

TAEHOON HA

☎ (267) 225-2588 | ✉ tah4002@med.cornell.edu | 🏠 taehoonh.me | 🔄 taehoonh | 🌐 taehoonha

Education

Weill Cornell Medicine

New York, NY

M.S., Biostatistics and Data Science

2018 – 2019

- Advisor: Xi Kathy Zhou, PhD
- Thesis: *Application of a Bayesian model averaging method to observational metabolomics data analysis*

Duke University

Durham, NC

M.S., Business Analytics

2017 – 2018

- Capstone project: Duke University Hospital (Duke Health)

Sungkyunkwan University

Seoul, Korea

B.B.A. with an emphasis on Quantitative Methods

2009 – 2017

- Dean's list with distinction
- Study-abroad: School of Arts and Sciences at the University of Pennsylvania (2014)

Research Experience

Weill Cornell Medicine

New York, NY

Research Assistant (Advisor: Xi Kathy Zhou, PhD)

04/2019 – Present

Application: Collaboration with Andrew J. Dannenberg, MD group

- Provide statistical consulting support to clinical (lab) and genomic data using R
- Collaborate with Andrew J. Dannenberg, MD group to identify the link along the obesity, inflammation, and breast cancer
- Update and customize R package software 'BTKR' which includes multiple functions that implement some commonly used biostatistics analysis methods for the summary of data

Methodology: Bayesian model averaging

- Assist the advisor with developing a new statistical method using Bayesian model averaging to identify differentially expressed genes associated with one or more phenotypes, as well as their interactions
- Develop R package 'BMASeq' using Bayesian model averaging to analyze observational gene-expression data
- Apply the Bayesian model averaging method to large scale public RNA-seq gene expression data
- Apply the Bayesian model averaging method ("BMA-seq") to observational metabolomics data to improve differentially expressed (DE) metabolites identification in high dimensional setting

Johns Hopkins Bloomberg School of Public Health

Baltimore, MD

Voluntary Researcher (Advisor: Bongsoo Park, PhD)

(Remote)

04/2019 – Present

Transcriptome and epigenome atlas for air pollution PM_{2.5}

- Align RNA sequences using STAR or TopHat2
- Construct analytical pipelines using EdgeR, DESeq2, or Limma/Voom to identify differentially expressed genes associated with the exposure to ultra-fine dust, PM_{2.5}
- Verify sample quality using Spearman's Rho correlation and hierarchical clustering methods

- Check the distribution by Relative Log Expression (RLE), and Principal Component Analysis (PCA)
- Normalize each sample and removed unwanted variances and filtered top N genes by p-values
- Perform DE (Differential Expression) analysis and Gene Ontology (GO) Term analysis on six different brain sub-areas and liver cells
- Conduct pathway analysis using Ingenuity Pathway Analysis (IPA) software

JB Lab & Clinic

Seoul, Korea

Research Scientist

(Remote)

08/2018 – 12/2019

- Identified the association of sodium intake and hypertension, metabolic syndrome, and ARB treatment effect from a 10K+ hypertension patients data acquired from a K-MetS study

Weill Cornell Medicine

New York, NY

Student Project

The Effect of Right Heart Catheterization (RHC) During the First 24 Hours on 30-day Mortality of Critically Ill Patients in Intensive Care Units

05/2019 – 08/2019

- Applied data adaptation method to estimate the propensity score
- Generated causal model estimands using multiple methods (random forest, GLM, elastic net, LASSO, and gradient boosting with SuperLearner)
- Conducted 5-fold cross-validation to evaluate each estimand's performance and coefficient in the ensemble estimator

Rate of General Anesthesia Use for Cesarean Delivery Among Anesthesiologists with and without Fellowship Training in Obstetric Anesthesia

01/2019 – 05/2019

- Fitted the logistic regression model to identify whether the fellowship-trained anesthesiologists are more or less likely to provide general anesthesia for non-routine C-section as compared to non-fellowship trained anesthesiologists
- Identified the significant difference between general and neuraxial anesthesia and the odds of using general anesthesia is 0.471 times lower in attending fellowship training anesthesiologists compared the non-fellowship training anesthesiologists

Cost-Effective Optimization of Model-Based Prediction of Cardiovascular Disease (CVD)

03/2019 – 05/2019

- Aimed to increase the accuracy of CVD diagnosis using a model-based approach
- Determined the demographic factors and medical tests that help predict the likelihood of heart disease using proportional odds model and logistics regression
- Identified a combination of necessary medical tests that help predict the probability of heart disease in a cost-effective manner and reduced the exam cost by \$110.17

Neuroendocrine Prostate Cancer (NEPC)

11/2018 – 12/2018

- Identified that there is no difference in the proportions of 3-month progression status between patients in the NEPC and non-NEPC group treated with alisertib
- Determined that there is no association between 3-month progression-free survival for all clinical characteristics and gene abnormalities
- Identified an association between PSA level and prior systemic therapies between NEPC and non-NEPC groups treated with alisertib

Major Risk Factors of Low Birth Weight Babies

10/2018 – 12/2018

- Determined that low birth weight is associated with the mother's premature labor history, race, smoking status, weight of the last menstrual period, and history of hypertension
- Fitted multiple generalized linear models with the model selection based on deviance and p-values

- Identified the primary injury factors of Ulnar Collateral Ligament Reconstruction for Major League Baseball pitchers by Statcast measures
- Designed a study to identify major factors of Ulnar Collateral Ligament Reconstruction (a.k.a. Tommy John Surgery) for Major League Baseball Pitchers by Statcast measurements

Teaching

Big Data in Medicine: Biomedical Imaging

Spring 2020

Teaching Associate for Prof. Elizabeth Sweeney, Weill Cornell Medicine

Big Data in Medicine: Genetics & Genomics

Teaching Associate for Prof. Davide Risso, Weill Cornell Medicine

Categorical and Censored Data Analysis

Fall 2019

Teaching Associate for Prof. Oleksandr Savenkov, Weill Cornell Medicine

- Lead lab sessions for 32 Master's candidate students to teach biostatistics methods with R
- Review and grade weekly homework and provide guidance on lab assignments
- Hold regular office hours regarding questions on course materials, assignments, and academic concerns

Publications

Submitted

- 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 (2020), *Effects of Obesity on Breast Aromatase Expression and Systemic Metabo-Inflammation in Women with BRCA1 or BRCA2 Mutations*, Submitted to Nature Cancer.
- Cho BA, Zhou XK, Morrow M, Giri DD, Sharaiha RZ, Kumar R, Yaghoobzadeh H, **Ha T**, Verma A, Elemento O, Pollak M, Laurence J, Iyengar NM, and Dannenberg AJ (2020), *Overexpression of Complement-related Genes in Adipose Tissues of Obese Individuals: Implications for the Pathogenesis of COVID-19*, Submitted to JCI Insight.
- David C. Montrose, Miguel Foronda, Suchandrima Saha, Erin M. McNally, Xi Kathy Zhou, **Taehoon Ha**, Jan Krumsiek, Akanksha Verma, Olivier Elemento, Rhonda K. Yantiss, Qiuying Chen, Steven S. Gross, Lorenzo Galluzzi, Lukas E. Dow and Andrew J. Dannenberg (2020), *Exogenous and Endogenous Sources of Serine Contribute to Colon Cancer Metabolism and Growth*, Submitted to Cancer Research.

In Preparation

- Bongsoo Park, Jeffrey A. DeIuliis, Rengasamy Palanivel, **Taehoon Ha**, Ji Eun Park, Sanjay Rajagopalan, and Shyam Biswal, *Sex-difference in the metabolic effects of air pollution exposure*.
- **Taehoon Ha**, Ji Eun Park, Rengasamy Palanivel, Sanjay Rajagopalan, Shyam Biswal, and Bongsoo Park, *Sex-difference in liver transcriptome with environmental exposure*.
- B Park, S Kim, **Taehoon Ha**, JE Park, V Vinayachandran, KD Hansen, B Paul, S Rajagopalan, and S Biswal, *Brain transcriptome map of air pollution PM_{2.5}*.

- Hanhan Wang, Lingsong Meng, **Tae-hoon Ha**, Xi Kathy Zhou, *A Bayesian model averaging approach for RNA-seq counts data (BMA-seq) and its application.*

Awards

Academic Excellence (Over 4.0 cumulative GPA), Weill Cornell Medicine	07/2019
Exchange Student Scholarship at the University of Pennsylvania (Travel Funding), Sungkyunkwan University	03/2015
Academic Excellence Scholarship, Sungkyunkwan University	01/2015 03/2014
Pursuit of Excellence Scholarship, Sungkyunkwan University	01/2014 01/2010 07/2009

Invited Talks

How to organize, manage, share, collaborate and process bio/healthcare data, Konkuk University Hospital	12/2018
RNA-seq data analysis 101, JB Lab & Clinic	08/2018
How to collaborate with a statistician, data analyst, and data scientist, Sungkyunkwan University	06/2017

Service

Nextstrain <i>Genomic analysis of COVID-19 spread: weekly situation report translation</i> • Translated weekly genomic analysis of COVID-19 spread situation reports into Korean	03/2020 – 05/2020
Prudential Foundation <i>Project CD34: Stem Cell Donation Trend Visualization</i> • Integrated and constructed the stem cell donation trend databases in Korea • Generated real-time dashboard to help the board's decision-making process	2015
S-ONE, Sungkyunkwan University <i>Data Analysis & Visualization Education Session Chief</i> • Led lab sessions for 40 students to teach statistical methods and data visualization tools when analyzing social science data	2013 – 2014
Samsung Dream Class Program <i>High School Mathematics Tutor</i> • Taught high school and pre-college math to 20 low-income students	2009 – 2010

Technical Skills

- **Programming:** R, SAS, Python
- **Database:** MySQL, SQL Server, Microsoft Access
- **Document:** LaTeX, Markdown
- **Cloud computing:** Google Cloud Platform, Amazon Web Services, Microsoft Azure
- **Platform:** Ubuntu (Linux)
- **Visualization:** Tableau Software

Membership

- American Statistical Association (ASA)
- Korean Statistical Society (KSS)
- American Heart Association (AHA)
- American Association for the Advancement of Science (AAAS)