

TAEHOON HA

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EDUCATION

- WELL CORNELL MEDICINE** | *M.S., Biostatistics and Data Science* New York, NY
• Academic Excellence (Over 4.0 cumulative GPA) Award
• Thesis: Application of a Bayesian Model Averaging Method to Observational Metabolomics Data Analysis
- DUKE UNIVERSITY** | *M.S., Business Analytics* Durham, NC
• Capstone project: Duke University Hospital (Duke Health)
- SUNGKYUNKWAN UNIVERSITY** | *B.B.A. with an emphasis on Quantitative Methods* Seoul, Korea
• Dean's list with distinction
• Study-abroad: School of Arts and Sciences at the University of Pennsylvania (2014) – Travel funding, Mar 2015
• Military Service: Republic of Korea Marine Corps (Rank: Sergeant, 2011 – 2013)

TECHNICAL SKILLS

- **Programming:** R, Python
- **Database:** MySQL, SQL Server, Microsoft Access
- **Platform:** MacOS, Windows, Ubuntu, Linux
- **Cloud/Distributed computing:** Amazon Web Services, Google Cloud Platform
- **Visualization:** Tableau Software, Prism Graphpad, Adobe Illustrator

RESEARCH EXPERIENCE

- COLD SPRING HARBOR LABORATORY** | *Biostatistician* Cold Spring Harbor, NY
Sep 2020 – Present
• Provide weekly office hours for researchers in need of statistical help or consultation
• Collaborate with Cancer Center researchers and Northwell Health on pre-clinical/clinical study design and complex statistical analyses
• Write statistical sections of research proposals, grant applications, and manuscripts
• Develop statistically rigorous workflows and analysis plans with Core Facility managers
• Assist faculty with developing and teaching educational seminars that include both theory and applications of statistics to biomedical research questions

- WELL CORNELL MEDICINE** | *Research Assistant – Biostatistics & Data Science (Advisor: Xi Kathy Zhou, PhD)* New York, NY
Apr 2019 – Sep 2020

Application: Collaboration with Andrew J. Dannenberg, MD group

- Collaborated extensively with investigators researching cancer, obesity, and metabolic diseases
- Provided statistical consulting support to clinical (lab) and genomic data using R
- Performed sample size and power calculations, designed and implemented database for clinical data collection
- Interpreted statistical analysis reports for investigators and wrote statistical method sections for scientific publication

Methodology: Application of Bayesian model averaging to better identify differentially expressed genes in high-dimensional setting

- Developed a new statistical method using Bayesian model averaging to identify DE genes associated with one or more patient characteristics (or phenotypes), as well as their interactions
- Built and improved R package 'BMAseq' using Bayesian model averaging to analyze observational gene-expression data
- Applied the Bayesian model averaging method to multiple types of datasets, from metabolomics data to NGS data, to check its performance

- JOHNS HOPKINS UNIVERSITY** | *Voluntary Researcher – Bioinformatics Analyst (Advisor: Bongsoo Park, PhD)* (Remote) Baltimore, MD
Apr 2019 – Present

Transcriptome and epigenome atlas for air pollution PM_{2.5}

- Generated a pipeline code to analyze liver single-cell RNA-seq data using R package Monocle to cluster the cells and predict cell types
- Constructed analytical pipelines using R and Python to identify DE genes associated with the exposure to particulate matter
- Checked sample quality by Spearman's Rho correlation, hierarchical clustering, and perform Principal Component Analysis (PCA)
- Performed Differential Expression analysis and Gene Ontology (GO) Term analysis on six different brain sub-areas and liver cells
- Conducted pathway analysis using Ingenuity Pathway Analysis (IPA) software
- Prepared tables and figures and wrote statistical methods sections for scientific publications

ADDITIONAL INFORMATION

PUBLICATIONS

Published

- CM Brennan, S Nadella, X Zhao, RJ Dima, N Jordan-Martin, BM Demestichas, SO Kleeman, M Ferrer, E Gablenz, N Mourikis, M Rubin, H Adnani, **T Ha**, S Prum, CB Schleicher, SS Fox, M Ryan, C Pili, J Poulard, G Goldberg, JM Crawford, S Goodwin, X Zhang, J Preall, S Costa, J Conigliaro, JR Masci, J Yang, DA Tuveson, KJ Tracey, T Janowitz (2022). *Oral Famotidine vs Placebo in Diverse Non-Hospitalized Patients with COVID-19: A Randomized Double-Blind, Data-Intense, Phase 2 Clinical Trial*. Gut.
- S Basu, C Liu, XK Zhou, N Ryohei, **T Ha**, J Chen, M Johncilla, RK Yantiss, DC Montrose, and AJ Dannenberg (2021). *GLUT5 is a Determinant of Dietary Fructose-mediated Exacerbation of Experimental Colitis*. AJP Gastrointestinal and Liver Physiology.
- JI Yang, **T Ha**, E Zhou, C Tzanavaris, CE Devoe, X Zhu, and J Boyd (2021). *Association of TP53 Mutation Status and GATA6 Amplification with Clinical Outcome of Pancreatic Cancer*. Journal of Clinical Oncology.
- DC Montrose, M Foronda, S Saha, EM McNally, XK Zhou, **T Ha**, J Krumsiek, A Verma, O Elemento, RK Yantiss, Q Chen, SS Gross, L Galluzzi, LE Dow and AJ Dannenberg (2021). *Exogenous and Endogenous Sources of Serine Contribute to Colon Cancer Metabolism and Growth*. Cancer Research.
- NM Iyengar, XK Zhou, H Mendieta, O El-Hely, DD Giri, L Winston, DJ Falcone, H Wang, L Meng, **T Ha**, M Pollak, CA Hudis, M Morrow, and AJ Dannenberg (2021). *Effects of Obesity on Breast Aromatase Expression and Systemic Metabo-Inflammation in Women with BRCA1 or BRCA2 Mutations*. npj Breast Cancer.

- R Nishiguchi, S Basu, HA Staab, N Ito, XK Zhou, H Wang, **T Ha**, M Johnchilla, RK Yantiss, DC Montrose, and AJ Dannenberg (2021). *Dietary Interventions to Prevent High Fructose Diet-associated Worsening of Colitis and Colitis-associated Tumorigenesis in Mice*. *Carcinogenesis*.
- EH Williams, TR Flint, CM Connell, D Giglio, H Lee, **T Ha**, E Gablenz, N Bird, JMJ Weaver, H Potts, CT Whitley, MA Bookman, AG Lynch, HV Meyer, S Tavaré, and T Janowitz (2020). *CamGFR v2: A New Model for Estimating the Glomerular Filtration Rate from Standardized or Non-Standardized Creatinine in Patients with Cancer*. *Clinical Cancer Research*.

Accepted

- S Bhatia, M Kramer, S Russo, P Naik, G Arun, K Brophy, P Andrews, C Fan, C Perou, J Preall, **T Ha**, D Plenker, D Tuveson, A Rishi, J Wilkinson, WR McCombie, K Kostroff, and D Spector (2021). *Patient-derived Triple Negative Breast Cancer Organoids Provide Robust Model Systems that Recapitulate Tumor Intrinsic Characteristics*. *Cancer Research*.

Submitted

- Y Gao, XY He, XS Wu, YH Huang, S Toneyan, JJ Ipsaro, **T Ha**, PK Koo, M Egeblad, L Joshua-Tor, and CR Vakoc (2021). *ETV6 Dependency in Ewing Sarcoma through Antagonism of EWS-FLI1-Mediated Enhancer Activation*. *Nature Cell*.

TEACHING EXPERIENCE

Big Data in Medicine: Biomedical Imaging | *Teaching Associate for Prof. Elizabeth Sweeney, Weill Cornell Medicine* *Spring 2020*

Big Data in Medicine: Genetics & Genomics | *Teaching Associate for Prof. Davide Risso, Weill Cornell Medicine* *Spring 2020*

Categorical and Censored Data Analysis | *Teaching Associate for Prof. Oleksandr Savenkov, Weill Cornell Medicine* *Fall 2019*

- Led lab sessions for 32 Master's candidate students to teach biostatistical methods with R
- Reviewed and graded weekly homework and provide guidance on lab assignments
- Held regular office hours regarding questions on course materials, assignments, and academic concerns

PRESENTATION & PRESS INTERVIEW

- Virtual Core Knowledge: Biostatistics Workshop, *Cold Spring Harbor Laboratory* *Jan 2021*
- Interview Article: Analysis of 3,600 COVID-19 sequences on Nextstrain, *Donga Science* *Apr 28th, 2020*
- The Single-cell Pathology Landscape of Breast Cancer, *Weill Cornell Medicine* *Mar 2020*
- Genomic Signatures Predict the Immunogenicity of BRCA-Deficient Breast Cancer, *Weill Cornell Medicine* *Dec 2019*
- Profound Perturbation of the Metabolome in Obesity Is Associated with Health Risk, *Weill Cornell Medicine* *Aug 2019*

SERVICE

Nextstrain | *Voluntary Technical Translator* *Mar 2020 – May 2020*

- Translated technical document and weekly genomic analysis of COVID-19 situation reports into Korean