BIOGRAPHICAL SKETCH

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NAME: Ha, Taehoon

eRA COMMONS USER NAME (credential, e.g., agency login): TAEHOONHA

POSITION TITLE: Biostatistician

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Sungkyunkwan University, Seoul	BS	07/2017	Business, Quantitative Methods
Duke University, Durham, NC	MS	05/2018	Quantitative Management
Weill Cornell Medicine, New York, NY	MS	12/2019	Biostatistics and Data Science

A. Personal Statement

My research interest is developing and applying novel statistical methods to better design biological, pre-clinical, and clinical studies related to cancer prevention, diagnosis, treatment, and prognosis. I have extensive experience analyzing biomarker expression and alterations in human cancer tissue and blood specimens and animal studies. In particular, I participated in multiple data analyses exploring correlations of key biomarkers in human tissue specimens with clinical characteristics such as tumor stage, subtype, obesity, and inflammation using univariate and multivariable analyses. As a biostatistician in this R01 proposal, I will provide statistical expertise in the design, analysis, and interpretation of results from all Aims. I will also assist with the writing of statistical sections of manuscripts.

1. Yang JI, Ha T, Zhou E, Tzanavaris C, Devoe CE, Zhu X, Boyd J (2021). Association of TP53 mutation status and GATA6 amplification with clinical outcome of pancreatic cancer, Journal of Clinical Oncology.
2. Iyengar NM, Zhou XK, Mendieta H, El-Hely O, Giri DD, Winston L, Falcone DJ, Wang H, Meng L, **Ha T**, Pollak M, Hudis CA, Morrow M, Dannenberg AJ (2021), Effects of Obesity on Breast Aromatase Expression and Systemic Metabo-Inflammation in Women with BRCA1 or BRCA2 Mutations, npj Breast Cancer.
3. Montrose DC, Saha S, Foronda M, McNally EM, Zhou XK, **Ha T**, Krumsiek J, Verma A, Elemento O, Yantiss RK, Chen Q, Gross SS, Galluzzi L, Dow LE, and Dannenberg AJ (2021), Exogenous and Endogenous Sources of Serine Contribute to Colon Cancer Metabolism and Growth, Cancer Research.
4. Williams EH, Flint TR, Connell CM, Giglio D, Lee H, **Ha T**, Gablenz E, Bird N, Weaver J, Potts H, Whitley CT, Bookman MA, Lynch AG, Meyer H, Tavaré S, Janowitz T (2021), CamGFR v2: A New Model for Estimating the Glomerular Filtration Rate from Standardized or Non-Standardized Creatinine in Patients with Cancer, Clinical Cancer Research.

B. Positions, Scientific Appointments, and Honors

Positions and Employment

2019 – 2020 Research Assistant: Biostatistics, Weill Cornell Medicine, New York, NY

2019 – 2020 Teaching Assistant, Weill Cornell Medicine, New York, NY

2019 – 2021 Voluntary Researcher: Bioinformatics Analyst, Johns Hopkins University, Baltimore, MD

2020 – Biostatistician, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY

Other Experience and Professional Memberships

2018 – 2019 Member, American Association for the Advancement of Science (AAAS)

2019 – Member, American Statistical Association (ASA)

Honors

2009 – 2015 Academic Excellence Scholarship, Sungkyunkwan University, Seoul

2019 – 2020 Academic Excellence Award, Weill Cornell Medicine, New York, NY

C. Contributions to Science

1. I have worked closely with investigators involved in diet and colon tumorigenesis. I collaborated with Andrew J. Dannenberg, MD, in the development of his high fructose diet research. I have performed multiple statistical analyses and was able to apply the techniques I learned during that time to numerous genetic association studies. The collaboration has led to collaborative papers of which a subset is listed below:

   - Basu S, Liu C, Zhou XK, Nishiguchi R, Ha T, Chen J, Johncilla M, Yantiss RK, Montrose DC, Dannenberg AJ (2021), GLUT5 is a Determinant of Dietary Fructose-mediated Exacerbation of Experimental Colitis, AJP Gastrointestinal and Liver Physiology.

   - Nishiguchi R, Basu S, HA Staab, Ito N, Zhou XK, Wang H, Ha T, J Melanie, KY Rhonda, Montrose DC, Dannenberg AJ (2021), Dietary Interventions to Prevent High Fructose Diet-associated Worsening of Colitis and Colitis-associated Tumorigenesis in Mice, Carciogenesis

2. I have been assisting Xi Kathy Zhou, Ph.D. with developing a new statistical method using Bayesian model averaging to identify differentially expressed genes associated with one or more patient characteristics (phenotypes), as well as their interactions. This project aims to apply the Bayesian model averaging method (BMA-seq) to observational gene-expression data to improve differentially expressed (DE) genes identification in high dimensional setting and develop R package software called '*BMAseq*.' The following manuscript is in preparation: Wang H, Meng L, **Ha T**, Zhou XK, A Bayesian model averaging approach for RNA-seq counts data (BMA-seq) and its application.

3. As a voluntary researcher, I have analyzed brain and liver transcriptome data to identify differentially expressed (DE) genes associated with the exposure to ultra-fine dust, $PM_{2.5}$, under the supervision of Bongsoo Park, Ph.D., at the National Institute of Health and Johns Hopkins Bloomberg School of Public Health. The following manuscripts are in preparation: Park B, Deiuliis J, Palanivel R, **Ha T**, Park JE, Rajagopalan S, and Biswal S, Sex-difference in the metabolic effects of air pollution exposure; **Ha T**, Park JE, Palanivel R, Rajagopalan S, Biswal S, and Park B, Sex-difference in liver transcriptome with environmental exposure; and Park B, Kim S, Ha T, Park JE, Vinayachandran V, Hansen KD, Paul B, Rajagopalan S, and Biswal S, Brain transcriptome map of air pollution $PM_{2.5}$.