

CURRICULUM VITAE

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Work

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EDUCATION

2014	PhD, Statistics, University of Wisconsin-Madison (Advisor: Karl W. Broman)
2008	MS, Statistics, Korea University, Seoul, Korea (Advisor: Myung-Hoe Huh)
2006	BS, Mathematics, Korea University, Seoul, Korea

PROFESSIONAL POSITIONS

2019	Assistant Professor, Department of Applied Statistics, College of Business & Economics, Chung-Ang University, Seoul, Korea
2017-2019	Staff Engineer, Samsung Research, Seoul R&D Campus, Seoul, Korea
2016-2017	Research Associate, Lillehei Heart Institute, University of Minnesota, US
2014-2016	Postdoctoral Associate, Division of Biostatistics School of Public Health, University of Minnesota, US

RESEARCH INTERESTS

- Real-world big data analysis: Develop new service that combines enterprise big data
- Biostatistics: statistical methodology and software development for bio-data analysis
- Development of Statistical Software tools
- Deep learning applications

PUBLICATIONS

Working Manuscripts

2020 **Kwak IY**, Kwag S, Lee J, Huh J, Jeon Y, Hwang J, Yoon J, Lee C. (2020) RESMAX: Detecting Voice Spoofing Attacks with Residual Network and Max Filter Map, On preparation

- 2020 Ahmed E, **Kwak IY**, Huh J, Kim I, Oh T, Kim H (2020) Void: A fast and light voice liveness detection system, USENIX Security Symposium, Boston, USA, 2020 (Accepted)
- 2019 **Kwak IY**, Huh J, Kim I, Han S, Yoon J. (2019) Voice Presentation Attack Detection through Text-Converted Voice Command Analysis, Proceedings of the 2019 CHI Conference on Human Factors in Computing Systems
- Magli A, Baik J, Mills LJ, **Kwak IY**, Dillon BS, Gonzalez RM, Stafford DA, Swanson SA, Stewart R, Thomson JA, Garry DJ, Dynlacht BD, Perlingeiro R, Time-dependent Pax3-mediated chromatin remodeling and cooperation with Six4 and Tead2 specify the skeletal myogenic lineage in developing mesoderm, *PLoS biology*, 17 (2), e3000153
- Magli A, Baik J, Pota P, Cordero CO, **Kwak IY**, Garry DJ, Love PE, Dynlacht BD, Perlingeiro R, Pax3 cooperates with Ldb1 to direct local chromosome architecture during myogenic lineage specification, *Nature Communications*, 10, 2316
- 2018 Gong W, **Kwak IY**(co-1st author), Pota P, Koyano-Nakagawa N, Garry DJ. (2018) DrImpute: imputing dropout events in single cell RNA sequencing data, *BMC Bioinformatics*, 19 (1), 220
- Gong W, **Kwak IY**, Koyano-Nakagawa N, Pan W, Garry DJ. (2018) TCM visualizes trajectories and cell populations from single cell data, *Nature Communications*, 9 (1), 2749
- 2017 **Kwak IY**, Pan W. (2017) Gene- and pathway-based association tests for multiple traits with GWAS summary statistics. *Bioinformatics*, 33 (1), 64-71.
- Chen Z, Zhu W, Bender I, Gong W, **Kwak IY**, Yellamilli A, Hodges TJ, Nemoto N, Zhang J, Garry DJ, Berlo JH (2017) Pathologic Stimulus Determines Lineage Commitment of Cardiac C-kit⁺ Cells. *Circulation* circulationaha. 117.030137
- 2016 Wei P, Cao Y, Zhang Y, **Kwak IY**, Xu Z, Crosby J, Boerwinkle E, Pan W. (2016) On Robust Association Testing for Quantitative Traits and Rare Variants. *G3*, 116.035485.
- Kwak IY**, Pan W. (2016) Adaptive Gene- and Pathway-Trait Association Testing with GWAS Summary Statistics. *Bioinformatics*, 32 (8), 1178-1184.
- 2015 Pan W, **Kwak IY**, Wei P. (2015) A Powerful Pathway-Based Adaptive Test for Genetic Association with Common or Rare Variants. *The American Journal of Human Genetics*, 97:86-98
- Kwak IY** Moore CR, Spalding EP, Broman KW. (2015) Mapping quantitative trait loci underlying function-valued traits using functional principal component analysis and multi-trait mapping. *G3*, 6 (1), 79-86.
- 2014 **Kwak IY**, Moore CR, Spalding EP and Broman KW. (2014) A simple regression-based method to map quantitative trait loci underlying function-valued phenotypes. *Genetics*, 197(4):1409-1416
- 2013 Moore CR, Johnson LS, **Kwak IY**, Livny M, Broman KW, Spalding EP (2013) High-throughput computer vision introduces the time axis to a quantitative trait map of a plant growth response. *Genetics* 195:1077–1086
- 2010 Billings T, Sargent EE, Szatkiewicz JP, Leahy N, **Kwak, IY**, Bektassova N, Walker M, Hassold T, Graber JH, Broman KW, Petkov PM (2010) Patterns of recombination activity on mouse chromosome 11 revealed by high resolution mapping. *PLoS One* 5:e15340
- 2008 **Kwak IY**, Huh MH (2008) Andrews' Plot for Extended Uses, *The Korean Communications in Statistics*, 15: 87–94
- Kwak IY**, Huh MH (2008) Parallel Coordinate Plots of Mixed-Type Data, *The Korean Communications in Statistics*, 15: 587–595
- Park MR, **Kwak IY**, Huh MH (2008) Applications of Parallel Coordinate Plots for Visualizing Gene Expression Data, *The Korean Journal of Applied Statistics*, 21(6): 911–921

SOFTWARE DEVELOPMENT

R/Drimpute	An R package for imputing dropout events. Many statistical methods in cell type identification, visualization and lineage reconstruction do not account for dropout events ('PCAReduce', 'SC3', 'PCA', 't-SNE', 'Monocle', 'TSCAN', etc). 'Drimpute' can improve the performance of such software by imputing dropout events.
R/aSPU	An R package for the (adaptive) Sum of Powered Score ('SPU' and 'aSPU') tests, inverse variance weighted Sum of Powered score ('SPUw' and 'aSPUw') tests and some gene-based and pathway based association tests (aSPUs, aSPUsPath, MTaSPUsSet, MTaSPUsSetPath, etc). (https://cran.r-project.org/web/packages/aSPU/index.html).
R/funqtl	An R package with add-on functions for the R/qlt package to deal with QTL mapping for function-valued traits. (github.com/ikwak2/funqtl).
R/xoi	Tools for analyzing crossover interference. (github.com/kbroman/xoi). Assisted Karl Broman to develop the package using C language.
R/APCP	An R package that plots Andrews type parallel coordinate plot. (github.com/ikwak2/APCP).

PRESENTATIONS

2019	Voice Presentation Attack Detection through Text-Converted Voice Command Analysis, 2019 CHI Conference on Human Factors in Computing Systems, Glasgow, UK
2017	Gene- and pathway-based association tests for multiple traits with GWAS summary statistics, 2017 ENAR spring meeting, Washington, DC
2016	Adaptive Gene- and Pathway-Trait Association Testing with GWAS Summary Statistics, 2016 ENAR spring meeting, Austin, TX
2015	Regression-Based Methods to Map Quantitative Trait Loci Underlying Function-Valued Phenotypes, 2015 ENAR spring meeting, Miami, FL
2015	Adaptive Gene- and Pathway-Trait Association Testing with GWAS Summary Statistics, <i>2015 3rd Annual BICB Symposium</i> , Minneapolis, MN
2013	QTL analysis with Function-valued Trait Data, <i>2013 ENAR Spring meeting</i> , Orlando, FL
2008	Parallel Coordinate Plots of Mixed-type Data, <i>2008 Korea-Japan Student Conference</i> , Seoul, Korea
2007	Andrews' Plot for Extended Uses, <i>Autumn Conference, The Korean Statistical Society</i> , Seoul, Korea

POSTERS

2016	Gene-based association tests for multiple traits with GWAS summary statistics, TC ASA Fall Research Meeting, Mounds View, MN
2015	Adaptive Gene- and Pathway-Trait Association Testing with GWAS Summary Statistics, TC ASA Fall Research Meeting, Rochester, MN
2013	QTL analysis with Function-valued Trait Data, Complex Trait Community annual meeting, Madison, WI

JOURNAL MANUSCRIPT REVIEWS

Molecular Ecology Resources, Scientific Reports, Biometrics, IEEE/ACM Transactions on Computational Biology and Bioinformatics