

# Brittany A. Baur, Ph.D. | Curriculum Vitae

330 N. Orchard St., Madison WI 53715, Room 3241D · 516-728-1226 · babaur@wisc.edu

## Education

---

**Ph.D., Computational Sciences** — Marquette University, Milwaukee, WI August 2013 — May 2017  
**Dissertation:** Identifying regulators from multiple types of biological data in cancer  
**Advisor:** Serdar Bozdog

**M.S., Bioinformatics** — Marquette University/Medical College of Wisconsin, Milwaukee, WI/Wauwatosa, WI August 2011 — May 2013  
**Thesis:** Genome-wide fine-mapping of diabetic traits  
**Advisor:** Leah Solberg-Woods (MCW)

**B.A., Mathematics and Biology** — Manhattanville College, Purchase, NY August 2007 — May 2011

## Work Experience

---

**Postdoctoral Research Associate** - University of Wisconsin-Madison June 2017-Present  
I work on methods to predict long-range regulatory interactions and interpret non-coding regulatory variation in the context of the 3D genome.

**Richard W. Jobling Research Assistant** — Marquette University August 2016 - May 2017  
I worked on methods to predict causal miRNA and copy number drivers for several types of cancer.

**Teaching Assistant** — Marquette University August 2011 - May 2013  
Calculus I (Fa 2011, Fa 2012, Fa 2015) August 2015 - May 2016  
Calculus II/III for Biomed and Civil Engineers (Sp 2012, Sp 2013)  
Modern Elementary Statistics (Sp 2016)  
Data Mining (Sp 2016)

**Research Assistant** — Marquette University August 2013 - May 2015  
I worked on Bayesian gene-regulatory network inference methods that incorporate copy number and DNA methylation data. I also worked on computing gene-centric methylation levels from 450K DNA methylation arrays.

**Summer Research Fellow** — Marquette University Summers 2014, 2015, 2016  
I was awarded a summer research fellowship to perform additional work on various research projects throughout graduate school.

**Software Development Intern** — Mackevision Corporation May 2012 - August 2012  
I developed software for production pipeline enhancements.

**Bio-Grid REU Fellow** — University of Connecticut, Storrs Campus Summer 2010  
Researched and benchmarked tools for identifying network motifs

**Tutor and Supplemental Instructor** — Academic Resource Center, Manhattanville College  
I tutored college students in Calculus I, II, biology and chemistry

January 2009 - May 2011

## Science Policy Publications

---

- Davis J, **Baur B**, Alexander S, Bachmann B. Policy options to mitigate the impacts of green gentrification when constructing new bike paths in the Madison area, *Journal of Science Policy and Governance*. September 2021
- McKetney J, Trujillo E, Tabbutt M, **Baur B**. Improving Bus Route Design using Stop Balancing and Community-level Data, *Journal of Science Policy and Governance*. March 2021

## Scientific Publications

---

- Baur B**, Lee D-I, Haag J, Chasman D, Gould M, Roy S. Deciphering the role of 3D genome organization in breast cancer susceptibility, *Frontiers in Genetics*. January 2022
- Baur B**, Shin J, Schreiber S, Zhang S, Zhang Y, Manjunath M, Song J, Noble WS, Roy S. Leveraging epigenomes and three-dimensional genome organization for interpreting regulatory variation, *BioRxiv*. August 2021
- Baur B**, Shin J, Zhang S, Roy S. Data integration for inferring context-specific gene regulatory networks, *Current Opinion in Systems Biology*. September 2020
- Zhang Y, Manjunath M, Yan J, **Baur B**, Zhang S, Roy S, Song J. The cancer-associated genetic variant rs3903072 modulates immune cells in the tumor microenvironment, *Frontiers in Genetics*. August 2019
- Keele GR, Prokop JW, He H, Holl K, Littrell J, Deal A, Francic S, Cui S, Gatti DM, Broman KW, Tschannen M, Tsaih S, Zagloul M, Kim Y, **Baur B**, Fox J, Robinson M, Levy S, Flister MJ, Mott R, Valdar W, Solberg Woods LC. Genetic Fine-Mapping and Identification of Candidate Genes and Variants for Adiposity Traits in Outbred Rats, *Obesity*. January 2018
- Baur B** and Bozdag S. ProcessDriver: A computational pipeline to identify copy number drivers and associated disrupted biological processes in cancer, *Genomics*. July 2017
- Baur B** and Bozdag S. A feature selection algorithm to compute gene centric methylation from probe level methylation data, *PLoS ONE*. February 2016
- Baur B** and Bozdag S. A canonical correlation analysis based dynamic Bayesian prior to infer gene regulatory networks from multiple types of biological data, *Journal of Computational Biology*. May 2015
- Wong E, **Baur B**, Quader S and Huang C. Biological Network Motif Detection: Principles and Practice, *Briefings in Bioinformatics*. 2011

## Oral Presentations

---

<b>Baur B</b> , Lee D, Haag J, Gould M, Roy S. Deciphering the role of 3D genome organization in breast cancer susceptibility. ISMB, Montreal, Canada (Virtual)	July 2020
<b>Baur B</b> , Schreiber J, Zhang S, Zhang Y, Manjunath M, Song J, Noble WS, Roy S. Leveraging public epigenomic datasets to examine the role of regulatory variation in the three-dimensional organization of the genome. Biology of Genomes, Cold Spring Harbor, NY (Virtual)	May 2020
<b>Baur B</b> , Schreiber J, Zhang S, Zhang Y, Manjunath M, Song J, Noble WS, Roy S. Leveraging public epigenomic datasets to examine the role of regulatory variation in the three-dimensional organization of the genome. Recomb RSG, New York, NY	November 2019
<b>Baur B</b> , Schreiber J, Zhang S, Zhang Y, Manjunath M, Song J, Noble WS, Roy S. Leveraging public epigenomic datasets to examine the role of regulatory variation in the three-dimensional organization of the genome. GLBIO, Madison, WI	May 2019
<b>Baur B</b> , Schreiber J, Zhang S, Zhang Y, Manjunath M, Song J, Noble WS, Roy S. Leveraging public epigenomic datasets to examine the role of regulatory variation in the three-dimensional organization of the genome. NHGRI Research Training and Career Development Annual Meeting, St. Louis, MO	April 2019
<b>Baur B</b> , Zhang S, Chasman D and Roy S. In silico prediction of high-resolution chromosomal contact counts in multiple cell lines. ISMB, Chicago, IL	July 2018
<b>Baur B</b> , Zhang S, Chasman D and Roy S. Computational analysis of long-range regulatory interaction dynamics across different cell types and species. CPCP Annual Retreat, Madison, WI	June 2018
<b>Baur B</b> and Bozdag S. A computational approach to identify copy number drivers and associated disrupted biological processes. Marquette University MSCS Colloquium Series. Milwaukee, WI	October 2016
<b>Baur B</b> and Bozdag S. A canonical correlation analysis based dynamic Bayesian prior to infer gene regulatory networks from multiple types of biological data, RECOMB RSG, San Diego, CA	November 2014
<b>Baur B</b> and Bozdag S. Computing gene centric DNA methylation from probe-level methylation arrays. Great Lakes Bioinformatics, Cincinnati, OH	May 2014

## Poster Presentations

---

<b>Baur B</b> , Taylor T, Lee D-I, Singh G, Wang L, Rathnakumar K, Wilson M, Mitchell J, Roy S. Assessing the predictive power of Hi-C interactions across species, ISMB/ECCB.	2021
<b>Baur B</b> , Schreiber J, Zhang S, Zhang Y, Manjunath M, Song J, Noble WS, Roy S. Leveraging public epigenomic datasets to examine the role of regulatory variation in the three-dimensional organization of the genome. Biology of Genomes, Cold Spring Harbor, NY	2019

## Brittany A. Baur

<b>Baur B</b> , Zhang S, Chasman D and Roy S. Leveraging public epigenomic datasets to examine the role of regulatory variation in the three-dimensional organization of the genome. UW Epigenetics Symposium, Madison, WI	2018
<b>Baur B</b> , Zhang S, Chasman D and Roy S. In silico prediction of high-resolution chromosomal contact counts in multiple cell lines. WID symposium, Madison, WI	2018
<b>Baur B</b> and Bozdag S. CARMMA: A computational pipeline to detect cancer-related miRNA-mRNA modules and associated disrupted biological processes. Great Lakes Bioinformatics, Chicago, IL.	2017
<b>Baur B</b> and Bozdag S. Reverse engineering gene regulatory networks from structural and epigenetic data. Great Lakes Bioinformatics, Toronto, ON, Canada	2016
<b>Baur B</b> and Bozdag S. Reverse engineering gene regulatory networks from structural and epigenetic data. RECOMB RSG, Philadelphia, PA	2015
<b>Baur B</b> and Bozdag S. A dynamic Bayesian approach for inferring gene regulatory networks from multiple types of biological data. ISMB, Boston, MA	2014
<b>Baur B</b> and Bozdag S. Computing gene centric DNA methylation from probe-level methylation arrays. Great Lakes Bioinformatics, Cincinnati, OH	2014
<b>Baur B</b> , Holl K, Valdar W and Solberg Woods LC. Genome wide fine-mapping of post-prandial glucose in heterogeneous stock rats. Complex Trait Community, Madison, WI	2013
Bettica A, <b>Baur B</b> and Tiruneh M. The antioxidant and neuroprotective efficacies of several common bioavailable polyphenolic flavonoids and terpenoids from <i>Ginkgo biloba</i> leaf extract against neurotoxin-induced Parkinson's disease. Neuroscience, San Diego, CA	2010

## Activities

<b>Communications Chair, Catalysts for Science Policy</b> , University of Wisconsin- Madison As Communications Chair of Catalysts for Science Policy, I manage the organization's social media accounts, website, and blog. I also serve as an editor for the newsletter and blog. I also organize monthly journal clubs where we discuss current science policy issues.	June 2021 - Current
<b>Editor-in-Chief, <i>Genomics: Insights</i></b> <i>Genomics: Insights</i> is an online publication on <a href="http://unlockinglifescode.org">unlockinglifescode.org</a> , a collaboration between the Smithsonian and the NHGRI that serves as a venue for undergrads, post-bacs, grad students and post-docs to communicate recent genomics research to a general audience. As Editor-in-Chief, I coordinate reviewer selection, organize Q&A sessions and workshops, correspond with authors, and coordinate new improvements to the review process and journal.	2018-Current
<b>Member, Catalysts for Science Policy</b> , University of Wisconsin-Madison	2020-Current

As a member of Catalysts for Science Policy, I worked on a project leveraging census data to identify communities that may be underserved by Madison Metro Transit. I also take part in other activities such as writing memos for WI state legislators and leading journal club discussions.

**Duchesne Scholar**, Duchesne Center, Manhattanville College

August 2007 - May 2011

I took part in various mentoring/tutoring initiatives in NYC to help children with Math and Science.

**Member**, Tri-Beta Biological Honor Society, Manhattanville College

April 2009 - May 2011

I helped organize events such as the Manhattanville Annual Science Competition.

## Workshop Presentations

---

Parker N, <b>Baur B</b> , Miller T, Hebner, Y. Writing Effective Science Policy Memos, National Science Policy Symposium, Virtual.	2021
<b>Baur B</b> , Gunter C. How to Write About Genomics So That People Will Want to Read It. NHGRI Virtual Event.	2020
Lee D, <b>Baur B</b> , Liu X, Ward H. Higher Understanding with Lower Dimensions. GLBIO, Madison, WI.	2019

## Awards

---

Genomic Sciences Training Program Postdoctoral Traineeship, UW-Madison	June 2018
Richard W. Jobling Distinguished Research Fellowship, Marquette University	August 2016
Computational Sciences Summer Research Fellow, Marquette University	Summers 2014, 2015, 2016
FASEB MARC Travel Award (RECOMB RSG), San Diego, CA	2014
FASEB MARC Travel Award (GLBio), Cincinnati, OH	2014
Biology Honors, Manhattanville College	2011
Ruth Alscher Memorial Award for Biology, Manhattanville College	2011
Duchesne Scholar, Manhattanville College	2007-2011
Board of Trustees Scholar, Manhattanville College	2007-2011
POLYED Undergraduate Award for Achievement in Organic Chemistry, Manhattanville College	2009

## Mentoring

---

Zhiwei Wang, Undergraduate at UW-Madison	Fall 2021-Current
Priya Brahmabhatt, Undergraduate at George Washington University	Summer 2018
Yuanhang Wang, Undergraduate at UW-Madison	Spring 2019-Spring 2020

## Service

---

Reviewer ISMB/ECCB	2021
Reviewer, PSB	2020
PC member, ACM-BCB (HPC-BOD)	2020
Reviewer, ISMB	2020
Reviewer, Recomb RSG	2019
Reviewer, ACM-BCB	2019
Reviewer, ISMB	2018
Reviewer, ACM-BCB	2015
Reviewer, ACM-BCB	2014

## Skills

---

**Programming languages:** Java, Python, Perl, Matlab, R, C++, SQL

**Other:** Proficient knowledge in parallel computing and databases