CURRICULUM VITAE

Il-Youp Kwak

Work

Samsung Research, Security Team
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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

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

EXPERIENCES & WORK HISTORY

July 2017 – present

Data Scientist (Staff Engineer) at Samsung Research
Working on researches in Data driven security (AI security).
- Authentication model or attack detection model using voice commands.
- Replay attack detection using deep learning.
- Trusted location project using WIFI data.

July 2016 – July 2017

Research Associate at Lillehei Heart Institute (PI: Daniel Garry)
Project on statistical methods for single cell RNA sequencing data.

Sep 2014 – July 2016

Postdoctoral Associate at University of Minnesota – Twin Cities (Mentor: Wei Pan)
Project on gene and pathway level association testing in GWAS data.
Studied the use of summary statistics in gene and pathway level testing.
Project on gene and pathway level association testing with multiple traits.

Fall 2008 – Sep 2014

Research Assistant
Project on statistical methods for the analysis of meiotic recombination
Project on quantitative trait locus mapping underlying function-valued phenotypes, in collaboration with Edgar Spalding (Botany, UW-Madison).

Feb 2007 – Oct 2008

Teaching Assistant (in Korea)
Exploratory Data Analysis (2007 Fall), Statistical Mathematics (2007 Spring, 2008 Spring).

Jan 2002 – Feb 2004

Military service (in Korea)
Served at Korean army (mandatory for Korean male).

PUBLICATIONS

Working Manuscripts

2019   **Kwak IY**, Huh J, Kim I, Han S, Yoon J. (2019) Voice Presentation Attack Detection through Text-Converted Voice Command Analysis, Accepted on CHI Conference on Human Factors in Computing System Proceedings

Ahmed E, **Kwak IY**, Huh J, Kim I, Kim H (2019) Void: Voice liveness detection through spectrogram analyses of voice commands, Submitted (on minor revision)

Journal Articles

2018   Gong W, **Kwak IY**(co-1st author), Pota P, Koyano-Nakagawa N, Garry DJ. (2017) 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. (2017) 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/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

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.