**CURRICULUM VITAE**

Kipoong Kim

**Address**

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**Research Interests**

Bioinformatics, Multi-source Data Integration, Variable Selection, Low-Rank Approximation, High-dimensional Statistics

**Academic and Professional Positions**

23.06~ : Postdoc. Department of Statistics, Seoul National University (Supervisor: Sungkyu Jung)

23.03~23.05: Visiting Scholar. College of Medicine, Yonsei University  
22.03~23.02: Postdoc. Department of Statistics, Seoul National University (Supervisor: Sungkyu Jung)

**Education**

2019~2022: Ph.D. Department of Statistics, Pusan National University (Advisor: Hokeun Sun)

2016~2017: M.S. Department of Statistics, Pusan National University (Advisor: Hokeun Sun)

2010~2016: B.S. Department of Statistics, Pusan National University

**Peer Reviewed Publications**

Kipoong Kim and Sungkyu Jung (2023). Integrative sparse reduced-rank regression via orthogonal rotation for analysis of high-dimensional multi-source data. Submitted.

Kipoong Kim, Taehwan Jun, Bokeun Ha, Shuang Wang and Hokeun Sun (2023). New statistical selection method for pleiotropic variants associated with both quantitative and qualitative traits. Submitted.

Kipoong Kim and Choongrak Kim (2023). A summary on the distance metric between two subspaces. The Korean Journal of Applied Statistics, 36(3), 271-277.

Kipoong Kim and Choongrak Kim (2022). A Review on the t-distributed stochastic neighbors embedding. The Korean Journal of Applied Statistics, 36(2), 167-173.

Kipoong Kim and Hokeun Sun (2020). Selection probability of multivariate regularization to identify pleiotropic variants in genetic association studies. Communications for Statistical Applications and Methods, 27(5), 535-546.

Kipoong Kim, Jajoon Koo, and Hokeun Sun (2020). An empirical threshold of selection probability for analysis of high-dimensional correlated data. Journal of Statistical Computation and Simulation, 90(9), 1606–17.

Kipoong Kim, and Hokeun Sun (2019). Incorporating genetic networks into case-control association studies with high-dimensional DNA methylation data. BMC Bioinformatics, 20(1), 510.

Kipoong Kim, Jiyun Choi, and Hokeun Sun (2016). Network-based regularization for analysis of high-dimensional genomic data with group structure. The Korean Journal of Applied Statistics, 29(6), 1117–28.

**Software**

[R] png.ukb: A data manipulation tool for large-scale UK biobank data

[R] CPCA: Compositional PCA for zero-inflated microbiome data

[R] iSRRR: Integrative Sparse Reduced-Rank Regression for multi-source data analysis

[R] UNISS: Unified Selection Score for multi-trait analysis

[R] CTGSA: Covariance Thresholding for Gene Set Analysis of Genetic Pathway Data

(Last Updated: Aug 25, 2023)