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 (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

2021.7   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.

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, Accepted.

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 Revie, 46(4), 61—76

2020   Yoon HY, **Kwak IY** (2020) Trends in FTA Research of Domestic and International Journal using Paper Abstract Data, Korea Trade Revie, 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/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

2021   DCLEAR: Reconstructing Single Cell Lineage Trees from CRSIPR recorders by Distance-based Methods, Keystone symposia on Molecular and Cellular Biology, Single Cell Biology (EK26), Virtual conference.
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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