

Tiffany Eulalio

Assistant Professor · University of South Florida

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Research Interests

Computational epigenetics, DNA methylation, statistical genetics, multi-omics, molecular epidemiology, cancer survivorship, and complex disease.

Education

- June 2024 **Doctor of Philosophy, Biomedical Informatics (Data Science)**, *Stanford University*, Stanford, CA.
Dissertation: *Insights Into the Cell Type-specific Epigenetic Landscape of Alzheimer's Disease: Integrating Genetics, DNA Methylation, and Data Science.*
- May 2018 **Bachelor of Science, Computer Science**, *University of Hawai'i at Mānoa*, Honolulu, HI.
Minor in Math
- May 2018 **Bachelor of Arts, Biology**, *University of Hawai'i at Mānoa*, Honolulu, HI.
- Dec 2014 **Associate of Science, Natural Science**, *Leeward Community College, University of Hawai'i*, Pearl City, HI.
- May 2012 **Associate of Arts, Liberal Arts**, *Kapi'olani Community College, University of Hawai'i*, Honolulu, HI.

Academic Appointments

- Jan 2026 – **Assistant Professor**, *University of South Florida*, Tampa, FL.
Present Health Informatics Institute, Morsani College of Medicine
Joint appointment, Bellini College of Artificial Intelligence, Cybersecurity and Computing
- June 2024 – **Postdoctoral Researcher**, *St. Jude Children's Research Hospital*, Memphis, TN.
Jan 2026 Epidemiology and Cancer Control, Wang Lab, Dr. Zhaoming Wang
- May 2025 – **Visiting Scholar**, *Johns Hopkins University*, Baltimore, MD.
Aug 2025 Biostatistics, Bloomberg School of Public Health, Chatterjee Lab, Dr. Nilanjan Chatterjee

Research Experience

- Sept 2018 – **Graduate Student**, *Stanford University*, Stanford, CA.
June 2024 Biomedical Data Science, Montgomery Lab, Dr. Stephen Montgomery
- Jan 2015 – **Undergraduate Researcher**, *University of Hawai'i at Mānoa*, Honolulu, HI.
Aug 2018 AlgoPARC: Algorithms and Parallel Computing Group, Information and Computer Science Department, Dr. Nodari Sitchinava
- May 2015 – **Laboratory Assistant**, *John A. Burns School of Medicine*, Honolulu, HI.
Dec 2015 Maunakea Laboratory, Dr. Alike Maunakea
- June 2014 – **Louis Stokes Alliance for Minority Participation (LSAMP) Summer Undergraduate Research Experience**, *University of Hawai'i at Mānoa*, Honolulu, HI.
May 2015 Blanchard Research Laboratory, Dr. Caroline Blanchard
- May 2013 – **Biology Lab Aide/Institutional Development Award (IDeA) Network for Biomedical Research Excellence (INBRE) Student Researcher**, *Leeward Community College, University of Hawai'i*, Honolulu, HI.
April 2014 Plant biology lab, Dr. Kabi Neupane

Teaching Experience

Jan 2021 – **Teaching Assistant**, *Stanford University*, Stanford, CA.
June 2021 Translational Biomedical Informatics, Dr. Dennis Wall

Jan 2014 – **Science, Technology, Engineering, and Mathematics (STEM) Peer Mentor**, *Leeward*
May 2015 *Community College, University of Hawai'i*, Pearl City, HI.
Organic Chemistry, Dr. Bradley Ashburn

Peer-Reviewed Publications

1. Meng X, **Eulalio T**, Oh K, Plonski N-M, Shelton K, Mulder HL, Easton J, Zhang J, Walker EV, Neale G, Srivastava DK, Howell RM, Mandelblatt JS, Ky B, Dixon SB, Armstrong GT, Hudson MM, Ness KK, Wang Z. Cancer treatment-related cardiotoxicity among survivors of childhood cancer: a comparative and integrated view of multiple measures of biological age acceleration. *Cancer Epidemiology, Biomarkers & Prevention*. 2026;35(5):718–727. doi:10.1158/1055-9965.EPI-25-1472
2. **Eulalio T**, Kim Y, Meng X, Plonski N-M, Shelton K, Mulder H, Plyler E, Easton J, Chen X, Zhang J, Walker E, Neale G, Ni M, Lucas JT Jr, Chatterjee N, Wang Z, Srivastava D, Ky B, Dixon SB, Ness KK, Hudson MM, Armstrong GT, Wang Z. Epigenome-wide analysis identifies DNA methylation mediators of treatment-related cardiometabolic risk in survivors of childhood cancer. *Nature Communications*. 2026;17:1979. doi:10.1038/s41467-026-68689-6
3. Meng X, **Eulalio T**, Kim Y, Easton J, Mulder HL, Walker E, Neale G, Song N, Shelton K, Howell RM, Xing M, Mirzaei S, Srivastava DK, Ky B, Dixon SB, Hudson MM, Ness KK, Armstrong GT, Wang Z. Epigenetic age acceleration mediates treatment effects on cardiometabolic and cardiovascular risk in childhood cancer survivors. *JACC: CardioOncology*. 2025. doi:10.1016/j.jacc.2025.06.001
4. **Eulalio T**, Sun MW, Gevaert O, Greicius MD, Montine TJ, Nachun D, Montgomery SB. *regionalpcs* improve discovery of DNA methylation associations with complex traits. *Nature Communications*. 2025;16:368. doi:10.1038/s41467-024-55698-6 *Selected for Nature Communications Editors' Highlights: Computational and Theoretical Biology (January 2025)*.
5. Nguyen M, **Eulalio T**, Marafino BJ, Rose C, Chen JH, Baiocchi M. Thick data analytics (TDA): an iterative and inductive framework for algorithmic improvement. *The American Statistician*. 2024;78:456–464. doi:10.1080/00031305.2024.2327535
6. Lang A-L, **Eulalio T**, Fox E, Yakabi K, Bukhari SA, Kawas CH, Corrada MM, Montgomery SB, Heppner FL, Capper D, Nachun D, Montine TJ. Methylation differences in Alzheimer's disease neuropathologic change in the aged human brain. *Acta Neuropathologica Communications*. 2022;10:174. doi:10.1186/s40478-022-01470-0
7. De Goede OM, Nachun DC, Ferraro NM, Gloudemans MJ, Rao AS, Smail C, **Eulalio TY**, Aguet F, Ng B, Xu J, Barbeira AN, Castel SE, Kim-Hellmuth S, Park Y, Scott AJ, Strober BJ, GTEx Consortium, Brown CD, Wen X, Hall IM, Battle A, Lappalainen T, Im HK, Ardlie KG, Mostafavi S, Quertermous T, Kirkegaard K, Montgomery SB. Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. *Cell*. 2021;184:2633–2648.e19. doi:10.1016/j.cell.2021.03.050
8. Nguyen M, Corbin CK†, **Eulalio T†**, Ostberg NP, Machiraju G, Marafino BJ, Baiocchi M, Rose C, Chen JH. Developing machine learning models to personalize care levels among emergency room patients for hospital admission. *Journal of the American Medical Informatics Association*. 2021;28:2423–2432. doi:10.1093/jamia/ocab118 †Co-second authors.
9. Teran NA, Nachun DC, **Eulalio T**, Ferraro NM, Smail C, Rivas MA, Montgomery SB. Nonsense-mediated decay is highly stable across individuals and tissues. *American Journal of Human Genetics*. 2021;108:1401–1408. doi:10.1016/j.ajhg.2021.06.008
10. Corces MR, Shcherbina A, Kundu S, Gloudemans MJ, Frésard L, Granja JM, Louie BH, **Eulalio T**, Shams S, Bagdatli ST, Mumbach MR, Liu B, Montine KS, Greenleaf WJ, Kundaje A, Montgomery SB, Chang HY, Montine TJ. Single-cell epigenomic analyses implicate candidate causal variants at inherited risk loci for Alzheimer's and Parkinson's diseases. *Nature Genetics*. 2020;52:1158–1168. doi:10.1038/s41588-020-00721-x
11. Balaan C, Corley MJ, **Eulalio T**, Leite-Ahyo K, Pang APS, Fang R, Khadka VS, Maunakea AK, Ward MA. Juvenile Shank3b-deficient mice present with behavioral phenotype relevant to autism spectrum disorder. *Behavioural Brain Research*. 2019;356:137–147. doi:10.1016/j.bbr.2018.08.005

Peer-Reviewed Consortium Publications

12. Chang CT, Farah H, Gui H, et al. Red teaming ChatGPT in medicine to yield real-world insights on model behavior. *npj Digital Medicine*. 2025;8:149. doi:10.1038/s41746-025-01542-0
13. Castel SE, Aguet F, Mohammadi P, et al.; GTEx Consortium. A vast resource of allelic expression data spanning human tissues. *Genome Biology*. 2020;21:234. doi:10.1186/s13059-020-02122-z
14. Demanelis K, Jasmine F, Chen LS, et al.; GTEx Consortium. Determinants of telomere length across human tissues. *Science*. 2020;369:eaaz6876. doi:10.1126/science.aaz6876
15. Ferraro NM, Strober BJ, Einson J, et al.; GTEx Consortium. Transcriptomic signatures across human tissues identify functional rare genetic variation. *Science*. 2020;369:eaaz5900. doi:10.1126/science.aaz5900
16. GTEx Consortium. The GTEx Consortium atlas of genetic regulatory effects across human tissues. *Science*. 2020;369:1318–1330. doi:10.1126/science.aaz1776
17. Jiang L, Wang M, Lin S, et al.; GTEx Consortium. A quantitative proteome map of the human body. *Cell*. 2020;183:269–283.e19. doi:10.1016/j.cell.2020.08.036
18. Kim-Hellmuth S, Aguet F, Oliva M, et al.; GTEx Consortium. Cell type-specific genetic regulation of gene expression across human tissues. *Science*. 2020;369:eaaz8528. doi:10.1126/science.aaz8528
19. Oliva M, Muñoz-Aguirre M, Kim-Hellmuth S, et al.; GTEx Consortium. The impact of sex on gene expression across human tissues. *Science*. 2020;369:eaba3066. doi:10.1126/science.aba3066

Open-Source Software

regionalpcs — Bioconductor R package that uses principal component analysis to summarize correlated DNA methylation measurements within genomic regions, improving detection of region-level associations.

[Bioconductor](#) · [GitHub](#) · [Package DOI](#)

Honors and Awards

- Jan 2024 St. Jude Children's Research Hospital Academic Program Special Postdoctoral Fellowship Awardee (2024 – 2026)
- Jan 2023 St. Jude Children's Research Hospital 2023 Future Fellow Research Conference Awardee
- Sept 2022 Annual Biomedical Research Conference for Minority Scientists (ABRCMS) Travel Award
- May 2018 Phi Beta Kappa Member, Alpha of Hawai'i Chapter
- April 2017 Undergraduate Research Opportunity Program Project Funding Award
- March 2017 2017-2018 Achievement Scholarship for Undergraduates
- March 2016 2016-2017 Achievement Scholarship for Undergraduates
- May 2014 Outstanding Student in Organic Chemistry II, American Chemical Society, Hawai'i Section
- Oct 2013 Best Poster Presentation in Bioinformatics, Third Biennial Western Regional IDEa Conference

Professional Service and Outreach

- Sept 2025 Abstract Reviewer, Computational and Systems Biology, Annual Biomedical Research Conference for Minority Scientists (ABRCMS) 2025, San Antonio, TX
- Nov 2022 Session Moderator and Conference Judge, Annual Biomedical Research Conference for Minority Scientists (ABRCMS)
- Oct 2022 Peer-to-peer student mentor for MS/PhD applicants from underrepresented backgrounds in STEM, Stanford University
- Oct 2022 Session Moderator, *Methods and databases: Open, benchmarked and FAIR*, American Society of Human Genetics (ASHG), Los Angeles, CA

Professional Service and Outreach (continued)

- April 2022 Conference Judge, *Computational and Systems Biology*, ABRCMS Spring Symposium
- Nov 2021 Conference Judge, *Computational and Systems Biology*, ABRCMS
- Aug 2021 Stanford Summer Research Program (SSRP)/AMGEN Scholars Symposium Judge
- Jan 2021 Faculty Search Committee Student Representative for Stanford's Department of Biomedical Data Science
- Oct 2020 Workshop Session Co-Leader, *Discount Knowledge at the "Junior" College: Turning perceived stigma into strength*, Society for Advancement of Chicanos/Hispanics and Native Americans in Science (SACNAS) Conference
- Nov 2019 Stanford Biosciences Minority Recruitment Ambassador, ABRCMS, Anaheim, CA
- 2014 – 2017 Leeward Regional Hawai'i State Science Olympiad Session Leader and Judge
- 2014 – 2017 Science Success Workshop Co-Host, Leeward Community College

Peer Review

- April 2026 Ad hoc reviewer, *Clinical Epigenetics* (DNA methylation deconvolution)

Mentoring

- May 2025 *Master's Committee Member - Elena Valencia-Barbosa*
Clinical Investigations Master's Program, Department of Epidemiology and Cancer Control, St. Jude Children's Research Hospital, Memphis, TN.

External Seminar

- Jan 2025 *Exploring Twist MethylSeq for epigenetic insights in survivors of childhood cancer*, Twist Human Methylome Solution Uses and Best Practices, Twist Bioscience Seminar, Memphis, TN.

Selected Oral Presentations

- Oct 2025 *Large-scale meQTL mapping reveals treatment-related differences in genetic regulation of DNA methylation in survivors of childhood cancer from the St. Jude Lifetime Cohort (SJLIFE)*, Knowledge in Data Science Symposium, St. Jude Children's Research Hospital, Memphis, TN.
- Sept 2022 *Regional Principal Components capture more disease-relevant genes in Alzheimer's disease*, Annual Biomedical Research Conference for Minority Scientists (ABRCMS) Graduate Symposium, Anaheim, CA.

Departmental Talks

- Jan 2021 *Capturing DNA methylation signal using principal component analysis*, Department of Biomedical Data Science Talks, Stanford, CA.
- April 2020 *Investigating the DNA methylation landscape in Alzheimer's disease*, Department of Biomedical Data Science Talks, Stanford, CA.
- May 2019 *Deep learning approach to automatically extract gene-phenotype relationships from unstructured literature data*, Department of Biomedical Data Science Talks, Stanford, CA.

Conference Poster Presentations

- Oct 2025 American Society of Human Genetics (ASHG), Boston, MA.
Epigenome-wide analysis identifies DNA methylation signatures linking cancer therapy to impaired pulmonary function in survivors of childhood cancer: A report from the St. Jude Lifetime Cohort.
- April 2025 American Association for Cancer Research (AACR), Chicago, IL.
Epigenome-wide analysis of DNA methylation mediators linking cancer treatments to cardiometabolic risks in survivors of childhood cancer.
- Nov 2023 American Society of Human Genetics (ASHG), Washington, D.C.
Regional principal components provide insight into cell type-specific DNA methylation, genomic variants, and Alzheimer's disease mechanisms.
- June 2023 St. Jude Children's Research Hospital 2023 Future Fellow Research Conference, Memphis, TN
Regional principal components provide insight into cell type-specific DNA methylation, genomic variants, and Alzheimer's disease mechanisms.
- Oct 2022 American Society of Human Genetics (ASHG), Los Angeles, CA.
Quantifying regional DNA methylation improves the detection of biologically relevant associations in Alzheimer's disease
- Sept 2022 Advances in Genome Biology (AGBT) Precision Health Meeting, San Diego, CA.
Quantifying regional DNA methylation improves the detection of biologically relevant associations in Alzheimer's disease
- June 2022 National Library of Medicine (NLM) Conference, Buffalo, NY.
Capturing DNA methylation signal using principal component analysis

Institutional Poster Presentations

- Nov 2025 2025 Faculty/Postdoctoral Poster Session, Memphis, TN.
Epigenome-wide analysis identifies DNA methylation mediators for cancer treatment-related cardiometabolic risks among survivors of childhood cancer: A report from the St. Jude Lifetime Cohort.
- Jan 2025 11th Annual Comprehensive Cancer Center Postdoctoral Symposium, Memphis, TN.
Epigenome-wide analyses of cardiometabolic risk factors and adverse cardiac outcomes in childhood cancer survivors.
- Sept 2023 Stanford's Biomedical Data Science Annual Retreat, Monterey Bay, CA.
Regional principal components provide insight into cell type-specific DNA methylation, genomic variants, and Alzheimer's disease mechanisms.
- Sept 2022 Stanford's Biomedical Data Science Annual Retreat, Santa Cruz, CA.
Quantifying regional DNA methylation improves the detection of biologically relevant associations in Alzheimer's disease
- May 2022 Department of Biomedical Data Science Fest Poster Session, Stanford, CA.
Capturing DNA methylation signal using principal component analysis
- Sept 2021 Stanford's Biomedical Informatics Annual Retreat, Virtual.
Utilizing PCA to capture complex methylation profiles
- Sept 2019 Stanford's Biomedical Informatics Annual Retreat, Monterey Bay, CA.
Predicting allelic imbalance to investigate regulators of nonsense-mediated decay
- December 2018 Department of Computer Science Poster Symposium, Stanford, CA.
Deep learning approach to automatically extract gene-phenotype relationships from unstructured literature data