

## Alex H. Wagner, PhD

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### Contact Information

480-ALEX-PHD  
awagner24@wustl.edu

### Research Interests

Bioinformatics, Cancer Genomics, Precision Medicine

### 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

Published Works

1. **AH Wagner**<sup>†</sup>, S Devarakonda<sup>†</sup>, ZL Skidmore, K Krysiak, A Ramu, L Trani, J Kunisaki, ..., M Griffith, OL Griffith, R Govindan (2018) "Recurrent WNT Pathway Alterations are Frequent in Relapsed Small Cell Lung Cancer". *Nature Communications*. doi: 10.1038/s41467-018-06162-9
2. BJ Ainscough<sup>†</sup>, EK Barnell<sup>†</sup>, KM Campbell, **AH Wagner**, TE Rohan, R Govindan, M Griffith, ER Mardis, SJ Swamidass, OL Griffith (2018) "A deep learning approach to automate refinement of somatic variant calling from cancer sequencing data". *Nature Genetics*. doi: 10.1038/s41588-018-0257-y
3. 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 (2018) "Standard operating procedure for somatic variant refinement of tumor sequencing data". *Genetics in Medicine*. doi: 10.1038/s41436-018-0278-z.
4. AM Danos<sup>†</sup>, DI Ritter<sup>†</sup>, **AH Wagner**, K Krysiak, ..., S Kulkarni, M Griffith, S Madhavan, OL Griffith (2018) "Adapting crowdsourced clinical cancer curation in CIViC to the ClinGen minimum variant level data community-driven standards". *Human Mutation*. doi: 10.1002/humu.23651.
5. K Cotto<sup>†</sup>, **AH Wagner**<sup>†</sup>, YY Feng, S Kiwala, AC Coffman, G Spies, A Wollam, NC Spies, OL Griffith, M Griffith (2017) "DGldb 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) "DGIdb 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, ..., TA Braun. (2011). "Sequencing and disease variation detection tools and techniques". *IEEE/ACS International Conference on Computer Systems and Applications (AICCSA)*. doi: 10.1109/AICCSA.2011.6126607

†Denotes Co-First Authorship

#### Interim Products

1. **AH Wagner**, B Walsh, G Mayfield, ..., M Griffith, OL Griffith, A Margolin (2018) "A harmonized meta-knowledgebase of clinical interpretations of cancer genomic variants". *bioRxiv*. doi: 10.1101/366856

- Submitted Publications
1. **AH Wagner**, B Walsh, G Mayfield, ..., M Griffith, OL Griffith, A Margolin (Under peer review, *Nature*) "A harmonized meta-knowledgebase of clinical interpretations of cancer genomic variants".
- Other Published Works
1. **AH Wagner**, K Krysiak, KM Campbell, EK Barnell "Cancer Genomics Primer: Tumor Heterogeneity" [Book Chapter] (Accepted). *Springer Publishing Group*.
- Funding
- Training Awards**
- *NHGRI K99* (Under consideration, impact score: 27)
  - *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 Nominee* 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 - Comp Bio* 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 †Oral Presentation; ††Invited talk

### External Presentations

- GA4GH 6th Annual Plenary, Basel, Switzerland October 2018
  - †† *The Variant Interpretation for Cancer Consortium*
- 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	<p><b>Teaching Assistant / Lecturer</b> Nov 2018 Advanced Sequencing Technologies and Applications Cold Spring Harbor Laboratories Cold Spring Harbor, NY</p> <p><b>Workshop Instructor</b> August 2018 Introduction to bioinformatics learning resources Cancer Genomics Consortium Annual Conference Nashville, TN</p> <p><b>Instructor</b> Fall 2017-Current Escape from Perlgatory: Developing in Python and Ruby McDonnell Genome Institute Saint Louis, MO</p> <p><b>Teaching Assistant / Lecturer</b> Nov 2017 Advanced Sequencing Technologies and Applications Cold Spring Harbor Laboratories Cold Spring Harbor, NY</p> <p><b>Workshop Instructor</b> Nov 2016 CIViC Hackathon Netherlands Cancer Institute (NKI) Amsterdam, NL</p> <p><b>Teaching Assistant / Lecturer</b> Nov 2016 Advanced Sequencing Technologies and Applications Cold Spring Harbor Laboratories Cold Spring Harbor, NY</p> <p><b>Teaching Assistant</b> Fall 2014 051:123 - Bioinformatics Techniques Instructor: Thomas L. Casavant Department of Biomedical Engineering University of Iowa</p>
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	<p><b>Guest Lecturer</b>  051:080 - Bioimaging and Bioinformatics  Instructor: Todd E. Scheetz  Department of Biomedical Engineering  University of Iowa</p>	Spring 2014
	<p><b>Teaching Assistant</b>  051:122 - Computational Genomics  Instructor: Thomas L. Casavant  Department of Biomedical Engineering  University of Iowa</p>	Spring 2014
	<p><b>Teaching Assistant</b>  051:123 - Bioinformatics Techniques  Instructor: Terry A. Braun  Department of Biomedical Engineering  University of Iowa</p>	Fall 2013
	<p><b>Instructor</b>  Introduction to Bioinformatics Computing with Python  Supplement to 051:123 - Bioinformatics Techniques  Department of Biomedical Engineering  University of Iowa</p>	Fall 2013
	<p><b>Teaching Assistant</b>  BIOL 313 - Principles of Genetics  Instructor: Jack Girton  Department of Biology  Iowa State University</p>	Fall 2006
Service	<p><b>Peer Review</b></p> <ul style="list-style-type: none"> <li>• Cancer Genetics</li> <li>• BMC Cancer</li> <li>• Genome Medicine</li> <li>• Nature Communications</li> <li>• Science Translational Medicine</li> </ul> <p><b>Editor</b>, CIViC Knowledgebase</p> <ul style="list-style-type: none"> <li>• Moderated curation of clinical interpretations of genomic variants from biomedical literature</li> <li>• Editor, with over 450 moderations (#6 all-time leader in moderations)</li> </ul> <p><b>Executive Committee</b>, Bioinformatics Training Grant Renewal</p> <ul style="list-style-type: none"> <li>• Assisted in curriculum development for proposed Bioinformatics PhD program</li> <li>• Researched student career development resources to be utilized by the program</li> <li>• Collaborated with co-PIs and others in writing the grant proposal to fund the program</li> </ul>	<p>August 2018  May 2018  April 2017  August 2016  August 2016</p> <p>2015-Present</p> <p>S13-F14</p>

**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:**

- Amazon Web Services (AWS), C, C++, Django, Docker, LSF, SQL, Perl, Python (PyCharm, Jupyter Notebooks), R (RStudio), Ruby on Rails (RubyMine), SGE, UNIX

**Common software (bioinformatics):**

- Bedtools, Ballgown, BWA, Cufflinks, GATK, GenVisR, GMS, HiSat2, Kallisto, IGV, Picard, Pizzly, RNA-SeQC, Samtools, Stringtie, Tophat, VCFTools

**Common software (other):**

- Anaconda, Git, GitHub, Homebrew, JIRA,  $\LaTeX$