CURRICULUM VITAE

**Il-Youp Kwak**

**Work**

Department of Applied Statistics

College of Business & Economics

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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**

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# 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

# Articles

*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/qtl package to deal with QTL mapping for function-valued traits. ([github.com/ikwak2/funqtl](http://github.com/ikwak2/funqtl)).

R/xoi Tools for analyzing crossover interference. ([github.com/kbroman/xoi](http://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](http://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, *2015 3rd Annual BICB Symposium*, Minneapolis, MN

*2013* QTL analysis with Function-valued Trait Data, *2013 ENAR Spring meeting*, Olando, FL

2008 Parallel Coordinate Plots of Mixed-type Data, *2008 Korea-Japan Student Conference*, Seoul, Korea

2007 Andrews’ Plot for Extended Uses, *Autumn Conference, The Korean Statistical Society*, 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