

# Jennifer Chang, Ph.D.

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CONTACT INFORMATION      **LinkedIn:** [www.linkedin.com/in/jenchang212](http://www.linkedin.com/in/jenchang212)  
**GitHub:** <http://github.com/j23414>

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*

- 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 the genetic diversity.
- 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, John Anderson, Jover Lee, John Huddleston

**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 recombination.
- 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-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., Polsky, 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