CURRICULUM VITAE

Name: Taesung Park

Email: tspark@stats.snu.ac.kr

Position: Professor

Institution: Seoul National University

Location: 1 Gwanak-ro, Gwanak-gu, Seoul, 08826

Education:

1980 - 1984, B.S., Department of Computer Science and Statistics

       Seoul National University, Korea

1984 - 1986, M.S., Department of Computer Science and Statistics

       Seoul National University, Korea

1986 - 1990, Ph. D., Department of Biostatistics, University of Michigan, USA

       Dissertation: Estimation of Nonresponse Models for Categorical Data

Representative Careers:

Professor	2001. 10 – present
Chair	2007. 9 – 2009. 8
Department of Statistics	
Seoul National University, Korea	

Fellow

American Statistical Association(ASA)   2018.8- present

Director

National Creative Research Laboratory of Bioinformatics and Biostatistics

Seoul National University, Korea   2012. 5 – 2016. 2

Visiting Professor

Department of Biostatistics

University of Washington   2009. 9 – 2010. 8

Specialty & Present Interest:

DNA Microarray Data Analysis, Genetic network DNA, Statistical Genetics, Gene-Gene interaction analysis

Missing Data Analysis, Repeated Measures Data and Longitudinal Data Analysis

Representative papers (up to 5):

- Paik S, Shak S, Tang G, Kim C, Baker J, Cronin M, Baehner FL, Walker MG, Watson D, **Park T**, Hiller W, Fisher ER, Wickerham DL, Bryant J and, Wolmark N (2004) A multigene assay to predict recurrence of tamoxifen-treated, node-negative breast cancer. New England Journal of Medicine, 351, 2817-2826

- Cho YS, Go MJ, and et. al (2009) A large-scale genome-wide association study of Asian populations uncovers genetic factors influencing eight quantitative traits. Nature Genetics, 41(5), 527-534

- Teslovich TM, Musunuru K, Smith AV, and et. al (2010) Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 466, 707–713

- Fuchsberger C, Flannick J, Teslovich TM, and et. al (2016) The genetic architecture of type 2 diabetes. Nature, doi:10.1038/nature18642

- Lek M, Karczewski KJ, Minikel EV, and et. al (2016) Analysis of protein-coding genetic variation in 60,706 humans. Nature, 536, 285-291