Jennifer Chang, Ph.D.

CONTACT
INFORMATION

LinkedIn: www.linkedin.com/in/jenchang212
GitHub: http://github.com/j23414

SUMMARY

Bioinformatics and workflow developer with 8+ years of experience. Written workflow orchestration pipelines (Snakemake, Nextflow, WDL, Slurm) and for public health workflows (Nextstrain, GATK). Track record of open-source contributions, cross-institution collaboration, and translating research into tools used by labs and agencies. Prior work includes developing C++ stand-alone software for systems biology network analysis, co-founding a tech startup, creating automated USDA flu in swine surveillance reports, and working at a Bioinformatic Core to support HPC scientific computing across USDA SCINet.

EDUCATION

Ph.D. in **Bioinformatics and Computational Biology**   *Aug 2011 – June 2017*
minor in **Statistics**

Dissertation: "Designing an integrated system for biological network exploration"

Iowa State University, Ames, Iowa 50010, USA

GPA: 3.71/4.00

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*
Contributed 300+ GitHub PRs to Nextstrain; authored tutorials and supported users via office hours, discussion board, and help email. While the major workflow language used in the project is Snakemake, minor wrapping of Nextstrain tools in WDL (for Terra.bio) and Nextflow as needed. Actively sought balance in standardization of workflows in a pathogen-repo-guide while allowing for bespoke solutions to help spin up various pathogen pipelines, including dengue, Lassa, WNV, mumps, and norovirus. Collaboratively produced seasonal influenza surveillance reports, integrating phylogenetics + antigenic data to inform projections. Delivered a Nextstrain workshop at VEME 2023; training 50+ researchers on real-time phylogenetics on location in South Africa. Published collaborative papers
40 hrs/wk. Supervisors: Trevor Bedford, Jover Lee

Bioinformatics Consultant (remote Nextstrain)   textslNov 2021 – Sept 2022
Remote contract work primarily contributing to the Nextstrain project. Implemented an initial Nextstrain pipeline in WDL, published it to Dockstore, and ran it on Terra.bio with the goal of providing accessible cloud computing for large-scale pathogen pipelines within Africa PGI. Collected initial benchmarks comparing compute costs and newly processed data, and created pipeline visualizations for feedback and documentation. Participated in regular online meetings, summarized research papers, while learning the teams coding and review practices. 40 hrs/wk. Supervisors: Trevor Bedford, John Huddleston

Bioinformatics Post-Doc, ORISE SCINet Fellow USDA-ARS   *Jun 2020 – Nov 2021*
ORISE SCINet Fellowship is part of the Big Data initiative to encourage cross-disciplinary, cross-location research: Contribute to and improve tutorials in the bioinformatics workbook (WGCNA). Participate in the development of and co-lead workshops on data analysis for USDA scientists. Collaborate with USDA scientists to analyze high-throughput sequencing datasets that lead to the publication of collaborative peer-reviewed publications. Designed and coordinated SCINet Corner starting in April 2021. SCINet Corner is a monthly virtual meeting space where USDA researchers from across the USA meet, share HPC best practices, listen to demos, and network. Drafted the GATK pipeline in Nextflow for Hufford Lab. Drafted the VGP Assembly pipeline in Nextflow for the ag100pest group.
`https://bioinformaticsworkbook.org/`
40 hrs/wk. Supervisors: Andrew Severin, Brian Scheffler

Post-Doctoral Computational Biologist, ORISE Fellow USDA-ARS   *Aug 2017 – Jun 2020*
Using R, Bash, and Perl in computational and statistical analysis of influenza A viruses (IAV) in swine. Collaborate with lab colleagues to develop scientific study designs for specific scientific objectives either in pigs or computational models. Prepare the quarterly surveillance report using Sweave every 3 months and present the information to scientists in multiple locations over conference calls. Select 21 virus for whole genome sequences each month which are later deposited and shared on NCBI GenBank.
40 hrs/wk. Supervisor: Amy Baker

Co-Founder Complex Computation, LLC; Ames, Iowa, USA   *July 2015 – August 2017*
Co-founder to market Mango Graph Studio where the company provides software solutions and workshops on network analysis. Served as PI for the DARPA SBIR Contract W911NF-15-P-0040 in 2015 and for the DARPA SBIR Contract W911NF-17-P-0014 in 2016 and prepared monthly progress reports on findings. Part of the first cohort of the Iowa State University StartUp Factory in 2016. Led a team of 3 software and electrical engineers to design and develop methods on signal analysis. 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*
Lucy2: updated the wxWidgets GUI, http://www.complex.iastate.edu/download/Lucy2/index.html
Since the update in 2013, Lucy2 has been downloaded over 700 times on all platforms (Mac, Windows, Linux)
Mango: designed and developed a network visualization software with a new graph exploration language (Gel). Won Plant Sciences Institute Scholar Grant in 2015. Presented and won awards at several conferences, see Conferences section. Mango has been licensed to Complex Computation, LLC.
20 hrs/wk. Supervisor: Hui-Hsien Chou

Teaching Assistant GEN 409 Molecular Genetics; Iowa State University   *Fall 2016*
The principles of molecular genetics: gene structure and function at the molecular level. Graded exams and homework and provided detailed feedback.
20 hrs/wk. Supervisor: Yanhai Yin

Teaching Assistant BCB 444 Introduction to Bioinformatics; Iowa State U. *Fall 2013, 2014, 2015*
Ran weekly 2-hour lab sections teaching bioinformatics command-line tools, perl, genome assembly, and genome annotation to a mixture of undergraduate and graduate students. Provided mentoring and remedial help outside of lab and class times. Graded weekly assignments and exams. Authored and presented the systems biology lecture. Occasionally answered questions on study design for graduate students depending on time available.
20 hrs/wk. Supervisor: Hui-Hsien Chou

Research Assistant Lab of Dr. Eve Wurtele; Iowa State U.   *Nov 2011 – Feb 2012*
Reprogrammed the Fuzzies game in the Unity3D environment. The game provides an interactive interface for learning basic genetic concepts.
20 hrs/wk. Supervisor: Eve Wurtele

Research Assistant Lab of Dr. Di Cook; Iowa State U.   *Sept 2011 – Nov 2011*
Proof-read biovizbase, a Bioconductor package. Developed an exon splicing visualization function for ggbio, written in R. Presented the results to peers in a statistical graphics group and a bioinformatics graduate student group.(https://github.com/j23414/Exon-Junction-Arches.git)
20 hrs/wk. Supervisor: Di Cook

Webteam Student Worker; Cornell College   *Aug 2007 – May 2011*
Update the college website, provide website development training to students and faculty.

Research Assistant Lab of Dr. Craig Tepper; Cornell College   *Mar 2011*
Performed Sanger sequencing of fire coral samples collected from the Bahamas for a conference publication. Wrote a protocol for using 4Sale, a tool for synchronous RNA sequence and secondary structure alignment and editing.

Programmer The Squirt Project: Building a Holonomic Turtle-Bot; Cornell College   *Aug 2008 – Apr 2009*

Worked in a team of four to design and build "Squirt," a holonomic tri-wheeled turtle-bot. A robot is holonomic if the number of degrees of freedom is greater than or equal to the total degrees of freedom. Squirt is holonomic because the drivetrain is composed of three omni-wheels mounted on the sides of an equilateral triangle. Programmed the Squirt to be autonomously and right-wall following and presented at the Cornell College Student Symposium.
part-time, varied hrs/week. Supervisor: Andy Wildenberg

Honours and Awards	Collegian Innovation and Leadership Winner, Iowa Women of Innovation	*2016*
	Teaching Excellence Award, Iowa State University	*2015*
	Dale W. Young and W.E. Loomis Award	*2015*
	James Cornette Fellowship	*2014*
	NSF IGERT Fellowship	*2011*
	Outstanding Junior Award, Cornell College	*2010*
	First Year Computer Science Student Achievement Award, Cornell College	*2008*
	State 2nd Place in Java Programming, Future Business Leaders of America,	*2007*

PUBLICATIONS   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. polishCLR: 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.

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

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.

Bioinformatics & Computational Biology Graduate Student Organization   *2011 − 2017*
Provide bioinformatics related consultant work on Iowa State University Campus. Mentored two students in a project converting R code to C code. In 2014 and 2015, helped design and run the Unix and Python Workshops, each workshop lasting 4 hours. Taught Advanced Unix in Spring 2016.

GDCB Technology Committee   *2013 − 2016*
For the Genetics, Development and Cellular Biology (GDCB) department, attended monthly meetings and provided website design feedback and outreach. Authored and distributed a form for student feedback.

Cornell College Computer Club   *Aug 2010 – May 2011*

Led one of three teams in an all-campus autonomous robot competition. Trained team members on programming VEX Robots.

Sustained Dialogue Campus Network

Head Moderator   *Aug 2010 – May 2011*

Provided training to student moderators. Led weekly moderator meetings to provide feedback and keep track of dialogue groups. Served as liason between e-board and moderators.

Vice-President   *Aug 2009 – May 2010*

Compiled and authored over 10 documents and workshops to train student moderators. Updated and interpreted internal files. Raised over $4000 to send 20 students to the National Conference at Princeton University. Held monthly phone conference calls with national headquarters located in Washington, DC. As a result of revitalizing the organization and increasing campus impact, received the 2010 Outstanding Junior Award.

PROGRAMMING   Snakemake, Nextflow, WDL, Bash, R, Python, Perl, C++, wxWidgets, OpenGL, Java

CONFERENCES
& WORKSHOPS

ACM SIGCHI Conference on Human Factors in Computing Systems   *May 5-10, 2012*

International Symposium on Bioinformatics Research and Applications   *May 21-23, 2012*

Danforth Center Fall Symposium   *Sept 26-28, 2012*
Poster: "Bioinformatics Laboratory (BCBLab)"

CRA-W Graduate Cohort Workshop   *Apr 5-6, 2013*

PSI Phenomics Workshop   *Nov 14,2014*
Talk: "Large biological graph data analysis using Mango"

Statistical Graphics Group Meeting   *Mar 5, 2015*
Talk: "Mango: an integrated environment for network visualization and exploration"

Bioinformatics and Computational Biology Retreat & Symposium   *Mar 27, 2015*
Poster: "Mango: an environment for analyzing and exploring multiple networks"

PAG Plant and Animal Genome Conference   *Jan 9-13 2016*
Poster: "Mango: an environment for combining heterogeneous networks"
Computer Demo: "Mango: an environment for combining heterogeneous networks"

BCBGSO Unix and Python Workshop Series   *Jan 28-30, 2016*
Talk: "Advanced Unix Workshop: working with grep, sed, and awk"

Statistical Graphics Group Meeting   *Feb 25, 2016*
Discussion Leader: "Michael Friendly paper 'The Golden Age of Statistical Graphics'"

Bioinformatics and Computational Biology Retreat & Symposium   *Mar 25, 2016*
Poster: "Mango: an environment for analyzing and exploring multiple networks"
Voted 1st place for Best Poster

3rd Annual Graduate & Professional Students' Research Conference   *April 12, 2016*
Innovative Inventions: "Mango: an environment for combining massive heterogeneous networks"
Outstanding Innovative Invention Award

Digital Agriculture Spoke All-Hands Meetings   *May 16-17, 2016*
Poster: "Mango: an environment for combining massive heterogeneous networks"

StartUp Factory Iowa State University Research Park   *Jun - Dec 2016*
http://www.isupark.org/news-events/news/startup-factory-provides-new-o
StartUp: Complex Computation, LLC
Attendees: **Jennifer Chang**, Hui-Hsien Chou, William Ash

DARPA/MTO M3IC Kick-Off Meeting Durham, NC   *Mar 29 - 30, 2017*
Magnetic Miniaturized and Monolithically Integrated Components (M3IC) meeting for the DARPA
SBIR Phase I Contract W911NF-17-P-0014
Talk: Complex Computation, LLC Phase I Progress Report

IEEE BIBM 2017 Kansas City, MO   *Nov 13 - 16, 2017*
IEEE International Conference on Bioinformatics and Biomedicine
Workshop: The 8th Integrative Data Analysis in Systems Biology
Workshop Paper: "Cavatica: a pipeline for identifying author adoption trends among software or
methods"
Authors: **Jennifer Chang**, Hui-Hsien Chou

NSF Cyber Carpentry Workshop Chapel Hill, NC   *Jul 16 - 27, 2018*
Data Lifecycle Training
Project Proposal: Cavatica. Led 2 teams to containerize Cavatica as Docker and Singularity images
over the course of a week. Each team composed of 5 graduate students or post doctorates from
different universities and fields ranging from biology, statistics to social science. Answered coding
questions as needed.

CANA: Center for Applied Network Analysis University of Southern California *Oct 12, 2018*
Valente directs the Center for Applied Network Analysis (CANA) which hosts a twice monthly, two-
hour, lab meeting in which students, post-docs, and faculty present work in progress. Connected to
the group via Anuja Majmundar from the 2018 NSF CyberCarpentry Workshop.
Talk: Mango Graph Studio and social network applications.

CRWAD: Conference of Research Workers in Animal Disease Chicago, IL *Dec 1 - 4, 2018*
Poster: "Spatial and temporal patterns of swine IAV gene constellations in the USA from 2010 to
2018"
Authors: **Jennifer Chang**, Tavis K. Anderson, Amy L. Vincent

Student Research Symposium San Diego State University   *Mar 1 - 2, 2019*
Grew out of a collaboration after meeting Anuja Majmundar at the 2018 NSF CyberCarpentry. They
used Cavatica to research E-Cigarettes and Social Media.
Poster: "Network Analysis of Social Media Data-Based Research on Electronic Cigarettes"
Authors: Taylor Perry, Christian Dominguez, **Jennifer Chang**, Anuja Majmundar, Erlinde Cornelis

Iowa State Research Day Iowa State University   *Mar 28, 2019*
Poster: "N2 NA coordinated evolution with HA increases influenza A virus genetic diversity in swine"
Authors: Micheal A. Zeller, **Jennifer Chang**, Tavis K. Anderson, Amy L. Vincent, Phillip C. Gauger

PyCon 2019: Python Software Foundation, Cleveland, OH   *May 1 - 9, 2019*
Poster: "Making Python libraries machine accessible"
Authors: Zebulun W. Arendsee, **Jennifer Chang**, Andrew Wilkey

CEIRS 10th CEIRS Annual Meeting, Baltimore, MD   *June 23-26, 2019*
Poster: "Spatial and temporal patterns of swine IAV gene constellations and reassortment in the USA from 2009 to 2019"
Authors: **Jennifer Chang**, Tavis K. Anderson, Amy L. Vincent
Talk: "Antigenic distance of North American swine influenza A virus (H3N2) and human H3N2 seasonal strains as an indication of risk to human populations"
Authors: Carine K. Souza, Divya Venkatesh, Tavis K. Anderson, **Jennifer Chang**, Nicola Lewis, Susan E. Detmer, Ignacio Mena, Marie Culhane, Martha Nelson, Adolfo Garcia-Sastre, Amy L. Vincent
Talk:"Molecular determinants facilitating sustained interspecies transmission of human H3N2 influenza A virus in United States pigs"
Authors: Joshua D. Powell, Eugenio J. Abente, Carine K. Souza, **Jennifer Chang**, Daniela S. Rajao, Tavis K. Anderson, Amy L. Vincent

CRWAD: Conference of Research Workers in Animal Disease Chicago, IL *Nov 2 - 5, 2019*
Talk: "Evolutionary diversification of clade 1A.3.3.3 H1 swine influenza A viruses and zoonotic risk in the United States"
Authors: Tavis K. Anderson, Kelly F. Hewitt, **Jennifer Chang**, Michael A. Zeller, Divya Venkatesh, Nicola S. Lewis, Amy L. Vincent

ISMB: 28th Conference on Intelligent Systems for Molecular Biology   *July 13 - 16, 2020*
Virtual Attendee: `https://iscb-ismb20.myconferencenow.com`

BCC2020: Bioinformatics Community Conference   *July 16 - 21, 2020*
Virtual Attendee: `https://bcc2020.sched.com`

Arthropod Genomics Symposium 2020   *July 21 - 23, 2020*
Virtual Attendee: `https://bcc2020.sched.com`

USDA-ARS Software Carpentry Workshop   *Aug 18 - 19, 2020*
Virtual Helper: `https://s-canchi.github.io/2020-08-18-USDA/`

SCINet Geospatial Workshop   *Aug 25 - 31, 2020*
Virtual Attendee: `https://kerriegeil.github.io/SCINET-GEOSPATIAL-RESEARCH-WG/`

9th Annual Geo for Good Summit   *Oct 20 - 21, 2020*
Virtual Attendee: `https://earthoutreachonair.withgoogle.com/events/geoforgood20`

GLBIO 2021: Great Lakes Bioinformatics Conference   *May 10 - 13, 2021*
Poster: "morloc: type-directed code generation can reduce the hassle of developing scientific software"
Authors: Zebulun Arendsee, **Jennifer Chang**
`https://www.iscb.org/glbio2021`

13th Annual SISMID 2021   *July 7- 23, 2021*
Summer Institute in Statistics and Modeling in Infectious Diseases
Module 2: "Mathematical Models of Infectious Diseases" Instructors: Micaela Martinez; Marc Lipsitch"
Module 5: "Spatial Statistics in Epidemiology and Public Health" Instructors: Jonathan Wakefield; Lance Waller"
Module 8: "MCMC I for Infectious Diseases" Instructors: Kari Auranen; M. Elizabeth Halloran; Vladimir Minin"
Module 13: "Pathogen Evolution, Selection, and Immunity" Instructors: Trevor Bedford; Sarah Cobey"
`https://si.biostat.washington.edu/suminst/sismid2021/modules`

SISMID and SISCER 2023 *July 10- 19, 2023*
Summer Institutes at University of Washington
CR2301: "Design and Analysis of Clinical Trials" Instructors: Michael Proschan, Pamela Shaw
CR2305: "Evaluation of Biomarkers and Risk Models" Instructors: Kathleen Kerr
MD2310: "Infectious Diseases, immunology and Within-Host Models" Instructors: Andreas Handel, Paul G Thomas

VEME 2023 Stellenbosch, South Africa *Aug 20 - 26, 2023*
The Virus Evolution and Molecular Epidemiology Workshop
Tutorial Teacher: "Real-time tracking of pathogen evolution using Nextstrain"
Teacher: **Jennifer Chang**, Tutorial Writer: John Huddleston, TA: Nashwa Ahmed
`https://veme.climade.health/`

PAG 2024 San Diego, CA, USA *Jan 12 - 17, 2024*
International Plant and Animal Genome
Poster: "GATK-Flow: Deploying GATK Best Practices for Variant Discovery through a Nextflow Workflow"
Authors: Viswanathan Satheesh, **Jennifer Chang**, Arun S. Seetharam, Matthew B. Hufford, Andrew J. Severin
Talk: "Deploying GATK Best Practices for Variant Discovery"
Speaker: Viswanathan Satheesh, **Jennifer Chang**, Arun S. Seetharam, Matthew B. Hufford, Andrew J. Severin
`https://www.intlpag.org/31/`

CRWAD 2024 Chicago, USA *Jan 20 - 23, 2024*
Conference of Research Workers in Animal Diseases
Talk: "Streamlining classification of PRRSV-2 ORF5 lineages and sublineages using Nextclade"
Presenter: Michael Zeller, Co-authors: **Jennifer Chang**, Phillip C Gauger, Jianqiang Zhang, Giovani Trevisan
`https://crwad.org/`

IVPS and ESPHM 2024 Leipzig, Germany *Jun 4 - 7, 2024*
27th International Pig Veterinary Society Congress, 15th European Symposium of Porcine Health Management
Poster: "Streamlining PRRSV-2 ORF5 classification using Nextclade"
Presenter: Giovani Trevisan, Co-authors: Michael Zeller, **Jennifer Chang**, Roger Main, Phillip C Gauger, Jianqiang Zhang
`https://www.ipvs2024.com/`

VGEB 2024 Wellcome Genome Campus, UK *Nov 6 - 8, 2024*
Virus Genomics, Evolution and Bioinformatics Conference
Poster: "New Nextstrain resources for real-time genomic surveillance of multiple pathogens"
Presentor: Kimberly R. Andrews, Co-authors: **Jennifer Chang**, Jover Lee, Cornelius Roemer, Laura Urbanska, Louise H. Moncla, Miguel Paredes, Marcela Torres, Ivan Aksamentov, James Hadfield, Emma B. Hodcroft, John Huddleston, Victor Lin, Thomas Sibley, John S.J. Anderson, Richard A. Neher, Trevor Bedford
`https://coursesandconferences.wellcomeconnectingscience.org/`

APVS 2025 Fukuoka, Japan *Nov 9-12, 2025*
Poster: Standardized classification of common porcine viral pathogens using Nextclade
Presenter: Michael A Zeller, **Jennifer Chang**, Giovani Trevisan, Pablo Pineyro, Phillip C Gauger, Jianqiang Zhang, Rodger G Main