

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
- 2003 – 2005 Purdue University, West Lafayette, IN
M.S., Dept. of Civil and Environmental Engineering
Advisors: Larry Nies and Suresh Rao
- 1999 – 2003 Purdue University, West Lafayette, IN B.S., Dept. of Mechanical
Engineering

RESEARCH EXPERIENCE

- 2015 - present Iowa State University, Ames, IA
Assistant Professor, Agricultural and Biosystems Engineering
Genomics and Environmental Research in Microbial Systems
<http://germslab.org>
- 2013 – 2015 Argonne National Laboratory, Argonne, IL
Assistant Computational Biologist, Computing and Life Sciences
- 2012 – 2015 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
- 2007 Chinese Academy of Sciences, Beijing, China
Research Center for Eco-Environmental
Sciences, NSF EAPSI Summer Internship
Supervisor: Guibin Jiang

PUBLICATIONS

1. **Howe, A.** and Chain, Patrick. Challenges and opportunities in understanding microbial communities with metagenome assembly (accompanied by IPython Notebook tutorial). 2015. *Frontiers in Microbiology*.
<http://journal.frontiersin.org/article/10.3389/fmicb.2015.00678>

2. Zifacakova, L., Vetrovsky, T., **Howe, A.**, Baldrian, P. 2015. Microbial activity in forest soil reflects the changes in ecosystem properties between summer and winter. *Environmental Microbiology*. doi: 10.1111/1462-2920.13026.
<http://onlinelibrary.wiley.com/doi/10.1111/1462-2920.13026>
3. 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>
4. 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>
5. 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>
6. **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>
7. 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>
8. 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>
9. 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>
10. **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>

11. **Chuang, A.S.** and Mattes, T.E. 2007. Identification of polypeptides expressed in response to vinyl chloride, ethene, and epoxyethane in *Nocardioides* 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>
12. 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 *Nocardioides* 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. PI: **Howe, A.** Microbial characterization of communities associated with manure pit foaming. September, 2015 – March, 2016. Subcontract, \$30,000 USD.
2. PIs: Soupir, Michelle and **Howe, A.** Metagenomic Analysis and Modeling of Environmental Resistance to Agricultural Antibiotics. University of Iowa, Center for Health Effects of Environmental Contamination. August 2015 – July 2016. \$30,000 USD.
3. 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 – August 2016. \$2,944,265 USD.
4. 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 – September 2014.
5. 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 – September 2014. \$20,000 USD.

PENDING GRANTS

1. PI: **Howe, A.** CAREER: Transforming water quality monitoring through microbial indicators. NSF. January 2016 to December 2020. Amount requested: 525,000 USD.
2. PI: **Howe, A.**, Sarkar, S., and Williams, R. QuBBD: Expert guided pattern discovery and inference for health and disease in human gut microbiomes. January 2016 – December 2016. Amount requested: 100,000 USD.
3. PI: **Howe, A.**, Soupir, M., Allen, H., Moorman, T., and Hinsa, S. Diversity of Antibiotic Resistance genes and Transfer Elements Quantitative Monitoring (DARTE-

QM) for Environmental Samples. January 2016 to December 2018. USDA-AFRI. Amount requested: 999,346 USD.

4. PI: **Howe, A.**, Tim, U., Que, L., Qiao, D., Sharma, S., and Mickelson, S. Cloud Nutrient Investigation and Analysis Ecosystem (Cloud NINE) and Integrated Sensor Technology. USDA. January 2016 to December 2018. Amount requested: 493,000 USD.

GRANTS NOT AWARDED

1. PI: **Howe, A.**, Downing, J., Filstrup, C. and Yang, F. MicroArray Value and Risk Chips (MAVeRiC) for non-use valuation of water quality in lakes. Water Quality Benefits, EPA. August 2015 to July 2018. Amount requested: 795,000 USD.
2. PI: **Howe, A.** Novel and transformative approaches to detect water pathogens to protect human health. Iowa State University Foundation, Galloway Fellowship. August 2015 – July 2016. Amount requested: \$41,266.
3. PI: Soupier, M., **Howe, A.**, O'Connor, A., Moorman, T., and Allen, H. Diversity of Antibiotic Resistance genes and Transfer Elements Quantitative Monitoring (DARTE-QM) for Environmental Samples. ISU PIIR. January 2016 – December 2018. Amount requested: \$409,940.
4. PI: Downing, J., Arbuckle, J., **Howe, A.**, Howe, M. Zhang, Z., Filstrup, C., Yang, F. Big Data at the Water-Food-Energy Nexus. ISU PIIR. January 2016 – December 2018. Amount requested: \$574,258.

SELECT ORAL PRESENTATIONS

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

1. Next generation sequencing analysis. May 2015. **Howe, A.** Laboratoria de Genomica, CIBNOR, La Paz, Mexico (invited presentation)
2. Metagenomic data analysis workshop. March, 2015. **Howe, A.** Environmental Microbial Genomics Group, Ecole Centrale de Lyon, Lyon, France. (invited presentation)
3. What to do in the event of a data deluge. December, 2014. **Howe, A.** EEMiS Workshop. EEMiS, Linnaeus University, Kalmar, Sweden. (invited presentation)
4. Riding the data tidal wave in microbiology. November, 2014. **Howe, A.** The future of big data. University of Nebraska-Lincoln, Lincoln, NE. (invited presentation)
5. 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)
6. 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)
7. 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)
 8. 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)
 9. Metagenomic data and its role in NEON. July, 2014. **Howe, A.** NEON metagenomic workshop, Boulder, CO. (invited presentation)
 10. Assembly of complex metagenomes. May, 2013. **Howe, A.C.** American Society of Microbiology, Denver, CO. (invited presentation)
 11. Big data (in biology): integrating large, fast, heterogeneous datasets. **Howe, A.C.** EAP Air Sensors 2013: Data Quality and Applications, Raleigh, NC. (invited presentation)
 12. Dirty little secrets for soil metagenomic assembly. August, 2012. **Howe, A.C.** International Society of Microbial Ecology, Seattle, WA (invited presentation)
 13. 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)
 14. The dirt on soil metagenomics assembly. May, 2012. **Howe, A.C.** SciLifeLab, Stockholm, Sweden. (invited presentation)
 15. Approaches for scaling de novo assembly of metagenomic sequencing. March, 2012. **Howe, A.C.** X-Gen Conference and Expo, San Diego, CA. (invited presentation)
 16. 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)
 17. 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)
 18. 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)
 19. 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 AND TRAINING EXPERIENCE

Instructor, Iowa State University, Ames, Iowa, Data Carpentry Workshop. 2015.

Instructor, Kellogg Biological Station, Hickory Corners, MI. Next generation sequencing course, 2015.

Instructor, Centro de Investigaciones Biologicas Del Noroeste. La Paz, Mexico. Sequencing bioinformatics, 2015.

Instructor, National Institute of Health, Bethesda, MD. Software carpentry workshop, 2015.

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: Phil Colgan, 2015 – present. Iowa State University, ABE.
PhD student, advisor

Student: Jared Flater, 2015 – present. Iowa State University, ABE.
MS student, advisor

Postdoc: Jin Choi, 2015 – present. Iowa State University, ABE.
Postdoc researcher, advisor

Postdoc: Ryan Williams, 2015 – present. Iowa State University, ABE.
Postdoc researcher, advisor

Postdoc: Fan Yang, 2015 – present. Iowa State University, ABE.
Postdoc researcher, advisor

PROFESSIONAL SERVICE

PeerJ, editor. (2015 – present)

Applied Environmental Microbiology, Editorial Board member. (2015 - present)

Panel Reviewer and ad-hoc reviewer *National Science Foundation* (2015 - present)

Steering Committee, Software Carpentry Foundation, 2015.

Instructor and developer, Data Carpentry Foundation, 2015-present.

Instructor and developer, Software Carpentry Foundation, 2015-present.

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.

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

Black and Veatch Building a World of Difference Faculty Fellowship