Claire E. Weber, PhD

Statistician and Bioinformatician, NEI, NIH
Special Volunteer, NCATS, NIH
301-272-5999 | claire.weber@nih.gov | cwebio.wordpress.com
ORCID: https://orcid.org/0000-0002-2352-8479

Work experience

October 25, 2020 to present

Statistician and Bioinformatician, Federal employee at The National Eye Institute, The National Institutes of Health. Carry out statistical and bioinformatics analysis pipelines for the Age Related Eye Disease Studies (AREDS/AREDS2) project in the laboratory of Dr. Emily Chew. High throughput omics data analysis including metabolomics, genetics, proteomics and integration with clinical data. Teach Medical Fellows in statistical analysis. Collaborate with NIH intra- and extramural colleagues in NCATS, NLM, NIEHS, and The Emmes Company, LLC.

January 23, 2018 to October 24, 2020

Bioinformatics Scientist, contractor through Kelly Services, at the Stem Cell Translation Laboratory (SCTL), The National Center for Advancing Translational Sciences (NCATS), The National Institutes of Health (NIH). Lead three other contractor bioinformaticians and one Special Volunteer in the analysis of bulk and single-cell RNA sequencing of induced pluripotent stem cells. Develop new methods to analyze such data. Project manager on a novel bioinformatics software tool, SEQUIN. SCTL is supported by The NIH Common Fund and the HEAL Initiative (Helping End Addiction Long-term).

December 1, 2015 to January 22, 2018

Research data analyst, Johns Hopkins University in the Data Analysis Core, Baltimore, MD, as part of the Atopic Dermatitis Research Network. Maintenance and analysis of whole genome sequencing data in a cluster computing environment. Data mining, statistical analysis, and visualization.

July 29, 2017 to November 29, 2017; and January 13, 2020 to March 7, 2020

SAS subcontractor, Malley Research Programming, Inc., Rockville, MD. SAS and R language data tasks to support clinical studies projects prior to FDA submission, including Random Forests analysis with cross-validation. Organization of patient metadata.

May-July 2013

Museum assistant, University of Michigan Museum of Paleontology, with Dr. Robyn J. Burnham. Created an online database for the CLIMBERS project,

Censusing Lianas in Mesic Biomes of Eastern Regions. Accessible at http://climbers.lsa.umich.edu.

March-July 2013
Herbarium assistant, University of Michigan Herbarium. Databasing of South American bryophytes in the collections, and handling of loan request samples.

2011-2012
Research assistant, Yin-Long Qiu lab, UM Department of Ecology and Evolutionary Biology. Research on evolution of bryophytes with respect to growing substrate, for ancestral state reconstruction. Included study of specimens and phylogenetic mapping.

2010 Intern, Kelsey Museum of Archaeology, Ann Arbor, MI. Museum Studies Program: Researched and curated Egyptian artifacts for permanent installation in the museum. Created website for the Mary Meader aerial photographs exhibition.

2007 Intern, National Science Foundation, Arlington, VA. Continued research on disabilities in ancient Egypt, culminating in a presentation to staff.

2006 Research Volunteer, National Institutes of Health, Bethesda, MD. Worked with the Physical Disabilities Branch to research disabilities and disease in ancient Egypt. Assisted in scientific research on imaging human gait.

Education

PhD Biosciences, George Mason University, Fairfax, VA. Cumulative GPA 4.000/4.000, graduated August 2024. Dissertation title: Integrative multi-omics investigation of biomarkers for Age-Related Macular Degeneration. Focus on bioinformatics.

MS Plant Biology and Conservation, Northwestern University, Evanston, IL. Cumulative GPA 3.800/4.000, graduated April 2016. Thesis title: Methods in orthology detection and application to the moss phylogeny. Focus on bioinformatics.

BS Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI. Cumulative GPA 3.411/4.000, graduated December 2012.

Smith College, studied Conservation Biology and Art History, Northampton, MA, 2008-2009.

Publications (née Malley)

ORCID: https://orcid.org/0000-0002-2352-8479

1. S. Ryu *et al.*, Stress-free cell aggregation by using the CEPT cocktail enhances embryoid body and organoid fitness. *Biofabrication* **16**, 015016 (2023).
2. L. Zelinger *et al.*, Ultra-rare complement factor 8 coding variants in families with age-related macular degeneration. *iScience* **26**, 106417 (2023).
3. **C. Weber** *et al.*, SEQUIN is an R/Shiny framework for rapid and reproducible analysis of RNA-seq data. *Cell Rep Methods* **3**, 100420 (2023).
4. C. A. Tristan *et al.*, Efficient and safe single-cell cloning of human pluripotent stem cells using the CEPT cocktail. *Nat Protoc* **18**, 58-80 (2023).
5. M. J. Song *et al.*, Bioprinted 3D outer retina barrier uncovers RPE-dependent choroidal phenotype in advanced macular degeneration. *Nat Methods* **20**, 149-161 (2023).
6. S. Ryu *et al.*, Stress-free cell aggregation by using the CEPT cocktail enhances embryoid body and organoid fitness. *Biofabrication* **16**, (2023).
7. V. M. Jovanovic *et al.*, A defined roadmap of radial glia and astrocyte differentiation from human pluripotent stem cells. *Stem Cell Reports* **18**, 1701-1720 (2023).
8. S. Ryu *et al.*, Human Pluripotent Stem Cells for High-Throughput Drug Screening and Characterization of Small Molecules. *Methods Mol Biol* **2454**, 811-827 (2022).
9. E. Y. Chew *et al.*, Long-term Outcomes of Adding Lutein/Zeaxanthin and omega-3 Fatty Acids to the AREDS Supplements on Age-Related Macular Degeneration Progression: AREDS2 Report 28. *JAMA Ophthalmol* **140**, 692-698 (2022).
10. C. A. Tristan *et al.*, Robotic high-throughput biomanufacturing and functional differentiation of human pluripotent stem cells. *Stem Cell Reports* **16**, 3076-3092 (2021).
11. Y. Chen *et al.*, A versatile polypharmacology platform promotes cytoprotection and viability of human pluripotent and differentiated cells. *Nat Methods* **18**, 528-541 (2021).
12. L. Bin *et al.*, Whole genome sequencing identifies novel genetic mutations in patients with eczema herpeticum. *Allergy* **76**, 2510-2523 (2021).
13. K. Kanchan *et al.*, Genomic integrity of human induced pluripotent stem cells across nine studies in the NHLBI NextGen program. *Stem Cell Res* **46**, 101803 (2020).
14. A. Winters *et al.*, The MALT1 locus and peanut avoidance in the risk for peanut allergy. *J Allergy Clin Immunol* **143**, 2326-2329 (2019).
15. M. G. Johnson, C. Malley, B. Goffinet, A. J. Shaw, N. J. Wickett, A phylotranscriptomic analysis of gene family expansion and evolution in the largest order of pleurocarpous mosses (Hypnales, Bryophyta). *Mol Phylogenet Evol* **98**, 29-40 (2016).

Honors and awards

- Travel Grant Recipient, American Macular Degeneration Foundation, for the Association for Research in vision and Ophthalmology (ARVO) Conference 2023
- Member, The Honor Society of Phi Kappa Phi 2022-present, invited to top 10% of graduate class at George Mason University
- NEI Director's Rookie of the Year Award 2021. Nominated by the NEI community, for demonstrating initiative, enthusiasm, and creativity in contributions to the institute's mission during the first year at NEI
- Kelly Government Solutions 2020 Distinguished Achievement award for group achievement towards the STOPS contract with NIH
- Two Kelly Government Solutions 2019 Distinguished Achievement awards for personal and group achievement towards the STOPS contract with NIH
- NCATS featured staff profile, August 2019
- M.S. thesis research funded by a grant from the National Science Foundation, DEB-1239992, as part of the 1000 Plants Initiative.
- The Shaw Fellowship, the Robert D. Hevey and Constance M. Filling Fellowship, and the Harris Foundation Fellowship, totaling $30,000 for tuition in the Program in Plant Biology and Conservation at Northwestern University, 2013-2014.
- The Underwood-Alger Scholarship through the Program in Biology, 2012
The K. L. Jones Award for 2012 for an undergraduate working in a plant biology laboratory
- James B. Angell Scholar, University of Michigan 2011
- University of Michigan Honors, 2009-2010
- Smith College Dean's List, 2008-2009
- Honors Meritorious for thesis in Humanities & Arts Signature Program, 2008

Technical skills

- Bioinformatics programming for data analysis, mining, and visualization in R, Python, Perl, and bash. Fluent in R with 9 years experience. R Shiny application development.
- Mining and analysis of large datasets from databases
- Summary statistics such as central tendency, mean, median, quartiles
- Parametric statistics and hypothesis testing using linear regression, *t*-test, ANOVA, MANOVA, chi-square test, Cox Proportional Hazards and survival models, Linear Mixed Effects
- Nonparametric statistics for data mining including Wilcoxon Rank Sum, Fisher's Exact, PCA, tSNE, UMAP clustering, Lasso regression
- Machine learning methods in feature selection: RandomForests, decision trees, XGBoost
- Statistical prioritization of biomarkers and molecules (chemicals, metabolites, genes, proteins) for disease association and/or response to treatment
- Use of bioinformatics and cheminformatics databases for retrieval and research i.e. UniProtKB/Swiss-Prot, PDB, PubChem; HMDB, GeneCards, UCSC Genome Browser, UK BioBank, NIH dbGaP both submissions process and data access

- High Performance Computing (HPC) systems including the NIH Biowulf and Johns Hopkins JHPCE. Slurm batch operations and parallelization to handle big data projects
- Amazon Web Services (AWS) cloud computing instances, storage management, and app hosting
- Versed in analysis of next-generation sequencing data, i.e. Illumina NextSeq and NovaSeq platforms and DRAGEN Server
- Human genome annotation using software and databases such as ANNOVAR, Enrichr, The 1000 Genomes Project, GSEA
- Genome wide association study (GWAS) approaches including PLINK software; linkage disequilibrium measurement
- Variant calling software including Platypus and GATK Best Practices
- Proficient in Windows 11, Mac OS, and Linux-based operating systems including Red Hat Enterprise Linux and Ubuntu
- Specific software: SAS IDE, R Studio IDE, SPSS, Adobe Photoshop and Illustrator, Microsoft Office suite, OpenOffice suite, Perkin Elmer Spotfire
- Hardware: enthusiast in PC building

Paper and poster presentations

2024 Poster at Association for Research in vision and Ophthalmology (ARVO) 2024 Conference. “Association of metabolites with late AMD in the AREDS/AREDS2.” An NCATS and NEI collaboration.

2024 Poster at American Society for Mass Spectrometry (ASMS) 2024 Conference. “High-throughput Workflow for Deep Analysis of Human Serum Proteome by Mass Spectrometry.” An NCATS and NEI collaboration.

2023 Poster at American Society for Human Genetics (ASHG) 2023 Conference. “SEQUIN: interactive web app for rapid, reproducible bulk and single cell RNA-Seq analysis.” NCATS project with SCTL. Also an invited session moderator.

2023 Paper presentation at Association for Research in vision and Ophthalmology (ARVO) 2023 Conference. “Metabolomics of age-related macular degeneration points to lipid dysregulation and inflammation: an AREDS pilot study.”

2022 Poster at Association for Research in vision and Ophthalmology (ARVO) 2022 Conference. “High HDL or low LDL, low total cholesterol confer greater risk of advanced age-related macular degeneration in Mendelian Randomization.”

2021 Paper presentation as well as co-author on posters at the Association for Research in Vision and Ophthalmology (ARVO) 2021 Virtual Conference. “Progression of Age-Related Macular Degeneration measured by Ultrawidefield Imaging in the AREDS2 10 Year Follow-On.”

2020 Posters at International Society for Stem Cell Research (ISSCR) Virtual Conference, June 24, 2020:
-Systematic analysis of the genetic determinants of human neural lineage commitment by small molecule-based transcriptomic profiling. Co-first author with P.H. Chu.
-Effect of Viscoelastic Extracellular Matrix Stiffness on Development of Cerebral Organoids. Co-author with Seungmi Ryu
-Controlled astrogliogenesis enables automated, high-throughput generation of astrocytes from human pluripotent stem cells. Co-author with Vukasin Jovanovic
-iPSC small molecule screening platform. Co-author with Carlos Tristan

2019 Single-cell analysis of human iPSCs and neural lineage entry to discover novel marker genes through a consensus pseudotime trajectory. C. Malley, P.H. Chu, C.P. Austin, A. Simeonov, I. Singeç. Presented at the International Society for Stem Cell Research conference, July 26, 2019.

2018 Time-course single-cell transcriptomic analysis of controlled neural conversion of human iPS cells. P.H. Chu, C. Malley, J. Braisted, C. Tristan, R. Bargaje, P. Ormanoglu, A. Simeonov, I. Singeç. Stem Cell Translation Laboratory (SCTL), National Center for Advancing Translational Sciences (NCATS), NIH, Rockville, MD, 20850. Presented at the National Institutes of Health Molecular Biology in Single Cells Symposium, April 23, 2018.

2017 Gene enrichment analysis of whole-genome sequenced patients to identify rare and deleterious genetic determinants of eczema herpeticum. Poster competition at Johns Hopkins University School of Public Health. Received 3rd place at M.S. level. Presented at ASHG 2016 as well.

2015 A comparison of ortholog detection methods and their application to the moss phylogeny. Recent topics poster at the Botanical Society of America Conference in Edmonton, Alberta, Canada.

Additional experience and skills

Large language models experimentation, i.e. ChatGPT, and digital artist using Stable Diffusion models. Member of the NIH GenAI Community of Practice (CIT/NLM).

Practical Genomics Workshop, Center for Computational Genomics at Johns Hopkins, August 14-17, 2017. A four-day intensive class addressing next-generation sequencing data analysis.

University of Michigan Biological Station, Pellston, MI, July-August 2011.
- Studied Evolution and Forest Ecosystems. Research on leaf morphology of Northern Red Oaks, with final paper and presentation.

- Determined shifts in oak dominance, mortality at Colonial Point, MI, with final presentation.

Foreign Language

Reading fluency in French.

References

- Dr. Emily Chew, Director, Division of Epidemiology and Clinical Applications, National Eye Institute, National Institutes of Health. echew@nih.gov

- Dr. Ewy Mathé, Director, Informatics, Division of Preclinical Innovation, National Center for Advancing Translational Sciences, National Institutes of Health. ewy.mathe@nih.gov

- Dr. Carlos Tristan, Director, Stem Cell Translation Laboratory, National Center for Advancing Translational Sciences, National Institutes of Health. carlos.tristan@nih.gov

- Dr. Ilyas Singec, Chief Scientific Officer, FUJIFILM Cellular Dynamics. ilyassingec@gmail.com