ERICH BAKER

CURRICULUM VITAE

CONTACT

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TRAINING

Doctor of Philosophy

University of Tennessee, Knoxville

1996 – 2000

Comparative and Experimental Medicine

Post-Doctoral Fellowship

Oak Ridge National Laboratories

2000 – 2002

Genome Annotation and System Modeling Group

ACADEMIC EXPERIENCE

8+ years of academic leadership

Citations: 1,118

h-index: 18

$4M+ in granting

Mentored 24 Ph.D. and master's students

PROFILE

I am a seasoned academic leader with a strong foundation in bioinformatics, data science, and computer science research and teaching, complemented by progressive and successful leadership roles, culminating in my current role as Vice Provost for Research and Strategic Initiatives. With extensive experience managing university centers and institutes, I bring faculty-centered leadership with a growth mindset to the dynamic landscape of higher education. My approach emphasizes innovation as a driving force to strengthen the mission of the university, positioning it as a positive influence in the world. Through executive leadership in a private university setting, I am committed to fostering academic excellence in a safe environment to enable every student to flourish.

LEADERSHIP EXPERIENCE

Vice Provost for Research & Strategic Initiatives

Belmont University 2023 - present

- Administration of university centers and institutes, including personnel, budgets, strategic goal setting, and mission alignment with Belmont's Aspirational Aim.
- Office of Sponsored Programs
- University Libraries
- Institutional Research and Strategic Analysis
- Institutional Review Board
- Academic Facilities
- University Policy Review Committee
- Center for Interprofessional Engagement and Simulation
- Belmont Collaborative for Data and AI
- Academic Liaison for Online Programs
- Faculty Personnel Issues
- Various strategic roles, including service as chair of the university task force for enrollment, chair of the university task force for libraries, program analysis, among others.

Interim Dean, School of Engineering and Computer Science

Baylor University 2022 - 2023

- Led the transition of the School of Engineering and Computer Science (ECS) from R2 to R1.
- Managed 56 faculty and 20 staff in three departments and auxiliary services spanning Computer Science, Electrical Engineering, and Mechanical Engineering, career placement, professional advising, marketing, and advancement.
- Managed a budget of approximately $77M, including personnel, operating expenses, and $50M in extramural support.
- Managed tenure and promotion decisions of junior and senior faculty
- Engaged in advancement to secure endowed professorships, student scholarships, and operational expenses.
- Supported online and in person degrees, for ~800 undergraduate students, ~30 master's students, and approximately 100 Ph.D. students.
- Oversaw efforts in strategic planning and accreditation.

Chair (including Interim), Department of Computer Science

Baylor University 2018 - 2022

- Supported a department of 22 FTE faculty, and 3 staff.
- Responsible for the implementation of BS, BA, MS, and Ph.D. programs across disciplines of bioinformatics, computer science, and data science.
- Started the Data Science degree.
- Supported and hired our first faculty in cybersecurity and raised $2M to start a cyber range.
- Started mentoring program.
- Started online degrees in computer science and software engineering.
- Oversaw ABET accreditation.
- Approximately 300 undergraduate and 50+ graduate students.

ACADEMIC APPOINTMENTS

Vice Provost for Research and Strategic Initiatives 2023 – present
Belmont University, Nashville, TN.

Professor, Computer Science, Department of Mathematics and Computer Science 2023 – present
Belmont University, Nashville, TN.

Interim Dean, School of Engineering and Computer Science 2022 – 2023
Baylor University, Waco, TX.

Chair, Department of Computer Science, School of Engineering and Computer Science 2019 – 2022
Baylor University, Waco, TX.

Interim Chair, Department of Computer Science, School of Engineering and Computer Science 2018 – 2019
Baylor University, Waco, TX.

Adjunct Professor, The Jackson Laboratories 2016 – present
Bar Harbor, ME.

Professor, Bioinformatics, Department of Computer Science, School of Engineering and Computer Science 2014 – 2023
Baylor University, Waco, TX.

Associate Professor, Bioinformatics, Department of Computer Science, School of Engineering and Computer Science 2008 – 2014
Baylor University, Waco, TX.

Assistant Professor, Bioinformatics, Department of Computer Science, School of Engineering and Computer Science 2002 – 2008
Baylor University, Waco, TX.

Post-Doctoral Research Associate in Bioinformatics 2000 – 2002
Graduate School of Genome Science and Technology; Computational Biology Section,
Genome Annotation and Systems Modeling Group, Division of Life Sciences
Oak Ridge National Laboratories, Oak Ridge, TN.

Graduate Research Assistant 1997 – 2000
Graduate Program in Comparative and Experimental Medicine, Department of Medical Genetics
University of Tennessee Medical Center, Knoxville, Knoxville, TN.

KEY PROFESSIONAL ACCOMPLISHMENTS

Belmont University

- Started Belmont’s Office for Sponsored Programs (OSP). (2023) As Belmont University transitions from a teaching university to one that supports extramural funding and professional education in the health sciences, such as the 2024 opening of the Frist College of Medicine, and existing thriving colleges of nursing and pharmacy, there was a need to vision, staff, and implement an Office of Sponsored Programs. This includes technical and administrative support for the entire granting life cycle, from ideation, pre-award, post-award, and grant close-out. It also included the development of compliant policies and procedures in COI, IRB, Tech Transfer, and IP among many others. Prior to the development of OSP, in FY2023, Belmont reported $2.7M in new grant awards. We were able to report $35M in FY24, and $60M currently in FY25.
- Started Belmont University Center for Interprofessional Engagement and Simulation (BUCIES). Embedded in the physical space of the Frist College of Medicine, the state-of-the-art BUCIES occupies 55,000+ sq ft of experiential simulation materials for training health-care professional across medicine, nursing, pharmacy, physical therapy, social work, and occupational therapy. I was tasked with developing and implementing a plan to purchase critical simulation materials, totaling more than $3M, and related personnel, including 15 individuals ranging from an executive director to a standardized patient theater coach to support our 90+ standardized patients. Recently opened, the center is expected to support 1,000+ students each academic and has an operating and personnel budget more than $2.5M per year.
- Belmont Collaborative for Data and AI (BCDAI). Previously called the Belmont Data Collaborative (BDC), I led out on re-imagining the scope of the university-funded center to include dedicated resources in AI. The mission of BCDAI is to support students, faculty, and researchers in their quest to become competent stewards and operators of Data and AI technologies. Staffed by data and AI professionals, the center’s aim is to enable Belmont to make an impact for good in our local and global community.

- As Interim dean at Baylor I drafted the strategic aim and corresponding grant that led to the development of a $2M cyber range. In addition to the physical range, I lead a team that positioned the university to gain CAE accreditation along with hiring critical personnel to implement a larger vision for cyber security.
- In response to changing demand in higher education, I led the effort to start an online master's degree program in computer science and software engineering while serving as chair of computer science at Baylor. The program involved an intensive self-study, market analysis, and operational framework to be successful in the crowded market.
- As a department chair, I crafted and implemented the university's first curriculum in data science. The new major quickly became the fastest growing program within the university as it brought together disciplines across the academy to examine data-driven problems.
- Belmont Policy Review Committee. In the summer of 2023, Belmont undertook an effort to systematically review all internal university policies. I was tasked with co-chairing the committee as we carefully review our practices, policies, and procedures to align with Belmont's current size and rate of growth. The committee plays a critical role in building trust between the faculty and administration.

EDUCATION

Ph.D., Comparative and Experimental Medicine August, 1996 - September, 2000
University of Tennessee, Knoxville, TN

M.S., Biomedical Science August, 1995 - August, 1996
Barry University, Miami, FL

B.A., Pre-professional Studies August, 1990 - August, 1994
University of Notre Dame, South Bend, IN

AWARDS

- Outstanding University Scholarship Award, Tenure-Track Faculty, 2005 – 2006, Baylor University
- Outstanding University Scholarship Award, Tenured Faculty, 2010 – 2011, Baylor University

JOURNAL PUBLICATIONS [PEER REVIEWED]

[1] From Foundational GNNs to Modern Variants: A Review of Architectural Inheritance, Evolution and Trends, Artificial Intelligence Review.

[2] Nowak, T., Gassen, J., Weaver, S., **Baker, E**., Muehlenbein, M. Cytokines and Estradiol Across Age and Reproduction. Adaptive Human Behavior and Physiology. Under review.

[3] Castaneda, E. and **Baker, E.J**. Spectral divergence prioritizes key classes, genes, and pathways between substance use disorder and its comorbidity. Frontiers in Neuroscience. Submitted for publication.

[4] Castaneda, E., Bubier, J., Grady, S., Langston, M., Chasler, E., **Baker, E.J**. Influence of multi-species data on prioritization of gene-disease associations in substance use disorder using random walk with restart models. PLOS One. In press.

[5] Grady, S.K., Peterson, K.A., Murray, S.A., **Baker, E.J**., Langston, Chesler. A graph theoretical approach to experimental prioritization in genome-scale investigations. Mamm Genome (2024). https://doi.org/10.1007/s00335-024-10066-z.

[6] Everest U Castaneda and **Erich J Baker**. KNeXT: A NetworkX-based topologically relevant KEGG parser. (2024) Frontiers in Genetics. 15(1). DOI: 10.3389/fgene.2024.1292394.

[7] Kearney S, Berger A, **Baker E**. Aon: a service to augment Alliance Genome Resource data with additional species. (2023) BMC Research Notes. 16(1). DOI: 10.1186/s13104-023-06577-8.

[8] Khanal, B., Orduz, J., Rivas, P., **Baker E**. Supercomputing leverages quantum machine learning and Grover's algorithm. (2023) J Supercomput 79, 6918–6940. https://doi.org/10.1007/s11227-022-04923-4.

[9] **Erich J. Baker**, Sharon Moore, Steven W. Gonzales, Kathleen A. Grant. Long-term Drinking Stability in the Open-Access Self-Administration Monkey Model. (2023) Alcohol. 113(41-48). DOI: 10.1016/j.alcohol.2023.07.002.

[10] Nowak, Hendderson, Gassen, Weaver, **Baker**, Muehlenbein. Is political affiliation a health risk factor during the COVID-19 pandemic? Attitudes toward vaccines, unapproved treatments, health recommendations, government response, and information sources. Journal of Health Politics, Policy, and Law. *submitted for publication.*

[11] Gassen, J., Nowak, T. J., Henderson, A. D., Weaver, S. P., **Baker, E. J**., & Muehlenbein, M. P. (2022). Longitudinal changes in COVID-19 concern and stress: Pandemic fatigue overrides individual differences in caution. *Journal of public health research*, *11*(3), DOI: 10.1177/22799036221119011.

[12] Muehlenbein, Gassen, Nowak, Henderson, Morris, Weaver, **Baker**. Age-Dependent Relationships Between Disease Risk and Testosterone Levels: Relevance to COVID-19 Disease. (2023) American Journal of Men's Health. doi.org/10.1177/15579883221130195.

[13] Gassen, Nowak, Henderson, Alexandria, Weaver, **Baker**, Muehlenbein. Exploring links between pathogen avoidance motivation, COVID-19 case counts, and immune function. (2022) American Journal of Human Biology. doi.org/10.1002/ajhb.23833. (2023).

[14] Muehlenbein, Gassen, Nowak, Henderson, Weaver, **Baker**. Waco COVID Survey: A Community-Based SARS-CoV-2 Serological Surveillance Study in Central Texas. (2022) Journal of Community Health. doi.org/10.1007/s10900-022-01143-y.

[15] Sattgast, Lara, Branscum, Adam, Newman, Natali, Gonzales, Steven, Benton, Mary Lauren, **Baker, Erich**, Grant, Kathleen, Turner, Russell, and Iwaniec, Urszula. Ethanol Alters the Relationship Between IGF-1 and Bone Turnover in Male Macaques. (2022) Journal of Endocrinology. doi.org/10.1530/JOE- 22-0075.

[16] Muehlenbein, Gassen, Nowak, Henderson, Weaver, **Baker**. Waco COVID Survey: A Community-Based SARS-CoV-2 Serological Surveillance Study in Central Texas. (2022) Journal of Community Health. doi.org/10.1007/s10900-022-01143-y.

[17] Huang, Duan, Xing, Gu, Wang, Sherali, **Baker**. A Fine-grained Video Traffic Control Mechanism in Software-Defined Networks. (2022) IEEE Transactions on Network and Service Management. Doi:10.1109/TNSM.2022.3164335.

[18] Sharon Moore, Ami Radunskaya, Elizabeth Zollinger, Kathleen A. Grant, Steven Gonzales, Nicole A. R. Walter, **Erich J. Baker.** (2022) Pairing Food and Drink: a physiological model of blood ethanol levels for a variety of drinking behaviors. Mathematical Biosciences. doi.org/10.1016/j.mbs.2022.108778.

[19] Mary Lauren Benton, Vanessa A. Jimenez, Natali Newman, Steven W. Gonzales, Kathleen A. Grant, Russell T. Turner, Urszula T. Iwaniec, and **Erich J. Baker.** (2022) Dose-response effects of alcohol on biochemical markers of bone turnover in non-human primates: effects of species, sex and age of onset of drinking. Bone Reports. vol. 66. doi.org/10.1016/j.bonr.2021.101159.

[20] Samuel J. Shenoi and **Erich J Baker.** (2021) Using hierarchical similarity to examine the genetics of Behçet's disease. BMC Research Notes 14(1). DOI: 10.1186/s13104-021-05767-6.

[21] Gassen Jeffrey, Nowak Tomasz J., Henderson Alexandria D., Weaver Sally P., **Baker Erich J.**, Muehlenbein Michael P. (2021) Unrealistic Optimism and Risk for COVID-19 Disease. Front. Psychol (12). doi.org/10.3389/fpsyg.2021.647461.

[22] Palmer RHC, Johnson EC, Won H, Polimanti R, Kapoor M, Chitre A, Bogue MA, Benca-Bachman CE, Parker CC, Ursu O, Verma A, Reynolds T, Ernst J, Bray M, Kwon SB, Lai D, Quach BC, Gaddis NC, Saba L, Chen H, Hawrylycz M, Zhang S, Zhou Y, Mahaffey S, Fischer C, Sanchez-Roige S, Bandrowski A, Qing L, Shen L, Philip V, Gelernter J, Bierut LJ, Hancock DB, Edenberg HJ, Johnson EO, Nestler EJ, Barr PB, Prins P, Smith DJ, Akbarian S, Thorgeirsson T, Walton D, **Baker E**, Jacobson D, Palmer AA, Miles M, Chesler EJ, Emerson J, Agrawal A, Martone M, Williams RW. Integration of Evidence across Human and Model Organism Studies: A Meeting Report. Genes Brain Behav. 2021 Apr 23:e12738. doi: 10.1111/gbb.12738. Epub ahead of print. PMID: 33893716.

[23] Reynolds, Timothy, Johnson, Emma C., Huggett, Spencer B., Bubier, Jason A., Palmer, Rohan H. C., Agrawal, Arpana, **Baker, Erich J.**, Chesler, Elissa J. Interpretation of psychiatric genome-wide association studies with multispecies heterogeneous functional genomic data integration. Neuropsychopharmacology (2020) 0:1–12; https://doi.org/10.1038/s41386-020-00795-5.

[24] Hill, D. P., Harper, A., Malcolm, J., McAndrews, M. S., Mockus, S. M., Patterson, S. E., Reynolds, T., **Baker, E. J.**, Bult, C. J., Chesler, E. J., & Blake, J. A. (2019). Cisplatin- resistant triple-negative breast cancer subtypes: Multiple mechanisms of resistance. BMC Cancer, 19(1), 1039. https://doi.org/10.1186/s12885-019-6278-9.

[25] Jason Bubier, David Hill, Gaurab Mukherjee, Timothy Reynolds, **Erich J. Baker**, Alexander Berger, Jake Emerson, Judith A Blake, Elissa J. Chesler. Curating Gene Sets: Challenges and Opportunities for Integrative Analysis. Database. Volume 2019. 2019, baz036, https://doi.org/10.1093/database/baz036.

[26] Bubier, Jason, Sutphin, George, Reynolds, Timothy, Korstanje, Ron, Fuksman-Kumpa, Axis, **Baker, Erich**, Langston, Michael, and Chesler, Elissa. Integration of heterogeneous functional genomics data in gerontology research identifies genes and pathway underlying aging across species. PLoS ONE 14(4): e0214523.. https://doi.org/10.1371/journal.pone.0214523.

[27] Moore, Sharon, **Baker, Erich**, Grant, Kathy, Gonzales, Steven, Zollinger, Elizabeth, and Radunskaya, Ami. Time for a Drink? A Mathematical Model of Non-Human Primate Alcohol Consumption. Frontiers in Applied Mathematics and Statistics. 2019 Feb 22. Vol. 5. https://doi.org/10.3389/fams.2019.00006.

[28] Dozier BL, Stull CA, **Baker EJ**, Ford MM, Jensen JP, Finn DA, and Grant KA. Chronic ethanol drinking increases during the luteal menstrual cycle phase in rhesus monkeys: implication of progesterone and related neurosteroids. Psychopharmacology (Berl). 2019 Jan 15. pp 1- 12. doi: 10.1007/s00213-019-5168-9.

[29] Phillips, Charles, Wang, Kai, **Baker, Erich**, Bubier, Jason, Chesler, Elissa, and Langston, Michael. On Finding and Enumerating Maximal and Maximum k-Partite Cliques in k-Partite Graphs. Algorithms. 2019, 12(1), 23. https://doi.org/10.3390/a12010023.

[30] S M Ashiqul Islam, Christopher Michel Kearney and **Erich Baker**. Classes, Databases, and Prediction Methods of Pharmaceutically and Commercially Important Cystine-Stabilized Peptides. Toxins. 2018, 10(6), 251. https://doi.org/10.3390/toxins10060251.

[31] S.M. Ashiqul Islam, Christopher Michel Kearney & **Erich J. Baker**. Assigning biological function using hidden signatures in cystine-stabilized peptide sequences. Scientific Reports volume 8, Article number: 9049 (2018). DOI:10.1038/s41598-018-27177-8.

[32] Islam SMA, Heil BJ, Kearney CM, **Baker EJ**. Protein classification using modified n-grams and skip- grams. Bioinformatics. 2017 Dec 22. doi: 10.1093/bioinformatics/btx823. PubMed PMID: 29309523.

[33] **Baker EJ**, Walter NA, Salo A, Rivas Perea P, Moore S, Gonzales S, Grant KA. Identifying Future Drinkers: Behavioral Analysis of Monkeys Initiating Drinking to Intoxication is Predictive of Future Drinking Classification. Alcohol Clin Exp Res. 2017 Mar;41(3):626-636. doi: 10.1111/acer.13327.

[34] Bubier JA, Langston MA, **Baker EJ**, Chesler EJ. Integrative Functional Genomics for Systems Genetics in GeneWeaver.org. Methods Mol Biol. 2017;1488:131-152.

[35] Akinyeke T, Weber SJ, Davenport AT, **Baker EJ**, Daunais JB, Raber J. Effects of alcohol on c-Myc protein in the brain. Behav Brain Res. 2017 Mar 1;320:356-364. doi: 10.1016/j.bbr.2016.11.009.

[36] Jason A. Bubier, Troy D. Wilcox, Jeremy J. Jay, Michael A. Langston, **Erich J. Baker**, Elissa J. Chesler. Cross-Species Integrative Functional Genomics in GeneWeaver Reveals a Role for Pafah1b1 in Altered Response to Alcohol. *Frontiers in Behavioral Neuroscience* 01/2016; 10.DOI:10.3389/fnbeh.2016.00001.

[37] **Erich Baker**, Jason A. Bubier, Timothy Reynolds, Michael A. Langston, Elissa J. Chesler. GeneWeaver: data driven alignment of cross-species genomics in biology and disease. *Nucleic Acids Research* 12/2015; 44(D1):gkv1329. DOI:10.1093/nar/gkv1329.

[38] S M Ashiqul Islam, Tanvir Sajed, Christopher Michel Kearney, **Erich J Baker**. *PredSTP: A highly accurate SVM based model to predict sequential cystine stabilized peptides*. BMC Bioinformatics 07/2015; 16(210):1. DOI:10.1186/s12859-015-0633-x.

[39] Jason A Bubier, Charles A Phillips, Michael A Langston, **Erich J Baker**, Elissa J Chesler. GeneWeaver: finding consilience in heterogeneous cross-species functional genomics data. *Mammalian Genome* 06/2015; 26(9). DOI:10.1007/s00335-015-9575-x.

[40] Speegle, G., **Baker, E.** Integration of Big Data Components for NoSQL Problems, *Proceedings of the 2014 International Conference on Advances in Big Data Analytics*, 2014. 128-134.

[41] **Erich J. Baker**, Jonathan Farro, Steven Gonzales, Christa Helms and Kathy grant. Chronic alcohol self- administration in monkeys shows long-term quantity/frequency categorical stability. *ACER.* 2014 Nov;38(11):2835-43.

[42] Charles A Phillips, **Erich J Baker**, Elissa J Chesler, Michael A Langston. Algorithmic tools for tripartite data analysis. *BMC Bioinformatics* 09/2014; 15(Suppl 10):P32-P32. DOI:10.1186/1471-2105-15-S10-P32.

[43] Pablo Rivas-Perea, **Erich Baker**, Greg Hamerly, Bryan F Shaw. Detection of leukocoria using a soft fusion of expert classifiers under non-clinical settings. *BMC Ophthalmology* 09/2014; 14(1):110.DOI:10.1186/1471-2415-14-110.

[44] **EJ Baker,** C Culpepper, C Philips, J Bubier, M Langston and EJ Chesler. Identifying common components across biological network graphs using a bipartite data model. GLBIO. *BMC Proceedings* 2014, 8(Suppl 6):S4*.*

[45] Daunais, Davenport, Helms, Gonzales, Hemby, Friedman, Farro, **Baker** and Grant. Monkey alcohol tissue research resource: banking tissues for alcohol research. *ACER.* 2014 Jul;38(7):1973-81.

[46] Yun Zhang, Charles A. Philips, Gary L. Rogers, **Erich J. Baker**, Elissa J. Chesler and Michael A. Langston. On finding bicliques in bipartite graphs: a novel algorithm and its application to the integration of diverse biological data types. *BMC Bioinformatics.* 2014. 15(1):110.

[47] Elissa J. Chesler and **Erich J. Baker**. Contributions of genomic and informatics approaches to understanding alcohol dependence: from genes to networks. *Neurobiology of Alcohol Dependence*. 2014:523-537.

[48] Jeremy J Jay, **Erich J Baker** and Elissa J Chesler. A Context-Driven Gene Prioritization Method for Web-based Function Genomics. *Bioinformatics Research and Applications*, Springer. 161-172, 2013.

[49] **Erich J. Baker**. The Bioinformatics of Behavioral Neuroscience. *International Review of Neurobiology.*2012. 103:19-38.

[50] **Erich J. Baker**, Jeremy Jay, Jason Bubier, Michael Langston and Elissa Chesler. The Ontological Discovery Environment: A web-based system for integrative functional genomics analysis. *Nucleic Acids Research.* 2012. 40(1) D1067-1076.

[51] **Erich J. Baker** and Elissa J. Chesler The importance of open source integrative genomics to drug discovery. *Current Opinions in Drug Discovery.* 2010. 13(3):310-316.

[52] **Erich J. Baker**, Zuopan Li, Jeremy Jay, Vivek Philip, Yun Zhang, Michael A. Langston, Elissa J. Chesler Ontological discovery environment: A system for integrating gene-phenotype associations. *Genomics,* 2009. 94:377-387.

[53] Baker, L.E. and **Baker, E.J.** Reuniting Families: using phenotypic and genotypic forensic evidence to identify unknown immigrant remains. *Journal of Forensic Science,* 2008 53(1).

[54] **Baker, E.J**., Lin, Guan, Liu, Huadong, and Kosuri, R. NFU-enabled FASTA: Distributing bioinformatics applications over wide-area networks. *Source Code for Biology and Medicine*, 2007 Nov 26;2:8.

[55] Kirov SA, Peng X, **Erich Baker**, Schmoyer D, Zhang B and Snoddy J. GeneKeyDB: A lightweight, gene- centric, relational database to support data mining environments for sets of genes and gene products. *BMC Bioinformatics*. 2005 Mar 24;6(1):72.

[56] **Erich Baker**, B. Jackson, L. Galloway, et. al. MuTrack: an on-line distributed database for phenotypic discovery in mutagenized mice. *BMC Bioinformatics*. 2004 5:11.

[57] **Baker, E.J.**, Gerrard, D., Bamberger, E.G., Lozzio, C.B., and Ichiki, A.T.. HL-60-conditioned media induces myeloperoxidase in K-562 leukemia cells. *Leukemia Research*, 26:1017-1025, 2002.

[58] **Baker, E.J.**, Ichiki, A.T., Day, N.E., Andrews, R.B., Bamberger, E.G., and Lozzio, C.B. Simultaneous flow cytometric measurement of K-562 megakaryocytic differentiation and CD56+ large granular lymphocyte cytotoxicity. *Journal of Immunological Methods*. 253(1-2):37-44, 2001.

[59] **Baker, E.J.**, Ichiki, A.T., Hodge J.W., Sugantharaj, D., Bamberger, E.G., and Lozzio, C.B. PMA-treated K- 562 leukemia cells mediate a TH2-specific expansion of CD4+ T cells in vitro. *Leukemia Research* 24:1049-1057, 2000.

[60] Ichiki, A.T., Langenberg, M., **Baker, E.J.**, Hodge, J.W., Bamberger, E.G., Gerard, D.A., and Lozzio, C.B. Differential regulation of IL-1α and IL-1β in K-562 cells. *Journal of Interferon and Cytokine Research* 18:1045-1050, 1998.

JOURNAL PUBLICATIONS [NON-PEER REVIEWED]

[1] Bubier, Jason, Sutphin, George, Reynolds, Timothy, Korstanje, Ron, Fuksman-Kumpa, Axis, **Baker, Erich**, Langston, Michael, and Chesler, Elissa. Integration of heterogeneous functional genomics data in gerontology research identifies genes and pathway underlying aging across species. BioRxiv, October, 2018. https://doi.org/10.1101/451013. [Preprint Server].

[2] Bubier, Jason, Vivek Philip, Christopher Quince, James Campbell, Yanjiao Zhou, Tatiana Vishnivetskaya, Suman Duvvuru, Rachael Hageman Blair, Juliet Ndukum, Kevin D Donohue, Charles Phillips, Carmen Foster, David Mellert, George Weinstock, Cymbeline T Culiat, **Erich J Baker**, Michael A Langston, Bruce O'Hara, Anthony V Palumbo, Mircea Podar, Elissa J Chesler. Systems Genetic Discovery of Host-Microbiome Interactions Reveals Mechanisms of Microbial Involvement in Disease. BioRxiv, January 1, 2018. https://doi.org/10.1101/349605. [Preprint Server].

CONFERENCE PROCEEDINGS

The artifacts listed in this section have met the criteria for peer review in their appropriate domains. However, like some areas of life science, bioinformatics conferences have an uneven history of providing indexed citations to meeting artifacts. Where possible, indexed proceedings are indicated. In other cases, a peer-reviewed abstract represents a short platform presentation.

[1] Jui, T.D., Benton, M.L., **Baker, E.** (2024). Node Classification with Multi-hop Graph Convolutional Network. In: Han, H. (eds) Recent Advances in Next-Generation Data Science. SDSC 2024. Communications in Computer and Information Science, vol 2158. Springer, Cham. *https://doi.org/10.1007/978-3-031-67871-4_14*.

[2] Tonni Das Jui, **Erich Baker**, Mary Lauren Benton. Assessing information influence for node attribute prediction. The 2024 World Congress in Computer Science, Computer Engineering, & Applied Computing (CSCE'24). Las Vegas, Nevada.

[3] T. D. Jui, **E. Baker** and M. L. Benton. From Static Graph Attention Generation to Dynamic Graph Attention Coefficient. Conference: Computational Science & Computational Intelligence (CSCI'24). Las Vegas, Nevada.

[4] T. D. Jui, **E. Baker** and M. L. Benton. "k-Hopped Link Prediction With Graph Embedding," 2023 Congress in Computer Science, Computer Engineering, & Applied Computing (CSCE), Las Vegas, NV, USA, 2023, pp. 600-607*, doi: 10.1109/CSCE60160.2023.00104.*

[5] Alibek Zhakubayev, Thomas Andersen, Annie Vesterby, Lene Warner Thorup Boel, Kathleen Grant, Urszula Iwaniec, Russell Turner, **Erich Baker**, Mary Lauren Benton. Image processing approach provides robust feature extraction for classification with small sample sizes. (2023). Proceedings of the 2023 7th International Conference on Information System and Data Mining (ICISDM) Atlanta, GA, USA. https://doi.org/10.1145/3603765.3603777.

[6] Javier Orduz-Ducuara*, Pablo Rivas, **Erich Baker**. Quantum Machine Learning Foundations and Applications: A Succinct Literature Review. (2021). Transactions on Computational Science & Computational Intelligence. *Accepted for publication.*

[7] Reynolds, T., Bubier, J. A., Agrawal, A., **Baker, E. J.**, & Chesler, E. J. Integrative cross-species analysis uncovers convergent genomic regulatory features associated with complex disease. NIDA Genetics and Epigenetics Cross-Cutting Research Team Meeting, Rockville, MD. January, 2019.

[8] Reynolds, T., Emerson, J., Berger, A., Bubier, J., **Baker, E. J.**, & Chesler, E. J., GeneWeaver.org: A RESTful service for multi-species data integration in functional ge- nomics. Intelligent Systems for Molecular Biology, Basel, Switzerland. August, 2019.

[9] S. Moore, A. Radunskaya, E. Zollinger, N. Walter, K. Grant, **E.Baker**. A mathematical model of blood ethanol concentration levels in rhesus macaques. 42nd Annual RSA Scientific Meeting, Minneapolis, MN. ACER 2019.43.issue-s1. doi.org/10.1111/acer.14056.

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[11] E.J. Chesler, T. Reynolds, J.A. Bubier, C.A. Phillips,M.A. Langston, **E.J. Baker**. Finding convergent behavioral features of alcohol use disorder through functional genomic comparison across species. 41st Annual RSA Scientific Meeting, San Diego, CA. ACER 2018.65.issue-s1.

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[23] **E. Baker**, J. Farro, S. Gonzales, J. Daunais, K. Grant. The Monkey Alcohol Tissue Research Resource (MATRR). 37th Annual Scientific Meeting of the Research-Society-on-Alcoholism; 06/2014.

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[25] **Erich Baker**, Jason Bubier, Jeremy Jay and Elissa Chesler. GeneWeaver: Building context-driven similarity on empirically-defined functional genomics relationships. *International ISMB Conference,* Berlin, DE, July, 2013.

[26] E. J. Chesler, J. J. Jay, M. A. Langston, **E. J. Baker**, J. A. Bubier. Cross species integrative functional genomics of alcohol related behaviors in the Geneweaver web based software system. 16th World Congress of the; 09/2012.

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[28] Jeremy Jay, **Erich Baker**, Jason Bubier, Elissa Chesler. GeneWeaver.org: a platform for the analysis of gene set associations. *International ISMB Conference,* Long Beach, CA, July, 2012.

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[34] Daunais JB, Chesler EJ, Davenport AT, **Baker EJ**, Hemby SE, Friedman DP, Grant KA. What's a MATRR?. MMM Meetings, Ann Arbor, MI, 2010.

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[46] Baker, L.E. and **Baker, E.J.** Reuniting Families: using phenotypic and genotypic forensic evidence to identify unknown immigrant remains. *Journal of Forensic Science Proceedings*. p. 297, 2004.

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[52] Lelslie Galloway, Barbara Jackson, Denise Schmoyer, **Baker, E.J.**, Fred Baas and Jay Snoddy. The TMGC Web Site and Mutrack. Tennessee Mouse Genome Consortium Meeting, Nashville, Tennessee, Jan, 2003.

[53] **Erich Baker**, Brynn Jones, Doug Hyatt, et al. Integrating Computational Analysis of Orthologous Gene Sequences and RNA Expression Analysis in the Mouse Skin. Cold Spring Harbor, Genome Sequencing and Biology. May, 2002. Supplement.

[54] **Erich Baker**, Doug Hyatt, Barbara Jackson, et al. Comparative and Collaborative Bioinformatics Required to Study the Gene Regulatory Networks that Create Phenotypes. Cold Spring Harbor, Genome Sequencing and Biology. May, 2002. Supplement.

[55] Philip LoCascio, Norman Doggett, **Erich Baker**, et al. U.S. Department of Energy National Laboratories Collaborative High Throughput Genome Analysis Framework. Cold Spring Harbor, Genome Sequencing and Biology. May, 2002. Supplement.

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[59] Brynn H. Jones, Jay R. Snoddy, Cymbeline T. Culiat, Mitchel J. Doktycz, Peter R. Hoyt, Denise D. Schmoyer, **Erich J. Baker**, et al. Functional Analysis of Gene Regulatory Networks Underlying Skin Biology and Environmental Susceptibility. DOE Genome Contractor-Grantee Workshop IX. p 39. January, 2002.

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[61] **Baker, E.J.**, Jackson, B., Chen G.L., Schmoyer D., Miller D., Snoddy J., and the Tennessee Mouse Genome Consortium**.** TMGC: MuTrack, A Collaborative Database for Integrated Computational and Experimental Research in the Tennessee Mouse Genome Consortium. Proceedings of the 15th Annual Mouse Genome Consortium. Edinburgh, Scotland, October, 2001.

[62] **Baker, E.J.**, Barbara Jackson, et al. TMGC:Mutrack, A Collaborative Database for Phenotype Screening in the Tennessee Mouse Genome Consortium. Cold Spring Harbor, Genome Sequencing and Biology. May, 2001. Supplement.

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[64] Schimmel, S., **Baker, E.J.**, Gerrard, D.A., Day, N.E., and Ichiki, A.T. Induction of K-562 cells to elongate and adhere. American Association of Cancer Research, New Orleans, LA, 2001. Supplement.

[65] **Baker, E.J.**, Day, N.E., and Ichiki A.T. Type 2 immune response mediated by PHA-treated K-562 leukemia cells. American Association of Cancer Research Annual Meeting, San Francisco, CA, 2000.

[66] Day, N.E., Gerard, D.A., **Baker, E.J.**, and Ichiki, A.T. Mononuclear cell-derived factors induce homotypic aggregation of K-562 cells. FASEB Journal. 2000.

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EDITED VOLUMES

[1] *Next Generation Data Science*. Eds: Henry Han & **Erich Baker**. Springer Nature. 2024, Volume 2113. ISBN : 978-3-031-61815-4.

[2] *The Recent Advances in Transdisciplinary Data Science*. Eds: Henry Han & **Erich Baker**. 2022, Volume 1725. ISBN : 978-3-031-23386-9.

GRANTS

- PI INIA U24 – INIAstress Computational and Statistical Analysis Core. NIAAA/NIH. $350,076 over 5 years.
- Co-PI. CDC SBIR II – CrossWalk. Partner with JSR Associates, Inc.-Behaviors. Year 2 funding of $47,500 total to Baylor. 8/30/20 – 7/29/22.
- Co-PI. CDC SBIR – CrossWalk. Partner with JSR Associates, Inc.-Behaviors. Year 1 funding of $47,500 total to Baylor. 8/30/18 – 7/29/19.
- Co-PI. NIH R01-R01 AA026289 - Complex systems analysis of the impact of alcohol on bone in non- human primates. $456,000 over 5 years (Sub-Contract only). 9/17/17 – 8/31/22.
- PI. Sanofi GeneWeaver Discovery Grant (Contract). $48,000. 6/1/2016 – 5/31/2017.
- Co-PI. NIH R24-Renewal of Monkey Alcohol Tissue Resource Repository (MATRR). $952,000 over five years (Sub-Contract only). 9/1/15-8/31/20.
- Co-PI. NIH R01-Renewal of A1018776-01 Data Structures, Algorithms and Tools for Ontological Discovery. $350,000 over 5 years (Sub-Contract only). (9/1/14-8/31/19).
- Co-PI. NIH R01 A1018776-01 Data Structures, Algorithms and Tools for Ontological Discovery. $199,498 over 4 years (Sub-Contract only). (9/1/10-8/31/14).
- Co-PI. NIH R24 Monkey Alcohol Tissue Resource Repository (MATRR). $982,000 over five years (Sub- Contract only). 9/1/10-8/31/15.
- Co-PI. CDMRP/TAMU. Root Cause of Post-traumatic and Developmental Stress Disorders. $60,000 over 3 years (8% effort, 5/08-2/11).
- PI. Baylor-URSA (Undergraduate Research) Bayesian classifier for the identification alternative splice regions in yeast. $8,600 (8/1/11-7/31/12).
- PI. Baylor-URC. High-performance graph mining using MapReduce. $4500 (6/1/10-5/31/11).
- Co-PI. NIH/NIAAA. U01 AA016669 Ontological Discovery for Ethanol Research (INIA project). Subcontract to Baylor $71,280 over 3 years. (10% effort, 6/18/07-8/31/10).
- Co-PI. Department of Energy. An Integrated Knowledge Resource for the *Shewanella* Federation. $168,000 over 3 years. (35% effort, 10/05 – 10/7).
- P.I. Baylor University NSF Grant Improvement Award. Exploring graph-based biological databases, $15,000, 2004-2005.
- Co-investigator. National Institutes for Health, Planning Grant for a National Center of Excellence in Bioinformatics Computing, in conjunction with the Bioinformatics Core of the Tennessee Mouse Genome Consortium, 5 years, $1.5 million total. Subcontract awarded to Baylor, $240,000 over 4 years. (50% effort ending 5/06)
- Physician's Medical Education Research Fund, Isolating the Factor for PMA-induced Adherence in K- 562 Cells, $8,000, 1999.
- Physician's Medical Education Research Fund, Analyzing the Effectiveness of DNA Transfection in K- 562 cells, $6,000, 1998.
- Physician's Medical Education Research Fund, Exploring the K-562 Phenotype and Genotype, $10,000, 1997.

SOFTWARE DEVELOPED

- PredSTP – An on-line SVM-based predictor of a novel class of cycteine-stabilized knottin proteins (STP/NTP).
- MATRR – An on-line data store and analysis application suite for tracking monkey tissue and alcohol disease states.
- RootCouseofPTSD.org – An on-line knowledgebase linking molecular and phenotypic relationships underpinning the development of PTSD.
- ODE: Ontological Discovery Environment and GeneWeaver – An on-line database and software package for correlating phenotype data with gene networks; GeneWeaver.org
- Mutrack(MouseTrack) – An integrated on-line distributed data system for discovery of novel phenotypes in mutagenized mice.
- GeneKeyDB – A lightweight metadata database representing collected data from community resources, including NCBI, Ensembl, and SwissProt.
- MOMA – A proprietary distributed LIMS for tracking SNP data in molecular forensic laboratories.

STUDENTS

Ph.D. Students

- Everest Casanada. TITLE FORTHCOMING. Department of Biology, mentor, 2020 - present
- Tonni Das Jui. TITLE FORTHCOMING. Department of Computer Science, mentor. 2022 - present
- Timothy Reynolds. Information condensation in Gene Set relationships, Ph.D. Candidate, Institute for Biomedical Studies, Baylor University, mentor, 2015 - 2021.
- Chi Yen Tseng, Influence of Environmental Factors and Contaminant Mixtures on Acute Toxicity and Molecular Responses: Studies from the lab and field. Department of Biology, committee member. 2017 – 2021.
- Jinyan Chan. Dr. Insight, A Novel Systematic Drug Repurposing Method. Institute for Biomedical Studies, committee member. 2016 - 2020.
- Mishu Islam, Automated Discovery of Knottins, Ph.D. Candidate, Institute for Biomedical Studies, Baylor University, co-mentor. 2015 - 2018.
- Timothy Zumwalt, Type I helper and cytotoxic T cell activity in microsatellite instable colorectal cancer, Ph.D. Candidate, Institute for Biomedical Studies, Baylor University, committee member.
- Jeremy Jay, Graph theory applications in functional genomics, Ph.D., 2014, Department of Computer Science, University of Maine, committee member.
- Sharath Rongali, Identification of germline and somatic cell specific genes essential for ovulation in *Caenorhabditis elegans*, Ph.D., 2011, Institute for Biomedical Studies, Baylor University, committee member.
- Baoqing Ding, On the Origin of Lake Malawi Cichlid Species and Mechanisms of their Maintenance, Ph.D., 2011, Department of Biology, Baylor University, committee member.
- Zun Liu, Determining the functionality of retroviral elements in nuclear export in plants for the improvement of a plant RNA virus vector. Ph.D., 2010, Institute for Biomedical Studies, Baylor University, committee member.
- Sushil Batra, Identification of phenotype in *caenorabhditis elegans* on the basis of sequence similarity. Ph.D., 2007, Institute for Biomedical Studies, Baylor University, co-mentor.

Master's Students

- Kelechi Fletcher, Identifying Phylogenetic Hierarchies and Functional Modules In Biological Networks Through Hierarchical Similarity Decomposition. M.S. Department of Computer Science, Baylor University, expected date – 2016 - present, mentor
- Alex Salo, Automated discovery of drinking categories in monkeys in a self-induced alcohol drinking protocol, M.S. Department of Computer Science, Baylor University, 2015 - 2016, mentor.
- Alvin Jude, Giving the users a hand: towards touchless hand gestures for the desktop, M.S., 2015, Department of Computer Science, committee member.
- Ryan Hennings, Automated Detection of Leukocoria, M.S. Computer Science, 2014, committee member.
- Maryuri Roca, Studies on Bovine γ-glutamylamine cycltransferase, M.S., Biomedical Studies, 2010, committee member.
- David Morillo, Bootstrapping bipartite graphs consisting of edges based on ontology terms occurring in scientific abstracts. M.S., Computer Science, 2010, mentor.
- Kristi DeLeon, Dynamics and interaction studies of angiotensin I and II: experiment and molecular modeling, M.S., Biomedical Studies, 2009, committee member.
- Stephen Bush, Automated sequence homology: using empirical correlations to create graph-based networks for the elucidation of protein relationships. M.S., Bioinformatics, 2008, mentor.
- Kevin Kastner, GeneKeyAPI: a set of tools for dynamically updating and accessing GeneKeyDB. M.S., Computer Science, 2008, mentor.
- Garvin Lee Chandler, Influenza hemagglutinin expression in *Nicotiana tabacum* and *Nicotiana benthamiana*. M.S., Biomedical Studies, 2007, committee member.
- Nick Lin, Distributing sequence similarity algorithms on scale-free networks, M.S., 2006, mentor.
- Ravi Kosuri, NFU-enabled FASTA. M.S., Computer Science, 2005, mentor.

Undergraduate Honor's Theses

- Sam Shenoi, Identification and Analysis of an Improved Beçhet's Disease Animal Model: A Computational Approach, 2021, mentor.
- Natasha Lie, Predication of novel genes involved in retinitis pigmentosa from GeneWeaver, B.S. Biochemistry, 2016, mentor.
- True Price, Analysis of resting state fMRI using Pearson-VII mixture modeling, B.S. Bioinformatics, 2013, mentor.
- Ali Beck, The semantic web: an alternative approach to dynamic data definition and integration in medical informatics systems, B.S., Computer Science, 2006, mentor.

TEACHING EXPERIENCE

Instructed at Baylor
CSI 4335 Database Design I, CSI 4v96 Special Topics in Computational Biology, CSI 5v93 Graduate Topics in Computational Biology, CSI 5321 Cloud Computing, BINF 4360 Bioinformatics Database Design, BINF 43C9 Bioinformatics Capstone Course, BINF 3360 Introduction to Computational Biology, BINF 3350 Genomics and Bioinformatics, BMS 5v96 Graduate Bioinformatics, BINF 5330 Systems Biology and Bioinformatics, DSC 3310 Cloud Computing, DSC 2300 Intro to Data Science, CSI 3335 Database Design

Instructed at University of Tennessee/ORNL
Bioinformatics and PERL, Genome Science and Technology I/II

Teaching Assistant
Advances in Immunology, Undergraduate Laboratory Research

PROFESSIONAL AND UNIVERSITY SERVICE

Belmont University

- 2023 – present: Founding Co-Chair, Belmont Policy Review Committee
- 2024 – present: Belmont Digital Steering Committee, MATRR
- 2023 – present: Chair, Belmont Digital Technology Network
- 2024 – present: University committee for the evaluation of ERP/HCM software transition
- 2024: Chair, University Task Force on Enrollment
- 2024: Chair, University Task Force on University Libraries
- 2025: Chair, University Task Force on Digital Technology
- 2025 – present: LCME Data Collection Instrument (DCI) Standard 5 Committee

Baylor University

- 2021 – 2022: ECS Dean Search Committee
- 2005-2008; 2012-2023: University Committee on Research
- 2012 – 2023: ECS Research Committee
- 2011 – 2023: Departmental Undergraduate Curriculum Committee
- 2013-2015: Chair, Departmental Search Committee
- 2010-2013: Chair, Departmental Chair Search Committee
- 2010-2012: Department Search Committee (non-chair position)
- 2010-2014: University *ad hoc* committee for electronic course evaluation
- 2010-2012: University Dean Search Committee
- 2009 - 2012: University Committee on Academic Freedom
- 2008-2010: ECS Building Committee
- 2007-2015: departmental subcommittee for ABET
- 2007-present: participated in the ECS Academy and various student recruiting activities (i.e. Presentations at University Recruitment seminars [Nat'l Merit Scholars], Brochure/ New Website development, I2E, etc.)
- 2005-2014: Student advisement for 50-60 bioinformatics majors per semester (Spring and Fall)
- 2003-present: Advisor for the Baylor Bioinformatics Club (ABB)
- 2003-present: Department Graduate Committee
- 2002-2008: CS departmental Committee for Retention
- 2002 - 2007: SACS and ABET assessment information for B.S. in Informatics (Bioinformatics) degree
- 2008-2011: Faculty Senate
- 2009-2010: Secretary, Executive Council of Faculty Senate
- 2008-2015: Advisor for Baylor Chapter of Up-till-Dawn which raised > $100k for St. Jude's children's hospital