BIOGRAPHICAL SKETCH

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NAME	POSITION TITLE
Yun Li	Assistant Professor of Genetics and Biostatistics
eRA COMMONS USER NAME yun_li	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
University of Michigan	PhD	2009	Biostatistics
Bowling Green State University	MS	2004	Applied Statistics
Bowling Green State University (BGSU)	MA	2002	Communication Studies
Shanghai JiaoTong University (SJTU), China	BS	2001	English, Computer Sci.

A. Personal Statement

The focus of my research is on the development of statistical methods and their application to the genetic dissection of complex diseases and traits. In particular, I have developed a genotype imputation method (implemented in software MaCH) that has become standard in the analysis of genome-wide association scans. I have developed methods for the analysis of rare variants and assessed different approaches to handle imputation uncertainty in subsequent association analysis. I have worked on genomewide scans for genetic variants underlying several metabolic, auto-immune and cardiovascular diseases and related quantitative traits. In addition, I have developed methods to accommodate low-coverage sequencing data and have been actively involved in a number of next-generation sequencing based studies including the 1000 Genomes Project (Project Leader on calling SNP genotypes from low-coverage pilot), targeted sequencing of selected exons in >14,000 individuals (GlaxoSmithKline QPOC sequencing project), the WHI whole exome sequencing project (WHISP), and whole genome sequencing based studies for type 2 diabetes, for cannabis and stimulant dependence, and for blood lipid levels.

B. Positions and Honors.

Professional Experience

2009- Assistant Professor, Department of Genetics, University of North Carolina
2009- Assistant Professor, Department of Biostatistics, University of North Carolina
2009- Faculty Member, Carolina Center for Genome Sciences, University of North Carolina
2009- Faculty Member, Biological and Biomedical Science Program, University of North Carolina
2004-2009 Research Assistant, Center for Statistical Genetics, University of Michigan

Other Experience and Professional Memberships

2002- Member, American Statistical Association
2003-2005 Member, American Society for Quality
2005- Member, American Society of Human Genetics
2007-2009 Member, American Association for the Advancement of Science
2007- Manuscript Reviewer, *Annals of Neurology*, *Bioinformatics*, *European Journal of Human Genetics*, *Genetic Epidemiology*, *Genome Research*, *Human Heredity*, *International Journal of Biostatistics*, *Journal of Bioinformatics and Computational Biology*, *PLoS Genetics*, *PLoS ONE*
2010- Review Editor, *Frontiers in Statistical Genetics and Methodology*

Honors and Awards

2008 Rackham Predoctoral Fellowship, University of Michigan
2008 2008 Trainee Award in Predoctoral Basic, American Society of Human Genetics
2008 Rackham One-Term Dissertation Fellowship, University of Michigan
2007 March of Dimes Scholarship on Medical and Experimental Mammalian Genetics
2005 Best Performance on the Qualifying Examination, Dept. of Biostatistics, University of Michigan
2004 Ronald Benton Scholarship, Toledo Section, American Society for Quality
2003 Wray Jackson Smith Scholarship, American Statistical Association

C. Selected peer-reviewed publications (in chronological order).

Li M, Atmaca-Sonmez P, Othman M, Branham KE, Khanna R, Wade MS, **Li Y**, Liang L, Zareparsi S, Swaroop A and Abecasis GR (2006) CFH haplotypes without the Y402H coding variant show strong association with susceptibility to age-related macular degeneration. *Nature Genetics* 38**:**1049-1054.

Scott LJ, Mohlke KL, Bonnycastle LL, Willer CJ, **Li Y**, Duren WL, Erdos MR, Stringham HM, Chines PS, Jackson AU, Prokunina-Olsson L, Ding CJ, Swift AJ, Narisu N, Hu T, Pruim R, Xiao R, Li XY, Conneely KN, Riebow NL, Sprau AG, Tong M, White PP, Hetrick KN, Barnhart MW, Bark CW, Goldstein JL, Watkins L, Xiang F, Saramies J, Buchanan TA, Watanabe RM, Valle TT, Kinnunen L, Abecasis GR, Pugh EW, Doheny KF, Bergman RN, Tuomilehto J, Collins FS, Boehnke M (2007) A genome-wide association study of type 2 diabetes in Finns detects multiple susceptibility variants. *Science* 316**:**1341-1345*.*

The International HapMap Consortium (2007) A second generation human haplotype map of over 3.1 million SNPs. *Nature* 449:851-861.

Willer CJ *et al.* (2008) Newly identified loci that influence lipid concentrations and risk of coronary artery disease. *Nature Genetics* 40:161-169.

Zeggini E *et al.* (2008) Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. *Nature Genetics* 40:638-645.

Chambers JC, Elliott P, Zabaneh D, Zhang W, **Li Y**, Froguel P, Balding D, Scott J, Kooner JS (2008) Common genetic variation near the melanocortin-4 receptor gene is associated with waist circumference and insulin resistance. *Nature Genetics* 40:716-718.

Gaulton KJ, Willer CJ, **Li Y**, Scott LJ, Conneely KN, Jackson AU, Duren WL, Chines PS, Narisu N, Bonnycastle LL, Luo J, Tong M, Sprau AG, Pugh EW, Doheny KF, Valle TT, Abecasis GR, Tuomilehto J, Bergman RN, Collins FS, Boehnke M, Mohlke KL (2008) Comprehensive association study of type 2 diabetes and related quantitative traits with 222 candidate genes. *Diabetes* 57:3136-3144.

Kathiresan S, Willer CJ, Peloso G, Demissie S, Musunuru K, Schadt E, Kaplan L, Bennett D, **Li Y**, *et al*. (2009) Common variants at 30 loci contribute to polygenic dyslipidemia. *Nature Genetics* 41:56-65*.*

Nair RP, Duffin KC, Helms C, Ding J, Stuart PE, Goldgar D, Gudjonsson JE, **Li Y**, Tejasvi T, Feng BJ, Ruether A, Schreiber S, Weichenthal M, Gladman D, Rahman P, Schrodi SJ, Prahalad S, Guthery SL, Fischer J, Liao W, Kwok PY, Menter A, Lathrop GM, Wise CA, Begovich AB, Voorhees JJ, Elder JT, Krueger GG, Bowcock AM, Abecasis GR; Collaborative Association Study of Psoriasis (2009) Genome-wide scan reveals association of psoriasis with IL-23 and NF-κB pathways. *Nature Genetics* 41:199-204*.*

Huang L, **Li Y**, Singleton AB, Hardy JA, Abecasis GR, Rosenberg NA, Scheet P (2009) Genotype imputation accuracy across worldwide human populations. *The American Journal of Human Genetics* 84:235-250.

Li Y, Willer CJ, Sanna S, Abecasis GR (2009) Genotype imputation. *Annual Review Genomics and Human Genetics* 10:387-406*.*

Chambers JC, Zhang W, **Li Y**, Sehmi J, Wass MN, Zabaneh D, Hoggart C, Bayele H, McCarthy MI, Peltonen L, Freimer NB, Srai SK, Maxwell PH, Sternberg MJ, Ruokonen A, Abecasis G, Jarvelin MR, Scott J, Elliott P, Kooner JS (2009) Genome-wide association study identifies variants in *TMPRSS6* associated with hemoglobin levels. *Nature Genetics* 41:1170-1172*.*

Dupuis J *et al.* (2010) New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics.* 42:105-116.

Lange LA, Croteau-Chonka DC, Marvelle AF, Qin L, Gaulton KJ, Kuzawa CW, McDade TW, Wang Y, **Li Y**, Levy S, Borja JB, Lange EM, Adair LS, Mohlke KL (2010) Genome-wide association study of homocysteine levels in Filipinos provides evidence for *CPS1* in women and a stronger *MTHFR* effect in young adults. *Human Molecular Genetics* 19:2050-2058.

Chambers JC, Zhang W, Lord GM, Lightstone L, Eggermann T, Schlieper G, van der Harst P, Abecasis GR, Ahmadi KR, Bakker SJ, Bilo HJG, Caulfield MJ, Cotlarciuc I, Hypponen E, Jarvelin MR, Lawlor DA, **Li Y**, *et*

al. (2010) Genetic loci influencing kidney function and chronic kidney disease. *Nature Genetics* 42:373-375.

Sanna S, Pitzalis M, Zoledziewska M, Zara I, Sidore C, Murru R, Whalen MB, Busonero F, Maschio A, Costa G, Melis MC, Deidda F, Poddie F, Morelli L, Farina G, **Li Y**, Dei M, Lai S, Mulas A, Cuccuru G, Porcu E, Liang L, Zavattari P, Moi L, Deriu E, Urru MF, Bajorek M, Satta MA, Cocco E, Ferrigno P, Sotgiu S, Pugliatti M, Traccis S, Angius A, Melis M, Rosati G, Abecasis GR, Uda M, Marrosu MG, Schlessinger D, Cucca F (2010) Variants within the immunoregulatory CBLB gene are associated with multiple sclerosis. *Nature Genetics* 42:495-497.

Willer CJ, **Li Y**, Abecasis GR (2010) METAL: fast and efficient meta-analysis of genomewide association scans. *Bioinformatics* 26:2190-2191.

Kapur K, Johnson T, Beckmann ND, Sehmi J, Tanaka T, Kutalik Z, Styrkarsdottir U, Zhang W, Marek D, Gudbjartsson DF, Milaneschi Y, Holm H, Diiorio A, Waterworth D, **Li Y**, Singleton AB, Bjornsdottir US, Sigurdsson G, Hernandez DG, Desilva R, Elliott P, Eyjolfsson GI, Guralnik JM, Scott J, Thorsteinsdottir U, Bandinelli S, Chambers J, Stefansson K, Waeber G, Ferrucci L, Kooner JS, Mooser V, Vollenweider P, Beckmann JS, Bochud M, Bergmann S (2010) Genome-wide meta-analysis for serum calcium identifies significantly associated SNPs near the calcium-sensing receptor (*CASR*) gene. *PLoS Genetics* 6:e1001035.

Wu Y, **Li Y**, Lange EM, Croteau-Chonka DC, Kuzawa CW, McDade TW, Qin L, Curocichin G, Borja JB, Lange LA, Adair LS, Mohlke KL (2010) Genome-wide association study for adiponectin levels in Filipino women identifies *CDH13* and a novel uncommon haplotype at *KNG1-ADIPOQ. Human Molecular Genetics* 19:4955-4964.

Ellinghaus E, Ellinghaus D, Stuart PE, Nair RP, Debrus S, Raelson JV, Belouchi M, Fournier H, Reinhard C, Ding J, **Li Y**, Tejasvi T, Gudjonsson J, Stoll SW, Voorhees JJ, Lambert S, Weidinger S, Eberlein B, Kunz M, Rahman P, Gladman DD, Gieger C, Wichmann HE, Karlsen TH, Mayr G, Albrecht M, Kabelitz D, Mrowietz U, Abecasis GR, Elder JT, Schreiber S, Weichenthal M, Franke A (2010) Genome-wide association study identifies a psoriasis susceptibility locus at *TRAF3IP2*. *Nature Genetics* 42:991-995.

Wassel CL, Lange LA, Keating BJ, Taylor KC, Johnson AD, Palmer CD, Ho LA, Smith NL, Lange EM, **Li Y**, Yang Q, Delaney JA, Tang W, Tofler G, Redline S, Taylor HA Jr, Wilson JG, Tracy RP, Jacobs DR Jr, Folsom AR, Green D, O'Donnell CJ, Reiner AP (2010) Association of genomic loci from a cardiovascular gene SNP array with fibrinogen levels in European Americans and African-Americans from six cohort studies: the Candidate gene Association Resource (CARe). *Blood*. [Epub ahead of print]

The 1000 Genomes Project. (2010) A map of human genome variation from population scale sequencing. *Nature* 467:1061-1073.

Li Y, Byrnes AE, Li M (2010) To identify associations with rare variants, just WHaIT: Weighted haplotype and imputation-based tests. *The American Journal of Human Genetics* 87:728-735.

Li Y, Willer CJ, Scheet P, Ding J, and Abecasis GR (2010) MaCH: using sequence and genotype data to estimate haplotypes and unobserved genotypes. *Genetic Epidemiology* 34:816-834.

Zawistowski M, Gopalakrishnan S, Ding J, **Li Y**, Grimm S, Zollner S. (2010) Extending rare variant testing strategies: analysis of non-coding sequence and imputed genotypes. *The American Journal of Human Genetics* 87:604-617.

Ding J, Gudjonsson JE, Liang L, Stuart PE, **Li Y**, Chen W, Weichenthal M, Ellinghaus E, Franke A, Cookson W, Nair RP, Elder JT, Abecasis GR (2010) Gene expression in skin and lymphoblastoid cells: refined statistical method reveals extensive overlap in cis-eQTL signals. *The American Journal of Human Genetics* 87:779-789.

Zheng J, **Li Y**, Abecasis GR, Scheet P (2011) A comparison of approaches to account for uncertainty in analysis of imputed genotypes. *Genetic Epidemiology* 35: 102-110.

D. Research Support

ACTIVE

3R01 DK078150-04(NCE) Mohlke (PI) 04/01/07-03/31/12
Genetic Epidemiology of Body Mass Index, Adiposity, and Weight Gain
The goals of this study are to test candidate genes for association with obesity-related traits and weight gain across 22 years in women from the Cebu Longitudinal Health and Nutrition Survey and to evaluate interactions with diet composition and physical activity.
Role: Co-Investigator

Subcontract No. 3001352222 Li (PI) 12/01/09-11/30/11
GlaxoSmithKline/UMichigan
The goal of this project is to develop and apply imputation based methodology to genome wide association and sequencing datasets.
Role: Subcontract PI

1RC2HL102924-01 Jackson, North (PI) 09/30/09-07/31/11
WHI Sequencing Project (WHISP)
The overall goal of this project submitted in response to NHLBI RC2 Topic 'Large-scale DNA Sequencing and Molecular Profiling of Well-phenotyped NHLBI Cohorts' (RFA-OD-09-004) is to identify putative functional variants for high-priority heart lung and blood phenotypes among American post-menopausal women from diverse ancestral and geographic backgrounds.
Role: Co-Investigator

1R01 DA030976-01 Wilhelmsen (PI) 09/30/10-05/31/15
Deep Sequencing Studies for Cannabis and Stimulant Dependence
The goal of this proposal is to identify genes that affect susceptibility to stimulant and cannabis dependence using whole genome sequencing with genotype imputation.
Role: Co-Investigator

3R01 CA082659-11S1 Lin (PI) 08/01/09-07/31/11
Statistical Methods in Cancer Research
The goal of this project is the development of statistical methods for the designs and analysis of clinical and epidemiological cancer studies.
Role: Co-Investigator

5P01HD031921-15 Whitsel (PI) 08/01/10-03/51/13
Modification of PM-mediated Arrhythmogenesis in Populations
The goal of the project is to examine susceptibility to the arrhythmogenic effects of particulate matter (PM) air pollution contributed by common genetic variation.
Role: Co-Investigator

U01 DA024413 Costello (PI) 09/01/07-06/30/12
A developmental model of gene-environment interplay in SUDs
The major goal of this study is to investigate genetic main effects and gene-environment interactions using GWAS data in longitudinal studies of substance initiation and progression.
Role: Co-Investigator

RD83272001 Wright (PI) 10/01/05-09/30/11
Computational Toxicology: Environmental Bioinformatics Research
Role: Co-Investigator

PAST

5R01 HL095396-02 Knowles (PI) 09/24/08-07/31/12
Molecular Phenotypes for Cystic Fibrosis Lung Disease
The goal of this project is to define a molecular phenotype for CF lung disease, which relates to prognosis, and new targets for therapy.
Role: Co-Investigator