

Alex H. Wagner, PhD

Contact Information

480-ALEX-PHD
awagner24@wustl.edu

Research Interests

Bioinformatics, Cancer Genomics, Machine Learning

Research Experience

Postdoctoral Research Scholar January 2015 to Present

McDonnell Genome Institute,
Washington University School of Medicine
Saint Louis, MO

Advisors:

[Obi L. Griffith, PhD](#)

[Ramaswamy Govindan, MD](#)

Graduate Research Assistant August 2010 to December 2014

Coordinated Laboratory for Computational Genomics,
University of Iowa College of Engineering
Iowa City, IA

Advisors:

[Terry A. Braun, PhD](#)

[Edwin M. Stone, MD, PhD](#)

Clinical Laboratory Technologist July 2008 to July 2010

Department of Laboratory Medicine and Pathology,
Mayo Clinic, Rochester, MN

Supervisors:

[Dianna Bowden](#)

[Thomas P. Moyer, PhD](#)

Biological Laboratory Aide Jan 2007 to Sep 2007

USDA Agricultural Research Service,
Iowa State University, Ames, IA
Supervisor: [David Grant, PhD](#)

Education

University of Iowa, Iowa City, IA

PhD, [Computational Genetics](#), December 2014

- Thesis Topic: *Computational Methods for Identification of Disease-Associated Variations in Exome Sequencing*
- Advisors: [Terry A. Braun, PhD](#) and [Edwin M. Stone, MD, PhD](#)
- **GPA: 3.90**

Graduate Certificate, [Bioinformatics](#), May 2013

- Advisor: [Terry A. Braun, PhD](#)
- **GPA: 3.96**

Iowa State University, Ames, IA

BS, **Biology**, May 2008

- Minor in **Mathematics**
- *Cum Laude*
- GPA: 3.51

Extracurricular Education

High Performance Computing, Gregory Howes, Iowa, Summer 2012

Machine Learning, Andrew Ng, Stanford (Online), Fall 2011

Intro to Databases, Jennifer Widom, Stanford (Online), Fall 2011

Bibliography

1. **AH Wagner**[†], S Devarakonda[†], ZL Skidmore, K Krysiak, A Ramu, L Trani, J Kunisaki, ..., M Griffith, OL Griffith, R Govindan (In Revision) "Recurrent WNT Pathway Alterations are Frequent in Relapsed Small Cell Lung Cancer". *Nature Communications*.
2. **AH Wagner**, K Krysiak, KM Campbell, EK Barnell (Submitted Chapter) "Cancer Genomics Primer: Tumor Heterogeneity". *Springer Publishing Group*.
3. BJ Ainscough[†], EK Barnell[†], KM Campbell, **AH Wagner**, TE Rohan, R Govindan, M Griffith, ER Mardis, SJ Swamidass, OL Griffith (Under Review) "Deep Learning to Refine Somatic Variants in Cancer". *Nature Genetics*.
4. EK Barnell, P Ronning, KM Campbell, K Krysiak, BJ Ainscough, C Ramirez, N Spies, J Kunisaki, ZL Skidmore, F Gomez, L Trani, M Matlock, **AH Wagner**, SJ Swamidass, M Griffith, OL Griffith (2017) "Standard operating procedure for somatic variant refinement of tumor sequencing data". *bioRxiv*. doi: 10.1101/266262
5. K Cotto[†], **AH Wagner**[†], YY Feng, S Kiwala, AC Coffman, G Spies, A Wollam, NC Spies, OL Griffith, M Griffith (2017) "DGIdb 3.0: a redesign and expansion of the drug-gene interaction database". *Nucleic Acids Research*. doi: 10.1093/nar/gkx1143.
6. M Griffith, NC Spies, K Krysiak, JF McMichael, AC Coffman, AM Danos, BJ Ainscough, CA Ramirez, DT Rieke, L Kujan, EK Barnell, **AH Wagner**, ..., OL Griffith (2017) "CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer". *Nature Genetics*. doi: 10.1038/ng.3774.
7. BJ Ainscough, M Griffith, AC Coffman, **AH Wagner**, J Kunisaki, MNK Choudhary, JF McMichael, RS Fulton, RK Wilson, OL Griffith, ER Mardis (2016) "DoCM: a database of curated mutations in cancer". *Nature methods*. doi: 10.1038/nmeth.4000.
8. M Griffith, OL Griffith, K Krysiak, ZL Skidmore, MJ Christopher, JM Klco, A Ramu, TL Lamprecht, **AH Wagner**, ..., TJ Ley (2016) "Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia". *Experimental hematology*. doi: 10.1016/j.exphem.2016.04.011.

9. ZL Skidmore, **AH Wagner**, R Lesurf, KM Campbell, J Kunisaki, OL Griffith, M Griffith (2016) “GenVisR: Genomic Visualizations in R”. *Bioinformatics*. doi: 10.1093/bioinformatics/btw325.
10. **AH Wagner**, AC Coffman, BJ Ainscough, NC Spies, ZL Skidmore, KM Campbell, K Krysiak, D Pan, JF McMichael, JM Eldred, JR Walker, RK Wilson, ER Mardis, M Griffith*, OL Griffith* (2016) “DGldb 2.0: mining clinically relevant drug?gene interactions”. *Nucleic Acids Research*. doi: 10.1093/nar/gkv1165.
11. SS Whitmore, **AH Wagner**, AP DeLuca, AV Drack, EM Stone, BA Tucker, S Zeng, TA Braun, RF Mullins, TE Scheetz (2014) “Transcriptomic analysis across nasal, temporal, and macular regions of human neural retina and RPE/choroid by RNA-Seq”. *Experimental Eye Research*. doi:10.1016/j.exer.2014.11.001
12. TP Sharma, CM McDowell, Y Liu, **AH Wagner**, D Thole, BP Faga, RJ Workinger, TA Braun, AF Clark (2014) “Optic nerve crush induces spatial and temporal gene expression patterns in retina and optic nerve of BALB/cJ mice”. *Molecular Neurodegeneration*. doi: 10.1186/1750-1326-9-14
13. TA Braun, RF Mullins, **AH Wagner**, J Andorf, R Johnston, B Bakall, AP DeLuca, G Fisherman, R Weleber, A Cideciyan, S Jacobson, V Sheffield, B Tucker, EM Stone (2013) “Non-exonic and synonymous variants in ABCA4 are an important cause of Stargardt disease”. *Human Molecular Genetics*. doi: 10.1093/hmg/ddt367
14. **AH Wagner**, KR Taylor, AP DeLuca, TL Casavant, RF Mullins, EM Stone, TE Scheetz, TA Braun (2013), “Prioritization of Retinal Disease Genes: An Integrative Approach.” *Human Mutation*. doi: 10.1002/humu.22317
15. **AH Wagner**, VN Anand, W Wang, JE Chatterton, D Sun, AR Shepard, N Jacobson, L Pang, AP DeLuca, TL Casavant, TE Scheetz, RF Mullins, TA Braun, AF Clark (2013) “Exon-level expression profiling of ocular tissues”. *Experimental Eye Research*. doi: 10.1016/j.exer.2013.03.004
16. AP DeLuca, **AH Wagner**, KR Taylor, B Faga, D Thole, VC Sheffield, EM Stone, TL Casavant, TE Scheetz, TA Braun (December 2011) “Sequencing and disease variation detection tools and techniques”. *9th IEEE/ACS International Conference on Computer Systems and Applications (AICCSA)*. doi: 10.1109/AICCSA.2011.6126607

†Denotes Co-First Authorship

Funding

Training Awards

- *NHGRI K99 Pathway to Independence (A1 in prep)* *Submit July 2018
- *NCI F32 Postdoctoral Fellowship* 2017–present
- *NCI T32 Postdoctoral Training in Cancer Biology* 2016–2017
- *NIGMS T32 Predoctoral Training Grant in Genetics* 2013–2014

- *NIGMS T32 Predoctoral Training Grant in Bioinformatics* 2011–2013
 - Consecutive annual awards granted for 2011-2012 and 2012-2013.

Travel Awards

- *1st Place Student/Trainee Travel Award, CGC* August 2018
- *AACR-Bristol Myers Squibb Scholar-in-Training Award, AACR* April 2018
- *NSF Travel Grant, ISMB* July 2013
- *Graduate Student Senate Travel Grant, ARVO* May 2013

Merit

Research Awards

- *ICTS Precision Medicine Abstract Award* January 16, 2018
 - Precision Medicine Symposium
Institute of Clinical and Translational Science
Washington University in Saint Louis
 - The most outstanding research was selected from more than 75 applicants to present to Eric Green, the director of the National Human Genome Research Institute (NHGRI).
- *D.C. Priestestersbach Dissertation Prize* 2015
 - Genetics Program Nomination
 - This biennial award recognizes excellence in doctoral research. Each of the twenty biological/life sciences programs at the University of Iowa nominates one dissertation submitted between July 1, 2013 and June 30, 2015 to compete for the award.
- *Outstanding Student Research Award* 2012–2013
 - This annual award recognizes a single student in the College of Engineering for exemplary research in the fields of bioinformatics and computational biology.

Oral Presentation Awards

- *Annual Bioinformatics Retreat, University of Iowa* August 16, 2013
 - *Best Student Talk*
- *Midwest Eye Research Symposium* July 6, 2012
 - *Outstanding Oral Presentation, 2nd Place*

Poster Presentation Awards

- *Interdisciplinary Health Research Poster Session* April 23, 2013
 - *Best Poster Award, Center on Aging*

Presentations

*Upcoming event; †Invited Talk

External Presentations

- Cancer Genomics Consortium, Nashville, TN *August 2018
 - †*Coordinating variant interpretation knowledgebases improves clinical interpretation of genomic variants in cancers*
- American Association for Cancer Research, Chicago, IL *April 2018
 - Standardization and coordination of variant interpretation knowledgebases improves clinical genome actionability*
- Curating the Clinical Genome, Hinxton, UK June 2016
 - The Drug Gene Interaction Database*

- AGBT Annual Conference, Orlando, FL February 2016
The Drug Gene Interaction Database
- ISMB Annual Conference, Berlin, Germany July 2013
Positive and Unlabeled Learning for Prioritization (PULP)
- ARVO Annual Conference, Seattle, WA May 2013
Positive and Unlabeled Learning for Prioritizing Candidate Variants in Retinal Degenerative Diseases
- BICB Industry Symposium, Minneapolis, MN May 2013
Positive and Unlabeled Learning for Prioritizing Candidate Variants in Retinal Degenerative Diseases
- ARVO Annual Conference, Ft. Lauderdale, FL May 2012
RNA Sequencing for Identification of Genetic Factors in Retinal Disease
- Joint Bioinformatics Retreat, Ames, IA Aug 2011
Using RNA Sequencing To Identify And Isolate Causative Genetic Factors In Retinal Disease

Washington University in Saint Louis

- ICTS Precision Medicine Symposium January 2018
Coordinating variant interpretation knowledgebases improves clinical interpretation of genomic variants in cancers
- Postdoctoral Research Symposium March 2017
The Drug Gene Interaction Database

University of Iowa

- Genetics Retreat 2014 October 2014
† *Active Phenotype Acquisition for the Genetic Characterization of Heritable Retinal Diseases*
- Engineering Research Open House 2014 April 2014
Positive and Unlabeled Learning for Prioritization (PULP)
- Genetics Retreat 2013 October 2013
Prioritizing Disease Genes in Exome Studies
- Joint Bioinformatics Retreat August 2013
† *Positive and Unlabeled Learning for Prioritization*
- Interdisciplinary Health Research Poster Session April 2013
Positive and Unlabeled Learning for Prioritizing Candidate Variants in Retinal Degenerative Diseases
- Genetics Retreat 2012 November 2012
Machine Learning Based Prioritization of Retinal Disease Genes
- Joint Bioinformatics Retreat October 2012
† *Prioritization of Retinal Disease Genes: An Integrative Approach*
- Midwest Eye Research Symposium July 2012
† *Machine Learning Based Prioritization of Eye Disease Genes*
- Genetics Retreat 2011 February 2012
Exon-level Expression Profiling of Ocular Tissues

Teaching
Experience

*Upcoming event

Workshop Instructor

Introduction to bioinformatics learning resources

*August 2018

Cancer Genomics Consortium Annual Conference
Nashville, TN

Instructor	Fall 2017-Current
Escape from Perlgatory: Developing in Python and Ruby McDonnell Genome Institute Saint Louis, MO	
Teaching Assistant / Lecturer	Nov 2017
Advanced Sequencing Technologies and Applications Cold Spring Harbor Laboratories Cold Spring Harbor, NY	
Workshop Instructor	Nov 2016
CIViC Hackathon Netherlands Cancer Institute (NKI) Amsterdam, NL	
Teaching Assistant / Lecturer	Nov 2016
Advanced Sequencing Technologies and Applications Cold Spring Harbor Laboratories Cold Spring Harbor, NY	
Teaching Assistant	Fall 2014
051:123 - Bioinformatics Techniques Instructor: Thomas L. Casavant Department of Biomedical Engineering University of Iowa	
Guest Lecturer	Spring 2014
051:080 - Bioimaging and Bioinformatics Instructor: Todd E. Scheetz Department of Biomedical Engineering University of Iowa	
Teaching Assistant	Spring 2014
051:122 - Computational Genomics Instructor: Thomas L. Casavant Department of Biomedical Engineering University of Iowa	
Teaching Assistant	Fall 2013
051:123 - Bioinformatics Techniques Instructor: Terry A. Braun Department of Biomedical Engineering University of Iowa	

	Instructor	Fall 2013
	Introduction to Bioinformatics Computing with Python Supplement to 051:123 - Bioinformatics Techniques Department of Biomedical Engineering University of Iowa	
	Teaching Assistant	Fall 2006
	BIOL 313 - Principles of Genetics Instructor: Jack Girton Department of Biology Iowa State University	
Service	Peer Review	
	• Genome Medicine	April 2017
	• Nature Communications	August 2016
	• Science Translational Medicine	August 2016
	Editor , CIViC Knowledgebase	2015-Present
	• Moderated curation of clinical interpretations of genomic variants from biomedical literature	
	• Proliferative editor, with over 450 moderations (#6 all-time leader in moderations)	
	Executive Committee , Bioinformatics Training Grant Renewal	S13-F14
	• Assisted in curriculum development for proposed Bioinformatics PhD program	
	• Researched student career development resources to be utilized by the program	
	• Collaborated with co-PIs and others in writing the grant proposal to fund the program	
	Planning Committee Chair , Ann. UI Bioinformatics Retreat	S13-F14
	• Planned logistics of the 2013 and 2014 annual bioinformatics retreats	
	• Invited selected extramural faculty to participate in the retreats	
Software Familiarity	Programming languages and environments:	
	• C, C++, Java, LSF, Matlab, SQL, Perl, Python (PyCharm / Jupyter Notebooks), R (RStudio), Ruby on Rails (RubyMine), SGE, UNIX	
	Common software (bioinformatics):	
	• Bedtools, Ballgown, Bowtie, BWA, Cufflinks, GATK, GenVisR, GMS, Kallisto, IGV, Picard, Pizzly, RNA-SeQC, Samtools, Stringtie, Tophat, UCSC Genome Browser, VCFTools	
	Common software (other):	
	• Git, GitHub, JIRA, L ^A T _E X	