

Alex H. Wagner, PhD

Contact Information

480-ALEX-PHD
awagner24@wustl.edu

Research Interests

Bioinformatics, Cancer Genomics, Precision Medicine

Research Experience

Instructor in Medicine

June 2019 to Present

Division of Oncology,
Washington University School of Medicine
Saint Louis, MO

Advisors:

[Obi L. Griffith, PhD](#)

[Timothy J. Ley, MD](#)

Postdoctoral Research Scholar

January 2015 to May 2019

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. 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 (2019) "Standard operating procedure for somatic variant refinement of tumor sequencing data". *Genetics in Medicine*. doi: 10.1038/s41436-018-0278-z.
2. **AH Wagner**[†], S Devarakonda[†], 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
3. BJ Ainscough[†], EK Barnell[†], 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
4. AM Danos[†], DI Ritter[†], **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[†], **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 Kico, 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/c 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". <i>bioRxiv</i> . doi: 10.1101/366856
Submitted Publications	1. AH Wagner , B Walsh, G Mayfield, ..., M Griffith, OL Griffith, A Margolin (Under secondary review, <i>Nature Genetics</i>) "A harmonized meta-knowledgebase of clinical interpretations of somatic cancer genomic variants".
Other Published Works	1. AH Wagner , K Krysiak, KM Campbell, EK Barnell (2019) "Cancer Genomics for the Clinician: Tumor Heterogeneity" [Book Chapter]. <i>Springer Publishing Group</i> . ISBN-13: 9780826168672
Funding	<p>Research Awards</p> <ul style="list-style-type: none"> • <i>NHGRI K99/R00</i> 2019–present • <i>NCI K12 Career Development in Clinical Oncology</i> (Declined for K99) <p>Training and Fellowship Awards</p> <ul style="list-style-type: none"> • <i>NCI F32 Postdoctoral Fellowship</i> 2017–2019 • <i>NCI T32 Postdoctoral Training in Cancer Biology</i> 2016–2017 • <i>NIGMS T32 Predoctoral Training Grant in Genetics</i> 2013–2014 • <i>NIGMS T32 Predoctoral Training Grant in Bioinformatics</i> 2011–2013 • Consecutive annual awards granted for 2011-2012 and 2012-2013. <p>Travel and Trainee Awards</p> <ul style="list-style-type: none"> • <i>CCG 2019 Trainee Abstract Award</i> May 2019 • <i>1st Place Student/Trainee Travel Award, CGC</i> August 2018 • <i>AACR-Bristol Myers Squibb Scholar-in-Training Award, AACR</i> April 2018 • <i>NSF Travel Grant, ISMB</i> July 2013 • <i>Graduate Student Senate Travel Grant, ARVO</i> May 2013
Merit	<p>Research Awards</p> <ul style="list-style-type: none"> • <i>ICTS Precision Medicine Abstract Award</i> January 16, 2018 <ul style="list-style-type: none"> • 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). • <i>D.C. Priestestersbach Dissertation Prize Nominee</i> 2015 <ul style="list-style-type: none"> • 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. • <i>Outstanding Student Research Award - Comp Bio</i> 2012–2013 <ul style="list-style-type: none"> • 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 Speaker; *Upcoming

External Presentations

- AMIA 2019 Annual Conference, Washington, D.C. *November 2019
 - †† *Panelist, computational representation of patient data*
- CGC 2019 Annual Conference, Nashville, TN *August 2019
 - †† *Community resources for clinical variant classification in cancers*
- CGC 2019 Annual Conference, Nashville, TN *August 2019
 - † *A new somatic variation model enables precise search strategies for clinical interpretations of patient tumors*
- Curating the Clinical Genome, Washington, D.C. May 2019
 - † *Somatic variant curation standards enable improved identification of relevant clinical interpretations for tumor variants*
- GA4GH Implementation Connect, Hinxton, UK April 2019
 - †† *Variant Interpretation for Cancer Consortium: Workstream Goals 2019*
- AACR Annual Conference, Atlanta, GA March 2019
 - Cancer genome interpretation with CIViCpy*
- GA4GH-AMED Symposium, Sendai, Japan March 2019
 - †† *The Variant Interpretation for Cancer Consortium, a Genomic Knowledge Workstream Driver Project of the GA4GH*
- 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

Workshop Instructor August 2019

Bioinformatics: Understanding what's Underneath the Hood.
Cancer Genomics Consortium Annual Conference
Nashville, TN

Workshop Leader March 2019

Genomic Knowledge Standards
AMED-GA4GH Workshop
Sendai, JP

Teaching Assistant / Lecturer Advanced Sequencing Technologies and Applications Cold Spring Harbor Laboratories Cold Spring Harbor, NY	Nov 2018
Workshop Instructor Introduction to bioinformatics learning resources Cancer Genomics Consortium Annual Conference Nashville, TN	August 2018
Instructor Escape from Perlatory: Developing in Python and Ruby McDonnell Genome Institute Saint Louis, MO	Fall 2017-Current
Teaching Assistant / Lecturer Advanced Sequencing Technologies and Applications Cold Spring Harbor Laboratories Cold Spring Harbor, NY	Nov 2017
Workshop Instructor CIViC Hackathon Netherlands Cancer Institute (NKI) Amsterdam, NL	Nov 2016
Teaching Assistant / Lecturer Advanced Sequencing Technologies and Applications Cold Spring Harbor Laboratories Cold Spring Harbor, NY	Nov 2016
Teaching Assistant 051:123 - Bioinformatics Techniques Instructor: Thomas L. Casavant Department of Biomedical Engineering University of Iowa	Fall 2014
Guest Lecturer 051:080 - Bioimaging and Bioinformatics Instructor: Todd E. Scheetz Department of Biomedical Engineering University of Iowa	Spring 2014
Teaching Assistant 051:122 - Computational Genomics Instructor: Thomas L. Casavant Department of Biomedical Engineering University of Iowa	Spring 2014

	Teaching Assistant 051:123 - Bioinformatics Techniques Instructor: Terry A. Braun Department of Biomedical Engineering University of Iowa	Fall 2013
	Instructor Introduction to Bioinformatics Computing with Python Supplement to 051:123 - Bioinformatics Techniques Department of Biomedical Engineering University of Iowa	Fall 2013
	Teaching Assistant BIOL 313 - Principles of Genetics Instructor: Jack Girton Department of Biology Iowa State University	Fall 2006
Service	Peer Review <ul style="list-style-type: none"> • Cancer Genetics • BMC Cancer • Genome Medicine • Nature Communications • Science Translational Medicine 	August 2018 May 2018 April 2017 August 2016 August 2016
	Editor , CIViC Knowledgebase • Moderated curation of clinical interpretations of genomic variants from biomedical literature • Editor, with over 450 moderations (#7 all-time leader in moderations)	2015-Present
	Executive Committee , Bioinformatics Training Grant Renewal • 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	S13-F14
	Planning Committee Chair , Ann. UI Bioinformatics Retreat • Planned logistics of the 2013 and 2014 annual bioinformatics retreats • Invited selected extramural faculty to participate in the retreats	S13-F14
Software Familiarity	Programming languages and environments: <ul style="list-style-type: none"> • 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): <ul style="list-style-type: none"> • Bedtools, Ballgown, BWA, CNVkit, Cufflinks, GATK, GenVisR, GISTIC, GMS, HiSat2, Kallisto, IGV, Picard, Pindel, Pizzly, RNA-SeQC, Samtools, SomaticSniper, Strelka, Stringtie, Tophat, VarScan, VCFTools 	

Common software (other):

- Anaconda, Git, GitHub, Homebrew, JIRA, L^AT_EX