

# WON LEE

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## SUMMARY

Motivated, insightful and creative neuroscientist with Ph.D. from Columbia University, 6 years of research experience and productive publication record. Proactively adopt leading-edge bioinformatics approaches in R, Python, and shell scripting to better characterize interaction among social environment, brain and physiology  
<https://github.com/veritasluxmea> • <http://wonlee-neuroscientist.com>

## HIGHLIGHTED SKILLS

Bioinformatics analysis – R, Python, shell scripting  
Bowtie2, Kallisto, Salmon, Samtools, MultiQC, Differential network analysis, WGCNA, ARACNe, DESeq2, edgeR, pandas, scikit-learn, dimensionality reduction, hub/key driver gene detection, RRHO, differentially expressed gene, gene ontology analysis (GO)

Statistical analysis  
Bayesian hierarchical modeling, social network analysis, mixed effects model  
Molecular/cellular techniques  
DNA/RNA extraction and library prep, qPCR, flow cytometry (multi-color, multi-panel design), in situ hybridization, IHC, ELISA

## EXPERIENCE

### Postdoctoral Researcher

June 2020 – Present

Champagne & Curley Social Neurobiology Lab, The University of Texas at Austin

Austin, TX

- Tackle challenges in analyzing brain transcriptome data encompassing heterogeneity across multiple brain regions by implementing machine learning and network-based modeling approach, aiming to identify key driver genes of stress resilience and metabolism shift upon social environment change
- Collaborate to develop library prep and data analysis pipeline for hydroxymethylation (5hmC) sequencing
- Lead collaborative bioinformatics analysis projects with three labs (Northwestern, NYU, UT Austin) via facilitating sample preparation and raw data processing for high-throughput tag-based RNA sequencing

### Graduate Research Fellow

April 2014 – May 2020

Champagne & Curley Social Neurobiology Lab, Columbia University & University of Texas at Austin

- Published 10 research articles (5 first-authored, 3 via inter-institution collaborations) highlighting social environment shift metabolism, immune system, neuropeptide signaling, and neural response
- Led statistical analysis applying hierarchical modeling, Bayesian statistics, and machine learning to properly model data associated with social behavior, metabolism, and stress resilience using R and Python
- Pivotal contribution in establishing a new lab at UT Austin resulting in 18% of saving from the original lab relocation budget (construction design, equipment purchase, recruitment, communication liaison)
- Designed and conducted time-sensitive experiments involving multiple state-of-art lab techniques to investigate the association among stress resilience, immune system, and brain gene expression
- Presented 4 times at prestigious conferences, invited to present in an international conference, initiated three new out-of-institution collaborations by actively networking at the conferences
- Trained 12 undergraduate students on animal handling, behavioral observation, wet lab protocols then assigned and supervised them to independent projects based on each student's talent and interest

### High school Biology Teacher

September 2013 – January 2014

Mae-tan High School

Suwon, South Korea

- Developed digital handouts and teaching materials for 11<sup>th</sup> Biology I and 12<sup>th</sup>-grade Biology II
- Supervised students on science portfolios, one team won the 1<sup>st</sup> prize in National Science Creativity Award

## EDUCATION

Columbia University, New York, NY

May 2020

PhD in Psychology, Visiting scholar at UT Austin (2017 – 2020)

Selected honors/awards: Samsung Scholarship (\$250,000), Dean's Fellow, Neuroscience Fellow

Teachers College, Columbia University, New York, NY

July 2015

MS in Neuroscience and Education

Seoul National University, Seoul, South Korea

August 2013

BS in Biology Education, minor in Psychology, University Medal, Valedictorian, Summa Cum Laude