Alex H. Wagner, PhD

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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 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
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".
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 Awards
- *NHGRI K99/R00* — 2019–present
- *NCI K12 Career Development in Clinical Oncology* — (Declined for K99)

Training and Fellowship Awards
- *NCI F32 Postdoctoral Fellowship* — 2017–2019
- *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 and Trainee Awards
- *CCG 2019 Trainee Abstract Award* — May 2019
- *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. 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.

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 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

Teaching Assistant   Fall 2006
BIOL 313 - Principles of Genetics
Instructor: Jack Girton
Department of Biology
Iowa State University

Service   **Peer Review**

- Cancer Genetics   August 2018
- BMC Cancer   May 2018
- 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
- Editor, with over 450 moderations (#7 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:**

- 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