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CURRICULUM VITAE

Sungho Won (Ph.D.)

RESEARCH INTEREST

Biostatistics
Bioinformatics
Genetic Epidemiology

CHRONOLOGY OF EMPLOYMENT

Full time instructor,	Dept of Applied Stat, Chung-Ang Univ	2009.09. – 2009.12.
Assist Prof,	Dept of Applied Stat, Chung-Ang Univ	2010.01. – 2014.02.
Assist Prof,	Dept of Public Health Science, Seoul National Univ	2014.03. – 2016.02
Assoc Prof,	Dept of Public Health Science, Seoul National Univ	2016.03. – now

EDUCATION

July 2009 ~ Aug 2009	**Research Associate** advised by Prof. Christoph Lange Dept of Biostatistics, School of Public Health, Harvard MA USA
July 2008 ~ June 2009	**Research Follow** advised by Prof. Christoph Lange Dept of Biostatistics, School of Public Health, Harvard MA USA
Aug 2004 ~ Aug 2008	**Ph.D.** advised by Prof. Robert C. Elston and Yuquo Luo Dept of Epidemiology and Biostatistics Case Western Reserve University, Cleveland Ohio USA
Mar 2000 ~ Aug 2004	**M.S.** advised by Prof. Taesung Park Dept of Statistics, Seoul National University, Korea
July 1996 ~ Feb 2000	**B.S.** Dept of Biological Education, Seoul National University, Korea

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AWARDS

Scholarships

2008	Intl Genetic Epi Society. St. Louis MI USA
2006	Genetic Analysis Workshop 15. Tampa Bay FL USA

EDITORIAL BOARDS

Associate editor, BMC Medical Genetics	2017.11.01 –
Editorial board, The Korean Journal of Applied Statistics	2012.01.01 –
Editorial board, Genes & genomics	2017.08.01 –

BOOK CHAPTER

1. Analysis of complex disease association studies *A practical guide*. Sham PC, *et al*. ELSEVIER 2011.
2. Statistical Human Genetics. Method and Protocol. Elston RC. Spring 2017. Chapter: Namkung J, Won S. Single Marker Family-Based Association Analysis Not Conditional on Parental Information (409-437).

PATENT

1. Alignment algorithm of sequence data. Registration Number: 10-1768122

SOFTWARES

1.	Tool for rare variant association analysis with GRM.	2013.03.05.	C-2013-004457
2.	Tool for estimating heritability with family-based samples.	2013.02.26.	C-2013-002696
3.	Software to analyze the copy number variation	2014.03.06.	C-2014-005311
4.	FARVATX	2014.07.22.	C-2014-018137
5.	WISARD	2015.01.20.	C-2015-001092
6.	FARVAT	2015.01.20.	C-2015-001093
7.	SelSAMPLE	2016.08.08.	C-2016-019299
8.	mFARVAT	2016.08.08.	C-2016-019300
9.	ONETOOL	2017.07.14.	C-2017-016439
10.	Rex-Pro		

PUBLICATIONS (* equally contributed, †: corresponding authors, underline: lab students)

1. **Won S**, Elston RC, Park T†. Extension of the Haseman-Elston regression model to longitudinal data. *Human Heredity* (SCI) 2006 May;61(2);111-119. 2.
2. **Won S**, Shinha R, Luo Y†. Fine-scale linkage disequilibrium mapping: A comparison of coalescent-based and haplotype-clustering-based methods. *BMC proceeding* (Proceeding) 2007 Nov;31(Suppl 1);S133. 3.
3. Igo RP, Londono D, Miller K, Parrado AR, Quade SRE, Sinha M, Kim S, **Won S**, Li J, Goddard KAB†. Density-based clustering in haplotype analysis for association mapping. *BMC proceeding* (Proceeding) 2007 Nov;31(Suppl 1);S27.
4. Ziegler A†, DeStefano AL, Konig IR, Bardel C, Brinza D, Bull S, Cai Z, Glaser B, Jiang W, Lee KE, Li CX, Li J, Li X, Majoram P, Meng Y, Nicodemus KK, Platt A, Schwarz DF, Shi W, Shugart YY, Stassen HH, Sun YV, **Won S**, Wang W, Wahba G, Zagaar UA, Zhao Z. Data mining, neural nets, trees — problems 2 and 3 of genetic analysis workshop 15. *Genetic Epidemiology* (SCI) 2007 Nov;31(Suppl 1);S51-60. 5.
5. De Andrade M†, Allen AS, Brinza D, Cheng R, Da Y, de Vries AR, Ewhida A, Feng Z, Jung H, Hsieh HJ, Kohler K, Liu Y, Liu-Marses W, Luan J, Marquard V, Nolte IM, Oh S, Platt A, Qin X, Yoo YJ, Yuan A, Tian X, **Won S**. 2007 Summary of contributions to GWA15 Group 13: candidate gene association studies. *Genetic Epidemiology* (SCI) 2007 Nov;31(Suppl 1);S110-117.

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6. **Won S**, Elston RC†. The power of independent types of genetic information to detect association in a case-control study design. *Genetic Epidemiology* (SCI) 2008 Dec;32(8); 731-756.
7. **Won S**, Morris N, Lu Q, Elston RC†. Choosing an optimal method to combine p-values. *Statistics in Medicine* (SCI) 2009 May;28(11);1537-1553.
8. **Won S**, Kim S., Elston RC†. Phase uncertainty in case-control association studies. *Genetic Epidemiology* (SCI) 2009 Sep;33(6);463-478.
9. Stein CM† , Zalwango SZ, Malone LL, **Won S**, Mayanja-Kizza H, Mugerwa RD, Leontiev DV, Thompson CL, Cartier KC, Elston RC, Iyengar SK, Boom WH, Whalen CC. 2008 Genome scan of M. tuberculosis infection and disease in Ugandans. *PLoS one* (SCIE) 2008 Dec;3(12):e4094.
10. Lu Q, Wang X, Song Y, **Won S**, Cui Y, Elston RC†. The effect of multiple genetic variants in predicting the risk of Type 2 Diabetes. *BMC proceeding* (Proceeding) 2009 Dec; 3 Suppl 7: S49. 11.
11. Lu Q, Obuchowski N, **Won S**, Zhu X, Elston RC†. Using the robust optimal receiver operating characteristic curve for predictive genetic tests. *Biometrics* (SCI) 2010; 66;586-593.
12. Kim S, Morris N, **Won S**, Elston RC†. Single-marker and two-marker association tests for unphased case-control genotype data, with a power comparison. *Genetic Epidemiology* (SCI) 2010; 34;67-77.
13. **Won S**, Wilk JB, Mathias R, O'Donnell C, Silverman EK, Barnes K, O'Connor G, Weiss ST, Lange C†. On the analysis of genome-wide association studies in family-based designs: A universal, robust analysis approach and an application to four genome-wide association studies. *Plos Genetics* (SCI) 2009 Nov; 5(11): e1000741.
14. **Won S**† , Bertram L, Tanzi RE, Lange C. Maximizing the power of genome-wide association studies: A novel class of powerful family-based association tests. *Stat in Bioscience* 2009 Nov; 1:125-143.
15. Lu Q, Song Y, Wang X, **Won S**, Cui Y, Elston RC† The effect of multiple genetic variants in predicting the risk of type 2 diabetes. *BMC Proceeding* (Proceeding). 2009 Dec;15;3 Suppl 7:S49.
16. Cho MH, Boutaoui N, Klanderman BJ, Sylvia JS, Ziniti JP, Hersh CP, Demeo DL, Hunninghake GM, Litonjua AA, Sparrow D, Lange C, **Won S**, Murphy JR, Beaty TH, Regan EA, Make BJ, Hokanson JE, Crapo JD, Kong X, Anderson WH, TalSinger R, Lomas DA, Bakke P, Gulsvik A, Pillai SG, Silverman EK†. Variants in FAM13A are associated with chronic obstructive pulmonary disease. *Nature Genetics* (SCI) 2010 Mar;42;200-202.
17. Lasky-Su J†, **Won S**, Mick E, Anney RJ, Franke B, Neale B, Biederman J, Smalley SL, Loo SK, Todorov A, Faraone SV, Weiss ST, Lange C. On genome-wide association studies for family-based designs: an integrative analysis approach combining ascertained family samples with unselected controls. *American Journal of Human Genetic* (SCI) 2010 Apr; 86(4):573-80.
18. Murphy A†, **Won S**, Rogers A, Chu JH, Raby BA, Lange C. On the genome-wide association analysis of copy number variants in family-based designs: methods for combining family-based and population-based information for testing dichotomous or quantitative traits, or completely ascertained samples. *Genetic Epidemiology* (SCI) 2010 Sep; 34:582-590.
19. Kim S, Morris NJ, **Won S**, Elston RC†. Single-marker and two-marker association tests for unphased case-control genotype data, with a power comparison. *Genetic Epidemioly* (SCI) 2010 Jan;34(1):67-77.
20. Wan ES, Cho MH, …, **Won S**, et al. Genome-wide association analysis of body mass in chronic obstructive pulmonary disease. *American Journal of Respiratory Cell and Molecular Biology* (SCI) 2011 Aug; 45(2): 304-310.
21. Yi H, Cho YJ, **Won S**, Lee JE, Jin Yu H, Kim S, Schroth GP, Luo S, Chun J†. Duplex-specific nuclease efficiently removes rRNA for prokaryotic RAN-seq. *Nucleic Acids Research* (SCI) 2011 Nov; 39(20): e140.
22. **Won S**, Morris N, Lu Q, Elston RC†. Authors' reply. *Statistics in Medicine* (SCI) 2011;30(11);2962-2964.
23. **Won S**†, Lu Q, Bertram L, Tanzi RE, Lange C. On the meta-analysis of genome-wide association studies: a robust and efficient approach to combine population and family-based studies. *Human Heredity* 2012 Mar;73(1):35-46.
24. Lee JH, Yi H, Jeon YS, **Won S**, Chun J†. TBC: A clustering algorithm based on prokaryotic taxonomy. *Journal of Microbiology* (SCIE) 2012 Apr;50(2):181-185.
25. Kim OS, Cho YJ, Lee K, Yoon SH, Kim M, Na H, Park SC, Jeon YS, Lee JH, Yi H, **Won S**, Chun J†. Introducing EzTaxone: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. *International Journal of Systematic and Evolutionary Microbiology* (SCI) 2012 Mar;62(Pt 3):716-721.

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26. Choi S, **Won S**†. Fine-scale mapping of disease susceptibility locus with Bayesian partition mode. *Genes & Genomics* (SCIE) 2012 Jun; 34(4):401-407.
27. Fier H†, **Won S**, Prokopenko D, AlChawa T, Ludwig KU, Fimmers R, Silverman EK, Pagano M, Mangold E, Lange C. Location, Location, Location': a spatial approach for rare variant analysis and an application to a study on non-syndromic cleft lip with or without cleft palate. *Bioinformatics* (SCI) 2012 Dec; 28(23);3027-3033.
28. Kim K, **Won S**, Kim J, Lee E, Kim K, Park S†. Meta-analysis of complication as a risk factor for early ambulation after percutaneous coronary intervention. *European Journal of Cardiovascular Nursing* (SSCI) 2013 Oct; 12(5):429-436.
29. Ryu HY†, Kim JW, Kim HS, Park HJ, Jeon HK, Park SY, Kim BR, Lang CC, **Won SH**. Second-look endoscopy is not associated with better clinical outcomes after gastric endoscopic submucosal dissection: a prospective, randomized, clinical trial analyzed on an as-treated basis. *Gastrointestinal Endoscopy* (SCI) 2013 Aug;78(2):285-294.
30. **Won S**†, Lange C. A general framework for robust and efficient association analysis in family-based designs: quantitative and dichotomous phenotypes. Statistics in Medicine (SCI) 2013 Nov; 32(25):4482-4498.
31. **Won S**†, Kwon M, Mattheisen M, et al. Efficient strategy for detecting gene × gene joint action and its application in schizophrenia. *Genetic Epidemiology* (SCI) 2014 Jan; 38(1): 60-71.
32. Sung YH, Cho MS, Kwon IG, Jung YY, Song MR, Kim K†, **Won S**. Evaluation of falls by inpatients in an acute care hospital in Korea using the Morse Fall Scale. *International Journal of Nursing Practice* (SSCI) 2014 Oct;20(5):510-517.
33. **Won** S†, Kim Y, Lange C. On rare-variant analysis in population-based designs: Decomposing the likelihood to two informative components. *Human Heredity* (SCI) 2014 April; 76(2):76-85.
34. Ryu HY†, Jeon HK, Cho MY, Kim HS, Kim JW, Park HJ, Kim MY, Baik SK, Kwon SO, Park SY, **Won SH**. A randomized trial to determine the diagnostic accuracy of conventional vs. jumbo forceps biopsy of gastric epithelial neoplasias before endoscopic submucosal dissection; open-label study. *Gastric Cancer* (SCI) 2014 Oct;17(4): 661-668.
35. Kim YK, Kim Y, Hwang MY, Shimokawa K, **Won S**, Kato N, Tabara Y, Yokota M, Han BG, Lee JH, Kim BJ†. Identification of a genetic variant at 2q12.1 associated with blood pressure in East-Asians by genome-wide scan including gene-environment interactions. *BMC Medical Genetics* (SCIE) 2014 Jun; 15(65).
36. **Won S**†. Book Review for 'Understanding Advanced Statistical Methods by WESTFALL, P. H. and HENNING, K. S. S. ChaOpman & Hall/CRC, Boca Raton, F' Biometrics (SCI) 2014 Jun; 70; 467-469. Book Review.
37. Choi S, Lee S, Nöthen MM, Lange C, Park T†, **Won S**†. FARVAT: a FAmily-based Rare Variant Association Test. *Bioinformatics* (SCI) 2014 Nov; 30(22):3197-3205.
38. Choi S, **Won S**†. Robust analysis with related samples under the presence of population substructure and its application to body mass index. *Genes & Genomics* (SCIE) 2014 Jul;36:643-654.
39. Jung JY, Choi DP, **Won S**, Lee Y, Kim YS, Kim SK, Oh YM, Suh I†, Lee SD†. Relationship of vitamin D binding protein polymorphisms and lung function in Korean chronic obstructive pulmonary disease. *Yonsei Medical Journal* (SCIE) 2014 Sep;55(5):1318-1325.
40. Majithia AR, Flannick J, Shahinian P, Guo M, Bray MA, Fontanillas P, Gabriel SB; **GoT2D Consortium**; NHGRI JHS/FHS Allelic Spectrum Project; SIGMA T2D Consortium; T2D-GENES Consortium, Rosen ED, Altshuler D†. Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. *Proceedings of the National Academy of Sciences of the United States of America* (SCI) 2014 Sep;11(36):13127-13132.
41. Bang SY, Na YJ, Kim K, Joo Y, Park Y, Lee J, Lee SY, Ansari AA, Jung J, Rhee H, Lee JY, Han BG, Ahn SM, **Won S**, Lee HS, Bae SC†. Targeted exon sequencing fails to identify rare coding variants with large effect in rheumatoid arthritis. *Arthritis Research & Therapy* (SCI) 2014 Sep;16(5):447.
42. Jason Flannick, Gudmar Thorleifsson, Nicola L Beer, Suzanne B R Jacobs, Niels Grarup, Noël P Burtt, Anubha Mahajan, Christian Fuchsberger, Gil Atzmon, Rafn Benediktsson, John Blangero, Don W Bowden, Ivan Brandslund, Julia Brosnan, Frank Burslem, John Chambers, Yoon Shin Cho, Cramer Christensen, Desirée A Douglas, Ravindranath Duggirala, Zachary Dymek, Yossi Farjoun, Timothy Fennell, Pierre Fontanillas, Tom Forsén, Stacey Gabriel, Benjamin Glaser, Daniel F Gudbjartsson, Craig Hanis, Torben Hansen, Astradur B Hreidarsson, Kristian Hveem, Erik Ingelsson, Bo Isomaa, Stefan Johansson, Torben Jørgensen, Marit Eika Jørgensen, Sekar Kathiresan, Augustine Kong, Jaspal Kooner, Jasmina Kravic, Markku Laakso, Jong-Young Lee, Lars Lind, Cecilia M Lindgren, Allan Linneberg, Gisli Masson, Thomas Meitinger, Karen

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43. Lee Y, Park S, Moon S, Lee J, Elston RC, Lee W†, **Won S**†. On the analysis of a repeated measure design in genome-wide association analysis. *International Journal of Environmental Research and Public Health* (SCIE) 2014 Nov;11(12):12283-12303.
44. Lim J, Sung J, **Won S**†. Efficient strategy for the genetic analysis of related samples with a linear mixed model. *Journal of Korean Data & Information Science Society* (학술진흥재단 등재지) 2014 Aug;25(5):1025-1038.
45. **Won S**† , Kim W, Lee S, Lee Y, Sung J, Park T† . Family-based association analysis: a fast and efficient method of multivariate association analysis with multiple variants. *BMC Bioinformatics* (SCIE) 2015 Feb;16(1):46.
46. Doo M, **Won S**, Kim Y†. Association between the APOB rs1469513 polymorphism and obesity is modified by dietary fat intake in Koreans. *Nutrition* (SCI) 2015 May;31(5):653-8.
47. **Won S***, Choi H*, Park S, Lee J, Park C†, Kwon S†. Evaluation of penalized and non-penalized methods for disease prediction with large-scale genetic data. *BioMed Research International* (SCIE) 2015 Jan; 605891.
48. Kim Y, Lee S, Kim NH, Kim YJ, Oh J, Lim J, Min H, Lee M, Seo HJ, Lee SH, Sung J, Cho NH, Kim BJ, Lee JY, Han BG, Elston RC, **Won S**†, Lee J†. On the estimation of Heritability with Family-based and Population-based Samples. *BioMed Research International* (SCIE) 2015 Jan;671349.
49. Kim J, Suh YJ, **Won S**, Nah JW, Lee W†. Gamma Mixed Model to Improve Sib-Pair Linkage Analysis. *The Korean Journal of Applied Statistics* (학술진흥재단 등재지) 2015 Apr;28(2):221-230.
50. Lim J, **Won S**†. Linear Mixed Models in Genetic Epidemiological Studies and Applications. *The Korean Journal of Applied Statistics* (학술진흥재단 등재지) 2015 Apr;28(2): 295-308.
51. Jaramillo JD, Wilson C, Stinson DJ, Lynch DA, Bowler RP, Lutz S, Bon JM, Arnold B, McDonald ML, Washko GR, Wan ES, DeMeo DL, Foreman MG, Soler X,Lindsay SE, Lane NE, Genant HK, Silverman EK, Hokanson JE, Make BJ, Crapo JD, Regan EA†; **COPDGene Investigators**. Reduced Bone Density and Vertebral Fractures in Smokers. Men and COPD Patients at Increased Risk. *Annals of the American Thoracic Society* 2015 May;12(5):648-656.
52. Lee SY, Kim DW†, Shin YK, Ihn MH, Lee SM, Oh HK, Ku JL, Jeong SY, Lee JB, Ahn S, **Won S**, Kang SB. Validation of Prediction Models for Mismatch Repair Gene Mutations in Koreans. *Cancer Research and Treatment* (SCI) 2016 Apr;48(2):668-75
53. Park S, Lee S, Lee Y, Lange C, **Won S**†. Adjusting heterogeneous ascertainment bias for genetic association analysis with extended families. *BMC Medical Genetics* (SCIE) 2015 Aug;16:62.
54. Kim SH, Huh K, **Won S**, Lee KW, Park MJ†. A Significant Increase in the Incidence of Central Precocious Puberty among Korean Girls from 2004 to 2010. *PLoS One* (SCIE) 2015 Nov 5;10(11):e0141844
55. Hardin M†, Cho MH, McDonald ML, Wan E, Lomas DA, Coxson HO, MacNee W, Vestbo J, Yates JC, Agusti A, Calverley PM, Celli B, Crim C, Rennard S, Wouters E, Bakke P, Bhatt SP, Kim V, Ramsdell J, Regan EA, Make BJ, Hokanson JE, Crapo JD, Beaty TH, Hersh CP; ECLIPSE and COPDGene Investigators; COPDGene Investigators—clinical centers; COPDGene Investigators-clinical centers. A genome-wide analysis of the response to inhaled β2-agonists in chronic obstructive pulmonary disease. Pharmacogenomics Journal (SCIE) 2015 Oct 27
56. Hayden LP†, Hobbs BD, Cohen RT, Wise RA, Checkley W, Crapo JD, Hersh CP; **COPDGene Investigators**. Childhood pneumonia increases risk for chronic obstructive pulmonary disease: the COPDGene study. Respiratory Research (SCIE) 2015 Sep 21;16(1):115. 57.
57. Regan EA†, Lynch DA, Curran-Everett D, Curtis JL, Austin JH, Grenier PA, Kauczor HU, Bailey WC, DeMeo DL, Casaburi RH, Friedman P, Van Beek EJ, Hokanson JE, Bowler RP, Beaty TH, Washko GR, Han MK, Kim V, Kim SS, Yagihashi K, Washington L, McEvoy CE, Tanner C, Mannino DM, Make BJ, Silverman EK, Crapo JD; **Genetic Epidemiology of COPD**

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(COPDGene) Investigators. Clinical and Radiologic Disease in Smokers With Normal Spirometry. *JAMA Internal Medicine* (SCI) 2015 Sep;175(9):1539-49.

58. Cho Y, Shin SY, **Won S**, Relton CL, Davey Smith G, Shin MJ†. Alcohol intake and cardiovascular risk factors: A Mendelian randomisation study. *Scientific Reports* (SCI) 2015 Dec 21;5:18422.
59. Kim YJ, Lee J, Kim BJ, **T2D-Genes Consortium**, Park T†. A new strategy for enhancing imputation quality of rare variants from next-generation sequencing data via combining SNP and exome chip data. *BMC Genomics* (SCIE). 2015 Dec 29;16(1)
60. Busch R, Han MK, Bowler RP, Dransfield MT, Wells JM, Regan EA, Hersh CP†, **COPDGene Investigators**. Risk factors for COPD exacerbations in inhaled medication users: the COPDGene study biannual longitudinal follow-up prospective cohort. *BMC Pulmonary Medicine* (SCIE). 2016 Feb 10;16:28.
61. Lee E, Lee SY, Kang MJ, Kim K, **Won S**, Kim BJ, Choi KY, Kim BS, Cho HJ, Kim Y, Yang SI, Hong SJ†. Clostridia in the gut and onset of atopic dermatitis via eosinophilic inflammation. *Annals of Allergy Asthma & Immunology* (SCI). 2016 Jul;117(1):91-92.e1.
62. Peddareddygari LR, Hanna PA, Igo RP, Jr., Lu YA, **Won S**, Hirano M, Grewa RP†. Autosomal Dominant Hereditary Spastic Paraplegia with Axonal Sensory Motor Polyneuropathy maps to Chromosome 21q 22.3 *International Journal of Neuroscience* (SCI) 2016;126(7):600-6
63. Choi S, Lee S, Qiao D, Hardin M, Cho MH, Silverman EK, Park T†, **Won S**†. FARVATX: FAmily-based Rare Variant Association Test for X-linked genes. *Genetic Epidemiology* (SCI) 2016 Sep;40(6):475-85
64. Wang L, Kim J, Lee S, Qiao D, Cho M, Elston RC, Silverman EK, **Won S**†. Family-based Rare Variant Association Analysis: a Fast and Efficient Method of Multivariate Phenotype Association Analysis. *Genetic Epidemiology* (SCI) 2016 Sep;40(6):502-11.
65. GBD 2015 HIV collarobrator, … , **Won S**, et al. Estimates of global, regional, and national incidence, prevalence, and mortality of HIV, 1980-2015: the Global Burden of Disease Study 2015. *The Lancet HIV*. 2016. Aug;3(8): :e361-87
66. Gim J, **Won S,** Park T†. LPEseq: Local-Pooled-Error Test for RNA Sequencing Experiments with a Small Number of Replicates. *PLoS One* (SCIE). 2016 Aug 17;11(8):e0159z182.
67. **GBD 2015 SDG Collaborators**. Measuring the health-related Sustainable Development Goals in 188 countries: a baseline analysis from the Global Burden of Disease Study 2015. *Lancet* (SCI). 2016 Oct 8;388(10053):1813-1850.
68. **GBD 2015 Mortality and Causes of Death Collaborators**. Global, regional, and national life expectancy, all-cause mortality, and cause-specific mortality for 249 causes of death, 1980-2015: a systematic analysis for the Global Burden of Disease Study 2015. *Lancet* (SCI). 2016 Oct 8;388(10053):1459-1544.
69. **GBD 2015 Disease and Injury Incidence and Prevalence Collaborators**. Global, regional, and national incidence, prevalence, and years lived with disability for 310 diseases and injuries, 1990-2015: a systematic analysis for the Global Burden of Disease Study 2015. *Lancet* (SCI). 2016 Oct 8;388(10053):1545-1602.
70. **GBD 2015 DALYs and HALE Collaborators**. Global, regional, and national disability-adjusted life-years (DALYs) for 315 diseases and injuries and healthy life expectancy (HALE), 1990-2015: a systematic analysis for the Global Burden of Disease Study 2015. *Lancet* (SCI). 2016 Oct 8;388(10053):1603-1658.
71. **GBD 2015 Risk Factors Collaborators.** Global, regional, and national comparative risk assessment of 79 behavioural, environmental and occupational, and metabolic risks or clusters of risks, 1990-2015: a systematic analysis for the Global Burden of Disease Study 2015. *Lancet* (SCI). 2016 Oct 8;388(10053):1659-1724.
72. **GBD 2015 Child Mortality Collaborators.** Global, regional, national, and selected subnational levels of stillbirths, neonatal, infant, and under-5 mortality, 1980-2015: a systematic analysis for the Global Burden of Disease Study 2015. *Lancet* (SCI). 2016 Oct 8;388(10053):1725-1774.
73. **GBD 2015 Maternal Mortality Collaborators.** Global, regional, and national levels of maternal mortality, 1990-2015: a systematic analysis for the Global Burden of Disease Study 2015. *Lancet* (SCI) 2016 Oct 8;388(10053):1775-1812.
74. Gim J, **Won S**, Park T. Conditional estimation of local pooled dispersion parameter in small-sample RNA-Seq data improves differential expression test. *Journal of Bioinformatics and Computational Biology* (SCIE). 2016 Oct;14(5):1644006.
75. Lim J, **Won S**, Park S, Kim J, Koo SH, and Kwon GC†. External Quality Assessment of Institutions and Instruments Using a Linear Mixed Model. *Journal of Laboratory Medicine and Quality Assurance* (국내학술지) 2016;38:43-51

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PRESENTATIONS (2014-now)

- Wang L, **Won S**. Comparing family-based rare variant association tests for dichotomous phenotypes. Genetic Analysis Workshop 19. *Genetic Analysis Workshop (Vienna, Austria)*. 2014/08/24-2014/08/27 (*Poster presentation*)
- Kim W, **Won S**. Incorporating family history to disease prediction and genome-wide association study. The 11th KOGO Winter Symposium 2015. *한국유전체학회 (대명리조트 서면)*. 2015/02/04-2015/02/06 (*Poster presentation*)
- Longfei W, **Won** S. Family-based rare variant association analysis: a fast and efficient method of multivariate phenotype association analysis. The 11th KOGO Winter Symposium 2015. *한국유전체학회 (대명리조트 서면)*. 2015/02/04-2015/02/06 (*Poster presentation*)
- Kim W, **Won S**. Incorporating family history to disease prediction and genome-wide association study. The 3rd International Symposium on Statistical Genetics. *International Symposium on Statistical Genetics (서울대학교)*. 2015/02/04-2015/02/06. (*Invited presentation*)
- **Won S**. Family-based association analysis: a fast and efficient method of multivariate association analysis with multiple variants. 2015 춘계학술대회. *한국통계학회* (*충북대학교*). 2015/05/29-2015/05/30. (*Platform presentation*)
- **Won S**. FARVAT: a Fast and Robust Approach for Extended Families. 2015 Chinese Institute of Probability and Statistics Annual Meeting. *Chinese Statistical Association* (*Changhua. Taiwan*). 2015/06/27-2015/06/28. (*Platform presentation*)
- **Won S.** Association Analysis of Repeatedly Observed RNA sequencing data. *한국생물정보시스템정보학회* (*서울대학교*) 2015/10/22. (Platform presentation)
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