

Ashley Mae Conard

Areas: interpretable machine learning, temporal and multi-omics data modeling, gene regulatory networks, visualization, reproducibility, platform development, high-performance computing, game theory ashleymaeconard@gmail.com www.linkedin.com/in/ashleymaeconard

Education

Ph.D. in Computational Biology, Computer Science track, Brown University (expected spring 2022) 2019-Current

Develop statistical and Bayesian methods and visualizations for longitudinal multi-omics studies to uncover gene regulation.
Formulate novel research directions, perform experimental design, develop interpretable methods, and aid in wet-lab validation.
Advisors: Drs. Lorin Crawford (biostatistics), Erica Larschan (molecular biology), and Charles Lawrence (applied math).

M.Sc. in Computer Science, Cancer Genomics concentration, Brown University and Princeton University 2015-2017

Built deep learning method to improve DNA single-cell sequencing data for large region mutation (copy-number) inference.
Created pipeline identifying subclonal mutations in bulk sequencing tumor samples. Advisor: Dr. Benjamin Raphael.

B.A. in Computer Science (Biochemistry concentration and French minor), GPA: 3.7, DePauw University 2010-2014

Computing & Technology Internship Experience (selected)

Computational Biology Researcher and Creator, Google Cloud, Palo Alto, CA Fall 2021

Developing new computational biology frameworks in collaboration with several biotech companies and Google Cloud.

Bayesian Inference Researcher, Biomedical Computing Team, Health Futures, Microsoft Research, WA Summer 2021

Built interpretable Bayesian models using temporal and multi-omics data to uncover dysregulation in cancer, ALS, Parkinson's.

Machine Learning Scholar, Department of Health, Stephen Morris, RI Fall 2018

Designed predictive model for a need in Rhode Island's hospital systems. Hope is to form state legislation based on findings.

Game Theory & Bioinformatics Researcher, Université Libre Bruxelles, Fulbright/BAEF Scholar, Dr. Tom Lenaerts, Belgium 2014-2015

Created a method utilizing cooperative game theory, machine learning and structural bioinformatics techniques to quantify the roles and regulatory dynamics of core amino acids in a FYN SH3 protein domain.

High Performance Computing Researcher, MIT Lincoln Laboratory, Drs. Jeremy Kepner & Darrell Ricke, MA Summers 2013, 2014

Developed a fast protein analysis algorithm, using Dynamic Distributed Dimensional Data Model (D4M), merging sparse algebra, associative and distributed arrays, and triplestore/NoSQL databases (Accumulo) for fast Big Data analysis.

Google Cambridge Arduino Workshop Creator, Google, Computer Science Summer Institute, Chelsea Pollen, MA Summers 2013, 2014

Created, recruited, implemented, and led Arduino workshop for 40 students at Summer Institute ([link](#)).

Chemical Inventory Database Creator (Senior Project), DePauw University, Dr. David Roberts, IN Spring 2014

Designed, built, deployed database (Parse) & front end (HTML, CSS). >2K users to catalog & distribute chemicals ([details](#), [users link](#))

Bioinformatics Research & Tutor, DePauw University, Dr. Chester Fornari, IN 2012-2014

Devised labs & tutored Bioinformatics and Cells & Genes. Research: Integrated MEGA and Chimera to analyze TP53.

Structural Biology & Drug Discovery Researcher, Vanderbilt University, Dr. Jens Meiler, TN January 2013

Method development assistant for new structure prediction algorithms in RosettaLigand program (simulations and design of macromolecules) and new machine learning techniques in Biochemical Library (BCL) drug discovery project.

DePauw Alumni Office Technology Associate, DePauw University, Mrs. Holly Enneking, IN 2011-2012

Provided IT solutions and built video presentations for award lectures and conducted interviews for alumni networking.

Quality Control & Technology Researcher, Elanco (Eli Lilly and Company), Mr. Scott Burd, IN Summer 2012

Identified problem, implemented and tested 2 deviation documentation and instrument control software programs. Former went GLOBAL for Elanco plants in 11/2012, the latter runs automatically daily. Wet-lab work: GC, AA, HPLC (see Relevant Skills).

Computational Biology & Machine Learning Researcher, Université Libre Bruxelles (ULB), Dr. Tom Lenaerts, Belgium Spring 2012

Utilized cooperative game theory, machine learning, and structural bioinformatics to define FYN protein binding specificities.

Technology Associate, IT Associate Program, DePauw University, Mrs. Angie Smock, IN 2010-2011

Project manager for team of 10 for IT solutions. Projects: virtual flashcard program, website, tech brochure, IT solutions.

Technology Sales & Marketing Associate, JDS Uniphase, Mr. William DeWeese, TX, NY Summer 2011

Researched, tested, taught, and marketed communication software, services, and solutions for Verizon, AT&T.

Inorganic Chemistry Researcher, Ionogel Analysis and Application, DePauw University, Dr. Hillary Eppley, IN Fall 2010

Synthesized ionogels and determined chemical and physical properties to use as a catalysts for biosensing, optics, electrolytes.

Organic Chemistry Researcher, Eli Lilly and Company, Dr. David Bender, IN Summer 2008

Assessed hydrolytic stability of cyclopropanecarboxylic acid esters as potential prodrugs. Synthesized an acyclovir prodrug and worked with a ghrelin O-acyltransferase inhibitor. This is viewed as a potential therapeutic target to treat obesity and diabetes.

Technology Skills

Languages: Bash, C++, CSS, HTML, Java, Julia, MATLAB, pMatlab, Markdown, Python, R, RShiny, SQL

Development Tools / Environments: Arduino IDE, BlueJ, Conda, Docker, Eclipse, Jupyter, Putty, RStudio, Visual Studio Code, Xcode

Big Data Tools: Apache Accumulo, Apache Hadoop, Azure, Cuda, MPI, OpenMP, Slurm

Application Programs / Platforms: ArcGIS, Arduino, Audacity, Azure Dev. Ops, Business Objects, Cytoscape, Chimera, Discoverant, Dreamweaver, Final Cut Pro, GIMP, Google Cloud Platform, Illustrator, Infopath, MakerBot, Raspberry Pie, Raven, RosettaLigand

Relevant Coursework & Skills

Chemistry and Biochemistry Skills: Nuclear Magnetic Resonance Spectroscopy (^{13}C and ^1H), Mass Spectroscopy, Infrared Spectroscopy, Chromatography, Polymerase Chain Reaction methods, Gel Electrophoresis, familiar with Microwave Acid Digestion Bomb methods, Gas Chromatography (GC), High Performance Liquid Chromatography (HPLC), Atomic Absorption (AA) Spectrometry.

Relevant Coursework: Computer Sci./ Mathematics: Bayesian Inference in Genomics & Molecular Biology, Advanced Probabilistic Methods, Systems, Computational Molecular Biology, Advanced Algorithms in Computational Biology, Topics in Computational Linguistics, Coalescent Theory, Statistical Inference, Bioinformatics, Object Oriented Software Dev., Data Structures, Algorithm Dev. & Graphics
Biochemistry/Biology: Genetics, Function & Structure Biomolecules, Ecology & Evolution, Cells & Genes, Enzyme Mechanisms.

Foreign Languages French (fluent), Spanish (fluent), Portuguese (beginner), Dutch (beginner)

Awards & Honors Accepted

NSF Graduate Research Fellowship: Machine Learning and Computational Biology (2014-Current)

Fulbright Research Scholar & Belgian American Education Foundation Fellowship: Computational Biology, Belgium 2014-2015

DePauw: Dean's List (each semester), Alpha Lambda Delta Award (2010), and Old Gold Award for academic excellence (2014)

Grace Hopper Int'l Celebration of Women in Computing: Poster Award 2013, (scholarships: **NSF** 2010, **Xerox** 2012, **Intel** 2013)

Honors Societies: Mortar Board (VP '14), Chi Alpha Sigma, Phi Eta Sigma, Order of Omega, National Society for Collegiate Scholars

Select Publications

co-first: *, corresponding: ‡

- **A. Conard**‡, N. Goodman, Y. Hu, N. Perrimon, R. Singh, C. Lawrence‡, E. Larschan‡. TIMEOR: a web-based tool to uncover regulatory mechanisms from temporal and multi-omics data. *NAR Web Server Issue*. 2021 ([link](#))
- **A. Conard**, R. Singh‡, L. Crawford‡. A Bayesian Inference Approach to Predicting and Interpreting Cancer Patient Gene Regulatory Networks from Multiple Data Types. (In preparation). 2021
- M. Ray*, **A. Conard***, E. Larschan‡. The CLAMP transcription factor regulates sex-specific splicing in the Drosophila early embryo. *Nature Communications*. (Under review). 2021 ([link](#))
- N. D'Silva*, K. McCullar*, **A. Conard**, et al. Neuromolecular and behavioral adaptation associated with alcohol deprivation. *Genetics*. (Under review). 2021. ([link](#))
- M. Tsarli, **A. Conard**, E. Larschan‡. Drosophila CLAMP regulates neurogenesis in the optic lobe. *Genetics*. (Under review). 2021 ([link](#))
- **A. Conard**, I. Nathoo, M. Tsarli, C. Lawrence, E. Larschan‡. XvsY: A Computational Approach to Distinguish the Temporal Sex-Specific Roles of Vital Co-Factors on Brain Development in Drosophila. *Cell Press STAR Protocols*. (In preparation). 2021
- **A. Conard***, A. DenAdel*, C. Lawrence‡. Lessons in Bayesian Inference in Genomics and Molecular Biology. (In preparation). 2021
- H. Yeh, **A. Conard**, L. Ding, L. Crawford‡. Efficient Multi-Trait Learning with Biologically Annotated Neural Networks. (In preparation)
- **A. Conard**, E. Cilia, T. Lenaerts‡. Game Theory and Feature Selection Show FYN Protein Domain Amino Acid Dependencies. (In prep). 2021
- **A. Conard**, B. Raphael. Identification of Subclonal Drivers and Copy-Number Variants from Bulk and Single-Cell DNA Sequencing of Tumors. *Thesis M.S. in C.S., Brown University*. 2019 ([link](#))
- Cuypers, A. Jacobsen, B. Siranosian, K. Schwahn, **A. Conard**, et al. Highlights from the ISCB Student Council Symposia in 2016. *F1000Research*. 2016, 5(ISCB Comm J):2852 ([link](#))
- **A. Conard**, S. Dodson, J. Kepner‡, D. Ricke‡. Using a Big Data Database to Identify Pathogens in Protein Data Space, *arXiv*. 2015 ([link](#))

Leadership, Activities, Teaching (selected)

Professional Organizations & Positions

ISCB, ISBA, IEEE, AAAS, ACS, SIAM member, made Chemistry Day Workshop ('10), ushered IEEE Computing Workshop ('13)	Current
Student of Vision Abie Award Judge and Co-creator: intl. award to CS student for building tech. solution to local problem	2015 -Current
Ambassador to France (to return every 5 years): selected to represent US for D-Day Embarkation Commemoration	2004-Current
Fulbright Board of Trustees: young professional board member (Finance & Conference Committee, Strategic Task Force)	2018-2020
Finance Chair for International Society of Computational Biology (ISCB) Student Symposium	2016-2018
Princeton Citizen Scientists executive team: group of scientists interested in policy, mobilizing at Princeton and beyond.	2016-2017
AnitaB.org Board of Trustees: Student Board Member working on program and strategies committees	2015-2017
US-EU-NATO Affairs Delegate: Fulbright grantee to engage in EU Seminar in int'l diplomacy with EU Commission	February 2015
Venture Crew President (2010), Vice President (2009), Venture Crew 1121, Boy Scouts of America, IN	2008-2013

Brown University

Reviewer: Assisted advisors to review: ISMB/ECCB (2021), AISTATS (2020), Nature Communications, and Genes and Development (2019)

Teaching: Statistical Inference II, Applied Math 0650, lecturer (2019)

Mentoring: Helen Xi, Lee Ding (ugrad., '21); Dominique Pablito (grad., '21); Isaac Nathoo (ugrad., '21); Nathaniel Goodman (ugrad. '20)

DePauw University

Co-founder Robotics Club: mostly Arduino and 3D printing, **University Athletics:** Soccer (2010-2012) and Women's Track (2013-2014)

Co-founder of DePauw Farm: 2-acre farm, 25% produce given to local Greencastle IN food pantry ([history](#), [website](#))

Several Interviews [PhD prgm](#), [GHC '16](#), [GHC '15](#) **Articles** [Tech women report](#), [AnitaB Board](#), [D-day Ambassador](#), [Fulbright](#), [DePauw senior](#)