

ADINA CHUANG HOWE, Ph.D.

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EDUCATION

- 2005 – 2009 University of Iowa, Iowa City, IA
Ph.D., Dept. of Environmental Engineering and Science
Advisor: Timothy Mattes
Doctoral dissertation: *Proteomic investigations of vinyl chloride-assimilating bacteria: from pure cultures to the environment*
- 2003 – 2005 Purdue University, West Lafayette, IN
M.S., Dept. of Civil and Environmental Engineering
Advisors: Larry Nies and Suresh Rao
Thesis: *Life cycle analysis of impacts of new construction*
- 1999 – 2003 Purdue University, West Lafayette, IN B.S., Dept. of Mechanical Engineering

RESEARCH EXPERIENCE

- January, 2015 Iowa State University, Ames, IA
Assistant Professor, Agricultural and Biosystems Engineering
Genomics and Environmental Research in Microbial Systems
<http://germslab.org>
- 2013 – present Argonne National Laboratory, Argonne, IL
Assistant Computational Biologist, Computing and Life Sciences
Project: *Metagenomic analysis of soil and human gut microbial communities*
- 2012 – present Michigan State University, East Lansing, MI
Adjunct Faculty, Dept. of Microbiology and Microbial Genetics
- 2012 – 2013 Argonne National Laboratory, Argonne, IL
Post-doctoral Researcher, Computing and Life Sciences
- 2009 – 2012 Michigan State University, East Lansing, MI
Post-doctoral Fellow, Dept. of Microbiology and Microbial Genetics
Advisors: C. Titus Brown and James Tiedje
Project: *Metagenomic investigations of soil microbial systems*
- 2007 Chinese Academy of Sciences, Beijing, China
Research Center for Eco-Environmental Sciences
Supervisor: Guibin Jiang
Project: *Development of vitellogenin protein biomarkers for endocrine disrupting chemicals in zebrafish*

ON-GOING RESEARCH PROJECTS

1. khmer: k-mer counting and filtering. Software project, at <http://github.com/ged-lab/khmer/>. Michael R. Crusoe, Greg Edverson, Jordan Fish, **Adina Howe**, Eric McDonald, Joshua Nahum, Kaben Nanlohy, Jason Pell, Jared Simpson, C. S. Welcher, Qingpeng Zhang, and C. Titus Brown. BSD license. Estimated 200 users; 32 GitHub stars (93-99%ile); 56 GitHub forks (97-100%ile).
2. Comparison of microbial communities in soil aggregates of various bioenergy crops. Collaborators: Kirsten Hofmockel, Iowa State University.
3. Microbial and viral drivers of obesity and gut diseases. Collaborator: Eugene Chang, University of Chicago.
4. Identification of pathogenic viral biomarkers in wastewater streams. Collaborators: Joan Rose and Tiong Gaw Am, Michigan State University.

PUBLICATIONS

1. Aw, T.G., **Howe, A.**, and Rose, J. Metagenomic approaches for direct and cell culture evaluation of the virological quality of wastewater. 2014. Journal of virological methods 210(15):15-21. doi:10.1016/j.viromet.2014.09.017 <http://www.sciencedirect.com/science/article/pii/S0166093414003723>
2. Williams, R.J., **Howe, A.**, and Hofmockel, K. 2014. Demonstrating microbial co-occurrence pattern analyses within and between ecosystems. Frontiers in Microbiology 5(358). doi: 10.3389/fmicb.2014.00358 <http://journal.frontiersin.org/Journal/10.3389/fmicb.2014.00358>
3. Zhang, Q.P., Pell, J., Canino-Koning, R., **Howe, A.C.**, and Brown, C. T. 2014. These are not the k-mers you are looking for: Efficient online k-mer counting using a probabilistic data structure. PLoS ONE 9(7): e1011271. doi: 10.1371/journal.pone.0101271. <http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0101271>
4. **Howe, A.C.**, Jansson, J., Malfattie, S., Tringe, S., Tiedje, J., and Brown, C.T. 2014. Tackling soil diversity with the assembly of large, complex metagenomes. PNAS. Accepted February 11, 2014. doi:10.1073/pnas.1402565111. <http://www.pnas.org/content/early/2014/03/13/1402564111.short>
5. Vital, M, **Howe, A.C.**, and Tiedje, J. 2014. Revealing the bacterial butyrate-synthesis pathways from (meta)genomic data. mBio 5(2):e00889-14. doi: 10.1128/mBio.00889-14. *Featured in Faculty of 1000 Prime.* <http://mbio.asm.org/content/5/2/e00889-14>

6. Schwarz, E., Korhonen, P., Campbell, B., Young, N., Jex, Aaron, Jabbar, A., Hall, R. Mondal, A., **Howe, A.C.**, Pell, J. Hofmann, A., Boag, P., Zhu, X., Gregory, T., Loukas, A., Williams, B., Antoshechkin, I., Brown, C.T., Sternberg, P., and Gasser, R. 2013. The genome and developmental transcriptome of the strongylid nematode *Haemonchus contortus*. *Genome Biology* 14(R89). doi:10.1186/gb-2013-14-8-r89. <http://genomebiology.com/2013/14/8/R89>
7. Pell, J., Hintze, A., Canino-Koning, R., **Howe, A.C.**, Tiedje, J.M., and Brown, C.T. 2012. Scaling metagenome sequence assembly with probabilistic de Bruijn graphs. *PNAS* 109(33):13272-13277. doi:10.1073/pnas.1121464109. <http://www.pnas.org/content/109/33/13272.full>
8. **Chuang, A.S.**, Jin, Y.O., Schmidt, L.S., Li, Y., and Mattes, T.E. 2010. Proteomic analysis of ethene-enriched groundwater microcosms from a vinyl chloride-contaminated site. *Environ. Sci. Technol.* 44(5):1594-1601. doi: 10.1021/es903033r. <http://pubs.acs.org/doi/abs/10.1021/es903033r>
9. **Chuang, A.S.** and Mattes, T.E. 2007. Identification of polypeptides expressed in response to vinyl chloride, ethene, and epoxyethane in *Nocardioide* sp. strain JS614 by using peptide mass fingerprinting. *Appl. Env. Microbiol.* 73(13):4368-4372. doi: 10.1128/AEM.00086-07. <http://aem.asm.org/content/73/13/4368.full>
10. Mattes, T.E., Coleman, N.V., **Chuang, A.S.**, Rogers, A., Spain, J.C., and Gossett, J.M. 2006. Mechanism controlling the extended lag period associated with vinyl chloride starvation in *Nocardioide* sp. strain JS614. *Arch. of Microbiol.* 187(3):217-226. <http://link.springer.com/article/10.1007%2Fs00203-006-0189-2>

CURRENT GRANTS AWARDED

1. PIs: Hofmockel, K.H., Howe, A.C., Meyer, F.M., and Orr, G. Microbial drivers of global change at the aggregate scale: linking genomic function to carbon metabolism and warming. Department of Energy. September, 2013. \$2,944,265 USD.
2. PIs: Hofmockel, K.H. and Howe, A.C. Development of novel approaches to target microbial drivers of C cycling in soil aggregates. Joint Genome Institute. October, 2013.
3. PIs: Howe, A.C. and Ringus, Daina. Going viral: The Role of the Phageome in Human Ulcerative Colitis. University of Chicago Digestive Diseases Research Core Center Pilot and Feasibility Grant. October, 2013. \$20,000 USD.

PAST GRANTS AWARDED

1. PI: Howe, A.C. Metagenomic investigations of rhizosphere microbial communities in bioenergy crop soils. National Science Foundation Postdoctoral Fellowship in Biology. 2009. Amount awarded: 123,000 USD.
2. PI: Howe, A.C. Development of bioinformatics tools for soil metagenomic sequencing. Michigan State University Office of the Provost. 2009. Amount awarded: 92,500 USD.
3. PI: Chuang, A.S. Identification of protein biomarkers in response to vitellogenin in local fish. National Science Foundation East Asia Pacific Studies Internship. 2007. Amount awarded: 10,000 USD.
4. PI: Chuang, A.S. Metaproteomic investigations for vinyl-chloride biomarkers in the environment. National Science Foundation Graduate Research Fellowship. 2006. Amount awarded: 100,000 USD.
5. PI: Chuang, A. University of Iowa Presidential Research Fellowship. 2005. Amount awarded: 100,000 USD. (*Awarded but declined due to alternative funding source.*)

SELECT ORAL PRESENTATIONS

(many are openly accessible on www.slideshare.net/adinachuanghowe)

1. What to do in the event of a data deluge. December, 2014. **Howe, A.** EEMiS Workshop. EEMiS, Linnaeus University, Kalmar, Sweden. (invited presentation)
2. Riding the data tidal wave in microbiology. November, 2014. **Howe, A.** The future of big data. University of Nebraska-Lincoln, Lincoln, NE. (invited presentation)
3. Riding the big data tidal wave in modern microbiology. November, 2014. **Howe, A.** Is adding more data always better? Field Museum, Chicago, IL. (invited presentation)
4. Is it time for a community effort towards a soil reference database? October, 2014. **Howe, A.** Argonne National Laboratory Soil Metagenomics Meeting, Chicago, IL. (invited presentation)
5. Contrasting recovery of viruses and bacteria in the gut microbiome to dietary perturbations in mice. August, 2014. **Howe, A.** International Society of Microbial Ecology General Meeting 15, Seoul, Korea. (invited presentation)
6. Is bigger better – advice as metagenomes grow. August, 2014. **Howe, A.** International Society of Microbial Ecology General Meeting 15, Seoul, Korea. (invited roundtable workshop organizer)
7. Metagenomic data and its role in NEON. July, 2014. **Howe, A.** NEON metagenomic workshop, Boulder, CO. (invited presentation)

8. Assembly of complex metagenomes. May, 2013. **Howe, A.C.** American Society of Microbiology, Denver, CO. (invited presentation)
9. Big data (in biology): integrating large, fast, heterogeneous datasets. **Howe, A.C.** EAP Air Sensors 2013: Data Quality and Applications, Raleigh, NC. (invited presentation)
10. Dirty little secrets for soil metagenomic assembly. August, 2012. **Howe, A.C.** International Society of Microbial Ecology, Seattle, WA (invited presentation)
11. In the event of an emergency: What to do in a data apocalypse. July, 2012. **Howe, A.C.** ICiS Summer workshop: Using large scale metagenomics to quantify the role of phages and viruses in the evolution of prokaryotes, Park City, UT. (invited presentation)
12. The dirt on soil metagenomics assembly. May, 2012. **Howe, A.C.** SciLifeLab, Stockholm, Sweden. (invited presentation)
13. Approaches for scaling de novo assembly of metagenomic sequencing. March, 2012. **Howe, A.C.** X-Gen Conference and Expo, San Diego, CA. (invited presentation)
14. Deep sequencing of soil microbial communities of bioenergy crops. October, 2011. **Howe, A.C.**, Garoutte, A., Guo, J., and Tiedje, J.M. 3rd Annual Argonne Soils Workshop, Argonne National Laboratories, Argonne, IL. (invited presentation)
15. Exploring soil diversity with next generation sequencing. October, 2011. **Howe, A.C.**, Brown, C., and Tiedje, J.M. Frontiers of Soil Science Seminar Series, University of Wisconsin, Department of Soil Science, Madison, WI. (invited presentation)
16. Breaking down big data with assembly of soil metagenomes. June, 2011. **Howe, A.C.**, Pell, J., Canino-Koning, R., Hintze, A., and Brown, C.T. Earth Microbiome Project General Meeting, Shenzhen, China. (invited presentation)
17. Breaking down big data in soil metagenomes. May, 2011. **Howe, A.C.**, Pell, J., Canino-Koning, R., Hintze, A., and Brown, C.T. 111th General Meeting of American Society of Microbiology, New Orleans, LA. (invited presentation)

TEACHING EXPERIENCE

Instructor, Iowa State University, Ames, IA. Software carpentry workshop, 2014.

Instructor, University of Pennsylvania, Philadelphia, PA. Software carpentry workshop, 2014.

Instructor, Kellogg Biological Station, Hickory Corners, MI. Next generation sequencing course, 2014.

Instructor, University of Iowa, Iowa City, IA. Software carpentry workshop, 2013.

Instructor, Kellogg Biological Station, Hickory Corners, MI. Next generation sequencing course, 2013.

Instructor, Howard Hughes Medical Institute, Chevy Chase, MD. Software carpentry workshop, 2013.

Instructor, Women in Science and Engineering, Boston, MA. Software carpentry workshop, 2013.

Instructor. Columbia University, New York, NY. Software carpentry workshop, 2013.

Teaching Assistant, Kellogg Biological Station, Hickory Corners, MI. Next generation sequencing course, 2012.

Teaching Assistant, University of Vancouver, Vancouver, Canada. Software carpentry workshop, 2012.

Teaching Assistant, Michigan State University, East Lansing, MI. Software carpentry workshop, 2012.

Instructor, Michigan State University, East Lansing, MI. Metagenomic de novo assembly workshop, 2011.

Instructor, Yonsei University, Seoul, Korea. Metagenomic sequencing and assembly workshop, 2010.

Instructor, Michigan State University, East Lansing, MI. Assembly of next generation sequencing short reads, 2010.

Instructor, University of Iowa, Iowa City, Iowa. Environmental Chemistry Laboratory, 2008.

Instructor, Purdue University, West Lafayette, Indiana. Microbiology Laboratory, 2004.

ADVISING EXPERIENCE

Student:	Aaron Garoutte, 2010 – present. Michigan State University. Graduate student, mentor.
Dissertation:	Metatranscriptomic investigations of plant-microbe interactions in bioenergy crop soils
Student:	Julian Yu, 2010 – 2012. Michigan State University. Undergraduate student, formal advisor.
Project:	Plant-microbe interactions in isolates from bioenergy crop soils.
Student:	Trish Eddie, 2010 – 2012. Michigan State University. Undergraduate student, formal advisor.

Project: Gene-targeted amplicon sequencing of soil communities

Student: Tobias Ortega-Knight, Summer, 2012. Michigan State University.
Undergraduate student, formal advisor.

Project: *De novo* assembly of human gut microbiome mock community

Student: Danny Lynch, Summer, 2012. Michigan State University.
Undergraduate student, formal advisor.

Project: *De novo* assembly of yeast genome with digital normalization and
Trinity assembler.

PROFESSIONAL SERVICE

Scientific Reviewer *BMC Bioinformatics*; *G3: Genes, Genomes, Genetics*,
International Society for Microbial Ecology; *Molecular Ecology Resources*; *PLOS ONE*; *Biotechnology Journal*; Bacteriophage; and French Genomique Infrastructure Program. Reviewer for Graduate Women in Science. Program Committee member for SciPy 2014. Instructor and volunteer for Software Carpentry.

INDUSTRIAL EXPERIENCE

Exxon Mobil Production Company, US/East Operations Technology, New Orleans, Louisiana

Cummins Engine Company, High Horsepower Service Engineering, Columbus, Indiana

Cummins Engine Company, Apex Engineering Plant, Columbus, Indiana

AWARDS AND HONORS

Young Investigator Award Invited Oral Presentation, ASM, 2011.

Center for Environmental Beneficial Catalysis Fellow, University of Iowa, 2004. Ross

Fellowship, Purdue University, 2003.

PROFESSIONAL AFFILIATIONS

American Society for Microbiology

International Society for Microbial Ecology

Association of Environmental Engineering and Science Professors

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