JULIANNE YANG, PhD

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SUMMARY

- Accomplished, versatile scientist utilizing computational and biochemical/molecular biology techniques to address research questions in clinical and preclinical studies at Genentech and the University of California
- Demonstrated experience with designing and executing analysis plans of next-generation sequencing data including shotgun metagenomics, 16S rRNA gene amplicon sequencing, synthetic full-length 16S rRNA gene sequencing, ITS gene sequencing, bulk RNA-sequencing, and metabolomics
- Excellent ability to interpret and communicate findings to key stakeholders, technical, and non-technical audiences

EXPERIENCE

Genentech

Bioinformatics Intern   **Jun 2022 - Sep 2022**

- Built shell scripts to interrogate quality of synthetic full length 16S rRNA gene sequencing and prepared a report; resulting in repeated library preparation for failed samples worth over $20,000 and enhanced read quality
- Preprocessed and analyzed shotgun metagenomic data from the GARDENIA clinical trial patient samples: contaminant filtering, taxonomic classification (Kraken/Bracken), functional profiling (Humann), de novo assembly (Megahit), virulence factor alignment, and statistical analysis and visualization in R to identify candidate microbes both associated with and predictive of biologics therapeutic response
- Curated and analyzed public metagenomics data (from the PRISM IBD cohort) utilizing internal pipelines to compare results with internal data, resulting in co-authorship on manuscript in review (Tamburini et al., under review)
- Correlated differentially expressed genes from bulk transcriptomic data with candidate microbe abundance

University of California Los Angeles   **Jan 2020 - current**

Bioinformatics Analyst for the Microbiome Core and *Graduate Student Researcher* in the Jacobs Lab

Software Development

- Employed multithreading, shell scripting, and high-performance computing on the UCLA Hoffman2 cluster for efficient preprocessing, denoising, and alignment of genomics data, reducing computation time for the Microbiome Core by over 80% (https://github.com/julianneyang/metagenomicsonhoffman)
- Developed R package "Microbiome.Biogeography" wrapping custom functions for data wrangling and visualization (https://github.com/jacobslabucla/microbiome.biogeography; Yang et al., under revision)
- Built an RShiny app to interact with collected behavioral data from mouse models
- Wrapped QIIME commands in custom shell scripts for efficient analysis of 16S rRNA gene sequencing data (https://github.com/julianneyang/fast-16s-analysis)
- Wrote Python code for rapid image quantification of confocal microscopy images implementing algorithms in scikit-image, reducing image processing time and experimenter bias

Bioinformatics Data Science

- Identified microbes, genes, and pathways associated with phenotypic outcomes, through performing differential abundance (microbe) and differential expression (gene) and gene set enrichment analyses in R
- Benchmarked batch correction strategies for a meta-analysis of gut biogeography integrating 1,046 samples collected in-house (Yang et al., under revision)
- Implemented and compared performance of disease classifiers built with supervised machine learning algorithms to predict outcomes of experimental interventions using microbiome count data as feature inputs
- Documented computational analyses with markdown and version control tools (Git) to accompany publications (e.g. https://github.com/julianneyang/biotindeficiency; Yang et al., *Nutrients* 2023)
- Curated sequencing data for public access via NCBI (publicly active records- PRJNA904819, PRJNA997603)
- Utilized clustering algorithms to identify patterns in high dimensional data
- Designed and executed bioinformatics analysis plans for colleagues in medicine and preclinical research, resulting in 6 co-authored articles

Researcher, Project Lead, and People Manager

- Discovered that a Crohn's and Parkinson's disease linked risk variant can induce intestinal inflammation through modulation of the gut microbiome and mediate susceptibility to preformed fibril or transgenic mouse models of Parkinson's disease
- Ensured compliance with institutional and ethical guidelines for animal research through writing detailed protocols and including power analyses, resulting in approval by the Animal Research Committee (IACUC)

- Performed behavioral testing, mouse brain cryosectioning, and immunohistochemical staining of tissue sections followed by confocal imaging to evaluate neuropathological features
- Designed and executed a whole intestinal microbiota transplant experiment in antibiotic-treated wild-type mice
- Led a team of 10 researchers, managing personnel coordination, organizing samples and data, spearheading collaborations with other labs, and ensuring deadlines were met with respect to project goals
- Conducted biochemical and molecular biology experiments including enzyme activity assays, next generation sequencing library preparation, Western blots, anaerobic culture, and flow cytometry sample preparation
- Trained colleagues ranging from undergraduate researchers to postdoctoral fellows in biochemical assays, molecular biology, and bioinformatics analyses
- Secured the Clinical and Translational Science Institute Award for an innovative research proposal, valued at $10,000
- Supervised the thesis project and writing of four senior undergraduates (one who received Highest Departmental Honors, another who received a scholarship valued at $4,000)
- Prepared manuscripts and contributed to manuscripts of collaborators, resulting in 4 first-author publications (2 published, 2 submitted to date) and 8 peer-reviewed articles to date

University of Illinois, Urbana   **Jan 2018 - May 2019**

Research Assistant in the Chung Lab
- Assessed neuronal expression of pathogenic mutations in ion channels using immunoblot, immunocytochemistry, and fluorescence microscopy techniques followed by data analysis in ImageJ
- Wrote and defended undergraduate research thesis to biochemistry faculty and was awarded the "William T. and Lynn Jackson Merit Award for an Outstanding Senior Thesis" (1 of 1 students) and "Highest Distinction in the Department of Biochemistry" (1 of 4 students)

Research Experience for Undergraduates (REU)   **May - Jul 2016, 17, 18**

Summer Intern
- University of Missouri, Columbia, 2018: Spearheaded a pilot RNA-sequencing study in human macrophages exposed to *Sutherlandia frutescens*, a widely used herbal medicine
- University of Missouri, Columbia, 2017: Quantified the anti-inflammatory and anti-oxidative character of highly purified metabolites from *S. frutescens* through exposing a reporter cell line to varied concentrations of metabolites
- Loyola University, 2016: Varied media pH and carbon source to evaluate their effects on protein acetylation in *E. coli*

EDUCATION
University of California, Los Angeles
- Ph.D. in Molecular, Cellular, and Integrative Physiology (completed, awaiting formal degree conferral **Dec 15, 2023**)
- Dissertation: Microbiome Quantitative Trait Loci Modulate Intestinal Inflammation and the Gut-Brain Axis
- Publication record: https://orcid.org/0000-0001-5898-7221

University of Illinois, Urbana-Champaign
- B.S., Biochemistry; Minor, Chemistry; Highest Distinction (1 of 4 students)
- Thesis: Pathogenic and Phosphomimetic Mutations in Kv7.2 Regulate its Expression in Hippocampal Neurons

SKILLS
- **Computational:** Bioinformatics, biostatistics, R, Python, Linux/Unix environments, bash scripting, machine learning algorithms, next-generation sequencing data analysis, gene set enrichment analysis, high performance computing (Slurm, Grid Engine), source control with Git, genome alignment (Bowtie), genome assembly (Megahit), format conversion (SAMtools)
- **Laboratory Techniques:** Mouse models, mammalian cell culture, transfection, transformation via heat shock, immunohistochemistry, immunocytochemistry, immunoblots, anaerobic chamber use, PCR, qPCR, gel electrophoresis, DNA/RNA extraction, sequencing library prep, lipid extraction, protein purification by column chromatography, confocal microscopy, enzyme activity assays, flow cytometry prep, gRNA/ssODN design (CRISPR/Cas)

SELECT PUBLICATIONS
- **Yang, JC** et al. Biogeography of the mouse gut microbiota is observed under specific-pathogen-free conditions and partially recapitulated in colonized germ-free mice. *The ISME Journal*. (Submitted, under revision)
- **Yang, JC** et al. Biotin deficiency induces intestinal dysbiosis associated with an inflammatory bowel disease-like phenotype. *Nutrients* 2023, 15, 264. (Featured on cover)
- Tamburini FB, Tripathi A, Gold MP, **Yang JC**, et al. Gut microbial species and endotypes associate with remission in IBD patients treated with anti-TNF or anti-integrin therapy. *Clinical Gastroenterology and Hepatology*. (Submitted, under review)