## 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 Grifith, 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-exomic 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
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". *bioRxiv*. doi: 10.1101/700179

Submitted Publications

1. **AH Wagner**, B Walsh, G Mayfield, ..., M Griffith, OL Griffith, A Margolin (Under secondary review, *Nature Genetics*) "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, *Genome Medicine*) "The CIViC knowledge model and standard operating procedures for curation and clinical interpretation of variants in cancer".

Other Published Works

1. **AH Wagner**, K Krysiak, KM Campbell, EK Barnell (2019) "Cancer Genomics for the Clinician: Tumor Heterogeneity" [Book Chapter]. *Springer Publishing Group*. ISBN-13: 9780826168672

Funding

**Research and Fellowship Awards**

- *NHGRI K99/R00* 2019–present
- *NCI F32 Postdoctoral Fellowship* 2017–2019

**Training Awards**

- *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.

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. Spriestersbach 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.

**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

†*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** — Nov 2018
Advanced Sequencing Technologies and Applications
Cold Spring Harbor Laboratories
Cold Spring Harbor, NY

**Workshop Instructor** — August 2018
Introduction to bioinformatics learning resources
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

**Variant Representation (VR) Group Lead**, GA4GH 2018-Present
- Co-Leader of the GA4GH Genomic Knowledge Standards VR subgroup
- Technical co-lead and maintainer of the GA4GH VR Specification

**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)

**Peer Review**

- 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