Angela Zhang

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EDUCATION

University of Washington *Expected 2022*
Seattle, WA
Ph.D., Biostatistics
Fellow in the Biostatistics, Epidemiologic and Bioinformatics Training in Environmental Health
(BEBTEH)

University of Iowa *August 2013 - May 2017*
Iowa City, IA
B.S. with High Distinction, Biochemistry and Statistics, 2017
Minor in Mathematics and Chemistry
Member of Phi Beta Kappa

SKILLS

Statistical and Programming Languages: R (tidyverse), SAS, Python, SQL
Statistical Expertise: Survival analysis, generalized linear regression models, statistical learning, clinical
trials analysis, kernel regression models, mixed effects models, experimental design
Markup Languages: HTML/CSS, Latex, Markdown
Design/Miscellaneous Programs: Adobe Creative Suite, Microsoft Office
Computational Biology: RNA-Seq, metagenomics, microbiome (QIIME2), whole genome shotgun
sequencing
Benchwork Methods: Protein assays, immunohistochemical staining, brain sectioning of
mouse models, gene purification, protein purification

RESEARCH

Department of Biostatistics September 2019 - Present
Research Assistant *Fred Hutchinson Cancer Research Center; Seattle, WA*

- **Project Title**: Weighted kernel method for integrative metabolomic and metagenomic pathway
  analysis (With Dr. Michael C. Wu)
- Developing a method integrating metabolomic and metagenomic data from the microbiome using a
  weighted kernel regression framework

Department of Environmental and Occupational Health Sciences September 2017 - Present
Research Assistant *University of Washington; Seattle, WA*

- **Project Title**: Critical lncRNA-PCGs pairs identified through transcriptome characterization of
  HepaRG cells exposed to PBDEs
- **Project Title**: Exposure to cadmium modulates the composition of short chain fatty acid-producing
  microbiota in an Alzheimer's disease mouse model
- Under Dr. Julia Yue Cui, developed a pipeline for RNA-Seq analysis of lncRNAs and protein coding
  genes

- Researched the global effects of cadmium exposure using metabolomics, metagenomics and transcriptomic data in an Alzheimer's disease mouse model; presented results in a national conference (manuscript in progress)
- Performed gene enrichment analysis on HepaRG cells subjected to environmental pollutants such as PBDEs.
- Collaborated and assisted other group members with R and UNIX command line packages for analyzing RNA-Seq data and microbiome data.

Department of Microbiology   March 2014 - July 2017
Undergraduate Research Assistant   *University of Iowa; Iowa City, IA*

- **Project Title**: Investigating *Staphylococcus aureus* extracellular phosphatase activity (Senior Project in Biochemistry)
- Under Dr. Alexander Horswill, developed a protein assay to quantify extracellular alkaline phosphatase activity in *Staphylococcus aureus* through colorimetric approaches
- Conducted administrative tasks, such as creating an organizational system for the laboratory shipments and reconciling purchases made each month

Neuroscience Department   June 2016 - August 2016
Summer Undergraduate Research Fellow   *Scripps Research Institute ; Jupiter, FL*

- 10 Week REU (Research Experience for Undergraduates) under Dr. Damon Page
- Examined the role that PTEN plays in the hyperconnectivity of the brain and how environmental enrichment rescues social behavior deficits that result from *Pten* haploinsufficiency
- Grant from NSF 1359369

Department of Psychiatry   October 2013 - May 2016
Undergraduate Research Assistant   *University of Iowa; Iowa City, IA*

- With Dr. Jacob Michaelson, worked on three different projects (Language: R)
  - Explored the effects of the *Npas3/Npas1* proteins on gene expression in order to elucidate the etiology of schizophrenia
  - Performed gene expression analysis on healthy and diseased brain tissue from epileptic patients
  - Discovered gene networks within psychiatric risk genes from GTEx using machine learning techniques such as elastic net regression
- Presented results to more than 200 people at the University of Iowa's Spring Undergraduate Research Festival
- Earned the ICRU Fellows grant in order to personally fund research

National Agricultural Statistics Service   June 2015 - August 2015
JPSM Junior Fellow   *United States Department of Agriculture*

- Created predictive linear models for future land usage in farm operations across the United States
- Analyzed trends in technology usage by the agricultural sector through the Computer Usage Survey
- Participated in weekly seminars covering a variety of aspects of survey methodology and the Federal Statistical System.

Boyce Thompson Institute for Plant Research   June 2014 - August 2014
Bioinformatics Intern (REU)   *Cornell University; Ithaca, NY*

- Research Experience for Undergraduates (REU) program under Dr. Lukas Mueller

- Developed pipelines for constructing and analyzing tomato genomes from large datasets in order to elucidate disease resistant genes for domesticated tomato breeding projects
- Constructed and annotated the genomes of several wild tomato species using UNIX command line tools
- Assisted in bioinformatics workshops that provided help in setting up and running analyses in R and other bioinformatic tools

PRESENTATIONS

NIEHS Superfund Research Program Meeting   November 2019
Poster Presentation   *Seattle, WA*

Exposure to cadmium modulates the composition of short chain fatty acid-producing microbiota in an Alzheimer's disease mouse model

Pacific Northwest Association of Toxicologists Annual Meeting   October 2019
Poster Presentation   *Boise, ID*

Transcriptomic profiling of PBDE-exposed HepaRG cells unveils critical lncRNA-PCGs pairs involved in intermediary metabolism

International Society for the Study of Xenobiotics   July 2019
Poster Presentation   *Portland, OR*

Exposure to cadmium modulates the composition of short chain fatty acid-producing microbiota in an Alzheimer's disease mouse model

Summer Undergraduate Research Festival   August 2016
Poster Presentation   *Scripps Research Institute; Jupiter, FL*

Environmental enrichment rescues social deficits caused by neuronal hyperconnectivity in Pten haploinsufficient mice

Spring Undergraduate Research Festival
Poster Presentation   *University of Iowa; Iowa City, IA*

2016: Rescue of adult hippocampal neurogenesis through a neuroprotective compound P7C3-A20

2015: Whole transcriptome analysis of healthy and diseased brain tissue from epileptic patients

Summer Student Symposium   August 2014
Poster Presentation   *Boyce Thompson Institute for Plant Research; Ithaca, NY*

Transcriptome characterization and evolution in cultivated and wild tomato species

PUBLICATIONS

1 Zhang, A., Li, Y. L., Kelly, E., J., Sheppard, L., Cui, J. Y. 2019. Coordinate regulation of long non-coding RNAs and protein-coding genes in germ-free mice. *PLOS One. Accepted.*

2 Dempsey, J., Zhang, A., Cui, J. Y. 2018. Coordinate regulation of long non-coding RNAs and protein-coding genes in germ-free mice. *BMC Genomics.* 19(1).

3 Michaelson, J. J., Shin, M. K., Koh, J. Y., Bruggeman, L, **Zhang, A.**, Katzman, A., Mcdaniel, L., Fang, M., Pufall, M., Pieper, A. A 2017. NPAS1 and NPAS3 are master regulators of neuropsychiatric risk genes. *Biological Psychiatry.* 82(3):213-223.

AWARDS AND SCHOLARSHIPS

Travel Award for the Annual Meeting of the American Association for the Advancement of Science (AAAS)	2020
Travel Award for the Women in Statistics and Data Science Conference	2019
Dean's List	2013 - 2017
Old Gold Scholarship	2013 - 2017
Rex Montgomery Biochemistry Scholarship	2016 - 2017
Statistics and Actuarial Science Department Scholarship	2015 - 2017
Autism Science Foundation Undergraduate Research Grant	2016
ICRU Research Fellow Award	2015 - 2016
Barry M. Goldwater Campus Nominee	2015

LEADERSHIP AND SERVICE

Equity, Diversity and Inclusion Committee Member   2018 - Present
University of Washington   *Seattle, WA*

Womxn in Biostatistics and Statistics Leadership Board   2018 - Present
University of Washington   *Seattle, WA*