Yong Seok Park

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University of Pittsburgh
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Education

Ph.D. Biostatistics, University of Michigan-Ann Arbor, December, 2011.

> Dissertation: *On estimation and inference under order restrictions*.

> Committee: Jeremy M.G. Taylor (co-chair), John D. Kalbfleisch (co-chair), Bin Nan, Ji Zhu.

M.S. Biostatistics, University of Michigan-Ann Arbor, April, 2007.

M.E. Mechanical Engineering, Tsinghua University, Beijing P.R.China.

B.E. Mechanical Engineering, Shanghai Jiao Tong University, Shanghai P.R.China.

Fields of research interest

High-throughput Genomic data analysis in cancer research; survival, nonparametric and Bayesian analysis; joint survival-longitudinal modeling.

Personal Statement

My current research focuses on epigenetic and high throughput genomic data analysis in cancer study. Since January 2012, I have focused on Bioinformatics research such as developing whole genome DNA methylation data analysis pipeline using novel statistical model, RNA sequencing data analysis, microarray and sequencing based gene expression data analysis. In addition, I have developed a web-based statistical tool to predict recurrence of prostate cancer for patients after radiation therapy using Bayesian joint survival-longitudinal modeling. My research interests also include other traditional Biostatistics research including survival analysis, nonparametric analysis and ordered statistics analysis.

Computing Skills

Statistical Packages: R, SAS.

Computing Languages: C/C++, Java, Perl, Fortran, Pascal.

Complier Languages: Lex, Yacc.

Operating Systems: Unix/Linux, Windows.

Teaching

BIOS 2083 – Linear Models: Role: Primary Instructor, Fall 2014, Fall 2015, Fall 2016, Fall 2017, Fall 2018, Fall 2019

BIOS 2025 – Biostatistics Seminar: Role: Instructor, Winter 2015, Fall 2015, Winter 2016

BIOS 2055 – Intro High-throughput Genomic Data Analysis I: Data Mining and Applications: Role: Guest Lecturer. Spring 2014, Spring 2015, Spring 2016.

Publications

Statistics or Bioinformatics Journal Articles

1. Huo Z, Tang S, Park Y, Tseng G. P-value evaluation, variability index and biomarker categorization for adaptively weighted Fisher's meta-analysis method in omics applications. Bioinformatics. 2019 Jul 29;. doi: 10.1093/bioinformatics/btz589. [Epub ahead of print] PubMed PMID: 31359040.

2. Liu P, Lin CW, **Park Y**, Tseng G. MethylSeqDesign: a framework for Methyl-Seq genome-wide power calculation and study design issues. Biostatistics. 2019 May 20;. doi: 10.1093/biostatistics/kxz016. [Epub ahead of print] PubMed PMID: 31107532.

3. Lin, C-W, Liao, G, Lee, M-L T, **Park, Y**, Tseng, GC. RNASeqDesign: A framework for RNA-Seq genome-wide power calculation and study design issues. 2018, Journal of the Royal Statistical Society C, 68(3), 683-704.

4. Xu Z, **Park Y**, Zhen B, Zhu B. Designing cancer immunotherapy trials with random treatment time-lag effect. Stat Med. 2018 Dec 30;37(30):4589-4609. doi: 10.1002/sim.7937. Epub 2018 Sep 10. PubMed PMID: 30203592; PubMed Central PMCID: PMC6279582.

5. Ma, T, Huo, Z, Kuo, A, Zhu, L, Fang, Z, Zeng, X, Lin, C-W, Liu, S, Wang,L, Liu, P, Rahman, T, Chang, L-C, Kim, S, Jia Li, **Park, Y**, Song, Oesterreich, SC, Sibille, E and Tseng, GC. MetaOmics: Analysis Pipeline and Browser-based Software Suite for Transcriptomic Meta-Analysis. Bioinformatics (Oxford, England). 2019, May 1;35(9):1597-1599. doi: 10.1093/bioinformatics/bty825. PMID: 30304367 PMCID:PMC6499246

6. Kim S, Kang D, Huo Z, **Park Y**, Tseng GC. Meta-analytic Principal Component Analysis in Integrative Omics Application. Bioinformatics. Volume 34, Issue 8, 15 April 2018, Pages 1321–1328. PMID: 29186328

7. Xu, Z., Zhen, B., **Park, Y.**, Zhu, B. (2017), Designing therapeutic cancer vaccine trials with delayed treatment effect. *Statistics in medicine*, 36, 592-605

8. Kim, S., Oesterreich, S., Kim, S., **Park, Y.**, Tseng, G.C. (2017), Integrative Clustering of Multi-level Omics Data for Disease Subtype Discovery using Sequential Double Regularization. *Biostatistics*, 18, 165-179.

9. Qin, Z., Li, B., Conneely, K. N., Wu, H., Hu, M., Ayyala, D, **Park, Y.**, Jin, V. X., Zhang, F., Zhang, H., Li, L., Lin, S. (2016), Statistical challenges in analyzing methylation and long-range chromosomal interaction data. *Statistics in biosciences*. 8, 284-309. NIHMSID: NIHMS766759.

10. **Park, Y**, Wu, H. (2016), Differential methylation analysis for BS-seq data under general experimental design. *Bioinformatics*, 32, 1446-53.

11. **Park, Y.**, Figueroa, M., Rozek, L. and Sartor, M.A. (2014), MethylSig: a whole genome methylation analysis pipline, *Bioinformatics*, 30, 2414-22. PMID: 24836530.

12. **Park, Y.**, Kalbfleisch, J.D. and Taylor, J.M.G (2014). Confidence intervals under order restriction. *Statistica Sinica*, 24, 429-445. PMCID: PMC3910006. PMID: 24505210.

13. Taylor, J.M.G., **Park, Y.**, and others (2013), Real-time individual predictions of prostate cancer recurrence using joint models. *Biometrics*, 69, 206–213. PMCID: PMC3622120. PMID: 23379600.

14. **Park, Y.**, Taylor J.M.G., Kalbfleisch J.D. (2012). Pointwise nonparametric maximum likelihood estimator of stochastically ordered survivor functions. *Biometrika*, 99, 327-343. PMCID: PMC3635706. PMID: 23843661.

15. **Park, Y.**, Kalbleisch JD, Taylor JMG (2012). Constrained nonparametric maximum likelihood estimator of stochastically ordered survivor functions. *Canadian Journal of Statistics*, 40, 22-39.

Other Journal Articles

1. Lee, S-Y, Kalimuthu, K., **Park, Y**, Makala, H, Watkins, S.C., Choudry, M. H. A., Bartlett, D., Kwon, Y.T., Lee, Y.J. (2020), Ferroptoticagent-induced endoplasmic reticulum stress response plays a pivotal role in the autophagic process outcome. Journal of Cellular Physiology.

2. Xu, Z, **Park, Y.**, Liu, K. Zhu, B. (2020), Treating non-responders: pitfalls and implications for cancer immunotherapy trial design. Journal of Hematology & Oncology.

3. Lee, Y.J., Lee, Y-S., **Park Y.S.**, Helvetica, M.H.A., MD; Bartlett, D.L.B.(2020), BAX-dependent mitochondrial pathway mediates the crosstalk between ferroptosis and apoptosis". Apoptosis.

4. Lee, Y-S., Lee, D-H., Jeong, S.Y., Park, S.H., Oh, S. C., **Park, Y.S.**, Yu, J., Choudry, H.A., Bartlett, D.L., Lee, Y.J.(2019) Ferroptosis-inducing agents enhance TRAIL-induced apoptosis through upregulation of death receptor 5. Journal of cellular biochemistry, 120, 928-939.

5. Cavalcante, R.G., Patil, S., **Park, Y.**, Rozek, L.S., and Sartor, M.A. (2017) Integrating DNA methylation and hydroxymethylation data with the mint pipeline. Cancer Research, 7(21):e27-e30.

6. Machicado JD, Gougol A, Stello K, Tang G, **Park, Y.**, Slivka A, Whitcomb DC, Yadav D, Papachristou GI. Acute Pancreatitis Has a Long-Term Deleterious Effect on Physical Quality of Life. Clin Gastroenterol Hepatol. 2017 Jun 1. pii: S1542-3565(17)30668-7. doi: 10.1016/j.cgh.2017.05.037. [Epub ahead of print] PubMed PMID: 28579182.

7. Seynnaeve, B., Lee, S., Borah, S., **Park, Y.**, Pappo, A., Kirkwood, J. M., Bahrami, A. (2017). Genetic and Epigenetic Alterations of TERT Are Associated with Inferior Outcome in Adolescent and Young Adult Patients with Melanoma. *Scientific Reports*, 7, 45704

8. Andersen, C.L., Sikora, M.J., Boisen, M.M., Ma, T., Christie, A., Tseng, G., **Park, Y.S.**, Luthra, S., Chandran, U., Haluska, P. and Mantia-Smaldone, G. (2017), Active estrogen receptor-alpha signaling in ovarian cancer models and clinical specimens. *Clinical Cancer Research*, clincanres-1501.

9. Gearhart, T. L., Montelaro, R. C., Schurdak, M. E., Pilcher, C. D., Rinaldo, C. R., Kodadek, T., **Park, Y.**, Islam, K., Yurko, R., Marques, E. T. A Jr. and Burke, D. S.(2016), Selection of a potential diagnostic biomarker for HIV infection from a random library of non-biological synthetic peptoid oligomers. *Journal of immunological methods*, 435, 85-9.

10. Zhang, X, Rao, A., Sette, P, Deibert, C. Pomerantz, A., Kim, W. J., Kohanbash, G, Chang, Y., **Park, Y.**, Engh, J. Choi, J., Chan, T. Okada, H. Lotze, M. Paola, G., Amankulor, N. (2016), IDH mutant gliomas escape natural killer cell immune surveillance by downregulation of NKG2D ligand expression. *Neuro-oncology*, 18, 1402-12.

11. Li, H., Wheeler, S., **Park, Y.**, Ju, Z., Thomas, S.M., Fichera, M., Egloff, A.M., Lui, V.W., Duvvuri, U., Bauman, J.E., Mills, G.B., Grandis, J.R.(2016), Proteomic Characterization of Head and Neck Cancer Patient-Derived Xenografts. *Molecular Cancer Research*, 278-86. PMID: 26685214. PMCID: PMC4794346.

Book Chapters

1. Qin, T., **Park, Y.**, Figueroa, M.E., Sartor, M.A. (2015), Ultra-Deep Sequencing of Bisulfite-Modified DNA. In *Epigenomics in Health and Disease*, 47-72.

2. Kim, S., Huo, Z., **Park, Y.**, Tseng, G.C. (2015), MetaOmics: Transcriptomic Meta-Analysis Methods for Biomarker Detection, Pathway Analysis and Other Exploratory Purposes. In *Integrating Omics Data*, 39-67.

Software

Web-based PSA calculator, http://psacalc.sph.umich.edu.
MethylSig R Package.

Appointment

Assistant professor, Department of Biostatistics, University of Pittsburgh, Sep. 2013 – present

Post-Doctoral Research Fellow, Department of Computational Medicine & Bioinformatics, University of Michigan-Ann Arbor, Jan. 2012 – Aug. 2013

Graduate Student Research Assistant, Department of Biostatistics, University of Michigan-Ann Arbor, Jan. 2006 - Dec. 2011.

Professional Experience

Senior Software Engineer, Intelligent Telecommunications Inc., Daejeong, South Korea

Software Engineer, LG Electronics, Anyang, Gyeonggi-do, South Korea

Assistant Researcher, Tsinghua University, Beijing, China

Disertation Committee Member

Chien-Wei (Masaki) Lin, Department of Biostatistics, University of Pittsburgh

Silvia (Shuchang) Liu, Computational Biology, University of Pittsburgh

Zhiguang (Caleb) Huo, Department of Biostatistics, University of Pittsburgh

Ying Shan, Department of Biostatistics, University of Pittsburgh

SungHwan Kim, Department of Biostatistics, University of Pittsburgh

Rui Chen, Department of Biostatistics, University of Pittsburgh

Lun-Ching Chang, Department of Biostatistics, University of Pittsburgh

Ge (Serena) Liao, Department of Biostatistics, University of Pittsburgh

Journal Reviewer

PLOS ONE

Statistics Surveys

BMC Medical Genomics

Cancer Biomakers

Entropy

Briefing in Bioinformatics

Scientific Reports

Journal of Statistical Computation and Simulation

Journal of Royal Statistical Society, B

Invitated presentations:

1. Designing cancer immunotherapy trials with random treatment time-lag effect. Presented at: Conference on Lifetime Data Science: Foundations and Frontiers; 2019 May 30; Pittsburgh, Pennsylvania.

2. Designing cancer immunotherapy trials with random treatment time-lag effect. Presented at: Biostatistics Department Seminar Series, University of Pittsburgh; 2018 Dec 6; Pittsburgh, Pennsylvania.

3. On Adaptive Weighting of omics meta-analysis. Presented at ICSA Applied Statistics Symposium; 2018 Jun 16; New Brunswick, NJ

4. Estimation and inference of bounded normal mean. Presented at JSM; 2017 Aug 3; Baltimore, Maryland.

5. Statistical Analysis of Single Cell DNA methylation. Presented at ICSA Applied Statistics Symposium; 2017 Jun 26; Chicago, Illinoi.

6. Integrative Clustering of Multi-level Omics Data for Disease Subtype Discovery Using Sequential Double Regularization. Presented at: 10th ICSA International Conference; 2016 Dec 19; Shanghai, China

7. Design Immunotherapy Trials with Delayed Effect. Presented at: 2016 ASA Biopharmaceutical Section Regulatory-Industry Statistics Workshop; 2016 Sep 20; Baltimore, Maryland

8. Differential methylation analysis for BS-seq data under general experimental design. Presented at: Statistics Department Seminar Series, University of Pittsburgh; 2016 Feb 19; Pittsburgh, Pennsylvania.

9. Differential methylation analysis for BS-seq data under general experimental design. Presented at: Joint 24th ICSA Applied Statistics Symposium and 13th Graybill Conference; 2015 Jun 15; Fort Collins, Colorado.

10. Statistical Analysis of DNA Methylation using Within-Fragment Information. Presented at: SAMSI in Research Triangle Park; 2015 Mar 10; 19 T.W. Alexander Drive, Research Triangle Park, NC 27709-4006

11. DNA methylation and data analysis. Presented at: University of Pittsburgh Cancer Institute; 2014 Oct 20; 203 Lothrop St, Pittsburgh, PA 15213

12. MethylSig: a method to identify and visualize differentially methylated regions from genome-wide bisulfite sequencing data, Department of Bioinformatics, University of Michigan, Dec. 19, 2013.

Conference Presentations: Contributed

Park, Y. and Taylor, J. M. G., Restricted confidence intervals for ordered binary and survival data. Oral presentation at 2014 International Biometric Society (ENAR) Conference: March 2014, Baltimore, MD.

Park, Y., Maureen A. Sartor, MethylSig: a whole genome DNA methylation analysis pipeline. Poster presentation at Genomics Research Conference: May 2013, Boston, MA.

Park, Y., Kalbfleisch, J.D. and Taylor, J.M.G., Confidence intervals under order restriction. Oral presentation at 2012 International Biometric Society (ENAR) Conference: March 2012, Washington DC.

Park, Y., Kalbfleisch, J.D. and Taylor, J.M.G., Pointwise nonparametric maximum likelihood estimator of survivor functions under stochastic ordering constraint. Oral presentation at 2010 the Joint Statistical Meetings: August 2010; Vancouver, BC, Canada.

Park, Y., Kalbfleisch, J.D. and Taylor, J.M.G., Constrained NPMLE of survivor functions under stochastic ordering in the one- and two-sample cases. Oral presentation at 2010 International Biometric Society (ENAR) Conference: March 2010; New Orleans, LA.

Park, Y., Constrained Survival Analysis. Oral presentation at 2009 International Biometric Society (ENAR) Conference: March 2009; San Antonio, TX.

Honors, Awards, & Fellowships

Richard G. Cornell Scholarship, University of Michigan-Ann Arbor, 2006

Guanghua Scholarship, Tsinghua University

Excellent Graduating Undergraduate Student of universities and colleges in Shanghai

Professional Societies

American Statistical Association (ASA), 2008 – Present

International Biometric Society (ENAR), 2008 – Present

Institute of Mathematical Statistics (IMS), 2008 – Present

International Chinese Statistical Association (ICSA), 2014 – Present

Korean International Statistical Society (KISS), 2014 – Present

$\sim\sim\sim$ Last updated: June 3, 2020$\sim\sim\sim$