Dr. Ashley Mae Conard

Health Futures
Microsoft Research
Cambridge, MA 02142, USA

Senior Researcher, Biomedical Computing Group
LinkedIn: `linkedin.com/in/ashleymaeconard`

Research theme

My general research theme is to build expert-centered interpretable methods and platforms to enable more effective decision-making in biomedical and clinical settings. After all, I believe for methods to be useful, they must be used.

Research interests

Temporal and multi-omics integration, rare disease research, interpretable statistical & Bayesian models, large language models, time-series models, human-in-the-loop computation, gene regulatory networks, visualization and perturbation, reproducibility, high-performance computing, game theory, protein binding prediction

Education

2022 **Biostatistics Department, Brown University, RI, USA.**
Post-doctoral researcher
Advisor: Dr. Lorin Crawford

2022 **Center for Computational and Molecular Biology, Brown University, RI, USA.**
Ph.D. Computer Science, Computational Biology
Thesis: *It's about time: developing interpretable models to uncover regulatory mechanisms from temporal and multi-omics data*
Advisors: Dr. Lorin Crawford, Dr. Erica Larschan, Dr. Charles Lawrence

2019 **Computer Science, Brown University RI, USA.**
M.S. in Computer Science
Thesis: *Identification of subclonal drivers and copy-number variants from bulk and single-cell DNA sequencing of tumors* [link]
Advisor: Dr. Benjamin Raphael

2014 **DePauw University, IN, USA.**
B.A. in Computer Science, Biochemistry specialization, minor French, *magna cum laude*

Professional Research and Computing Experience

2023–current **Health Futures, Microsoft Research,**
Cambridge, MA, USA.
Senior researcher Build novel methods and pipelines to improve rare disease solve and diagnostic rates in partnership with the Broad Institute of MIT and Harvard, and the Center for Population Genomics, Australia [link].

2022 **Biostatistics Department, Brown University,**
Providence, RI, USA.
Post-doctoral researcher Develop interpretable Bayesian machine learning and statistical models from multi-omics data.

2019–2022 **Center for Computational and Molecular Biology (CCMB), Brown University,**
Providence, RI, USA.
Ph.D. Computer Science, Computational Biology Developed interpretable Bayesian machine learning models for longitudinal multi-omic studies and platforms to understand gene regulation. I formulated novel research directions, perform experiment design, method development, result and wet-lab validation.

Spring 2022 **Phenome Health, Deloitte,**
San Francisco, CA, USA.
Computational Biologist, Data Infrastructure, Machine Learning. Developing scientific and business strategy for healthcare and life science start-up under Dr. Leroy Hood.

Fall 2021 **Google Cloud,**
Palo Alto, CA, USA.
Researcher and Creator. Developing new computational biology frameworks in collaboration with several biotech companies and Google Cloud.

Summer 2021 **Biomedical Computing, Health Futures, Microsoft Research,**
Redmond, WA, USA.
Research Intern. Developed three interpretable Bayesian inference models leveraging temporal and multi-omic data to uncover dysregulation in breast cancer, ALS, and Parkinson's disease.

Fall 2018 **Department of Health, RI, USA.**
Machine Learning Scholar. Designed predictive model to address a need in Rhode Island's hospital systems. The hope is to form state legislation based on findings.

2015–2017 **Department of Computer Science, Princeton University, Brown University, MA, RI, USA.**
Graduate Student. Designed deep learning model to improve DNA single-cell sequencing data for large region mutation (copy-number) inference. Developed pipeline to identify subclonal driver mutations in bulk sequencing cancer tumor samples across nine cancer types.

2014–2015 **Department of Computer Science, Université Libre de Bruxelles, Belgium.**
Game Theory Researcher. Created a method to uncover binding specificities in SH3 protein domain using machine learning, cooperative game theory, and structural bioinformatics.

Summer 2013, 2014 **Massachusetts Institute of Technology Lincoln Laboratory, MA, USA.**
Bioinformatics Researcher. Developed a fast protein analysis algorithm using Dynamic Distributed Dimensional Data Model (by Dr. Jeremy Kepner), merging sparse algebra, associative and distributed arrays, and triplestore/NoSQL databases (Accumulo).

Summer 2013 **Department of Chemistry, DePauw University, IN, USA.**
Chemical Inventory Database Creator – Senior Project. Designed, built, and deployed database (Parse Platform) and front end (HTML, CSS). ∼2000 users for many departments [link].

January 2013 **Center for Structural Biology, Vanderbilt University, TN, USA.**
Visiting Scholar. Assisted in development of new structure prediction algorithms in RosettaLigand program (simulations and design of macromolecules) and proposed new machine learning techniques in Biochemical Library (BCL) drug discovery project.

2011–2012 **Technology Associate of Alumni Office, DePauw University, IN, USA.**
Student Worker. Provided information technology solutions for faculty and staff. Built video presentations for award lectures and conducted interviews for alumni networking.

Summer 2012 **Eli Lilly and Company (Elanco), IN, USA.**
Quality Control Researcher. Designed, tested and implemented two software programs. One for deviation documentation and the other instrument control. The former went GLOBAL for Elanco plants in Nov. 2012, the latter runs automatically daily. Learned how to use Gas Chromatography, Atomic Absorption Spectroscopy, and High Performance Liquid Chromatography.

Spring 2012 **Department of Computer Science, Université Libre de Bruxelles, Belgium.**
Visiting Scholar. Analyzed the role of core amino acids in a FYN SH3 protein domain using structural bioinformatics and game theory techniques.

2010–2011 **Information Technology Help Desk, Information Technology Associates Program, DePauw University, IN, USA.**
Technology Associate. Project manager for team of ten that implemented technology solutions for students and faculty, including revamping websites and software troubleshooting.

Summer 2011 **JDS Uniphase, TX, NY, USA.**
Technology Sales and Marketing Associate. Researched, tested, taught, and marketed communication software, services, and solutions for Verizon, AT&T.

Summer 2011 **Department of Biology, Science Research Fellowship Program, DePauw University, IN, USA.**
Behavioral Ecology Researcher. Developed procedures to test and analyze different advertisement and aggressive calling patterns of *Acris blanchardi*. Tested parachuting behavior of *Hyla chrysosclis, Acris blanchardi, and Anaxyrus fowleri*.

Fall 2010 **Department of Chemistry, Science Research Fellowship Program, DePauw University, IN, USA.**
Inorganic Chemistry Researcher. Synthesized ionogel and determined chemical and physical properties to use as a catalyst for biosensing, optics, and electrolytes.

Summer 2008 **Eli Lilly and Company, IN, USA.**
Inorganic Chemistry Researcher. Assessed hydrolytic stability of cyclopropanecarboxylic acid esters as potential prodrugs. Synthesized an acyclovir prodrug and worked with a ghrelin O-acyltransferase inhibitor to evaluate use as a potential therapeutic target to treat obesity and diabetes.

Honors and Awards

International and National

2014–2019 ○ National Science Foundation Graduate Research Fellowship Program (NSF GRFP)
2014–2015 ○ Fulbright Research Scholar, Machine Learning and Game Theory, Belgium
2015 ○ Belgian American Education Foundation Fellow, Machine Learning and Game Theory, Belgium
2014 ○ Science Mathematics and Research for Transformation (SMART). Declined due to NSF GRFP.
2010–2014 ○ Grace Hopper International Celebration of Women in Computing: Poster Award 2013, (scholarships: NSF 2010, Xerox 2012, Intel 2013)
2011 ○ Ohio Celebration of Women in Computing (OCWiC), scholarship to attend
○ National Society of Collegiate Scholars (NSCS)
2010 ○ Science National Honor Society
2009 ○ Indiana High School Athletic Association Role Model: gave speeches to promote drug-free living

DePauw University

2014 ○ Old Gold Award: academic excellence and high achievement

2012 ○ Internships in Francophone Europe: fellowship to study in Belgium and conduct research

2010–2014 ○ Dean's List (every semester)

○ Information Technology Associates Program (ITAP) - selective honors program

○ Science Research Fellows (SRF) - selective honors program

○ *Honors Societies*: Mortar Board, Chi Alpha Sigma, Phi Eta Sigma, Order of Omega, National Society for Collegiate Scholars, Alpha Lambda Delta

Publications

Co-first author: *, corresponding author: ‡.

2023 H. Xi, L. Crawford‡, **A. Conard**‡. Multioviz: an interactive platform for *in silico* perturbation and interrogation of gene regulatory networks. *BMC Bioinformatics*. (Under review).

V. Sriram, L. **A. Conard**, I Rosenberg, D. Kim, A. Hall‡. Accelerating precision medicine: a proposed framework for large-scale multiomic data integrity, interoperability, analysis, and collaboration in biomedical discovery. *PLOS Digital Health*. (In submission).

A. Mastrianni, H. Twede, A. Sarcevic, J. Wander, C. Austin-Tse, S. Saponas, H. Rehm, **A. Conard**‡, A. Hall‡. AI-Enhanced Sensemaking: Exploring the Design of a Generative AI-Based Assistant to Support Whole Genome Sequencing Analysis. *CHI*. (In submission).

A. Conard‡, I. Nathoo, M. Tsarli, C. Lawrence, E. Larschan. XvsY: pipeline to identify shared and distinct genomic signatures from multiple expression and protein-DNA interaction information over time. *Cell Press STAR Protocols*. (In submission).

N. D'Silva*, K. McCullar*, **A. Conard**, T. Blackwater, R. Azanchi, U. Heberlein, E. Larschan, K. Kaun‡. Neuromolecular and behavioral adaptation associated with alcohol deprivation. *Genetics*. (Under review).

2022 **A. Conard***, A. DenAdel*, L. Crawford‡. A spectrum of explainable and interpretable machine learning approaches for genomic studies. *WIREs Computational Statistics*.

A. Conard‡. It's About Time: Interpretable Methods and Associated Interactive Platforms to Uncover Regulatory Mechanisms from Temporal and Multi-Omics Data. *Brown University Ph.D. Thesis, Computer Science and Computational Biology*.

A. M. Bronikowski, R. P. Meisel, P. R. Biga, J. R. Walters, J. E. Mank, E. Larschan, G. S. Wilkinson, N. Valenzuela, **A. Conard**, J. P. de Magalhaes, J. Duan, A. E. Elias, T. Gamble, R. M. Graze, K. E. Gribble, J. A. Kreiling, and N. C. Riddle‡. Sex-specific aging in animals: Perspective and future directions. *Aging Cell*.

2021 **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*.

M. Ray*, **A. Conard***, E. Larschan‡. The CLAMP transcription factor regulates sex-specific splicing in the *Drosophila* early embryo. *eLife*.

2020 M. Tsarli, **A. Conard**, E. Larschan‡. The *Drosophila* CLAMP protein regulates neurogenesis in the optic lobe. *Genetics*. (Under review).

2019 **A. Conard**‡, B. Raphael‡. Identification of subclonal drivers and copy-number variants from bulk and single-cell DNA sequencing of tumors. *Brown University Department of Computer Science*.

2016 B. Cuypers, A. Jacobsen, B. Siranosian, K. Schwahn, **A. Conard**, N. Aben, M. Hassan, N. Fatima, S. Hermans, M. Woghiren, P. Meysman, F. Rahman, A. Jigisha. Highlights from the ISCB Student Council Symposia in 2016. *F1000Research*. 2016, 5(ISCB Comm J):2852

2015 **A. Conard**, S. Dodson, J. Kepner‡, D. Ricke‡. Using a Big Data Database to Identify Pathogens in Protein Data Space, *arXiv*:1501.05546.

Skills and Experience

Programming Languages	Bash, C++, C, CSS, HTML, Julia, Java, MATLAB, pMatlab, Markdown, Python, R, RShiny, SQL
Dev. Tools/ Environments	Azure Dev Ops, Arduino IDE, BlueJ, Conda, Docker, Eclipse, Jupyter, Putty, RStudio, Terminal, Visual Studio Code, Xcode
Big Data Tools	Apache Acculumo, Apache Hadoop, Azure, MPI, OpenMP, Slurm
Programs/ Platforms	ArcGIS, Arduino, Audacity, Business Objects, Cytoscape, Chimera, Discoverant, Dreamweaver, Final Cut Pro, GIMP, Google Cloud Platform, Illustrator, Infopath, MakerBot, Raspberry Pie, Raven, RosettaLigand
Foreign Languages	French (fluent), Spanish (fluent), Dutch (beginner), Portuguese (beginner)

Selected Presentations

Invited Talks

September 2023 **A spectrum of explainable and interpretable machine learning approaches for genomic studies**
ACM Conference on Bioinformatics, Comp. Biology, & Health Informatics (ACM BCB), TX, USA.

November 2020 **BIOGRINN: Bayesian model to interpret and predict genomics features from multi-omics data**
International Society for Bayesian Analysis (ISBA), Virtual.

November 2020 **TIMEOR: a web-based tool to uncover temporal regulatory mechanisms from multi-omics data**
Biological Data Science Conference, Cold Spring Harbor Laboratory, Virtual.

March 2020 **TIMEOR: web-based tool to uncover regulatory mechanisms from temporal & multi-omics data**
Adelman-Bender-Cole-Kuroda-Larschan Joint Lab Meeting, Harvard University, MA, USA.

January 2020 **Trajectory Inference and Mechanism Exploration with Omics Data in R. A computational method to uncover regulatory mechanisms of transcription factors during development**
Perrimon Lab Group Meeting (collaborator), Harvard University, MA, USA.

October 2019 **Trajectory Inference and Mechanism Exploration with Omics Data in R. Its about time!**
Epigenomics Club, Brown University, RI, USA.

August 2019 **Trajectory Inference and Mechanism Exploration with Omics Data in R - A method to uncover regulatory mechanisms over time**
Dana-Farber Cancer Institute, MA, USA.

August 2019 **Time course model of alcoholism in neural development of *Drosophila melanogaster***
Kaun Lab Group Meeting, Brown University, RI, USA.

June 2019 **Trajectory Inference and Mechanism Exploration with Omics Data in R - A method to analyze how transcription factors influence development**
Boston Area Drosophila Meeting, Brown University, RI, USA. *Flash talk*.

June 2019	**Trajectory Inference and Mechanism Exploration with Omics Data in R - A method to analyze how transcription factors influence development** Adelman-Bender-Cole-Kuroda-Larschan Joint Lab Meeting, Harvard University, MA, USA.
March 2019	**KO or OK? A pipeline to analyze how the CLAMP transcription factors influences development** Epigenomics Club, Brown University, RI, USA.
October 2019	**Student of Vision Abie Award** Grace Hopper Celebration, FL, USA. *Moderator and panelist*.
October 2018	**Student of Vision Abie Award** Grace Hopper Celebration, TX, USA. *Moderator and panelist*.
October 2016	**Subclonal Driver Events Across 9 Cancer Types** IB^2 Student Day, Université Libre de Bruxelles, Belgium.
August 2015	**Applying for National and International Awards** DePauw University, IN, USA.
December 2014	**Determining winning SH3 coalition using Game Theory** Benelux Bioinformatics Conference, Belgium.
June 2015	**Determining the winning SH3 Coalition with Game Theory** Regional Student Group, Belgium.
December 2014	**Determining winning SH3 coalition using Game Theory** Benelux Bioinformatics Conference, Belgium.
May 2014	**Chemical Inventory Database System and School-Wide Integration** DePauw University, IN, USA. *Presentation and poster* [link].
January 2014	**Essential Residues within Fyn SH3 Protein Domain using Game Theory** Indiana Women in Computing Conference (InWIC), IN, USA. *Won 1st prize* [link].
January 2014	**No Fomo - User Experience Challenge** Microsoft International Imagine Cup, DePauw University, IN. *Honorable mention* [link].
May 2012	**Coalitional Game Theory and Feature Selection to Describe the Dependencies Between Amino Acids Within the SH3 FYN Protein Domain** Chicago Women in Computing (ChiWIC), IL, USA.
May 2012	**Synergistic & Antagonistic Dependencies Analyzed via Game Theory in FYN Protein Domain** (Presented in French and English). Thesis in French. Université Libre de Bruxelles, Belgium.
June 2011	**Censorship between China and Google** Ohio Celebration of Women in Computing (OCWiC), OH, USA.

Posters

March 2021	**XvsY: tool to identify shared and distinct genomic signatures from multiple expression and protein-DNA interaction information over time** Annual Drosophila Meeting, Virtual.
April 2020	**TIMEOR: web-based tool to uncover regulatory mechanisms from temporal & multi-omics data** The Allied Genetics Conference (TAGC), Virtual.
November 2019	**TIMEOR: method to uncover regulatory mechanisms from temporal and multi-omics data** Fulbright Association Conference, DC, USA.
May 2019	**Method characterize how transcription factors influence development with RNA & ChIP-seq** RECOMB, DC, USA.

March 2019	**Method characterize how transcription factors influence development with RNA & ChIP-seq** Annual Drosophila Meeting, TX, USA.
November 2017	**Determining the winning SH3 coalition: how cooperative game theory reveals the importance of domain residues in peptide binding** Fulbright Association Conference, DC, USA.
October 2016	**Coalitional Game Theory and Feature Selection to Describe the Dependencies Between Amino Acids Within the SH3 FYN Protein Domain** Grace Hopper Celebration, TX, USA.
July 2015	**Determining the winning SH3 Coalition with Game Theory** International Society for Molecular Biology (ISMB), Ireland. *Won RSCB PDB Prize* [link].
January 2015	**Using a Big Data Database to Identify Pathogens in Protein Data Space** New England Database Day, MA, USA.
January 2014	**Creation and Implementation of D4M Algorithm for Protein Analysis** Indiana Women in Computing Conference (InWIC), IN, USA. *Won 1st prize* [link].
October 2013	**Creation and Implementation of D4M Algorithm for Protein Analysis** OurCS Conference, Carnegie Mellon, PA, USA. *Won 1st prize* [link].
September 2011	**Male-Male Cricket Frog Aggressive Behavior** DePauw University Summer Research, Science Research Fellow, IN, USA. [link].
September 2011	**Parachuting Arboreal Frogs** DePauw University Summer Research, Science Research Fellow, IN, USA. [link].

Student Mentorship

2023	Angela Mastrianni, graduate student, ‘AI-Enhanced Sensemaking: Exploring the Design of a Generative AI-Based Assistant to Support Whole Genome Sequencing Analysis’
	Shadi Zabad, graduate student, ‘Leveraging Genome-wide Complex Trait Association Signals to Inform Variant Prioritization in Rare Disease’
2021	Helen Xi, undergraduate student, ‘Multi-omic Visualization of Interpretable Biological Neural Neworks’
	Lee Ding, undergraduate student, ‘Efficient Multi-Trait Learning with Biologically Annotated Neural Networks’
2020	Dominique Pablito, graduate student, ‘Uncovering temporal sex-specific differences across multiple species’
	Isaac Nathoo, undergraduate student, ‘Regulation of alternate sex specific splicing by DNA binding protein CLAMP during early embryonic development determines transcriptome heterogeneity between sexes’
2019	Nathaniel Goodman, undergraduate student, ‘TIMEOR: a web-based tool to uncover regulatory mechanisms from temporal and multi-omics data’

Academic Service and Memberships

Journal and conference reviewer	○ IEEE HPEC, 2023 ○ Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB), 2021 (assisted advisor) ○ AISTATS, 2020 (assisted advisor) ○ Nature Communications, 2019 (assisted advisor) ○ Genes and Development, 2019 (assisted advisor)
Conference service	○ Grace Hopper Celebration, 2015–present ○ Fulbright Conference, 2019, 2020, 2021 ○ International Society of Computational Biology (ISCB) Student Council Symposium, 2016–2018 ○ Indiana Women in Computing Conference (InWIC), 2014
Memberships	○ Institute of Electrical and Electronics Engineers (IEEE), 2020–present ○ International Society for Computational Biology (ISCB), 2015–2016, 2020–present ○ Association for Computing Machinery (ACM), 2010, 2020–present ○ American Association for the Advancement of Science (AAAS), 2017–present ○ Fulbright Association, 2016–present ○ AnitaB.org, 2012–present ○ International Society for Bayesian Analysis (ISBA), 2021–2023 ○ Institute for Mathematical and Statistical Innovation (IMSI), 2021–2023 ○ Genetics Society for America (GSA), 2019–2023 ○ Society for Industrial and Applied Mathematics (SIAM), 2020–2023 ○ American Society for Biochemistry and Molecular Biology (ASBMB), 2018–2023 ○ National Science Policy Network (NSPN), 2020–2023
Ph.D. program service	○ CCMB Presenter Series founder, CCMB, Brown University, 2019–2022 ○ Graduate student recruiting, CCMB, Brown University, 2018–2022

Teaching Experience

Spring 2021	**Applied Math 2080, Inference in Genomics and Molecular Biology:** graduate and undergraduate course **Brown University**. Assisted in course content creation for Fall 2021.
Spring 2019	**Applied Math 0650, Statistical Inference II:** undergraduate course at **Brown University**. Lecture on causation and estimation calculations.
Summer 2013, 2014	**Arduino Programming:** student workshop for **Google's Computer Science Summer Institute**. Created, recruited, implemented, and led Arduino workshop for more than 40 students at Google's Computer Science Summer Institute [link].
2012–2014	**Biology 325, Bioinformatics Teacher's Assistant:** undergraduate course at **DePauw University**. Devised laboratory sessions, homework, helped grade, and tutored students.
2011–2014	**Tutor:** Created personalized lesson plans to tutor students (10 overall) in classes in the departments of Chemistry, Computer Science, Biology, French and Spanish, at **DePauw University**.

Software

Fall 2023 **Multioviz** [link]
Multioviz is a platform for the interactive assessment of gene regulatory networks.
Implementation details: Bash, R, R Shiny

Spring 2021 **time2splice** [link]
time2splice is a method to find temporal and sex-specific alternative splicing from multi-omics data.
Implementation details: Bash, Python, R

Fall 2020 **TIMEOR (Trajectory Inference and Mechanism Exploration using Omics data in R)** [link]
TIMEOR is a web server and Dockerized command line tool to identify gene regulatory networks and assign mechanism from temporal and multi-omics data.
Implementation details: Bash, Python, R, R Shiny

Summer 2014 **PRIPS (Pathogen Rapid ID from Protein Sequences)** (property of MIT Lincoln Laboratory)
A fast protein analysis algorithm, using Dynamic Distributed Dimensional Data Model (D4M-by Dr. Jeremy Kepner), merging triplestore/NoSQL databases (Accumulo) with associative and distributed array representations of proteomic sequences for fast genomic big data analysis using sparse linear algebra. Our approach efficiently extracts statistical patterns to relate protein sequences, with the end goal of rapidly identifing novel pathogens.
Implementation details: Matlab

Spring 2014 **Chemical Inventory Database** [description link], (property of DePauw [login link])
Web-based inventory management system used in many academic departments, mainly chemistry. Users log in and use a phone to scan barcodes for automatic item entry. The application uses the Parse Platform as a relational database to house inventory for DePauw University. This system has been updated by the maintainer Dr. Dave Roberts.
Implementation details: HTML, CSS, Parse Platform

2013, 2014 **Arduino-CSSI** (Computer Science Summer Institute at Google) [link]
Set of Arduino workshop modules and Fritzing diagrams to teach students how to program as part of the Google Computer Science Summer Institute (CSSI).
Implementation details: C

Summer 2012 **Instrument Control** (property of Eli Lilly and Elanco)
Online internal system to monitor product batch data. Batch data is extracted from Eli Lilly's Data Mart and Data Warehouse databases and then visualized for the researcher (such as potency, and solubility fluctuations). This system **continues to be run automatically daily**, enabling employees to easily inspect and verify internal processes, saving significant money and time.
Implementation details: SQL, Discoverant, and Business objects

Summer 2012 **Deviation Identification and Reporting** (property of Eli Lilly and Elanco)
Online internal system for deviation reporting with automatic alerts, excel exports, and editing options to identify malfunctioning manufacturing products and machines across the plant. These reports were previously on paper. This system was adopted **globally for all Elanco plants** in November, 2012.
Implementation details: SharePoint, Discoverant, and Business objects

January 2011 **INcitizenconnect** [link]
Website to keep updated with local legislation in the 2011 Indiana General Assembly.
Implementation details: Wordpress

Leadership and Activities

Professional Organizations and Positions

2022–present	**Models, Inference, and Algorithms (MIA) Steering Committee**. Broad Institute of MIT and Harvard's MIA is a prestigious talk and workshop series that supports learning and collaboration across the interface of biology and medicine with mathematics, statistics, machine learning, and computer science [link].
2015–present	**Student of Vision Abie Award Judge and Co-creator**. International award honors students committed to creating a future where the people who envision and build technology mirror the people and societies for which they build. Winners receive a $7000 prize and the chance to go to Grace Hopper [link].
2004–present	**D-Day Ambassador to France**. Selected to represent U.S. for D-Day Commemoration, and to return every 4 years until the 100th anniversary of World War II. *International School of Indiana*.
2018–2020	**Fulbright Board of Directors**. Young professional board member [link], [profile]. *Fulbright Assoc.*
2018	**Science Writer**. Wrote two articles on scientific advances targeted at advanced high school students. *Infobase Learning, Science News Today*.
2017–2018	**Princeton Citizen Scientists member**. Helped grow a group of scientists interested in policy, mobilizing at Princeton and beyond to advocate for science. *Princeton University*.
2016–2018	**International Society of Computational Biology (ISCB) Student Symposium Finance Chair**. Led a team to build new strategies bringing four new and important sponsors. We gave >20 scholarships to support international and domestic travel to the conference. *ISCB*
2015–2017	**AnitaB.org Board of Trustees**. Student board member in program and strategies committees. Focused efforts to build the Student of Vision Awards (an Abie Award), BRAID, Top Companies, and ABI.local. *AnitaB.org* [link, see Board Emeritus]
February 2015	**US-EU-NATO Affairs Delegate**. Fulbright grantee to engage in EU Seminar in international diplomacy. *Fulbright and EU Commission*.
2008–2011	**Venture Crew President (2010)**. Vice President in 2009. Venture Crew 1121. *Boy Scouts of America*.

DePauw University Organizations and Positions

2014	**Mortar Board Vice President**. Helped establish structure for new society focused on achievement in scholarship, leadership, and service. *DePauw University*.
2011–2014	**DePauw Organic Farm Co-founder**. Founded and built business plan for $\sim$2-acre farm, where 25% of produce is given to local Greencastle Indiana food pantries. *DePauw University* [link].
2011–2013	**Robotics Club Co-founder & Vice President**. Students are provided with free tools to make whatever they wish. We visit local schools for outreach days. *DePauw University*.
January 2011	**DePauw Environmental Policy Program**. Testified scientific bills, Indiana Statehouse, created website [link]. *DePauw University*.
2010–2014	**University Athletics**. Soccer (2010-2012) and Track (2013-2014). *DePauw University*.

Service and Outreach

November 2019	**Lifetime Achievement Award to President of Croatia Kolinda Grabar-Kitarović, NPR's Melissa Block, and Architect James S. Polshek**. Presented award with Fulbright Board of Directors. *Fulbright Association* [link].

November 2019	**Fulbright Talks host (similar to TEDx)**. *Fulbright Association* [link].
January 2019	**Fulbright Prize to German Chancellor Angela Merkel**. Presented award with Fulbright Board of Directors. *Fulbright Association* [link] [photo].
October 2019	**Advocating the "Value and Impact of the Fulbright Program" with U.S. Senator Chris Van Hollen (D-MD)**. *Fulbright Association* [link].
June 2018	**Raspberry Pi robotics outreach**. Taught ∼20 students in Roanoke VA. They got to keep their Raspberry Pi. *Virginia Tech Philosophy and Physical Computing Workshop* [link].
October 2016	**Presented Top Companies award (audience of ∼15,000)**. *AnitaB.org* [link].
October 2013	**IEEE High Performance Computing Conference (HPEC)**. Served as usher and attended. *IEEE*.
2012–2014	**STARS Computing Corps**. Student-led regional outreach group to broaden participation in computing. *DePauw University*.
November 2012	**National Chemistry Week High School Competition**. Organized, and executed a video and essay competition for high school students to come to the Children's Museum of Indianapolis for a day of chemistry, fun and to view undergraduate institutions. *American Chemical Society*.
Summer 2010	**Service Trip to Costa Rica**. Created a septic tank for 'Estación de las tortugas', worked on pineapple plantation, and helped record nesting behavior of Leather Back and Green Sea Turtles hatchlings. *Servicio en Las Américas Program, DePauw University*.

Media

November 2021	**Women and People of Color Still Experience Difficulty Advancing in Technology** - *I assisted Grace Hopper Celebration co-Founder and former CEO of AnitaB.org, Telle Whitney in report* [link].
July 2019	**Center for Computational and Molecular Biology Ph.D. Program** - *Brown University* [link].
July 2019	**Remembering D-Day** - *Fulbright Association* [link].
January 2019	**Alumni Profile: Ashley Mae Conard** - *Fulbright Association* [link].
May 2017	**An Insider's Look at Student Board Membership** - *AnitaB.org* [link].
October 2016	**Grace Hopper Interview as AnitaB.org Board Member** - *The Cube* [link].
October 2016	**Women Who Reign: Ashley Conard** - *ReigningIt* [link].
November 2015	**Meet Ashley Conard, AnitaB.org's New Student Board Member** - *AnitaB.org* [link].
October 2015	**Putting women and computer science in every field** - *SiliconANGLE* [link].
October 2015	**Grace Hopper Interview as AnitaB.org Board Member** - *The Cube* [link].
October 2015	**Ashley Conard '14 Will Conduct Computational Biology Research in Belgium with Fulbright Award** - *DePauw University* [link].
October 2015	**All of the Above** - *DePauw University* [link].

References

Academic

Professor Lorin Crawford (Ph.D. advisor)
Senior Researcher Microsoft Research
RGSS Assistant Professor of Biostatistics
Center for Computational Molecular Biology (CCMB)
Brown University School of Public Health
121 S Main St, Box G-S121-7
Providence, RI 02912
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Professor Erica Larschan (Ph.D. advisor)
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Department of Molecular Biology, Cellular Biology and Biochemistry
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External

Dr. Telle Whitney
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tel: 408-505-1083
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Biomedical Computing Senior Researcher, Microsoft Research
Health Futures
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DeDe Long
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