

Alex H. Wagner, PhD

Contact Information

480-ALEX-PHD
awagner24@wustl.edu

Research Interests

Cancer Genomics, Precision Medicine, Medical Informatics

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 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	<ol style="list-style-type: none"> 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 2. AM Danos[†], K Krysiak[†], EK Barnell[†], ..., AH Wagner, S Madhavan, M Griffith, OL Griffith (2019) "The CIViC knowledge model and standard operating procedures for curation and clinical interpretation of variants in cancer". <i>bioRxiv</i>. doi: 10.1101/700179
Submitted Publications	<ol style="list-style-type: none"> 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". 2. AM Danos[†], K Krysiak[†], EK Barnell[†], ..., AH Wagner, S Madhavan, M Griffith, OL Griffith (Under primary review, <i>Genome Medicine</i>) "The CIViC knowledge model and standard operating procedures for curation and clinical interpretation of variants in cancer".
Other Published Works	<ol style="list-style-type: none"> 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 and Fellowship Awards</p> <ul style="list-style-type: none"> • <i>NHGRI K99/R00</i> 2019–present • <i>NCI F32 Postdoctoral Fellowship</i> 2017–2019 <p>Training Awards</p> <ul style="list-style-type: none"> • <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.
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. Priestersbach 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

- This annual award recognizes a single student in the College of Engineering for exemplary research in the fields of bioinformatics and computational biology.

Travel and Trainee Awards

- *Trainee Abstract Award* May 2019
 - Curating the Clinical Genome Annual Conference Washington D.C.
- *1st Place Student/Trainee Travel Award* August 2018
 - Cancer Genomics Consortium Annual Conference Nashville, TN
- *AACR-Bristol Myers Squibb Scholar-in-Training Award* April 2018
 - American Association for Cancer Research Annual Conference Chicago, IL
- *NSF Travel Grant* July 2013
 - International Society for Computational Biology Intelligent Systems for Molecular Biology Annual Conference Berlin, Germany
- *Graduate Student Senate Travel Grant* May 2013
 - Association for Research in Vision and Ophthalmology Annual Conference Seattle, WA

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

	<ul style="list-style-type: none"> [†]<i>Positive and Unlabeled Learning for Prioritization</i> • Interdisciplinary Health Research Poster Session April 2013 <i>Positive and Unlabeled Learning for Prioritizing Candidate Variants in Retinal Degenerative Diseases</i> • Genetics Retreat 2012 November 2012 <i>Machine Learning Based Prioritization of Retinal Disease Genes</i> • Joint Bioinformatics Retreat October 2012 [†]<i>Prioritization of Retinal Disease Genes: An Integrative Approach</i> • Midwest Eye Research Symposium July 2012 [†]<i>Machine Learning Based Prioritization of Eye Disease Genes</i> • Genetics Retreat 2011 February 2012 <i>Exon-level Expression Profiling of Ocular Tissues</i>
Teaching Experience	<p>Guest Lecturer December 2019</p> <p>Variant Interpretation Introduction to Bioinformatics Instructor: Michael Baudis University of Zurich Zurich, Switzerland</p> <p>Workshop Instructor August 2019</p> <p>Bioinformatics: Understanding what's Underneath the Hood Cancer Genomics Consortium Annual Conference Nashville, TN</p> <p>Workshop Leader March 2019</p> <p>Genomic Knowledge Standards AMED-GA4GH Workshop Sendai, Japan</p> <p>Teaching Assistant / Lecturer Nov 2018</p> <p>Advanced Sequencing Technologies and Applications Cold Spring Harbor Laboratories Cold Spring Harbor, NY</p> <p>Workshop Instructor August 2018</p> <p>Introduction to bioinformatics learning resources Cancer Genomics Consortium Annual Conference Nashville, TN</p> <p>Instructor Fall 2017-Summer 2019</p> <p>Escape from Perl-gatory: Developing in Python and Ruby McDonnell Genome Institute Saint Louis, MO</p> <p>Teaching Assistant / Lecturer Nov 2017</p> <p>Advanced Sequencing Technologies and Applications Cold Spring Harbor Laboratories Cold Spring Harbor, NY</p>

	Workshop Instructor CIViC Hackathon Netherlands Cancer Institute (NKI) Amsterdam, Netherlands	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	Variant Representation (VR) Group Lead , GA4GH • Co-Leader of the GA4GH Genomic Knowledge Standards VR subgroup • Technical co-lead and maintainer of the GA4GH VR Specification	2018-Present

Co-Director, Variant Interpretation for Cancer Consortium 2018-Present

- Led the design and execution of the [VICC knowledge harmonization effort](#)
- Developed the VICC research objectives ([summary image](#)) and organized [eight expert-led Working Groups](#) to achieve them

Editor, CIViC Knowledgebase 2015-Present

- Moderated curation of clinical interpretations of genomic variants from biomedical literature
- Editor, with over 450 moderations (#7 all-time leader in moderations)

Workshop Co-chair, HemOnc / VICC Hackathon January 2020

- Pre-conference Workshop to *AACR Advancing Precision Medicine Drug Development*

Peer Review

- Nucleic Acids Research October 2019
- Cancer Genetics August 2018
- BMC Cancer May 2018
- Genome Medicine April 2017
- Nature Communications August 2016
- Science Translational Medicine August 2016

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, 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, \LaTeX