

CURRICULUM VITAE

Il-Youp Kwak

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 (focus on voice classifications)

DATA COMPETITIONS

2022.1	[3 rd] Our CAU_KU team (Il-Youp Kwak, Jonghoon Yang, Yerin Lee, Sunmook Choi and SeungSang Oh) ranked 3rd place at the ICASSP 2022 Grand Challenge on Audio Deepfake Detection Track 1 (Low quality fake audio detection).
2021.7	[6 th] Our CAU team (Hyejin Won, Baekseung Kim, Il-Youp Kwak and Changwon Lim) ranked 6th place at the IEEE AASP challenge on Detection and Classification of Acoustic Scenes and Event (DCASE) Task 6 on Audio Captioning.

- 2020.7 [7th and 9th] 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
- 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

PUBLICATIONS

International

- 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
- Lee Y, Lim S, **Kwak IY** (2021) CNN-Based Acoustic Scene Classification System, *Electronics*, 10(4), 371,
- Kim K, **Kwak IY**, Min H (2021) Particulate Matter 10 (PM10) Is Associated with Epistaxis in Children and Adults, *International Journal of Environmental Research and Public Health*, 18(9), 4809,
- Gong W, Granados A, Hu J, Jones M, Raz O, Martinez IS, Zhang H, Chow KK, **Kwak IY**, ... , Meyer P. (2021) Benchmarked approaches for cell lineage reconstructions of in vitro dividing cells and in silico models of *Caenorhabditis elegans* and *Mus musculus* developmental trees, *Cell Systems*, 12, 1-17.
- Park J, **Kwak IY**, Lim C (2021) A Deep Learning Model with Self-Supervised Learning and Attention Mechanism for COVID-19 Diagnosis Using Chest X-ray Images, *Electronics*, 10(16), 1996.
- Won H, Kim BS, **Kwak IY** and Lim C (2021) Transformer Followed by Transfer Learning for Audio Captioning, The 6th Workshop on Detection and Classification of Acoustic Scenes and Events (DCASE2021), Online.
- 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.
- 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*, Glasgow, UK.
- 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

Domestic

- 2021 Yang JH, **Kwak IY** (2021) Research trends in statistics for domestic and international journal using paper abstract data, *The Korean Journal of Applied Statistics*, 34(2), 267—278

Choi HJ, **Kwak IY** (2021) Data augmentation in voice spoofing problem, *The Korean Journal of Applied Statistics*, 34(3), 435—446

Yoon HY, **Kwak IY** (2021) Analysis of Shipping and Logistics News Articles using Topic Modeling, *Korea Trade Review*, 46(4), 61—76

Lim SY, **Kwak IY** (2021) Light weight architecture for acoustic scene classification, *The Korean Journal of Applied Statistics*, 34(6), 979—993

- 2020 Yoon HY, **Kwak IY** (2020) Trends in FTA Research of Domestic and International Journal using Paper Abstract Data, *Korea Trade Review*, 45(5), 37—53

Yoon HY, **Kwak IY** (2020) The Association Modeling on Keywords and Documents of Korea International Trade Research using Paper Abstract data, *Korea International Commerce Review*, 35(2), 45—64

- 2019 Yoon HY, **Kwak IY** (2019) The Association Modeling on Keywords and Documents of Logistics Research using Paper Abstract data, *Korea International Commerce Review*, 34(3), 147—166

- 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/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

2020	RESMAX: Detecting Voice Spoofing Attacks with Residual Network and Max Filter Map, <i>Spring Conference, The Korean Statistical Society</i> , Cheonan, Korea
2019	A survey on voice spoofing detection methods, <i>Autumn Conference, The Korean Statistical Society</i> , Seoul, Korea
2019	Voice Presentation Attack Detection through Text-Converted Voice Command Analysis, <i>Spring Conference, The Korean Statistical Society</i> , Kangwon, Korea
2019	Voice Presentation Attack Detection through Text-Converted Voice Command Analysis, <i>2019 CHI Conference on Human Factors in Computing Systems</i> , Glasgow, UK
2017	Gene- and pathway-based association tests for multiple traits with GWAS summary statistics, <i>2017 ENAR spring meeting</i> , Washington, DC
2016	Adaptive Gene- and Pathway-Trait Association Testing with GWAS Summary Statistics, <i>2016 ENAR spring meeting</i> , Austin, TX
2015	Regression-Based Methods to Map Quantitative Trait Loci Underlying Function-Valued Phenotypes, <i>2015 ENAR spring meeting</i> , 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

- 2021 RESMAX: Detecting Voice Spoofing Attacks with Residual Network and Max Filter Map, 25th International Conference on Pattern Recognition (ICPR2020), Milan, Italy
- 2021 DCLEAR: Reconstructing Single Cell Lineage Trees from CRSIPR records by Distance-based Methods, Keystone symposia on Molecular and Cellular Biology, Single Cell Biology (EK26), Virtual conference.
- 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