CURRICULUM VITAE

Il-Youp Kwak

Work
Department of Applied Statistics
College of Business & Economics
Chung-Ang University
84, Heukseok-ro, Dongjak-gu
Seoul, 06974, Republic of Korea

Phone: 82-10-5652-1534
Email: ikwak2@cau.ac.kr
Web: https://ikwak2.github.io/

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 (focus on voice classifications)

DATA COMPETITIONS

2020.3	[Winner of a Biomedical Data Competition] Our team (Il-Youp Kwak and Wuming Gong) won both Subchallenges 2 and 3 of the Allen Institute Cell Lineage Reconstruction DREAM Challenge
2020.7	Our CAU-ET team (Yerin Lee, Soyoung Lim and Il-Youp Kwak) ranked 7th and 9th place at the IEEE AASP challenge on Detection and Classification of Acoustic Scenes and Event (DCASE) Task 1 subtask B and A

PUBLICATIONS

Working Manuscripts

>   Gong W, Raz O, Salvador-Martinez I, **Kwak IY**, Jones MG, Khodaverdian A, Zhang R, Rao S, Wang R, Yosef N, Hu J, Liu Z, Zhang H, Guan Y, Retkute R, Garry DJ, Peng J, Han L, Shang X, Chung V, Mason M, DREAM consortium, Shendure J, Elowitz M, Telfold M, Shapiro E, Meyer P (2020+) Benchmarked machine learning approaches for reconstructions of large cell lineage trees in C.elegans and mouse (Submitted)

Published Papers

2021 **Kwak IY**, Kwag S, Lee J, Huh J, Jeon Y, Hwang J, Yoon J, Lee C. (2021) RESMAX: Detecting Voice Spoofing Attacks with Residual Network and Max Filter Map, 25th International Conference on Pattern Recognition (ICPR2020), Milan, Italy

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

>   Yoon HY, **Kwak IY** (2020) Association Modeling on Keyword and Abstract Data in Korean Port Research, Journal of Korea Trade, 25 (5), 71-86

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 (2019) 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 (2019) 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/DCLEAR   An R package for R package for Distance based Cell LinEAge Reconstruction (DCLEAR). These codes are created during the participation of Cell Lineage Reconstruction DREAM challenge. Our team achieved the best performance on subchallenges 2 and 3 of the competition.

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).

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

2020   RESMAX: Detecting Voice Spoofing Attacks with Residual Network and Max Filter Map, *Spring Conference, The Korean Statistical Society*, Cheonan, Korea

2019   A survey on voice spoofing detection methods, *Autumn Conference, The Korean Statistical Society*, Seoul, Korea

2019   Voice Presentation Attack Detection through Text-Converted Voice Command Analysis, *Spring Conference, The Korean Statistical Society*, Kangwon, Korea

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

2021   RESMAX: Detecting Voice Spoofing Attacks with Residual Network and Max Filter Map, 25th International Conference on Pattern Recognition (ICPR2020), Milan, Italy

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, Bioinformatics, Journal of Korean Statistical Society, Communications for Statistical Applications and Methods, iScience, IEEE Transactions on Mobile Computing