

# Jennifer Chang, Ph.D.

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## CONTACT INFORMATION

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## SUMMARY

**Bioinformatics and workflow developer** with 8+ years of experience.

## EDUCATION

Ph.D. in **Bioinformatics and Computational Biology** Aug 2011 – June 2017  
minor in **Statistics**, dissertation on "Designing an integrated system for biological network exploration"  
Iowa State University, Ames, Iowa 50010, USA

B.A. in **Computer Science and Biochemistry** Aug 2007 – May 2011  
Cornell College, Mount Vernon, Iowa 52314, USA

## PROFESSIONAL EXPERIENCE

**Bioinformatics Analyst III (Nextstrain)** Fred Hutch Cancer Center Nov 2021 – present

- Remote Contractor from November 2021 to September 2022, after which I became a full-time employee
- Delivered 300+ GitHub PRs across Nextstrain tooling and pathogen-specific repositories, improving performance, modularity, and long-term maintainability.
- Developed and maintained Snakemake workflows, with support in WDL (Terra.bio) and Nextflow as needed, enabling scalable and reproducible genomic analysis.
- Balanced standardization of heterogeneous pathogen pipelines under the pathogen-repo-guide with bespoke automation for dengue, Lassa, WNV, mumps, and norovirus pipelines summarizing trends.
- Ran harmonization of HI titer data integrating antigenic data with phylogenetics for seasonal influenza surveillance reports and global projections.
- Delivered a Nextstrain workshop at VEME 2023 (South Africa), training 50+ researchers on real-time phylogenetics analysis.
- Co-authored collaborative publications advancing open genomic surveillance.

40 hrs/wk. Supervisors: Trevor Bedford, Jover Lee

**Bioinformatics Post-Doc, ORISE SCINet Fellow USDA-ARS**

Jun 2020 – Nov 2021

- Developed Nextflow pipelines for GATK (Hufford Lab) and VGP Assembly (ag100pest) projects, improving automation, documentation, and reproducibility across collaborative genomic projects
- Founded and organized SCINet Corner, a monthly virtual HPC knowledge-sharing series engaging participants across USDA locations
- Co-authored and maintained tutorials in the Bioinformatic Workbook (e.g. WGCNA), increasing accessibility of analytical methods
- Contributed analyses that supported two peer-reviewed genomic publications

40 hrs/wk. Supervisors: Andrew Severin, Brian Scheffler

**Post-Doctoral Computational Biologist, ORISE Fellow USDA-ARS**

Aug 2017 – Jun 2020

- Performed large-scale statistical and genomic analysis (R, Bash, and Perl) of influenza A viruses (IAV) in swine, supporting national surveillance efforts, with a particular emphasis on reassortment.
- Collaborated with experimental and computational teams to design studies for swine or computation
- Produced quarterly IAV surveillance reports using Sweave, presenting trends and actionable findings to multi-site scientific teams.
- Selected a curated monthly set of 21 virus for whole genome sequences and deposition into NCBI GenBank, supporting public data availability.

40 hrs/wk. Supervisor: Amy Baker

**Co-Founder** Complex Computation, LLC; Ames, Iowa, USA

July 2015 – August 2017

- Co-developer of Mango Graph Studio, a C++ software for massive heterogeneous multi-network analysis
- Co-Founder leading efforts for the company to provide software solutions and workshops on network analysis.
- Served as Principal Investigator on two DARPA SBIR Contracts (W911NF-15-P-0040 in 2015 and W911NF-17-P-0014 in 2016), delivering monthly technical reports and providing findings to program managers.
- Presented the findings in-person to DARPA at a conference in Durham, NC.
- Collaborated with scientists and researchers at Iowa State University and other locations to develop network analysis pipelines to answer a variety of biological questions.

Varied from 20 to 40 hrs/wk Supervisor: Hui-Hsien Chou

**Research Assistant** Complex Computational Laboratory; Iowa State Univ.

Feb 2012 – Aug 2017

- Modernized the Lucy2 C++ wxWidgets GUI (2013), increasing usability and contributing to the subsequent 700+ cross-platform (Mac, Windows, Linux) downloads.
- Developed Mango Graph studio, a multi-network visualization and exploration software with a custom graph exploration language (Gel); later commercialized by licensing to Complex Computation, LLC.
- Awarded the Plant Sciences Institute Scholar Grant (2015) and received multiple conference awards for software and research presentations or posters.

20 hrs/wk. Supervisor: Hui-Hsien Chou

SELECTED  
PUBLICATIONS

Zeller, M.A., **Chang, J.**, Trevisan, G., Main, R., Gauger, P.C. and Zhang, J., Rapid PRRSV-2 ORF5-based lineage classification using Nextclade. *Frontiers in Veterinary Science*, 11, p.1419340.

Huddleston, J., Bedford, T., **Chang, J.**, Lee, J., and Neher, R. A., 2024. Seasonal influenza circulation patterns and projections for February 2024 to February 2025. Zenodo. <https://doi.org/10.5281/zenodo.10846007>

**Chang, J.**, Stahlke, A.R., Chudalayandi, S., Rosen, B.D., Childers, A.K. and Severin, A.J., 2023. polish-CLR: a Nextflow workflow for polishing PacBio CLR genome assemblies. *Genome Biology and Evolution*, 15(3), p.evad020.

Anderson, T.K., **Chang, J.**, Arendsee, Z.W., Venkatesh, D., Souza, C.K., Kimble, J.B., Lewis, N.S., Davis, C.T. and Vincent, A.L., 2020. "Swine Influenza A Viruses and the Tangled Relationship with Humans." *Cold Spring Harbor Perspectives in Medicine*, p.a038737.

**Chang, J.**, Anderson, TK., Zeller, MA., Gauger, PC., Vincent, AL., "OctoFLU: Automated classification to evolutionary origin of influenza A virus gene sequences detected in U.S. swine," 2019 bioRxiv: ASM Journal Microbiology Resource Announcements (MRA)

Duwell, M., Feldman, K., Blythe, D., Radebaugh, M., Kough, E., Bachaus, B., Crum, D., Perkins, K., Blanton, L., Davis, C., Jang, Y., Vincent, A., **Chang, J.**, Abney, D., Gudmundson, L., Brewster, M., Polksy, L., Rose, D., "Influenza A(H3N2) Variant Virus Outbreak at Three Fairs – Maryland, 2017", *MMWR Morb Mortal Wkly Rep* 2018;67:1167-1173. DOI: <http://dx.doi.org/10.15585/mmwr.mm6742a1>

**Chang, J.** and Chou, J., "Cavatica: A pipeline for identifying author adoption trends among software or methods," 2017 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Kansas City, MO, USA, 2017, pp. 2145-2150. doi:10.1109/BIBM.2017.8217990

**Chang, J.**, Cho, H., and Chou, H., "Mango: combining and analyzing heterogeneous biological networks", *BioData Mining*, August 2016

- Janzen, G.M., Inderski, B.T., **Chang, J.**, Arendsee, Z.W., Janas-Martindale, A., Torchetti, M.K., Baker, A.L. and Anderson, T.K. Sources and sinks of influenza A virus genomic diversity in swine from 2009 to 2022 in the United States. 2025 Journal of Virology, pp.JVI-00541-25.
- Zeller M.A., **Chang J.**, Trevisan G, Gauger PC, Zhang J. Nextclade data set for the ORF5-based lineage classification of PRRSV-1. Microbiology resource announcements. 0:e00303-25.
- Zeller, M.A., **Chang, J.**, Trevisan, G., Main, R., Gauger, P.C. and Zhang, J., Rapid PRRSV-2 ORF5-based lineage classification using Nextclade. Frontiers in Veterinary Science, 11, p.1419340.
- Huddleston, J., Bedford, T., **Chang, J.**, Lee, J., and Neher, R. A., 2024. Seasonal influenza circulation patterns and projections for February 2024 to February 2025. Zenodo. <https://doi.org/10.5281/zenodo.10846007>
- Chang, J.**, Stahlke, A.R., Chudalayandi, S., Rosen, B.D., Childers, A.K. and Severin, A.J., 2023. polish-CLR: a Nextflow workflow for polishing PacBio CLR genome assemblies. Genome Biology and Evolution, 15(3), p.evad020.
- Stahlke, A.R., **Chang J.**, Chudalayandi, S., Heu, C.C., Geib, S.M., Scheffler, B.E., Childers, A.K. and Fabrick, J.A., 2023. Chromosome-scale genome assembly of the pink bollworm, *Pectinophora gossypiella*, a global pest of cotton. G3: Genes, Genomes, Genetics, 13(4), p.jkad040.
- Venkatesh D, Anderson TK, Kimble JB, **Chang J**, Lopes S, Souza CK, Pekosz A, Shaw-Saliba K, Rothman RE, Chen KF, Lewis NS., Baker ALV, Antigenic characterization and pandemic risk assessment of North American H1 influenza A viruses circulating in swine. Microbiology Spectrum. 2022 Nov 1:e01781-22.
- Arendsee, Z., **Chang, J.** and Wurtele, E.S., 2022. rmonad: pipelines you can compute on. R Journal, 14(1).
- Stahlke, A.R., **Chang, J.**, Tembrock, L.R., Sim, S.B., Chudalayandi, S., Geib, S.M., Scheffler, B.R., Perera, O.P., Gilligan, T.M., Childers, A.K. and Hackett, K.J., A chromosome-scale genome assembly of a *Bacillus thuringiensis* Cry1Ac insecticidal protein resistant strain of *Helicoverpa zea*. 2022 Genome Biology and Evolution.
- Souza, C.K., Anderson, T.K., **Chang, J.**, Venkatesh, D., Lewis, N.S., Pekosz, A., Shaw-Saliba, K., Rothman, R.E., Chen, K.F. and Vincent, A.L., Antigenic distance between North American swine and human seasonal H3N2 influenza A viruses as an indication of zoonotic risk to humans. 2022 Journal of Virology, pp.JVI-01374.
- Arendsee, Z.W., **Chang, J.**, Hufnagel, D.E., Markin, A., Janas-Martindale, A., Vincent, A.L. and Anderson, T.K., octoFLUshow: an Interactive Tool Describing Spatial and Temporal Trends in the Genetic Diversity of Influenza A Virus in US Swine. 2021 Microbiology Resource Announcements, 10(50), pp.e01081-21.
- Kaplan, B.S., Anderson, T.K., **Chang, J.**, Santos J., Perez, D., Lewis, N.S., and Vincent, A.L., 2021. Evolution and antigenic advancement of N2 neuraminidase of swine influenza A viruses circulating in the United States following two separate introductions from human seasonal viruses. Journal of Virology.
- Powell, J.D., Abente, E.J., **Chang, J.**, Souza, C.K., Rajao, D.S., Anderson, T.K., Zeller, M.A., Gauger, P.C., Lewis, N.S. and Vincent, A.L., 2021. Characterization of contemporary 2010.1 H3N2 swine influenza a viruses circulating in United States pigs. Virology.
- Zeller, M.A., **Chang, J.**, Vincent, A.L., Gauger, P.C. and Anderson, T.K., 2021. Spatial and temporal coevolution of N2 neuraminidase and H1 and H3 hemagglutinin genes of influenza A virus in US swine. Virus Evolution, 7(2), p.veab090.
- Kaplan, B.S., Kimble, J.B., **Chang, J.**, Anderson, T.K., Gauger, P.C., Janas-Martindale, A., Killian, M.L., Bowman, A.S. and Vincent, A.L., 2020. Aerosol transmission from infected swine to ferrets of an H3N2 virus collected from an agricultural fair and associated with human variant infections. Journal of Virology.

Anderson, T.K., **Chang, J.**, Arendsee, Z.W., Venkatesh, D., Souza, C.K., Kimble, J.B., Lewis, N.S., Davis, C.T. and Vincent, A.L., 2020. "Swine Influenza A Viruses and the Tangled Relationship with Humans." Cold Spring Harbor Perspectives in Medicine, p.a038737.

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Dowell, M., Feldman, K., Blythe, D., Radebaugh, M., Kough, E., Bachaus, B., Crum, D., Perkins, K., Blanton, L., Davis, C., Jang, Y., Vincent, A., **Chang, J.**, Abney, D., Gudmundson, L., Brewster, M., Polksy, L., Rose, D., "Influenza A(H3N2) Variant Virus Outbreak at Three Fairs – Maryland, 2017", *MMWR Morb Mortal Wkly Rep* 2018;67:1167-1173. DOI: <http://dx.doi.org/10.15585/mmwr.mm6742a1>

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Tepper, C., Gaynor, S. and **Chang, J.**, "Cryptic Speciation or Intragenomic Variation: Implications for the Millepores (Fire Coral)", *14th Symposium on the Natural History of the Bahamas.*, pp.20, 2011.