

# Thomas Hsu

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## EDUCATION

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**Warren Alpert Medical School of Brown University, Providence, Rhode Island**  
Doctor of Medicine candidate, Class of 2022

Aug 2017 - present

**Brown University, Providence, Rhode Island**  
Bachelor of Arts in Biology, focus in Bioinformatics, Class of 2015  
Program in Liberal Medical Education, Class of 2015

Sept 2011 - May 2015

## SKILLS

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**Programming:** (*Proficient*) Python, C#, (*Familiar*) Javascript, Java, C++, HTML, R, MATLAB

**Data Management:** MySQL, Excel

**Charting and Clinical Documentation:** EPIC Electronic Health Records, VistA Electronic Health Records

## PROFESSIONAL EXPERIENCE

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**Dept. of Radiology, Alpert Medical School at Brown University - Researcher** Jan 2018 - Oct 2019

- Wrote and reviewed case reports on the radiologic and clinical findings of rare cancers seen throughout the hospital
- Gave presentations to departmental staff regarding best care practices and significant clinical markers of said cancers
- Made significant contributions on several papers pending publication.

**Dept. of Radiology, New York University Langone Medical Center - Research Data Associate** Aug 2016 - June 2017

- Designed study protocol to evaluate the difference in brain activity while breathing different concentrations of oxygen
- Wrote code to filter and correct for overflow errors in measurements of cerebral blood flow on CT scans
- Programmed algorithms to automatically delineate and measure infarcted brain tissue on diffusion-weighted MRI imaging
- Analyzed the developmental impact of induced strokes in newborn mice and compared tissue recovery against the extent of tissue infarct

**Dept. of Epidemiology, Brown University - Data Analyst for Yen-Tsung Huang, MD, MPH** Sept 2013 - May 2015

- Analyzed genomic data and created mathematical models relating biological factors to incidence and severity of disease
- Performed a 264-subject case analysis using novel statistical methods to compare the copy number variations of over 1800 gene pathways in smoking and non-smoking populations and identify several pathways of interest in the development of smoking-induced lung cancers
- Performed full epigenomic analysis of 511 subject evaluating the impact of tobacco use on the methylation of lung tissue in patients who developed lung squamous cell cancer or adenocarcinoma

## PEER-REVIEWED PUBLICATIONS

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Freeman, J., Chu, S., **Hsu, T.**, & Huang, Y.-T. (2016). Epigenome-wide association study of smoking and DNA methylation in non-small cell lung neoplasms. *Oncotarget*, 7(43), 69579-69591.

Huang, Y.-T., **Hsu, T.**, and Christiani, D. C. (2014). TEGS-CN: A Statistical Method for Pathway Analysis of Genome-Wide Copy Number Profile. *Cancer Informatics* 13.Suppl 4: 15-23. PMC.

Huang, Y.-T., **Hsu, T.**, Kelsey, K. T. and Lin, C.-L. (2015), Integrative Analysis of Micro-RNA, Gene Expression, and Survival of Glioblastoma Multiforme. *Genet. Epidemiol.*, 39: 134-143. doi: 10.1002/gepi.21875