Curriculum Vitae

Yun Ju Sung PhD
04/12/2021

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Present Position: Associate Professor of Psychiatry and Biostatistics, Washington University School of Medicine

Education:

1991-1995	BS in Mathematics, Pohang University of Science and Technology, Korea
1997-2001	MS in Statistics, University of Minnesota, Minneapolis, MN
2001-2003	PhD in Statistics, University of Minnesota, Minneapolis, MN

Academic Positions/Employment:

1998-2003	Teaching Assistant, Research Assistant, Consultant, School of Statistics, University of Minnesota, Minneapolis, MN
2001-2002	Instructor, School of Statistics, University of Minnesota, Minneapolis, MN
2003-2006	Postdoctoral Fellow, Division of Medical Genetics, University of Washington, Seattle, WA
2006-2014	Assistant Professor, Division of Biostatistics, Washington University School of Medicine, St Louis, MO
2015-2019	Associate Professor, Division of Biostatistics, Washington University School of Medicine, St Louis, MO
2020-present	Associate Professor, Department of Psychiatry, Washington University School of Medicine, St Louis, MO

Honors and Awards:

1999-2000	School of Statistics Alumni Fellowship, University of Minnesota
2001-2002	Graduate School Doctoral Dissertation Fellowship, University of Minnesota

Editorial Responsibilities:

Ad Hoc Journal Review: Genetic Epidemiology, Human Heredity, BMC Bioinformatics

Professional Societies and Organizations:

Memberships:

2005-present	American Society of Human Genetics
2006-present	International Genetic Epidemiology Society

Meeting Talks:

1. **Sung YJ** and Geyer CJ. Misspecification error in missing data models. *The Eastern North American Region (ENAR) Meeting*, April 1, 2003.
2. **Sung YJ** and Geyer CJ. Model misspecification error for mutation accumulation experiments. *Joint Statistical Meeting*, August 6, 2003.

3. **Sung YJ**, Thompson EA and Wijsman EM. MCMC-based multipoint linkage analysis for two loci plus a polygenic component and general pedigrees. *American Society of Human Genetics (ASHG) Meeting*, October 28, 2005.
4. **Sung YJ**, Thompson EA and Wijsman EM. MCMC-based multipoint linkage analysis for two loci plus a polygenic component and general pedigrees. *3rd Seattle Symposium in Biostatistics*, November 21, 2005.
5. **Sung YJ**, Thompson EA and Wijsman EM. MCMC linkage analysis for two genes and a polygenic component on general pedigrees. *9th Meeting of New Researchers in Statistics and Probability*, August 3, 2006.
6. **Sung YJ**, Thompson EA and Wijsman EM. Accounting for epistasis in linkage analysis of general pedigrees. *International Genetic Epidemiology Society (IGES) 15th Annual Meeting*, November 16, 2006.
7. **Sung YJ** and Rao DC. Imprinting effects in linkage analysis. *The Western North American Region (WNAR) Meeting*, June 26, 2007.
8. **Sung YJ** and Rao DC. Ignoring imprinting effects can severely jeopardize detection of linkage. *American Society of Human Genetics (ASHG) Meeting*, October 23, 2007.
9. **Sung YJ** and Rao DC. Model selection criteria in Bayesian networks. *International Genetic Epidemiology Society (IGES) 17th Annual Meeting*, September 15, 2008.
10. **Sung YJ**. Group 3: Multistage analysis strategies for GWA studies. *Genetic Analysis Workshop (GAW) 16*, September 17, 2008. Group presentation.
11. **Sung YJ**, Duan Y, Rice TK, Rankinen T, Bourchard C, and Gu CC. Evaluation of imputation strategies for family data. *International Genetic Epidemiology Society (IGES) 18th Annual Meeting*, October 19, 2009.
12. Ziegler A, **Sung YJ**, and Sun Y. Group 15: Collapsing methods for multiple rare variants. *Genetic Analysis Workshop (GAW) 17*. October 14, 2010. Group presentation.
13. Engelman C and **Sung YJ**. Collapsing methods. *Genetic Analysis Workshop (GAW) 18*, October 15, 2012. Group presentation
14. **Sung YJ**, Schwander K, Arnett D, Kardia S, Rankinen T, Bourchard C, Boerwinkle E, Hunt SC, Rao DC. How effective is meta-analysis as compared to mega-analysis of the pooled data for identifying gene-environmental interactions? *International Genetic Epidemiology Society (IGES) 22nd Annual Meeting*, September 17, 2013.
15. de las Fuentes L, Sitlani CM, Sun F, **Sung YJ** on behalf of Pharmacogenetics Working Group. Genome-wide meta-analysis of SNP-by-loop diuretic interactions as modulators of triglyceride levels for European and African ancestry in CHARGE. *Washington, DC CHARGE Investigator Meeting* on November 12-13, 2014.
16. **Sung YJ**, de las Fuentes L, Sitlani CM, Sun F. Genome-wide meta-analysis of SNP-by-loop diuretic interactions as modulators of triglyceride levels for European and African ancestry in CHARGE. *Third Annual Cardiovascular Research Day* on November 7, 2014 Washington University School of Medicine, St Louis.

17. **Sung YJ**, Winkler T, Bentley A, Brown MR. Meta-analysis of gene-smoking interactions in blood pressure using 1000 Genomes imputed data from four ethnic groups. Platform presentation at *Jackson, MS CHARGE Investigator Meeting* on July 1-2, 2015.

18. **Sung YJ**, Winkler TW, Manning AK, Kardia S, Zhu X, Rice K, Borecki IB, Rao DC, Gauderman WJ, Cupples LA. An empirical comparison of interaction and stratified models to GxE interaction analysis: Smoking and systolic blood pressure in the CHARGE Gene-Lifestyle Interactions Working Group. Platform presentation at *International Genetic Epidemiology Society (IGES) 24nd Annual Meeting*, October 4-6, 2015

19. **Sung YJ**, Winkler T, Bentley A, Brown MR, …, Borecki IB, Cupples LA, Rao DC, Morrison A on behalf of the CHARGE Gene-Lifestyle Interactions Working Group. Meta-analysis of gene-smoking interactions in blood pressure using 1000 Genomes imputed data from four ethnic groups. Platform presentation at *American Society of Human Genetics (ASHG) Meeting*, October 7-10, 2015

20. **Sung YJ**. Gene-Smoking interactions in blood pressure. Division Seminar at Division of Biostatistics, Washington University, March 4, 2016

21. Kraja AT, Chasman DI, **Sung YJ**, Aschard H, Manning AK, Feitosa MF, Winkler T, Zhu X, Province MA on behalf of the CHARGE Gene-Lifestyle Interactions Working Group. Blood pressure gene x alcohol exposure interactions capture association pleiotropy. Poster presented at the 25th Annual International Genetic Epidemiology Society (IGES) Meeting, Toronto, Canada. October 24-26,2016.

22. Cushing KC, Chiplunker AJ, Li A, **Sung YJ**, Geisman T, Chen LS, Cresci S, Gutierrez AC. Smoking interacts with CHRNA5, a nicotine acetylcholine receptor subunit gene, to influence the risk of IBD related surgery. Presented a poster on at *Digestive Disease Week*, May 7-9, 2017 DOI: http://dx.doi.org/10.1016/S0016-5085(17)33340-1

23. Laville V, **Sung YJ**, Province M, Gauderman J, Chasman DI. Rao DC, Aschard H, on behalf of the CHARGE Gene-Lifestyle Interactions Working Group. Estimating the heritability of gene-environment interactions. *International Genetic Epidemiology Society (IGES) 26nd Annual Meeting*, September 9-11, 2017

24. **Sung YJ** on behalf of the CHARGE Gene-Lifestyle Interactions Working Group. Multi-ancestry genome-wide study incorporating gene-smoking interactions identifies 139 genome-wide significant loci for systolic and diastolic blood pressure. Selected for travel award and platform presentation at *Boston, MA CHARGE Investigator Meeting*, September 27-28, 2017.

25. Laville V, **Sung YJ**, Province M, Gauderman J, Chasman DI, Rao DC, Aschard H, on behalf of the CHARGE Gene-Lifestyle Interactions Working Group. Estimating the heritability of gene-environment interactions. *American Society of Human Genetics (ASHG) Meeting*, October 17-21, 2017

26. Kraja AT, Feitosa MF, Chasman D, **Sung YJ**, …, Rao DC, Zhu X, and Province MA on behalf of the CHARGE Gene-Lifestyle Interactions Working Group. Pleiotropic effects on blood pressure traits using genome-wide analysis of gene-alcohol interactions. *American Heart Association* 2017

27. **Sung YJ**, Winkler TW, de las Fuentes L, …, Rao DC, Chasman DI, on behalf of the CHARGE Gene-Lifestyle Interactions Working Group. Multi-ancestry genome-wide study incorporating gene-smoking interactions identifies 139 genome-wide significant loci for systolic and diastolic blood pressure. *American Society of Human Genetics (ASHG) Meeting*, October 17-21, 2017

28. Bentley AR, … **Sung YJ**, … Rotimi CN, and Cupples LA, on behalf of the CHARGE Gene-Lifestyle Interactions Working Group. Multi-ethnic genome-wide association study of gene × smoking interactions identifies novel lipids loci. Platform presentation at *American Society of Human Genetics (ASHG) Meeting*, October 17-21, 2017

29. **Sung YJ**, Schwander KL, and de las Fuentes L on behalf of the CHARGE Gene-Lifestyle Interactions Working Group. Multi-ancestry genome-wide study accounting for gene-smoking interactions identifies multiple novel loci for pulse pressure and mean arterial pressure. Selected to Poster Bliz at *Rotterdam, the Netherlands CHARGE Investigator Meeting*, April 18-19, 2018

30. Schwander KL, de las Fuentes L, Winkler T, **Sung YJ** on behalf of the CHARGE Gene-Lifestyle Interactions Working Group. Multi-ancestry Genome-wide meta-analysis in 413,324 individuals accounting for gene-education interactions identifies novel loci for blood pressure. *Rotterdam, the Netherlands CHARGE Investigator Meeting*, April 18-19, 2018

31. Laville V, **Sung YJ**, Winkler T, Province M, Rice K, Kardia SLR, Gauderman J, Rao DC, Aschard H, on behalf of the CHARGE Gene-Lifestyle Interactions Working Group. Can gene-environment interaction analysis tell us about mechanisms in multifactorial diseases? Platform presentation at *American Society of Human Genetics (ASHG) Meeting*, October 15-19, 2018

32. **Sung YJ**, Schwander KL, Kilpeläinen T, Aschard H, de las Fuentes L on behalf of the CHARGE Gene-Lifestyle Interactions Working Group. Multi-ancestry genome-wide meta-analysis accounting for gene-education interactions in up to 227,850 individuals identifies novel lipid loci. *St Louis, the CHARGE Investigator Meeting*, June 26-28, 2019

33. **Sung YJ**, Schwander KL, Bentley AR, de Vries P, Kilpeläinen T, Noordam R, Musani SK, Aschard H, de las Fuentes L on behalf of the CHARGE Gene-Lifestyle Interactions Working Group. Multi-ancestry genome-wide meta-analysis accounting for gene-education interactions in up to 227,850 individuals identifies several novel lipid loci. *International Genetic Epidemiology Society (IGES) 26nd Annual Meeting*, October 12-14, 2019

34. Laville V, Majarian T, **Sung YJ**, Feitosa MF, Chasman D, Bentley AR, Rotimi CN, Cupples AL, de Vries PS, Brown MR, Morrison AC, Kraja AT, Province M, Schwander K, Gauderman J, DC Rao, Manning A, Aschard H. Large-scale multi-ancestry gene-environment

interaction screenings point towards different genetic mechanisms by population and exposure. *American Society of Human Genetics (ASHG) Meeting*, October 15-19, 2019

35. Chen H, Wang X, Manning AK, **Sung YJ**, Rao DC, Morrison AC, Boerwinkle E. Efficient gene-environment interaction tests for large biobank-scale sequencing studies. *American Society of Human Genetics (ASHG) Meeting*, October 15-19, 2019

36. **Sung YJ**, Yang C, Rhinn H, Norton J, Wang F, Bradley J, Farias F, Benitez BA, Harari O, Cruchaga C. Multi-tissue high-throughput proteomics profiling for neurodegenerative disease. *Keystone Symposia on Proteomics in Cell Biology and Disease,* September 21-23, 2020.

37. Westerman KE, Pham DT, Hong L, Chen Y, Sevilla-González M, **Sung YJ**, Sun YV, Morrison AC, Chen H, Alisa K. Manning AK. Scalable gene-environment interaction analysis and application to waist-hip ratio in the UK Biobank. *American Society of Human Genetics (ASHG) Meeting*, October 27-30, 2020

38. **Sung YJ**, Yang C, Rhinn H, Norton J, Wang F, Bradley J, Farias F, Benitez BA, Harari O, Cruchaga C. Multi-tissue proteomic signatures of genetically defined Alzheimer disease cases: a window into precision medicine. *The 15th International Conference on Alzheimer's and Parkinson's Diseases*, March 9-14, 2021

Research Support:

a) Governmental:

PI, Statistical Methods for Genomic Dissection of Cardiovascular Diseases NIH K25HL121091. 7/1/2014 to 6/30/2020 (NCE). $137,407. This mentored career development grant application proposes a training program to integrate my previous research in statistical genetics into cardiovascular disease (CVD). The research objective is to decipher the genetic and environmental architecture of cardiometabolic traits by incorporating GxE interactions and regulatory annotation information.

Teaching Title and Responsibilities:

a) Current Teaching:

1. Course Master of **Fundamentals of Genetic Epidemiology** (M21-515), 2007-present
2. Course Master of **Introduction to R for Data Science** (M21-506), 2013-present
3. Instructor of PRIDE Summer Institute in Cardiovascular Genetic Epidemiology: Genome-wide association studies and hands-on practice using PLINK, 2012-present

b) Past Teaching:

1. Teaching Assistant, University of Minnesota, 1998—2000
   Introductory Statistics for Engineers (Stat 3021)
   Master's-level **Theoretical Statistics (Stat 5122/5132/5133)**
   Master's-level **Design of Experiments (Stat 5303)**
2. Instructor, University of Minnesota, Spring 2001, Summer 2001, Fall 2002
   Introductory Statistics for Liberal Education Requirement (Stat 1001)
3. Instructor, Washington University, 2008-2013
   Computational Statistical Genetics (M21-621)
   Biostatistics II (M21-570)

c) Research Supervision (Master's-level):

1. Gabroel Alejandro de Erausquin (2008) Hypodopaminergic state as a quantitative trait in schizophrenia: Identification of SNP clusters by decision tree machine learing and QTLs by association.
2. Olivia Levi Knowles (2010) Methods for defining salt sensitivity and discovering genetic associations in GenSalt.
3. Visali Immidisetti (2010) Genome wide assocation analysis of responses to exercise training in fasting glucose.
4. Carlos Gonzalez (2011) Genome-wide association study of smoking in the genetic epidemiology network of salt sensitivity (GenSalt) study.
5. Lihua Wang (2011) Rare variant analysis for simulated phenotypes using the Genetic Analysis Workshop 17 family data.
6. Sonia Kalathiveetil (2012) The role of SNP-loop diuretic interaction in hypertension across ethnic groups in HyperGEN.
7. Cates Mallaney (2012) A test of methods for rare variant analysis on blood pressure in 147 unrelated individuals in the GAW18 dataset.
8. Nuo Cheng (2013) Role of rare variants in systolic blood pressure: Analysis of exome chip data in HyperGEN African American study.
9. Yize Li (2015) Evaluating the role of gene-smoking interactions in the known blood pressure loci.

Committees:

1998-2000	Salary Equity Task Force, University of Minnesota
2002-2003	Faculty Search Committee, School of Statistics, University of Minnesota
2006-2009	Seminar Organizer, Division of Biostatistics, Washington University
2009-present	Curriculum Committee, Division of Biostatistics, Washington University
2011-present	Admission Committee, Division of Biostatistics, Washington University
2014-2015	Faculty Search Committee, Department of Mathematics, Washington University
Summer 2015	Abstract Reviewer of American Society of Human Genetics Meeting 2015

Publications (published or in press):

1. **Sung YJ**, Dawson G, Munson J, Estes A, Schellenberg GD, Wijsman EM. Genetic investigation of quantitative traits related to autism: Use of multivariate polygenic models with ascertainment adjustment. *American Journal of Human Genetics*. 2005;76:68-81
2. Sieh W, Basu S, Fu AQ, Rothstein JH, Scheet PA, Stewart WC, **Sung YJ**, Thompson EA, Wijsman EM. Comparison of marker types and map assumptions using MCMC-based linkage analysis of COGA data. *BMC Genetics*. 2005;6 Suppl 1:S11
3. Schellenberg GD, Dawson G, **Sung YJ**, Estes A, Munson J, Rosenthal E, Rothstein J, Flodman P, Smith M, Coon H, Leong L, Yu CE, Stodgell C, Rodier PM, Spence MA, Minshew N, McMahon WM, Wijsman EM. Evidence for multiple loci from a genome scan of autism kindreds. *Molecular Psychiatry*. 2006;11:1049-1060, 1979
4. **Sung YJ**, Geyer CJ. Monte Carlo likelihood inference for missing data models. *Annals of Statistics*. 2007;35:990-1011
5. **Sung YJ**, Thompson EA, Wijsman EM. MCMC-based linkage analysis for complex traits on general pedigrees: Multipoint analysis with a two-locus model and a polygenic component. *Genetic Epidemiology*. 2007;31:103-114

6. **Sung YJ**, Wijsman EM. Accounting for epistasis in linkage analysis of general pedigrees. *Human Heredity*. 2007;63:144-152
7. **Sung YJ**, Di Y, Fu AQ, Rothstein JH, Sieh W, Tong L, Thompson EA, Wijsman EM. Comparison of multipoint linkage analyses for quantitative traits in the CEPH data: Parametric lod scores, variance components lod scores, and Bayes factors. *BMC Proceedings*. 2007;1 Suppl 1:S93
8. Wijsman EM, **Sung YJ**, Buil A, Atkinson E, Bastone L, Christensen GB, Diao G, Feng T, Franceschini N, Huang S, Kan D, Kerner B, Lantieri F, Lee E, Papachristou C, Paterson A, Rangrej J, Wang S, Xing C, Zhu X. Summary of Genetic Analysis Workshop 15: Group 9 linkage analysis of the CEPH expression data. *Genetic Epidemiology*. 2007;31 Suppl 1:S75-85
9. **Sung YJ**, Rao DC. Model-based linkage analysis with imprinting for quantitative traits: Ignoring imprinting effects can severely jeopardize detection of linkage. *Genetic Epidemiology*. 2008;32:487-496
10. Xiong C, Gao F, Yan Y, Luo J, **Sung YJ**, Shi G. On measuring overall heterogeneity in meta-analysis: Application to CSF biomarker studies in Alzheheimer's disease. *Journal of Modern Applied Statistical Methods*. 2008;7:286-296
11. **Sung YJ**, Rice TK, Shi G, Gu CC, Rao D. Comparison between single-marker analysis using Merlin and multi-marker analysis using lasso for Framingham simulated data. *BMC Proceedings*. 2009;3 Suppl 7:S27
12. Rice TK, **Sung YJ**, Shi G, Gu CC, Rao D. Genome-wide association analysis of Framingham Heart Study data for the Genetics Analysis Workshop 16: Effects due to medication use. *BMC Proceedings*. 2009;3 Suppl 7:S52
13. Neuman RJ, **Sung YJ**. Multistage analysis strategies for genome-wide association studies: Summary of Group 3 contributions to Genetic Analysis Workshop 16. *Genetic Epidemiology*. 2009;33 Suppl 1:S19-23
14. **Sung YJ**, Rice TK, Rao DC. Application of collapsing methods for continuous traits to the Genetic Analysis Workshop 17 exome sequence data. *BMC Proceedings*. 2011;5 Suppl 9:S121
15. Sun YV, **Sung YJ**, Tintle N, Ziegler A. Identification of genetic association of multiple rare variants using collapsing methods. *Genetic Epidemiology*. 2011;35 Suppl 1:S101-106
16. Bouchard C, Sarzynski MA, Rice TK, Kraus WE, Church TS, **Sung YJ**, Rao DC, Rankinen T. Genomic predictors of the maximal oxygen uptake response to standardized exercise training programs. *Journal of Applied Physiology*. 2011;110:1160-1170
17. Kato N, Takeuchi F, Tabara Y, Kelly TN, Go MJ, …, **Sung YJ**, …,Wu JY, Teo YY, Tai ES, Cho YS, He J. Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. *Nature Genetics*. 2011;43:531-538
18. **Sung YJ**, Wang L, Rankinen T, Bouchard C, Rao DC. Performance of genotype imputations using data from the 1000 Genomes Project. *Human Heredity*. 2012;73:18-25
19. **Sung YJ**, Gu CC, Tiwari HK, Arnett DK, Broeckel U, Rao DC. Genotype imputation for African Americans using data from Hapmap Phase II versus 1000 Genomes Projects. *Genetic Epidemiology*. 2012;36:508-516

20. Rankinen T, **Sung YJ**, Sarzynski MA, Rice TK, Rao DC, Bouchard C. Heritability of submaximal exercise heart rate response to exercise training is accounted for by nine SNPs. *Journal of Applied Physiology*. 2012;112:892-897

21. Rice TK, Sarzynski MA, **Sung YJ**, Argyropoulos G, Stutz AM, Teran-Garcia M, Rao DC, Bouchard C, Rankinen T. Fine mapping of a QTL on chromosome 13 for submaximal exercise capacity training response: The HERITAGE Family Study. *European Journal of Applied Physiology*. 2012;112:2969-2978

22. Chen LS, Saccone NL, Culverhouse RC, Bracci PM, Chen CH, …, **Sung YJ**, …, Wiencke JK, Wu JY, Yokota J, Amos CI, Bierut LJ. Smoking and genetic risk variation across populations of European, Asian, and African American ancestry: a meta-analysis of chromosome 15q25. *Genetic Epidemiology*. 2012;36:340-351

23. David SP, Hamidovic A, Chen GK, Bergen AW, Wessel J, …, **Sung YJ**, …, Ziegler RG, Zonderman AB, Jorgenson E, Haiman CA, Furberg H. Genome-wide meta-analyses of smoking behaviors in African Americans. *Translational Psychiatry*. 2012;2:e119

24. Wu Y, Waite LL, Jackson AU, Sheu WH, Buyske S, …, **Sung YJ**, …, Assimes TL, Crawford DC, Hsiung CA, North KE, Mohlke KL. Trans-ethnic fine-mapping of lipid loci identifies population-specific signals and allelic heterogeneity that increases the trait variance explained. *PLoS Genetics*. 2013;9:e1003379

25. Franceschini N, Fox E, Zhang Z, Edwards TL, Nalls Michael A, **Sung YJ**, …, Chakravarti A, Reiner AP, Levy D, Keating BJ, Zhu X. Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. *American Journal of Human Genetics*. 2013;93:545-554

26. Ghosh S, Vivar J, Sarzynski M, **Sung YJ**, Timmons J, Bouchard C, T. R. Integrative pathway analysis of a genome-wide association study of VO2max response to exercise training. *Journal of Applied Physiology*. 2013;115:1343-1359.

27. He J, Kelly T, Zhao Q, Li H, Huang J, Wang L, Jaquish C, **Sung YJ**, Shimmin L, Lu F, Mu J, Hu D, Ji X, Shen C, Guo D, Ma J, Wang R, Shen J, Li S, Chen J, Mei H, Chen C-S, Chen S, Chen J, Li J, Cao J, Lu X, Wu Z, Rice TK, Gu CC, Schwander K, Hamm L, Liu D, Rao DC, Hixson J, Gu D. Genome-wide association study identifies eight novel loci associated with blood pressure responses to interventions in Han Chinese. *Circulation: Cardiovascular Genetics.* 2013; 6:598-607.

28. de las Fuentes L*, **Sung YJ***, Schwander K, Kalathiveetil S, Hunt SC, Arnett DK, Rao DC. The role of SNP-loop diuretic interactions in hypertension across ethnic groups in HyperGEN. *Frontiers in Genetics*. 2013;4:304. doi: 10.3389/fgene.2013.00304. *Co-first authors

29. Simino J, **Sung YJ**, Kume R, Schwander K, Rao DC. Gene-alcohol interactions identify several novel blood pressure loci including a variant near SLC16a9. *Frontiers in Genetics*. 2013; 4:277. doi: 10.3389/fgene.2013.00277.

30. **Sung YJ**, Simino J, Kume R, Basson J, Schwander K, Rao DC. Comparison of two methods for analysis of gene-environment interactions in longitudinal family data: The Framingham Heart Study. *Frontiers in Genetics*. 2014;5:9. doi: 10.3389/fgene.2014.00009

31. Basson J, **Sung YJ**, Schwander K, Kume R, Simino J, de Las Fuentes L, Rao DC. Gene-education interactions identify novel blood pressure loci in the Framingham Heart Study. *American Journal of Hypertension*. 2014; 27: 431-444. doi:10.1093/ajh/hpt283

32. **Sung YJ**, Schwander K, Arnett D, Kardia S, Rankinen T, Bourchard C, Boerwinkle E, Hunt SC, Rao DC. An empirical comparison of meta-analysis and mega-analysis of individual participant data for identifying gene-environment interactions. *Genetic Epidemiology*. 2014; 38: 369-378.

33. **Sung YJ**, Basson J, Rao DC. Whole genome sequence analysis of the simulated SBP in Genetic Analysis Workshop 18 family data: Long term average and collapsing methods. *BMC Proceedings*. 2014; 8 (Suppl 1)**:**S12. doi:10.1186/1753-6561-8-S1-S12

34. Malllaney C, **Sung YJ***. Rare variant analysis of blood pressure phenotypes in the Genetic Analysis Workshop 18 whole genome sequencing data using SKAT. *BMC Proceedings*. 2014; 8 (Suppl 1):S10. doi:10.1186/1753-6561-8-S1-S10 *Corresponding author

35. **Sung YJ**, Korthauer KD, Swartz MD, Engelman CD. Methods for collapsing multiple rare variants in whole-genome sequence data. *Genetic Epidemiology*. 2014; 38 Suppl 1:S13-S28

36. Wang YJ, Tayo BO, Bandyopadhyay A, Wang H, Feng T, Franceschini N, Tang H, Gao J, **Sung YJ**, COGENT BP consortium, Elston RC, Williams SM, Cooper RS, Mu TW, Zhu X. The association of the Vanin-1 N131S variant with blood pressure is mediated by endoplasmic-reticulum-associated degradation and loss of function. *PLoS Genetics*. 2014; 10: e1004641. doi: 10.1371/journal.pgen.1004641

37. Wood AR, Esko T, Yang J, Vedantam S, Pers TH, Gustafsson S, Chu AY, Estrada K, … , **Sung YJ**, ... , Chasman DI, Goddard ME, Visscher PM, Hirschhorn JN, Frayling TM. Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*. 2014; 46: 1173–1186. doi:10.1038/ng.3097.

38. **Sung YJ**, de las Fuentes L, Schwander K, Simino J, Rao DC. Gene-smoking interactions identify several novel blood pressure loci in the Framingham Heart Study. *American Journal of Hypertension*. 2015; 28: 343–354. doi:10.1093/ajh/hpu149

39. Shungin D, Winkler TW, Croteau-Chonka DC, Ferreira T, Locke AE, …, **Sung YJ**, ... , Loos RJF, Cupples LA, Morris AP, Lindgren CM, Mohlke KL. New genetic loci link adipose and insulin biology to body fat distribution. *Nature*. 2015; 518: 187–196. doi:10.1038/nature14132

40. Locke AE, Kahali B, Berndt SI, Justice AE, Pers TH , … , **Sung YJ**, ... , North KE, Ingelsson E, Hirschhorn JN, Loos RJF, Speliotes EK. Large-scale genetic studies of body mass index provide insight into the biological basis of obesity. *Nature*. 2015; 518: 197–206. doi:10.1038/nature14177

41. **Sung YJ**, Basson J, Cheng N, Nguyen KD, Nandakumar P, Hunt SC, Arnett D, Davila-Roman V, Rao DC, Chakravarti A. Role of rare variants in systolic blood pressure: Analysis of exome chip data in HyperGEN African Americans. *Human Heredity*. 2015; 79: 20-27. DOI: 10.1159/000375373

42. Basson J*, **Sung YJ***, de Las Fuentes L, Schwander K, Cupples AL, Rao DC. Influence of smoking status and intensity on discovery of blood pressure loci through gene-smoking interactions. *Genetic Epidemiology*. 2015;39: 480–488. doi: 10.1002/gepi.21904 *Co-first authors

43. Tran NT, Aslibekyan S, Tiwari HK, Zhi DZ, **Sung YJ**, Rao DC, Hunt SC, Broeckel U, Arnett DK, Judd S, Muntner P, Kent ST, Irvin R. PCSK9 variation and association with blood pressure in African Americans: preliminary findings from the HyperGEN and REGARDS studies. *Frontiers in Genetics*. 2015; 6:136. doi: 10.3389/fgene.2015.00136

44. Winkler TW, Justice AE, Graff M, Barata L, Feitosa MF, Chu S, …, **Sung YJ**, ..., Heid IM, North KE, Borecki IB, Kutalik Z, Loos RJF. The influence of age and sex on genetic associations with adult body size and shape: a large-scale genome-wide interaction study. *PLoS Genetics*. 2015; 11:e1005378 DOI: 10.1371/journal.pgen.1005378

45. Sarzynski MA, Davidsen PK, **Sung YJ**, Hesselink MKC, Schrauwen P, Rice TK, Rao DC, Falciani F, Bouchard C. Genomic and transcriptomic predictors of triglyceride response to regular exercise. *British Journal of Sports Medicine*. 2015; 49:1524–1531. doi:10.1136/bjsports-2015-095179

46. **Sung YJ***, Pérusse L*, Sarzynski MA, Fornage M, Sidney S, Sternfeld B, Rice T, Terry G, Jacobs DR, Katzmarzyk P, Carr JJ, Ghosh S, Rankinen T, Rao DC, Bouchard C. Genome-wide association studies suggest sex-specific loci associated with abdominal and visceral fat. *International Journal of Obesity*. 2016; 40:662–674; doi:10.1038/ijo.2015.217 *Co-first authors

47. Basson J*, **Sung YJ***, de Las Fuentes L, Schwander K, Vazquez A, Rao DC. Three approaches to modeling gene-environment interactions in longitudinal family data: Gene-smoking interactions in blood pressure. *Genetic Epidemiology.* 2016; 40:73-80. doi: 10.1002/gepi.21941.

48. Kilpeläinen TO, Carli JFM, Skowronski AA, …., **Sung YJ**, …, Lindgren CM, Leibel RL, Loos RJF. Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. *Nature Communications*. 2016; 7:10494. doi:10.1038/ncomms10494

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