Ehnholm C, Eriksson J, Toivanen L, Vidgren G, Nylund SJ, Tuomilehto-Wolf E, Ross EH, Demirchyan E, Hagopian WA, Buchanan TA, Tuomilehto J, Bergman RN, Collins FS, Boehnke M (2000) The Finland-United States investigation of non-insulin-dependent diabetes mellitus genetics (FUSION) study. II. An autosomal genome scan for diabetes-related quantitative-trait loci. *American Journal of Human Genetics* 67:1186–1200 (PMID 11032784; PMC1288561)

3. **Li C**, Scott LJ, Boehnke M (2004) Assessing whether an allele can account in part for a linkage signal: The Genotype-IBD Sharing Test (GIST). *American Journal of Human Genetics* 74:418–431 (PMID 14872409; PMC1182256) (Software at http://biostat.mc.vanderbilt.edu/GIST)

4. Silander K, Scott LJ, Valle TT, Mohlke KL, Stringham HM, Wiles KR, Duren WL, Doheny KF, Pugh EW, Chines P, Narisu N, White PP, Fingerlin TE, Jackson AU, **Li C**, Ghosh S, Magnuson VL, Colby K, Erdos MR, Hill JE, Hollstein P, Humphreys KM, Kasad RA, Lambert J, Lazaridis KN, Lin G, Morales-Mena A, Patzkowski K, Pfahl C, Porter R, Rha D, Segal L, Suh YD, Tovar J, Unni A, Welch C, Douglas JA, Epstein MP, Hauser ER, Hagopian W, Buchanan TA, Watanabe RM, Bergman RN, Tuomilehto J, Collins FS, Boehnke M (2004) A large set of Finnish affected sibling pair families with type 2 diabetes suggests susceptibility loci on chromosomes 6, 11, and 14. *Diabetes* 53:821–829 (PMID 14988269)

5. Silander K, Mohlke KL, Scott LJ, Peck EC, Hollstein P, Skol AD, Jackson AU, Deloukas P, Hunt S, Stavrides G, Chines PS, Erdos MR, Narisu N, Conneely KN, **Li C**, Fingerlin TE, Dhanjal SK, Valle TT, Bergman RN, Tuomilehto J, Watanabe RM, Boehnke M, Collins FS (2004) Genetic variation near the hepatocyte nuclear factor-4α gene predicts susceptibility to type 2 diabetes. *Diabetes* 53:1141–1149 (PMID 15047633)

6. Ren Z, Cai Q, Shu XO, Cai H, **Li C**, Yu H, Gao YT, Zheng W (2004) Genetic polymorphisms in the *IGFBP3* gene: Association with breast cancer risk and blood IGFBP-3 protein levels among Chinese women. *Cancer Epidemiology, Biomarkers & Prevention* 13:1290–1295 (PMID 15298948)

7. McCauley JL, **Li C**, Jiang L, Olson LM, Crockett G, Gainer K, Folstein SE, Haines JL, Sutcliffe JS (2005) Genome-wide and ordered-subset linkage analyses provide support for autism loci on 17q and 19p with evidence of phenotypic and interlocus genetic correlates. *BMC Medical Genetics* 6:1

(PMID 15647115; PMC546213)

8. Epstein MP, Veal CD, Trembath RC, Barker JN, **Li C**, Satten GA (2005) Genetic association analysis using data from triads and unrelated subjects. *American Journal of Human Genetics* 76:592–608 (PMID 15712104; PMC1199297)
9. Sutcliffe JS, Delahanty RJ, Prasad HC, McCauley JL, Han Q, Jiang L, **Li C**, Folstein SE, Blakely RD (2005) Allelic heterogeneity at the serotonin transporter locus (*SLC6A4*) confers susceptibility to autism and rigid-compulsive behaviors. *American Journal of Human Genetics* 77:265–279 (PMID 15995945; PMC1224529)
10. **Li C**, Boehnke M (2006) Haplotype association analysis for late onset diseases using nuclear family data. *Genetic Epidemiology* 30:220–230 (PMID 16470533)
11. Kurnik D, Muszkat M, **Li C**, Sofowora GG, Solus J, Xie HG, Harris PA, Jiang L, McMunn C, Ihrie P, Dawson EP, Williams SM, Wood AJ, Stein CM (2006) Variations in the α_{2A}-adrenergic receptor gene and their functional effects. *Clinical Pharmacology & Therapeutics* 79:173–185 (PMID 16513442)
12. Yi Y, **Li C**, Miller C, George AL Jr (2007) Strategy for encoding and comparison of gene expression signatures. *Genome Biology* 8:R133 (PMID 17612401; PMC2323223)
13. Statnikov A, **Li C**, Aliferis CF (2007) Effects of environment, genetics and data analysis pitfalls in an esophageal cancer genome-wide association study. *PLoS One* 2:e958 (PMID 17895998; PMC1978529)
14. **Li C**, Li M, Lange EM, Watanabe RM (2008) Prioritized subset analysis: Improving power in genome-wide association studies. *Human Heredity* 65:129–141 (PMID 17934316; PMC2858373)
15. **Li C**, Li M (2008) GWAsimulator: A rapid whole genome simulation program. *Bioinformatics* 24:140–142 (PMID 18006546) (Software at http://biostat.mc.vanderbilt.edu/GWAsimulator)
16. Leon A, Donahue SP, Morrison DG, Estes RL, **Li C** (2008) The age-dependent effect of anisometropia magnitude on anisometropic amblyopia severity. *Journal of AAPOS* 12:150–156 (PMID 18155938)
17. Recchia FM, Chen E, **Li C**, Maguluri S (2008) Use of COX-2 inhibitors in patients with retinal venous occlusive disease. *Retina* 28:134–137 (PMID 18185149)
18. Cai Q, Kataoka N, **Li C**, Wen W, Smith JR, Gao YT, Shu XO, Zheng W (2008) Haplotype analyses of *CYP19A1* gene variants and breast cancer risk: Results from the Shanghai Breast Cancer Study. *Cancer Epidemiology, Biomarkers & Prevention* 17:27–32 (PMID 18199708; PMC2633134)
19. Li M*, **Li C***, Guan W (2008) Evaluation of coverage variation of SNP chips for genome-wide association studies. *European Journal of Human Genetics* 16:635–643 (PMID 18253166) (* **co-first author**)
20. **Li C**, Li M, Long JR, Cai Q, Zheng W (2008) Evaluating cost efficiency of SNP chips in genome-wide association studies. *Genetic Epidemiology* 32:387–395 (PMID 18271056; PMC2650398)
21. Menon R, Thorsen P, Vogel I, Jacobsson B, Morgan N, Jiang L, **Li C**, Williams SM, Fortunato SJ (2008) Racial disparity in amniotic fluid concentrations of tumor necrosis factor (TNF)-α and soluble TNF receptors in spontaneous preterm birth. *American Journal of Obstetrics and Gynecology* 198:533.e1–10 (PMID 18279834)
22. Schwarz UI, Ritchie MD, Bradford Y, **Li C**, Dudek SM, Frye-Anderson A, Kim RB, Roden DM, Stein CM (2008) Genetic determinants of response to warfarin during initial anticoagulation. *New*

England Journal of Medicine 358:999–1008 (PMID 18322281)

23. Jiang S, Moriarty-Craige SE, **Li C**, Lynn MJ, Cai J, Jones DP, Sternberg P (2008) Associations of plasma-soluble fas ligand with aging and age-related macular degeneration. *Investigative Ophthalmology & Visual Science* 49:1345–1349 (PMID 18385048)
24. O'Day DM, **Li C** (2008) First-time failure rates of candidates for board certification: An educational outcome measure. *Archives of Ophthalmology* 126:548–553 (PMID 18413528) (**Associated Editorial** by John G. Clarkson, *Arch Ophthalmol.* 2008, 126:562–563)
25. Parbhu KC, Galler KE, **Li C**, Mawn LA (2008) Underestimation of soft tissue entrapment by computed tomography in orbital floor fractures in the pediatric population. *Ophthalmology* 115:1620–1625 (PMID 18440640)
26. Li M, **Li C** (2008) Assessing departure from Hardy-Weinberg equilibrium in the presence of disease association. *Genetic Epidemiology* 32:589–599 (PMID 18449919) (Software at http://biostat.mc.vanderbilt.edu/HWECC and http://biostat.mc.vanderbilt.edu/HWETRIO)
27. Ryckman KK, Jiang L, **Li C**, Bartlett J, Haines JL, Williams SM (2008) A prevalence based association test for case-control studies. *Genetic Epidemiology* 32:600–605 (PMID 18473366)
28. Beeghly-Fadiel A, Long JR, Gao YT, **Li C**, Qu S, Cai Q, Zheng Y, Ruan ZX, Levy SE, Deming SL, Snoddy JR, Shu XO, Lu W, Zheng W (2008) Common *MMP-7* polymorphisms and breast cancer susceptibility: A multistage study of association and functionality. *Cancer Research* 68:6453–6459 (PMID 18648013; PMC2718434)
29. Kurnik D, **Li C**, Sofowora GG, Friedman EA, Muszkat M, Xie HG, Harris PA, Williams SM, Nair UB, Wood AJ, Stein CM (2008) Beta-1-adrenoceptor genetic variants and ethnicity independently affect response to beta-blockade. *Pharmacogenetics and Genomics* 18:895–902 (PMID 18794726; PMC2757009)
30. Campbell DB, **Li C**, Sutcliffe JS, Persico AM, Levitt P (2008) Genetic evidence implicating multiple genes in the MET receptor tyrosine kinase pathway in autism spectrum disorder. *Autism Research* 1:159–168 (PMID 19360663; PMC2678909)
31. Beeghly-Fadiel A, Shu XO, Long J, **Li C**, Cai Q, Cai H, Gao YT, Zheng W (2009) Genetic polymorphisms in the *MMP-7* gene and breast cancer survival. *International Journal of Cancer* 124:208–214 (PMID 18798254; PMC2597698)
32. **Li C**, Schwarz UI, Ritchie MD, Roden DM, Stein CM, Kurnik D (2009) Relative contribution of *CYP2C9* and *VKORC1* genotypes and early INR response to the prediction of warfarin sensitivity during initiation of therapy. *Blood* 113:3925–3930 (PMID 19074728; PMC2673121)
33. Li M, Wang K, Grant SF, Hakonarson H, **Li C** (2009) ATOM: A powerful gene-based association test by combining optimally weighted markers. *Bioinformatics* 25:497–503 (PMID 19074959; PMC2642636) (Software at http://biostat.mc.vanderbilt.edu/ATOM)
34. Zheng W, Long J, Gao YT, **Li C**, Zheng Y, Xiang YB, Wen W, Levy S, Deming SL, Haines JL, Gu K, Fair AM, Cai Q, Lu W, Shu XO (2009) Genome-wide association study identifies a new breast cancer susceptibility locus at 6q25.1. *Nature Genetics* 41:324–328 (PMID 19219042; PMC2754845)
35. Parl FF, Egan KM, **Li C**, Crooke PS (2009) Estrogen exposure, metabolism, and enzyme variants in a model for breast cancer risk prediction. *Cancer Informatics* 7:109–121 (PMID 19718449; PMC2730178)
36. Zheng W, Cai Q, Signorello LB, Long J, Hargreaves MK, Deming SL, Li G, **Li C**, Cui Y, Blot WJ

(2009) Evaluation of 11 breast cancer susceptibility loci in African American women. *Cancer Epidemiology, Biomarkers & Prevention* 18:2761–2764 (PMID 19789366; PMC2759857)

37. Kurnik D, Cunningham AJ, Sofowora GG, Kohli U, **Li C**, Friedman EA, Muszkat M, Menon UB, Wood AJ, Stein CM (2009) *GRK5* Gln41Leu polymorphism is not associated with sensitivity to β_1-adrenergic blockade in humans. *Pharmacogenomics* 10:1581–1587 (PMID 19842931; PMC2820245)

38. Zheng W, Wen W, Gao YT, Shyr Y, Zheng Y, Long J, Li G, **Li C**, Gu K, Cai Q, Shu XO, Lu W (2010) Genetic and clinical predictors for breast cancer risk assessment and stratification among Chinese women. *Journal of the National Cancer Institute* 102:972–981 (PMID 20484103; PMC2897876)

39. Long J, Cai Q, Shu XO, Qu S, **Li C**, Zheng Y, Gu K, Wang W, Xiang YB, Cheng J, Chen K, Zhang L, Zheng H, Shen CY, Huang CS, Hou MF, Shen H, Hu Z, Wang F, Deming SL, Kelley MC, Shrubsole MJ, Khoo US, Chan KY, Chan SY, Haiman CA, Henderson BE, Le Marchand L, Iwasaki M, Kasuga Y, Tsugane S, Matsuo K, Tajima K, Iwata H, Huang B, Shi J, Li G, Wen W, Gao YT, Lu W, Zheng W (2010) Identification of a functional genetic variant at 16q12.1 for breast cancer risk: Results from the Asia Breast Cancer Consortium. *PLoS Genetics* 6:e1001002 (PMID 20585626; PMC2891809)

40. Colburn JD, Morrison DG, Estes RL, **Li C**, Lu P, Donahue SP (2010) Longitudinal follow-up of hypermetropic children identified during preschool vision screening. *Journal of AAPOS* 14:211–215 (PMID 20603055)

41. Joos KM, **Li C**, Sappington RM (2010) Morphometric changes in the rat optic nerve following short-term intermittent elevations in intraocular pressure. *Investigative Ophthalmology & Visual Science* 51:6431–6440 (PMID 20688743; PMC3055763)

42. Long J, Shu XO, Cai Q, Gao YT, Zheng Y, Li G, **Li C**, Gu K, Wen W, Xiang YB, Lu W, Zheng W (2010) Evaluation of breast cancer susceptibility loci in Chinese women. *Cancer Epidemiology, Biomarkers & Prevention* 19:2357–2365 (PMID 20699374; PMC2936687)

43. Liu BH, Yu H, Tu K, **Li C**, Li YX, Li YY (2010) DCGL: an R package for identifying differentially coexpressed genes and links from gene expression microarray data. *Bioinformatics* 26:2637–2638 (PMID 20801914; PMC2951087)

44. Shu XO, Long J, Cai Q, Qi L, Xiang YB, Cho YS, Tai ES, Li X, Lin X, Chow WH, Go MJ, Seielstad M, Bao W, Li H, Cornelis MC, Yu K, Wen W, Shi J, Han BG, Sim XL, Liu L, Qi Q, Kim HL, Ng DP, Lee JY, Kim YJ, **Li C**, Gao YT, Zheng W, Hu FB (2010) Identification of new genetic risk variants for type 2 diabetes. *PLoS Genetics* 6:e1001127 (PMID 20862305; PMC2940731)

45. **Li C**, Shepherd BE (2010) Test of association between two ordinal variables while adjusting for covariates. *Journal of the American Statistical Association* 105:612–620 (PMID 20882122; PMC2946253; MR2724846) (Software at http://biostat.mc.vanderbilt.edu/OrdinalRegression)

46. He J, Wang K, Edmondson AC, Rader DJ, **Li C**, Li M (2011) Gene-based interaction analysis by incorporating external linkage disequilibrium information. *European Journal of Human Genetics* 19:164–172 (PMID 20924406; PMC3025792)

47. Wang X, Zhu X, Qin H, Cooper R, Ewens W, **Li C**, Li M (2011) Adjustment for local ancestry in genetic association analysis of admixed populations. *Bioinformatics* 27:670–677 (PMID 21169375; PMC3042179)

48. Cai Q, Wen W, Qu S, Li G, Egan KM, Chen K, Deming SL, Shen H, Shen CY, Gammon MD, Blot WJ, Matsuo K, Haiman CA, Khoo US, Iwasaki M, Santella RM, Zhang L, Fair AM, Hu Z, Wu PE,

Signorello LB, Titus-Ernstoff L, Tajima K, Henderson BE, Chan KY, Kasuga Y, Newcomb PA, Zheng H, Cui Y, Wang F, Shieh YL, Iwata H, Le Marchand L, Chan SY, Shrubsole MJ, Trentham-Dietz A, Tsugane S, Garcia-Closas M, Long J, **Li C**, Shi J, Huang B, Xiang YB, Gao YT, Lu W, Shu XO, Zheng W (2011) Replication and functional genomic analyses of the breast cancer susceptibility locus at 6q25.1 generalize its importance in women of Chinese, Japanese, and European ancestry. *Cancer Research* 71:1344–1355 (PMID 21303983; PMC3083305)

49. Kurnik D, Muszkat M, **Li C**, Sofowora GG, Friedman EA, Scheinin M, Wood AJ, Stein CM (2011) Genetic variations in the α_{2A}-adrenoreceptor are associated with blood pressure response to the agonist dexmedetomidine. *Circulation: Cardiovascular Genetics* 4:178–187 (PMID 21325151; PMC3080459)

50. Kohli U, Hahn MK, English BA, Sofowora GG, Muszkat M, **Li C**, Blakely RD, Stein CM, Kurnik D (2011) Genetic variation in the presynaptic norepinephrine transporter is associated with blood pressure responses to exercise in healthy humans. *Pharmacogenetics and Genomics* 21:171–178 (PMID 21412203; PMC3065933)

51. Edwards TL, Song Z, **Li C** (2011) Enriching targeted sequencing experiments for rare disease alleles. *Bioinformatics* 27:2112–2118 (PMID 21700677; PMC3137214) (Software at http://biostat.mc.vanderbilt.edu/SampleSeq)

52. Yu H, Liu BH, Ye ZQ, **Li C**, Li YX, Li YY (2011) Link-based quantitative methods to identify differentially coexpressed genes and gene pairs. *BMC Bioinformatics* 12:315 (PMID 21806838; PMC3199761)

53. Cai Q, Long J, Lu W, Qu S, Wen W, Kang D, Lee JY, Chen K, Shen H, Shen CY, Sung H, Matsuo K, Haiman CA, Khoo US, Ren Z, Iwasaki M, Gu K, Xiang YB, Choi JY, Park SK, Zhang L, Hu Z, Wu PE, Noh DY, Tajima K, Henderson BE, Chan KY, Su F, Kasuga Y, Wang W, Cheng JR, Yoo KY, Lee JY, Zheng H, Liu Y, Shieh YL, Kim SW, Lee JW, Iwata H, Le Marchand L, Chan SY, Xie X, Tsugane S, Lee MH, Wang S, Li G, Levy S, Huang B, Shi J, Delahanty R, Zheng Y, **Li C**, Gao YT, Shu XO, Zheng W (2011) Genome-wide association study identifies breast cancer risk variant at 10q21.2: results from the Asia Breast Cancer Consortium. *Human Molecular Genetics* 20:4991–4999 (PMID 21908515; PMC3221542)

54. Brantley MA Jr, Osborn MP, Sanders BJ, Rezaei KA, Lu P, **Li C**, Milne GL, Cai J, Sternberg P Jr (2012) Plasma biomarkers of oxidative stress and genetic variants in age-related macular degeneration. *American Journal of Ophthalmology* 153:460–467 (PMID 22035603; PMC3288635)

55. Shu XO, Long J, Lu W, **Li C**, Chen WY, Delahanty R, Cheng J, Cai H, Zheng Y, Shi J, Gu K, Wang WJ, Kraft P, Gao YT, Cai Q, Zheng W (2012) Novel genetic markers of breast cancer survival identified by a genome-wide association study. *Cancer Research* 72:1182–1189 (PMID 22232737; PMC3294129)

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70. Samuels DC*, **Li C***, Li B, Song Z, Torstenson E, Clay HB, Rokas A, Thornton-Wells TA, Moore JH, Hughes TM, Hoffman RD, Haines JL, Murdock DG, Mortlock DP, Williams SM (2013) Recurrent tissue-specific mtDNA mutations are common in humans. *PLoS Genetics* 9:e1003929 (* **co-first author**) (PMID 24244193; PMC3820769)
71. **Li C**, Williams SM (2013) Human somatic variation: It's not just for cancer anymore. *Current Genetic Medicine Reports* 1:212–218
72. Zhang Y, Long J, Lu W, Shu XO, Cai Q, Zheng Y, **Li C**, Li B, Gao YT, Zheng W (2014) Rare coding variants and breast cancer risk: Evaluation of susceptibility loci identified in genome-wide association studies. *Cancer Epidemiology, Biomarkers & Prevention* 23:622–628 (PMID 24470074; PMC3976694)
73. Cheng KF, Lee JY, Zheng W, **Li C** (2014) A powerful association test of multiple genetic variants using a random-effects model. *Statistics in Medicine* 33:1816–1827 (PMID 24338936; PMC4008649)
74. Zhang B, Jia WH, Matsuda K, Kweon SS, Matsuo K, Xiang YB, Shin A, Jee SH, Kim DH, Cai Q, Long J, Shi J, Wen W, Yang G, Zhang Y, **Li C**, Li B, Guo Y, Ren Z, Ji BT, Pan ZZ, Takahashi A, Shin MH, Matsuda F, Gao YT, Oh JH, Kim S, Ahn YO; Genetics and Epidemiology of Colorectal Cancer Consortium (GECCO), Chan AT, Chang-Claude J, Slattery ML; Colorectal Transdisciplinary (CORECT) Study, Gruber SB, Schumacher FR, Stenzel SL; Colon Cancer Family Registry (CCFR), Casey G, Kim HR, Jeong JY, Park JW, Li HL, Hosono S, Cho SH, Kubo M, Shu XO, Zeng YX, Zheng W (2014) Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. *Nature Genetics* 46:533–542 (PMID 24836286)

In Press

75. Chung C, Solus J, Oeser A, **Li C**, Raggi P, Smith J, Stein C (2014) Genetic variation and coronary atherosclerosis in patients with systemic lupus erythematosus. *Lupus* (in press) (PMID 24699314)

Submitted

76. **Li C** (2013) A new coefficient of determination for regression models. To *American Statistician*
77. Chen JH, Cheng KF, Wang IK, **Li C** (2011) Combining information from case-control and matched case-control studies. To *Epidemiology*
78. Solus JF, Chung CP, Oeser A, **Li C**, Rho YH, Bradley KM, Kawai VK, Smith JR, Stein CM (2013) Serum concentrations of IL-6 and TNFα are associated with susceptibility candidate gene polymorphisms in systemic lupus erythematosus, rheumatoid arthritis and controls. To *PLoS ONE*
79. Guan W, **Li C** (2013) Design of DNA pooling to allow incorporation of covariates in rare variants analysis. To *Human Heredity* (revision submitted)
80. Zhang Y, Long J, Cai Q, Shu XO, Gao YT, **Li C**, Zheng W (2013) Whole-exome sequencing

identifies novel somatic mutations in Chinese breast cancer patients. To *Breast Cancer*

81. Cai Q, Zhang B, Sung H, Low SK, Kweon SS, Shi J, Wen W, Choi JY, Takahashi A, Lu W, Gao YT, Noh DY, Teo SH, Shen CY, Matsuo K, Kim MK, Khoo US, Iwasaki M, Ashikawa K, Matsuda K, Shin MH, Zheng Y, Xiang YB, Ji BT, Wang W, Park SK, Kang P, Wu PE, Ito H, Ahn SH, Chan SY, Iwata H, Nakamura Y, Kubo M, Park MH, Mariapun S, Hsiung CN, Kasuga Y, Kang HS, Man EPS, Tsugane S, The DRIVE GAME-ON Consortium, Delahanty RJ, Zhang Y, Li B, **Li C**, Long J, Shu XO, Kang D, Zheng W (2013) Identification of novel breast cancer susceptibility loci at 1q32.1, 5q14.3, and 15q26.1: Results from the Asia Breast Cancer Consortium. To *Nature Genetics*
82. Kawai VK, Cunningham A, Vear SI, Van Driest SL, Oginni A, Xu H, Jiang M, **Li C**, Denny JC, Shaffer C, Bowton E, Gage BF, Ray WA, Roden DM, Stein CM (2014) Genotype and risk of major bleeding after the warfarin initiation phase. To *Thrombosis and Haemostasis*
83. Yang A, Guan W, Xiao R, Tang WHW, Moravec CS, Margulies KB, Cappola TP, **Li C**, Li M (2014) Differential isoform expression analysis in RNA-Seq using random-effects meta-regression. To *BMC Bioinformatics*
84. Shepherd BE, **Li C**, Liu Q (2014) Probability-scale residuals for continuous, discrete, and censored data. To *Journal of the American Statistical Association*
85. Newman JH, Holt TN, Cogan J, Womack B, Phillips JA, **Li C**, Hamid R (2014) Increased prevalence of an *EPAS1* (*HIF2α*) variant haplotype in cattle with high altitude pulmonary hypertension: brisket gene? To *Nature Communications*
86. Wanga V, Venuto C, Morse GD, Daar ES, Haas DW, **Li C**, Shepherd BE (2014) Genome-wide association study of tenofovir pharmacokinetics and creatinine clearance in AIDS Clinical Trials Group Protocol A5202. To *Journal of Infectious Diseases*
87. Chung CP, Solus JF, Oeser A, **Li C**, Raggi P, Smith JR, Stein CM (2014) A variant in the osteoprotegerin gene is associated with coronary atherosclerosis in patients with rheumatoid arthritis: results from a candidate gene study.
88. Li B, Zhan X, Wei Q, Zhong X, Chen W, **Li C**, Haines J (2014) Leveraging identity-by-descent for accuracy genotype inference in family sequencing data. To *PLoS Genetics*

Letter to the Editor

89. Statnikov A, **Li C**, Aliferis CF (2008) A statistical reappraisal of the findings of an esophageal cancer genome-wide association study. (Letter to the Editor) *Cancer Research* 68:3074-3075 (PMID 18413779)

Book Chapters, Society Transaction

90. **Li C** (2005) Detecting gene-gene interaction in linkage analysis. In *Current Protocols in Human Genetics*, edited by Dracopoli NC, Haines JL, Korf BR, Morton CC, Seidman CE, Seidman JG, Smith DR. Chapter 1, Unit 1.15. John Wiley & Sons (PMID 18428369)
91. O'Day DM, **Li C** (2006) The failure rate of candidates for board certification: An educational outcome measure. *Transactions of the American Ophthalmological Society* 104:129-142 (PMID 17471333; PMC1809893)
92. Airey DC, **Li C** (2011) Initial identification and confirmation of a QTL gene. In *Gene Discovery for Disease Models*, edited by Gu W, Wang Y. Chapter 19 (pp. 403-423). John Wiley & Sons, Inc.

Invited Talks/Lectures at Conferences/Workshops/Courses

April 6, 2004 — Genetic Analysis of Quantitative Traits
Genetic Analysis of Complex Human Diseases (April 4-7, 2004), Durham, North Carolina

June 13, 2004 — *Connecting Linkage and Association Results: An Integration*
SIAM Conference on Discrete Mathematics (June 13-16, 2004), Nashville, Tennessee

May 17, 2005 — *Genetic Analysis of Quantitative Traits*
Genetic Analysis of Complex Human Diseases (May 15-18, 2005), Durham, North Carolina

June 14, 2006 — *Genetic Analysis of Quantitative Traits*
Genetic Analysis of Complex Human Diseases (June 12-15, 2006), Durham, North Carolina

August 21, 2006 — *Genome-Wide Association Studies: Issues and Approaches*
Conference on Analysis of Complex Data Sets, Nashville, Tennessee

May 5, 2008 — *Genetic Linkage Analysis*
May 6, 2008 — *Genetic Analysis of Quantitative Traits*
Genetic Analysis of Complex Human Diseases (May 5-8, 2008), Coconut Grove, Florida

October 4, 2008 — *Coverage Variation and Cost Efficiency in Genome-wide Association Studies*
Biostatistics and Bioinformatics Workshop for High-Dimensional Data Analysis (October 3-5, 2008), Tamkang University, Tamsui, Taiwan

April 21, 2009 — *Genetic Analysis of Quantitative Traits*
Genetic Analysis of Complex Human Diseases (April 20-23, 2009), Miami Beach, Florida

July 7, 2012 — *Detection of Somatic Mutations Using Next-Generation Sequencing*
Tenth International Bioinformatics Workshop (July 7-8, 2012), Changchun, China

Seminars

February 5, 2002 — *Association Analysis for Mapping Genes Using Affected Sibships*
Department of Statistics, University of California, Berkeley, California

February 14, 2002 — *Association Analysis for Mapping Genes Using Affected Sibships*
Program in Human Genetics, Deparment of Molecular Physiology and Biophysics, Vanderbilt University, Nashville, Tennessee

February 18, 2002 — *Association Analysis for Mapping Genes Using Affected Sibships*
Division of Statistical Genetics, Department of Biostatistics, University of Iowa, Iowa City, Iowa

February 21, 2002 *Association Analysis for Mapping Genes Using Affected Sibships*
Division of Biostatistics, Washington University, St. Louis, Missouri

February 25, 2002 *Association Analysis for Mapping Genes Using Affected Sibships*
Department of Biostatistics, University of North Carolina, Chapel Hill, North Carolina

March 4, 2002 *Association Analysis for Mapping Genes Using Affected Sibships*
Department of Human Genetics, Emory University, Atlanta, Georgia

March 27, 2002 *Association Analysis for Mapping Genes Using Affected Sibships*
Division of Biostatistics, Department of Preventive Medicine, University of Southern California, Los Angeles, California

April 18, 2002 *Association Analysis for Mapping Genes Using Affected Sibships*
Department of Human Genetics, Genome Therapeutics Corporation, Waltham, Massachusetts

January 30, 2003 *Design and Data Analysis for Genetic Studies for Complex Diseases*
Program in Human Genetics, Vanderbilt University, Nashville, Tennessee

April 17, 2003 *Allele-Sharing Linkage Analysis on Subsets of Families Stratified Based on an Associated Allele*
Division of Biostatistics, Vanderbilt-Ingram Cancer Center, Nashville, Tennessee

October 5, 2004 *Connecting Linkage and Association Results: The Genotype-IBD Sharing Test (GIST)*
Section on Biostatistics, Department of Public Health Sciences, Wake Forest University, Winston-Salem, North Carolina

May 25, 2005 *Evaluation of Ophthalmology Residency Training Programs in the U.S.: Rank them or not?*
Department of Biostatistics, Vanderbilt University, Nashville, Tennessee

June 15, 2005 *A Discussion of Bayesian and Frequentist Statistics*
Department of Biostatistics, Vanderbilt University, Nashville, Tennessee (Co-Presentor: Dr. Sebastien Haneuse)

July 26, 2006 *Association Analysis in Human Genetics Studies*
Kennedy Center for Research on Human Development, Vanderbilt University, Nashville, Tennessee

October 24, 2006 *Issues in Genome-Wide Association Studies*
Center for Health Services Research, Vanderbilt University, Nashville, Tennessee

May 23, 2007 *What is Interaction? & A New Approach to Detecting Gene-Gene Interactions in Case-Control Studies*
Department of Biostatistics, Vanderbilt University, Nashville, Tennessee

September 19, 2007	*What is Interaction for A Binary Outcome?* Kennedy Center for Research on Human Development, Vanderbilt University, Nashville, Tennessee
February 12, 2008	*Issues in Genome-wide Association Studies: Coverage, Efficiency, and Prioritized Subset Analysis* Department of Biostatistics and Epidemiology, University of Pennsylvania, Philadelphia, Pennsylvania
April 1, 2008	*Coverage Variation and Cost Efficiency in Genome-wide Association Studies* Vanderbilt Epidemiology Center, Institute for Medicine and Public Health, Vanderbilt University, Nashville, Tennessee
April 14, 2008	*Genome-wide Association Studies: Coverage, Efficiency, and Prioritized Subset Analysis* Shanghai Cancer Institute, Shanghai, China
April 16, 2008	*Coverage Variation and Cost Efficiency in Genome-wide Association Studies* Department of Bioinformatics and Biostatistics, Shanghai Jiao Tong University, Shanghai, China
April 17, 2008	*Empirical Bayes in Action: Evaluation of Ophthalmology Residency Training Programs in the U.S.* Department of Statistics, Nankai University, Tianjin, China
August 15, 2008	*Genome-wide Association Approach for the Shanghai Breast Cancer Study* Cancer Biostatistics Workshop, Vanderbilt University, Nashville, Tennessee
April 8, 2009	*Test of Association between Two Ordinal Variables while Adjusting for Covariates* Department of Biostatistics, Vanderbilt University, Nashville, Tennessee
May 6, 2009	*Powerful Association Tests for Genome-Wide Association Studies Using Admixed Populations* Biostatistics Center, China Medical University, Taichung, Taiwan
May 7, 2009	*Powerful Association Tests for Genome-Wide Association Studies Using Admixed Populations* Department of Statistics, National Chengkung University, Tainan, Taiwan
May 13, 2009	*Association Test for Two Ordinal Variables with Covariate Adjustment* Biostatistics Center, China Medical University, Taichung, Taiwan
April 14, 2010	*A New Residual for Ordinal Outcomes* Department of Biostatistics, Vanderbilt University, Nashville, Tennessee
May 13, 2010	*Moving Towards Sequencing: Subject Selection Strategies for Targeted Sequencing* Shanghai Institute of Biological Sciences, Shanghai, China

May 26, 2010 *Moving Towards Sequencing: Subject Selection Strategies for Targeted Sequencing*
Biostatistics Center, China Medical University, Taichung, Taiwan

November 17, 2010 *A New Measure of Coefficient of Determination for Regression Models*
Department of Biostatistics, Vanderbilt University, Nashville, Tennessee

March 16, 2011 *Normal-Tumor Comparison using Next-Generation Sequencing Data*
Biostatistics Center, China Medical University, Taichung, Taiwan

March 23, 2011 *A New Measure of Coefficient of Determination for Regression Models*
Biostatistics Center, China Medical University, Taichung, Taiwan

July 12, 2012 *Detection of Somatic Mutations Using Next-Generation Sequencing*
Shanghai Center for Bioinformation Technology, Shanghai, China

October 3, 2012 *Optimized Selection of Unrelated Subjects for Whole Genome Sequencing Studies*
Biostatistics Center, China Medical University, Taichung, Taiwan

October 8, 2012 *Recurrent Tissue-specific mtDNA Mutations are Common in Humans*
Biostatistics Center, China Medical University, Taichung, Taiwan

February 13, 2013 *A New Measure of Coefficient of Determination for Regression Models*
Department of Community and Family Medicine, Dartmouth Medical School, Hanover, New Hampshire

October 2, 2013 *Recurrent Tissue-specific mtDNA Mutations are Common in Humans*
Department of Epidemiology and Biostatistics, Case Western Reserve University, Cleveland, Ohio

Presentations at Meetings

August 6, 2003 *Allele-Sharing Linkage Analysis on Subsets of Families Stratified Based on an Associated Allele*
Joint Statistical Meetings, San Francisco, California

November 4, 2003 *Haplotype Association Analysis for Late Onset Diseases Using Nuclear Family Data*
International Genetic Epidemiology Society, Redondo Beach, California

March 31, 2004 *A Uniform Measure of Linkage Disequilibrium for Markers with Two or More Alleles*
International Biometric Society (ENAR), Pittsburgh, Pennsylvania

March 21, 2005 *Combining Evidence from Linkage and Association Studies Using Dempster-Shafer Theory*
International Biometric Society (ENAR), Austin, Texas

March 29, 2006 *ArrayBLAST: Data Mining Tool for Gene Expression Signatures*
International Biometric Society (ENAR), Tampa, Florida

October 12, 2006 *Prioritized Subset Analysis in Genome-wide Association Studies*
American Society of Human Genetics, New Orleans, Louisiana

Other Talks

December 17, 2004 *Genetic Data Analysis and the Genetic Data Analysis Core*
GCRC Research Skills Workshop Series, Vanderbilt University

November 16, 2006 *Association Analysis in Human Genetics Studies*
MS Statisticians meeting, Department of Biostatistics, Vanderbilt University

May 17, 2007 *Haplotype Analysis*
MS Statisticians meeting, Department of Biostatistics, Vanderbilt University

January 17, 2013 *Ordinary Logistic Regression*
MS Statisticians meeting, Department of Biostatistics, Vanderbilt University