Alex H. Wagner, PhD

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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**[†], 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

2. 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

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 Grififth, 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[†], 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 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 (2019) "Cancer Genomics for the Clinician: Tumor Heterogeneity" [Book Chapter]. *Springer Publishing Group*. ISBN-13: 9780826168672

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. 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 talk

External Presentations
- 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		

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
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
  (#6 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