Henry E. Miller

PhD Candidate, F31 NIA/NIH Fellow

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Personal statement

My long-term research focus is to understand the factors which drive epigenetic aging and rejuvenation to develop novel therapies for aging and age-related diseases. During the remainder of my PhD training, I will continue to solidify my skills as a bioinformatician. After graduating (expected Dec. 2022), I hope to leverage these skills to address fundamental questions in epigenetic aging and rejuvenation. Success in this research direction may yield deeper insights into the aging epigenome, novel aging clocks, and drug targets for clinical translation.

Education

Aug 2018 – Current	**UT Health San Antonio** *Doctor of Philosophy* Biology of Aging **GPA: 4.0** **Qualifying exam: Passed with distinction**
Aug 2016 – May 2018	**SUNY University at Buffalo** *Master of Science* Biomedical Engineering **GPA: 3.8**
Aug 2012 – May 2016	**Christopher Newport University** *Bachelor of Science* Double major, Neuroscience and Philosophy **GPA: 3.1**

Research Experience

2018 - Current	**Bishop Laboratory** Supervisor: Alexander Bishop, DPhil *UT Health San Antonio* As a PhD candidate, I use bioinformatics to understand the role of R-loops in cancer, development, and aging.
2018 - 2018	**Chen Laboratory** Supervisor: Yidong Chen, PhD *UT Health San Antonio* As a rotation student, I benchmarked methodologies for RNA-Seq splicing analysis.
2018 - 2018	**Frost Laboratory** Supervisor: Bess Frost, PhD *UT Health San Antonio* As a rotation student, I analyzed calcium-dependent transcriptional signatures and transposable-element expression in human, mouse, and fly RNA-Seq data.

2017 - 2017	**Lovell Nanomedicine Laboratory** Supervisor: Jonathan Lovell, PhD *SUNY University at Buffalo* I generated three peanut allergy mouse models and formulated a novel drug based on phosphatidylserine liposomes designed to attenuate peanut allergies.
2017 - 2017	**Engineered Theranostics Laboratory** Supervisor: Yun Wu, PhD *SUNY University at Buffalo* I completed a short project which involved designing and fabricating microfluidic chips to enhance the interaction of liposome nanoparticles and lung-cancer cell-derived exosomal miRNAs.
2015 - 2016	**Eye-blink Conditioning Laboratory** Supervisor: Matthew Campolattaro, PhD *Christopher Newport University* As an undergraduate research student, I assisted the Campolattaro laboratory with data collection, tissue histology, and perfusion. Additionally, I performed rodent stereotaxis surgery and learned post-operative care methods.
2015 - 2016	**Velkey Fish Behavior Laboratory** Supervisor: Andrew Velkey, PhD *Christopher Newport University* As an undergraduate research student, I assisted the Velkey laboratory with running behavioral trials and collecting data.

Publications

2022

- **Miller HE** & Mahmud S, Movasati A, Shafiha R, Vines A, Bishop A & Venkitaraman A. BRCA2 and PAF1 coordinate in the regulation of transcriptional pausing. (**In preparation**).
- Borbeck, J, **Miller HE**, Shekhovtsov, S, Montemayor, D, Bernstein, M, Bishop A. autoPLIER: a pathway-constrained autoencoder for biologically interpretable low-dimensional embedding. (**In preparation**).
- Romero JC, Tonapi S, Loranc E, Bassani N, Lawrence LA, **Miller HE**, Robledo DG, Cao L, Nie J, Kanda K, Gorthi A, Lane AN, Fan TWN, Zha S, Musi N, Bishop AJR. ATM protein kinase regulates CD98HC dependent antiport activities to control cell metabolism. (**Under revision, Molecular Cell**).
- **Miller HE**, Ilieva1 M, Bishop AJR, Uchida S. Current Status of Epitranscriptomic Marks Affecting lncRNA Structures and Functions. **Non-coding RNA**. 2022, Mar 28;8(2):23. doi: https://doi.org/10.3390/ncrna8020023.
- Ilieva1 M, **Miller HE**, Agarwal A, Paulus GK, Madsen GH, Bishop AJR, Kauppinen S, Uchida S. Expression analysis of protein-coding and long non-coding RNA genes in fibrosis. **Non-coding RNA**. 2022, Jan 28;8(1):13. doi: https://doi.org/10.3390/ncrna8010013.

2021

- **Miller HE**, Montemayor D, Li J, Levy SA, Pawar R, Hartono S, Sharma K, Frost B, Chedin D, Bishop AJR. Exploration and analysis of R-loop mapping data with RLBase. **bioRxiv**; doi: https://doi.org/10.1101/2021.11.01.466854. (**preprint**).
- **Miller HE**, Montemayor D, Abdul J, Vines A, Levy SA, Hartono S, Sharma K, Frost B, Chedin D, Bishop AJR. Quality-controlled R-loop meta-analysis reveals the characteristics of R-Loop consensus regions. **bioRxiv**; doi: https://doi.org/10.1101/2021.11.01.466823. (**preprint, Under Revision, Nucleic Acids Res.**).
- **Miller HE**, Bishop AJR. Correlation AnalyzeR: functional predictions from gene co-expression correlations. **BMC Bioinformatics**. 2021 Apr 20;22(1):206. doi: 10.1186/s12859-021-04130-7. PMID: 33879054; PMCID: PMC8056587.

2020
- **Miller HE**, Gorthi A, Bassani N, Lawrence LA, Iskra BS, Bishop AJR. Reconstruction of Ewing Sarcoma Developmental Context from Mass-Scale Transcriptomics Reveals Characteristics of EWSR1-FLI1 Permissibility. **Cancers**. 2020 Apr 11;12(4):948. doi: 10.3390/cancers12040948. PMID: 32290418; PMCID: PMC7226175.
- Pan H, Jin M, Ghadiyaram A, Kaur P, **Miller HE**, Ta HM, Liu M, Fan Y, Mahn C, Gorthi A, You C, Piehler J, Riehn R, Bishop AJR, Tao YJ, Wang H. Cohesin SA1 and SA2 are RNA binding proteins that localize to RNA containing regions on DNA. **Nucleic Acids Res.** 2020 Jun 4;48(10):5639-5655. doi: 10.1093/nar/gkaa284.
- Mahoney R, Ochoa Thomas E, Ramirez P, **Miller HE**, Beckmann A, Zuniga G, Dobrowolski R, Frost B. Pathogenic Tau Causes a Toxic Depletion of Nuclear Calcium. **Cell Rep.** 2020 Jul 14;32(2):107900. doi: 10.1016/j.celrep.2020.107900. PMID: 32668249; PMCID: PMC7428851.
- Iskra B, Davis L, **Miller HE**, Chiu YC, Bishop AJR, Chen Y, Aune GJ.Assessing the heterogeneity of cardiac non-myocytes and the effect of cell culture with integrative single cell analysis. **bioRxiv**; doi: https://doi.org/10.1101/2020.03.04.975177. (**preprint**).

Conference presentations and speaking engagements

2020
Sarcoma Working Group Meeting
Greehey Children's Cancer Research Institute
Presented **talk** entitled "Reconstruction of Ewing Sarcoma Developmental Context from Mass-Scale Transcriptomics Reveals Characteristics of EWSR1-FLI1 Permissibility"

2020
Mikiten Research Symposium
UT Health San Antonio
Presented **talk**, "Bioinformatics for Biologists."

2017
Northeast Bioengineering Conference
New Jersey Institute of Technology
Presented **poster**, "Slit-based linear-array photoacoustic tomography system for vascular imaging in human."

Funding

Sep 2021 - Current | NIA/NIH F31 predoctoral fellowship (F31AG072902).

Sep 2020 - Sep 2021 | Greehey Foundation predoctoral fellowship

Work Experience

Mar 2017 - May 2018
Technology Research Intern
University of Buffalo School of Engineering

The University of Buffalo School of Engineering hired me as an Entrepreneurship Intern. In this experience, I developed a business plan and marketing materials for a new internet technology startup.

Mar 2017 - May 2018
Lead Venture Coach
Blackstone Launchpad at The University of Buffalo

Blackstone Launchpad at The University of Buffalo provides training and guidance for student and faculty entrepreneurs. As the Lead Venture Coach, I recruited, trained, and led a team of eight student entrepreneurs to coach more than 100 entrepreneurs.

Apr 2017 - May 2018	**Chief Communications Officer** *POP Biotechnologies Inc* POP Biotechnologies Inc is a Buffalo startup developing nanomedicine therapeutics for treating cancer and infectious diseases. As Chief Communications Officer, I handled business development activities, such as pitching investors, issuing press releases, and executive recruitment.
Aug 2016 - Dec 2017	**Director of Operations** *Sonioptix LLC* Sonioptix LLC is a Buffalo startup creating cutting-edge cancer screening devices. As director of operations, I handled all business development activities, such as pitching investors. During my tenure, Sonioptix LLC recieved funding to begin clinical studies in Western New York for their breast cancer screening device.
May 2016 - Aug 2016	**Environmental Health Technician** *Fairfax County Health Department* I was a summer employee for the Environmental Health division of Fairfax County Health Department. In this position, I assisted with surveillance, trapping, and analysis of mosquitoes and ticks in local parks. I also provided technical assistance in repairing broken traps.
Jan 2016 - May 2016	**Biochemistry Course Tutor** *Professor Lasseter, Christopher Newport University* I was a tutor for the Biochemistry for Pre-Medical Students course at Christopher Newport University. In this capacity, I met with students for one-on-one tutoring sessions in which I assisted them in mastering challenging course topics.
Aug 2014 - May 2016	**Philosophy Department Tutor** *Christopher Newport University* I was the department tutor for the Philosophy and Religious Studies department at Christopher Newport University. In this capacity, I met with students for one-on-one tutoring sessions in which I assisted them in mastering challenging topics from a variety of department courses. I also substitute lectured for several classes.
May 2014 - Aug 2014	**Environmental Health Technician** *Fairfax County Health Department* I was a summer employee for the Environmental Health division of Fairfax County Health Department. In this position, I performed health and safety inspections of local public pools and water parks.

Leadership and Volunteer Experience

Oct 2020 - Current	**Founder and President** *Bioinformatics Research Network* The Bioinformatics Research Network (BRN) is a 501(c)(3) non-profit dedicated to making high-quality bioinformatics training and professional opportunities accessible to all people. It provides free online bioinformatics training and project opportunities. I founded BRN in 2020 and have guided it as president of the board since September 2021. Under my leadership, BRN has reached a membership of 400 people, completed five research project, published two pre-prints and one peer-reviewed article, and helped eight members achieve professional opportunities or PhD positions in bioinformatics.

May 2020 - Nov 2021	**Co-Founder and Training Chair**
	BIG Bioinformatics
	BIG Bioinformatics is a UT Health student club that provides free online bioinformatics workshops. I co-founded BIG Bioinformatics in 2020 and have led the development of five full-length workshops. During my tenure as training chair, I created five workshops which were attended by more than 300 participants in total. The video recordings from these workshops have approximately 500 subscribers, 15k views, and 2k hours of watch time.

Professional Organizations

2020 - Current	**Member**, The International Society for Computational Biology (ISCB)
2020 - 2021	**Graduate student representative**, Bioinformatics Curriculum Committee, UT Health San Antonio
2017 - 2018	**Member**, Project Management Institute
2017 - 2018	**Member**, Biomedical Engineering Society
2017 - 2018	**Member**, Institute of Electrical and Electronics Engineers

Academic and Professional Honors

2022	**VitaDAO Longevity Fellowship Award**, Decentralized / Online
2020	**Passed qualifying exam with distinction**, UT Health San Antonio
2016	**Induction in Omicron Delta Kappa**, Christopher Newport University
2013	**Dean's List**, Christopher Newport University

Open-source software, analyses, and web applications

*Software on which I am the primary developer/maintainer

- **autoPLIER** (under development): An python package for using the autoPLIER pathway-constrained autoencoder. ⬤ Source code
- **FibroDB***: An R-Shiny app for exploring results from fibroblast RNA-Seq studies. ⬤ Web App ⬤ Source code
- **RLBase***: An R-Shiny app for exploring and analyzing R-loop mapping datasets. ⬤ Web App ⬤ Source code
- **RLSeq***: An R/Bioconductor package for analyzing R-loop mapping datasets. ⬤ Bioconductor page ⬤ Source code
- **RLHub***: An R/Bioconductor ExperimentHub package containing useful data resources for R-loop data analysis. ⬤ Bioconductor page ⬤ Source code
- **RLPipes***: An CLI/Bioconda package for upstream processing of R-loop data. ⬤ Bioconda page ⬤ Source code
- **onto-lib**: A python library for loading, querying, and processing biomedical ontologies from OBO files. ⬤ Source code
- **Correlation Analyzer***: An R-Shiny app for exploration of gene co-expression correlation data. ⬤ Web app ⬤ Source code
- **correlationAnalyzeR***: An R package for exploration and analysis of gene co-expression correlation data. ⬤ Vignette ⬤ Source code
- **Miller et al., Cancers 2020***: Reproducible analysis from published study, *Miller et al., Cancer 2020*. ⬤ Study link ⬤ Source code
- **Miller et al., bioRxiv 2021***: Reproducible analysis from preprint, *Miller et al., bioRxiv 2021*. ⬤ Study link ⬤ Source code

Research skills, tools, techniques

*__Bold__ indicates comprehensive skill and knowledge of a tool, data type, or technique.

Analysis techniques

__Transcriptomics__: __Differential gene expression__, __differential transcript usage__, differential splicing, *de novo* isoform prediction, __pathway enrichment__, __GSEA__, pausing index prediction, fusion-gene detection, transposon analysis, transcriptomic alignment, splice-aware genomic alignment, RNA-Seq data mining. scRNA-Seq analysis: upstream processing, scRNA-Seq data mining, __quality control__, integration, cell type prediction, __dimensionality reduction__, imputation, gene module scoring, trajectory analysis, differential expression analysis.

__Epigenomics__: Genomic alignment, __peak calling__, coverage analysis, __differential binding analysis__, differential accessibility analysis, motif analysis, __peak location meta-analysis and enrichment testing__, data mining, signal track correlation and clustering analysis, building custom UCSC browser sessions and track hubs. scATAC-Seq analysis: quality control, integration with scRNA-Seq, dimensionality reduction, differential accessibility.

__Other bioinformatics techniques:__ __Integrative multiomics data analyses__, GWAS analysis, mutation/CNV calling, mass-spectrometry analysis, nanostring analysis, survival analysis.

__Other data sci techniques:__ __Dimensionality reduction__, clustering, imputation, __data viz__, __interactive data reporting__, classification models, regression models, regular expressions.

Data types and technologies

__Languages__: __R__, python, bash, __markdown__, YAML, HTML, CSS (minor), JS (minor), LaTeX (minor).

__Data types__: __mRNA-Seq__, lncRNA-Seq (ribo-depleted), sRNA-Seq, __scRNA-Seq (10X, fluidigm c1)__, ATAC-Seq, scATAC-Seq, HiC-Seq, __ChIP-Seq (and variants)__, WGS, RRBS, WGBS, __DRIP-Seq (and variants)__, __R-ChIP (and variants)__, microarray, bulk mass spectrometry, CyTOF, nanostring.

__Bioinformatics technologies/tools__: R/Bioconductor packages: __DESeq2__, EdgeR, limma, __seurat__, single-cell experiment, SGSeq, DiffBind, phateR, Rmagic, __ChIPpeakAnno__, __ChIPseeker__, GenomicRanges/GenomicFeatures, valr, clusterProfiler, fgsea, msigdbr, annotationDBI (and related packages), BiomaRt, __ExperimentHub/AnnotationHub (usage and development of a hub)__, rtracklayer, tximport, SummarizedExperiment, SingleR, monocle, SRAdb, Biostrings, enrichR, flowCore, groHMM, nanostringr, RUVSeq, PLIER, regioneR, recount, Rsubread, __Bioconductor (general usage & package development)__. Command Line: SRA Toolkit, bedtools, __bioconda (general usage & package development)__, samtools, bwa, STAR, salmon, HISAT2, StringTie, MACS2/3, EPIC2, deepTools, Homer, MEME-Suite, TEtoolkit, fastp. GUI/Web: __UCSC Table/Genome Browser__, IGV, __GEO__, __SRA__, DAVID, __enrichr__, StringDB, cbioportal, GEPIA2.

__Data sci technologies/tools__: __R Markdown__, Rhtml, Jupyter Notebook, __conda__, __R-tidyverse (dplyr, ggplot2, etc)__, python-Saucie, python-pandas, python-numpy, python-sklearn, python-keras, __snakemake__, R-caret, R-pheatmap, R-ComplexHeatmap, plotly, R-DBI, R-DT, R-kableExtra, R-rstatix, R-Rtsne, R-uwot, R-SuperExactTest, R-xgboost.

__Other computational and web technologies/tools__: git, GitHub, CI/CD (GitHub actions), Linux server admin, NGINX, Wordpress, AWS (EC2, S3, RDS, DynamoDB, IAM), __R-shiny__, python-dash, python-flask, python-sqlalchemy, python-pytest, python-coverage python-click, R-devtools, R-parallel, R-future, R-httr, R-jsonlite, R-lintr, R-callr, R-renv.

Bench techniques

__Molecular biology__: Cell culture, Western blot, plasmid prep, protein extraction, RNA extraction, Bradford assay, ELISA, exosome isolation, transfection, nucleofection, nanodrop analysis.

__Biomedical engineering__: Liposome formulation, liposome extrusion, nanosight analysis, UV Vis, Autodesk CAD/Inventor, stereolithography/extrusion 3D printing, PDMS-based microfluidics.

__Animal techniques__: Neural cannulation, stereotaxis surgery, animal post-op care, perfusion, oral gavage, tissue histology.