

Curriculum Vitae: Wonji Kim

CONTACT DETAILS

Interdisciplinary Program of Bioinformatics, Seoul National University, Seoul, Korea

Channing Division of Network Medicine, Department of Medicine, Brigham and Women's Hospital and Harvard Medical School, Boston, MA, 02115, USA

Permanent Email: dnjswlzz11@gmail.com

RESEARCH INTERESTS

- Bioinformatics & Biostatistics
- Genome-wide association study
- Family-based association study

EDUCATION

Seoul National University

Seoul | S. Korea

Ph.D. candidate in Interdisciplinary Program of Bioinformatics

- Courses include bioinformatics, survival analysis, generalized linear model, categorical data analysis, and biostatistics (linkage analysis, segregation analysis, GWAS, genotype imputation etc.)

Chung-Ang University

Seoul | S. Korea

M.S. in Department of Statistics

Feb. 2015

- Courses include advanced mathematical statistics, longitudinal data analysis, multivariate data analysis, structural equation modeling, and statistical decision theory

B.S. in Department of Statistics

Feb. 2013

- Courses include mathematical statistics, regression analysis, data mining, time series analysis, clinical data analysis

PUBLICATIONS

Journal Articles

1. Wonji Kim, Krinio Giannikou, Sunho Won, John R. Dreier, Sanghun Lee, Magdalena Tyburczy, Edwin K Silverman, Elzbieta Radzikowska, Shulin Wu, Chin-Lee Wu, Elizabeth P. Henske, Gary Hunninghake, Miquel Pujana, Joel Moss, David J. Kwiatkowski "A Genome Wide Association Study (GWAS) implicates *NR2F2* in Lymphangioleiomyomatosis (LAM) Pathogenesis" *European Respiratory journal* (Under review)
2. Wonji Kim, Sungho Won "Heritability Estimation of Dichotomous Phenotypes Using a Liability Threshold Model on Ascertained Family-based Samples" *Genetic Epidemiology* (Under review)
3. Wonji Kim, Sungho Won, Duck-Woo Kim, Sung Il Kang, Il Tae Son, Heung-Kwon Oh, Sung-Bum Kang, Ji Won Park, Seung-Bum Ryoo, Seung-Yong Jeong, Kyu Joo Park "The Relevance of Family History to Increased Risk of Colorectal Cancer in Korea" (in progress)
4. Wonji Kim, Dandi Qiao, Michael H. Cho, Soo Heon Kwak, Kyong Soo Park, Edwin K. Silverman, Pak Sham, Sungho Won "Selecting cases and controls for DNA sequencing studies using family histories of disease." *Statistics in medicine* 36.13 (2017): 2081-2099.
5. Sujin Kim, Yoon Hee Cho, Inae Lee, Wonji Kim, Sungho Won, Ja-Lok Ku, Hyo-Bang Moon, Jeongim Park, Sungkyoon Kim, Gyuyeon Choi, Kyungho Choi "Prenatal exposure to persistent organic pollutants and methylation of LINE-1 and 1 imprinted genes in placenta: a CHECK cohort study", *Environment international*, 119, 398-406.
6. Donghe Li, Wonji Kim, Longfei Wang, Kyong-Ah Yoon, Boyoung Park, Charny Park, Sun-Young Kong, Yongdeuk Hwang, Daehyun Baek, Eun Sook Lee, and Sungho Won "Comparison of INDEL Calling Tools

with Simulation Data and Real Short-Read Data”, *Transactions on Computational Biology and Bioinformatics (TCBB)*, 2018.

7. Jungsoo Gim, Wonji Kim, Soo Heon Kwak, Hosik Choi, Changyi Park, Kyong Soo Park, Sunghoon Kwon, Taesung Park and Sungho Won **“Improving Disease Prediction by Incorporating Family Disease History in Risk Prediction Models with Large-Scale Genetic Data.”** *Genetics* 207.3 (2017): 1147-1155.
8. Tamar Sofer, Quenna Wong, Fernando P. Hartwig, Kent Taylor, Helen R. Warren, Evangelos Evangelou, Claudia P. Cabrera, Daniel Levy, Holly Kramer, Leslie A. Lange, Bernardo L. Horta, COGENT-BP consortium, Kathleen F. Kerr, Alex P. Reiner & Nora Franceschini **“Genome-wide association study of blood pressure traits by Hispanic/Latino background: the hispanic community health study/study of Latinos.”** *Scientific reports* 7.1 (2017): 10348.
9. Jingjing Liang, Thu H. Le, Digna R. Velez Edwards, Bamidele O. Tayo, Kyle J. Gaulton, Jennifer A. Smith, Yingchang Lu, Richard A. Jensen, Guanjie Chen, Lisa R. Yanek, Karen Schwander, Salman M. Tajuddin, Tamar Sofer, Wonji Kim, James Kayima, Colin A. McKenzie, Ervin Fox, Michael A. Nalls, J. Hunter Young, Yan V. Sun, Jacqueline M. Lane, Sylvia Cechova, Jie Zhou, Hua Tang, Myriam Fornage, Solomon K. Musani, Heming Wang, Juyoung Lee, Adebawale Adeyemo, Albert W. Dreisbach, Terrence Forrester, Pei-Lun Chu, Anne Cappola, Michele K. Evans, Alanna C. Morrison, Lisa W. Martin, Kerri L. Wiggins, Qin Hui, Wei Zhao, Rebecca D. Jackson, Erin B. Ware, Jessica D. Faul, Alex P. Reiner, Michael Bray, Joshua C. Denny, Thomas H. Mosley, Walter Palmas, Xiuqing Guo, George J. Papanicolaou, Alan D. Penman, Joseph F. Polak, Kenneth Rice, Ken D. Taylor, Eric Boerwinkle, Erwin P. Bottinger, Kiang Liu, Neil Risch, Steven C. Hunt, Charles Kooperberg, Alan B. Zonderman, Cathy C. Laurie, Diane M. Becker, Jianwen Cai, Ruth J. F. Loos, Bruce M. Psaty, David R. Weir, Sharon L. R. Kardia, Donna K. Arnett, Sungho Won, Todd L. Edwards, Susan Redline, Richard S. Cooper, D. C. Rao, Jerome I. Rotter, Charles Rotimi, Daniel Levy, Aravinda Chakravarti, Xiaofeng Zhu, Nora Franceschini **“Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations.”** *PLoS genetics* 13.5 (2017): e1006728.
10. Min Jung Koh, Wonji Kim, Jee In Kang, Kee Namkoong, Se Joo Kim **“Lack of association between oxytocin receptor (OXTR) gene polymorphisms and alexithymia: Evidence from patients with obsessive-compulsive disorder.”** *PloS one* 10.11 (2015): e0143168.
11. Sungho Won, Wonji Kim, Sungyoung Lee, Young Lee, Joohon Sung and Taesung Park **“Family-based association analysis: a fast and efficient method of multivariate association analysis with multiple variants.”** *BMC bioinformatics* 16.1 (2015): 46.

Conferences

1. Wonji Kim, Sungho Won **“Estimation of Heritability of the Disease on the Binary Trait using Liability Threshold Model”**, *International Genetic Epidemiology Society* 2017, Cambridge, United Kingdom.
2. Wonji Kim, Sungho Won **“Estimation of Heritability of the Disease on the Binary Trait using Liability Threshold Model”**, *The Korean Society of Health Informatics and Statistics* 2018, Seoul, South Korea.
3. Wonji Kim, Sungho Won **“Incorporating Family History to Disease Prediction and Genome Wide Association Study”**, *The 11th KOGO Winter Symposium* 2016, Hongcheon, South Korea. (Best Poster Presentation Award)

RESEARCH PROJECTS

1. A Genome Wide Association Study (GWAS) implicates *NR2F2* in Lymphangioliomyomatosis (LAM) Pathogenesis
 - Conducted genome wide association study
 - Discovered LAM pathogenesis using Hi-C data and Epigenetics

Jun. 2014 – Jun. 2018
2. The Relevance of Family History to Increased Risk of Colorectal Cancer (CRC) in Korea
 - Estimated prevalence and heritability of non-hereditary CRC in Korea population

- Estimated the relative risk of family history of CRC
 - Conducted survival analysis to estimate hazard ratio of family history of CRC
- Jun. 2015 – Aug. 2018
3. A multiomics approach to identify risk factors for atopy
 - Calculated genetic risk scores for atopy using reported variants
 - Performed genome wide association studies

Mar. 2018 – Dec. 2018
 4. Development of Automated Procedure for Genotype Imputation
 - Packaged overall procedures for genotype imputation including pre-imputation and post-imputation filtering
 - Developed automated method of strand alignment for SNPs with ambiguous allele (A/T or C/G) using genotype imputation technique

Mar. 2015 – Dec. 2017
 5. Development of a Risk Prediction Model for the Breast Cancer in Korea Population based on the Family History of Diseases
 - Performed segregation analysis to find genetic model for the breast cancer in Korea population
 - Compared imputation tools and INDEL calling tools for family-based genetic data

Feb. 2015 – Dec. 2017
 6. The Relevance of Oxytocin Receptor (OXTR) Gene Polymorphisms and Alexithymia of Obsessive-Compulsive disorder
 - Conducted multivariate ANOVA (MANOVA) for reported SNPs
 - Performed simulation studies

Nov. 2014 – Mar. 2015

SOFTWARES

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| 1. selSAMPLE | Aug. 2016 |
| <ul style="list-style-type: none"> - Tools for selecting cases and controls for DNA sequencing studies using family histories of disease - Written with R language | |
| 2. REx | Jan. 2018 |
| <ul style="list-style-type: none"> - Tools for comprehensive statistical computing on Excel spread sheet - Written with R language | |
| 3. LTMH | Dec. 2018 |
| <ul style="list-style-type: none"> - Tools for heritability estimation of binary trait - Written with R language | |

AWARD

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| 1. Best Poster Award
<i>The 11th KOGO Winter Symposium 2016</i> | Feb. 2016 |
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TEACHING EXPERIENCE

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- | Teaching Assistant | |
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| 1. Mathematical Statistics
<i>Department of Statistics, Chung-Ang University</i> | Sep. 2013 – Dec. 2013 |
| 2. Categorical data analysis
<i>Department of Statistics, Chung-Ang University</i> | Mar. 2014 – Jun. 2014 |
| 3. Mathematical Statistics | Mar. 2014 – Jun. 2014 |

Graduate School of Statistics, Chung-Ang University

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| 4. | Categorical data analysis, Mathematical Statistics
<i>Graduate School of Public Health, Seoul National University</i> | Mar. 2014 – Jun. 2014 |
| 5. | Introduction to Health Statistics and Bioinformatic
<i>Graduate School of Public Health, Seoul National University</i> | Mar. 2015 – Jun. 2015 |

COMPUTATIONAL SKILLS & MORE

- Programming: Python
- Statistical Tools : R, SAS
- Bioinformatics Tools : PLINK, IMPUTE2, SHAPEIT, Minimac