

Louise Hillier Moncla

Curriculum vitae

H318, Hill Pavilion
University of Pennsylvania
380 South University Ave
Philadelphia, PA, 19104
(1)412-848-3244
lhmoncla@upenn.edu
lhmoncla@gmail.com
Github: github.com/lmoncla
Twitter: @LouiseHMoncla

I. Education and employment

- 2022-** **Assistant Professor (tenure-track)**
Department of Pathobiology, School of Veterinary Medicine
University of Pennsylvania, Philadelphia, PA
- 2017-2022** **Post-doctoral Research Fellow**
Mentor: Dr. Trevor Bedford
Fred Hutchinson Cancer Research Center, Seattle, WA
- 2012-2017** **Ph.D. in Microbiology**
Mentor: Dr. Thomas Friedrich
Thesis title: "Disentangling the relative contributions of selection and stochastic processes in RNA virus evolution"
University of Wisconsin-Madison, Madison, WI
- 2008-2012** **Bachelor of Science in Biology**, Genetics and Development (Distinction and Honors)
Bachelor of Musical Arts (High Distinction)
Mentor: Dr. Beth Shapiro (2010-2012)
Honors thesis title: "An Examination of Polar Bear and Brown Bear Phylogeny Using Nuclear Genes as Molecular Markers"
The Pennsylvania State University, University Park, PA

II. Research

Research grants

- 2023-2024 **Center for Research on Coronaviruses and Other Emerging Pathogens Pilot and Feasibility Grant**
"Developing a framework for H5N1 sequencing and transmission inference in Pennsylvania"
Direct costs: \$50,000, **Role: PI**
- 2022-2024 **Margaret Q. Landenberger Research Foundation Grant**
"Reconstructing the ecological and evolutionary drivers of H5Nx cross-species transmission."
Direct costs: \$200,000, **Role: PI**
- 2022-2025 **CDC Broad Agency Announcement: "Applied Research to Address Emerging Public Health Priorities"**
"Impact of local differences in vaccine uptake on SARS-CoV-2 evolution and spread across three Upper Midwestern states"
Direct costs to lab: \$195,277, **Role: Co-Investigator**
- 2020-2024 **K99/R00 Pathway to Independence Award, NIAID/NIH**, impact score: 10
"Quantifying the genetic and environmental factors driving avian influenza spillover"
Direct costs: \$555,962, **Role: PI**

Peer-reviewed publications

‡ denotes corresponding author, * denotes equal contribution, [Google Scholar link](#)

1. Katarina M. Braun*, Luis A. Haddock III*, Chelsea M. Crooks, Gabrielle L. Barry, Joseph Lalli, Gabriele Neumann, Tokiko Watanabe, Masaki Imai, Seiya Yamayoshi, Mutsumi Ito, **Louise H. Moncla**, Katia Koelle, Yoshihiro Kawaoka, Thomas C. Friedrich. "Avian H7N9 influenza viruses are evolutionarily constrained by stochastic processes during replication and transmission in mammals." **Virus Evolution**, January 19, 2023, 2023, DOI:10.1093/ve/vead004.
2. Claudia P Arevalo, Marcus J Bolton, Valerie Le Sage, Naiqing Ye, Colleen Furey, Hiromi Muramatsu, Mohamad-Gabriel Alameh, Norbert Pardi, Elizabeth M Drapeau, Kaela Parkhouse, Tyler Garretson, Jeffrey S Morris, **Louise H Moncla**, Ying K Tam, Steven HY Fan, Seema S Lakdawala, Drew Weissman, Scott E Hensley. "A multivalent nucleoside-modified mRNA vaccine against all known influenza virus subtypes". **Science**, November 25, 2022, DOI: 10.1126/science.abm0271.
3. Katarina Braun*, Gage Moreno*, Cassia Wagner, Molly A. Accola, William M. Rehrauer, David Baker, Katia Koelle, David H. O'Connor, Trevor Bedford, Thomas C. Friedrich‡, **Louise H. Moncla‡**. "Acute SARS-CoV-2 infections harbor limited within-host diversity and transmit via tight transmission bottlenecks." **PLOS Pathogens**, August 23, 2021, DOI: 10.1371/journal.ppat.1009849. ‡ **Corresponding author**
4. **Louise H. Moncla*‡**, Allison Black*, Chas DeBolt, Misty Lang, Nicholas R. Graff, Ailyn C. Pérez-Osorio, Nicola F. Müller, Dirk Haselow, Scott Lindquist, Trevor Bedford‡. "Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State." **eLife**, April 19, 2021, DOI: 10.7554/eLife.66448. *‡ **Co-first and co-corresponding author**
5. Nicola F. Müller‡, Cassia Wagner*, Chris D. Frazar*, Pavitra Roychoudhury*, Jover Lee, **Louise H. Moncla**, Benjamin Pelle, Matthew Richardson, Erica Ryke, Hong Xie, Lasata Shrestha, Amin Addetia, Victoria M. Rachleff, Nicole A. P. Lieberman, Meei-Li Huang, Romesh Gautom, Geoff Melly, Brian Hiatt, Philip Dykema, Amanda Adler, Elisabeth Brandstetter, Peter D. Han, Kairsten Fay, Misja Ilcisin, Kirsten Lacombe, Thomas R. Sibley, Melissa Truong, Caitlin R. Wolf, Michael Boeckh, Janet A. Englund, Michael Famulare, Barry R. Lutz, Mark J. Rieder, Matthew Thompson, Jeffrey S. Duchin, Lea M. Starita, Helen Y. Chu, Jay Shendure, Keith R. Jerome, Scott Lindquist, Alexander L. Greninger‡, Deborah A. Nickerson‡, Trevor Bedford‡. "Viral genomes reveal patterns of the SARS-CoV-2 outbreak in Washington State". **Science Translational Medicine**, May 3, 2021, DOI: 10.1126/scitranslmed.abf0202.
6. Bedford T, Greninger AL, Roychoudhury P, Starita LM, Famulare M, Huang ML, Nalla A, Pepper G, Reinhardt A, Xie H, Shrestha L, Nguyen TN, Adler A, Brandstetter E, Cho S, Giroux D, Han PD, Fay K, Frazar CD, Ilcisin M, Lacombe K, Lee J, Kiavand A, Richardson M, Sibley TR, Truong M, Wolf CR, Nickerson DA, Rieder MJ, Englund JA, Hadfield J, Hodcroft EB, Huddleston J, **Moncla LH**, Müller NF, Neher RA, Deng X, Gu W, Federman S, Chiu C, Duchin J, Gautom R, Melly G, Hiatt B, Dykema P, Lindquist S, Queen K, Tao Y, Uehara A, Tong S, MacCannell D, Armstrong GL, Baird GS, Chu HY, Shendure J, Jerome KR. "Cryptic Transmission of SARS-CoV2 in Washington State." **Science**, October 30, 2020, DOI: 10.1126/science.abc0523
7. **Louise H. Moncla‡**, Trevor Bedford, Philippe Dussart, Srey Viseth Horm, Sareth Rith, Philippe Buchy, Erik A. Karlsson, Lifeng Li, Yongmei Liu, Huachen Zhu, Yi Guan, Thomas C. Friedrich, Paul F. Horwood‡. "Quantifying within-host diversity of H5N1 influenza viruses in humans and poultry in Cambodia." **PLOS Pathogens**, January 17, 2020, DOI: 10.1371/journal.ppat.1008191. ‡ **Co-corresponding author**
8. Allison Black*, **Louise H. Moncla***, Katherine Laiton-Donato, Barney Potter, Lissethe Pardo, Angelica Rico, Catalina Tovar, Diana P. Rojas, Ira M. Longini, M. Elizabeth Halloran, Dioselina

Peláez-Varvajal, Juan D. Ramírez, Marcela Mercado-Reyes, Trevor Bedford[‡]. [“Genomic Epidemiology supports multiple introductions and cryptic transmission of Zika virus in Colombia.”](#) **BMC Infectious Diseases**, November 12, 2019. * **Co-first author**

9. YQ Shirleen Soh, **Louise H. Moncla**, Rachel Eguia, Trevor Bedford, Jesse D. Bloom. [“Comprehensive mapping of the avian influenza polymerase protein PB2 to humans.”](#) **eLife**, April 30, 2019.
10. Mauricio A. Salvo, Mathew T. Aliota, **Louise H. Moncla**, ID Velez, AL Trujillo, Thomas C. Friedrich, Jorge E. Osorio[‡]. [“Tracking dengue virus type 1 genetic diversity during lineage replacement in an hyperendemic are in Colombia.”](#) **PLOS One**, March 7, 2019.
11. Hirotaka Imai, Jorge M. Dinis, Gongxun Zhong, **Louise H. Moncla**, Tiago J.S. Lopexs, Ryan McBride, Andrew J. Thompson, Wenjie Peng, Mai thi Q. Le, Anthony Hanson, Michael Lauck, Yuko Sakai-Tagawa, Shinya Yamada, Julie Eggenberger, David H. O’Connor, Yasuo Suzuki, Masato Hatta, James C. Paulson, Gabriele Neumann, Yoshihiro Kawaoka[‡]. [“Diversity of influenza A\(H5N1\) viruses in infected humans, northern Vietnam, 2004-2010.”](#) **Emerging Infectious Diseases** 24, 7, July 2018.
12. Katherine S. Xue, **Louise H. Moncla**, Trevor Bedford, Jesse D. Bloom[‡]. [“Within-host evolution of human influenza virus.”](#) **Trends in Microbiology**, March 10, 2018.
13. Maki Kiso, Kiyoko Iwatsuki-Horimoto, Seiya Yamayoshi, Ryuta Uraki, Mutsumi Ito, Eiryō Kawakami, Yuriko Tomita, Satoshi Fukuyama, Tiago J.S. Lopes, Tokiko Watanabe, **Louise H. Moncla**, Thomas C. Friedrich, Gabriele Neumann, Yoshihiro Kawaoka[‡]. [“Emergence of oseltamivir-resistant H7N9 influenza viruses in immunosuppressed cynomolgus macaques.”](#) **Journal of Infectious Diseases**, Volume 216, issue 5, September 1, 2017.
14. **Louise H. Moncla**, Nicholas W. Florek, Thomas C. Friedrich[‡]. [“Influenza evolution: new insights into an old foe.”](#) **Trends in Microbiology**, June 25, 2017. PMID: 28478941.
15. **Louise H. Moncla**, Andrea M. Weiler, Gabrielle Barry, Jason Weinfurter, Jorge M. Dinis, Olivia Charlier, Michael Lauck, Adam Bailey, Jens Kuhn, Victoria Wahl-Jensen, Joshua C. Johnson, Peter B. Jahrling, Tony L. Goldberg, David H. O’Connor, Thomas C. Friedrich[‡]. [“Within-host evolution of simian arteriviruses in crab-eating macaques.”](#) **Journal of Virology**, August 12, 2016.
16. Elizabeth A. Caine, **Louise H. Moncla**, Monica Ronderos, Thomas C. Friedrich, Jorge E. Osorio[‡]. [“A Single Mutation in the VP1 of Enterovirus 71 is Responsible for Increased Virulence and Neurotropism in Adult Interferon Deficient Mice.”](#) **Journal of Virology**. July 20, 2016. PMID: 27440896.
17. Dudley DM, Aliota MT*, Mohr EL*, Weiler AM, Lehrer-Brey G, Weisgrau KL, Mohns MS, Breitbach ME, Rasheed MN, Newman CM, Gellerup DD, **Moncla LH**, Post J, Schultz-Darken N, Schotzko ML, Hayes JM, Eudailey JA, Moody MA, Permar SR, O’Connor SL, Rakasz EG, Simmons HA, Capuano S, Golos TG, Osorio JE, Friedrich TC, O’Connor DH[‡]. [“A rhesus macaque model of Asian-lineage Zika virus infection.”](#) **Nature Communications**; 7:12204. Jun 28, 2016.
18. **Louise H. Moncla**, Gongxun Zhong, Chase W. Nelson, Austin L. Hughes, James Mutschler, Tokiko Watanabe, Yoshihiro Kawaoka, Thomas C. Friedrich[‡]. [“Selective bottlenecks shape evolutionary pathways taken during mammalian adaptation of a 1918-like avian influenza virus.”](#) **Cell Host and Microbe** 19, 169-190, February 10, 2016. **(Featured Article)**
19. Victoria Wahl-Jensen, Joshua Johnson*, Michael Lauck, Jason Weinfurter, **Louise Moncla**, Andrea Weiler, Olivia Charlier, Oscar Rojas, Russell Byrum, Dan Ragland, Louis Huzella, Erika Zommer, Melanie Cohen, John Bernbaum, Yíngyún Cai, Hannah Sanford, Steven Mazur, Reed Johnson, Gustavo Palacios, Adam Bailey, Peter Jahrling, Tony Goldberg, David O’Connor,

Thomas Friedrich, and Jens Kuhn[‡]. “Divergent simian arteriviruses cause simian hemorrhagic fever of different severity in macaques.” **MBio**. 2016 February 23; 7(1).

20. Jorge M. Dinis, Nicholas W. Florek*, Omolayo O. Fatola, **Louise H. Moncla**, James P. Mutschler, Jennifer K. Meece, Edward A. Belongia, Thomas C. Friedrich[‡]. “Deep sequencing reveals potential antigenic drift variants at low frequency in influenza A-infected humans.” **Journal of Virology**. 2016 January 6.
21. Nelson CW, **Moncla LH**, Hughes AL[‡]. “SNPGenie: estimating evolutionary parameters to detect natural selection using pooled next-generation sequencing data.” **Bioinformatics**. 2015 July 29.
22. **Louise H. Moncla**, Ted M. Ross*, Jorge M. Dinis, Jason T. Weinfurter, Tatum D. Mortimer, Nancy Schultz-Darken, Kevin Brunner, Saverio V. Capuano III, Carissa Boettcher, Jennifer Post, Michael Johnson, Chalise E. Bloom, Andrea M. Weiler, Thomas C. Friedrich[‡]. “A novel nonhuman primate model for influenza transmission.” **PLOS One** 8, e78750. November 14, 2013.

Submitted preprints

1. Miguel I. Paredes*, Amanda C. Perofsky, Lauren Frisbie, **Louise H. Moncla**, Pavitra Roychoudhury, Hong Xie, Shah A. Mohamed Bakhsh, Kevin Kong, Isabel Arnould, Tien V. Nguyen, Seffir T. Wendm, Pooneh Hajian, Sean Ellis, Patrick C. Mathias, Alexander L. Greninger, Lea M. Starita, Chris D. Frazar, Erica Ryke, Weizhi Zhong, Luis Gamboa, Machiko Threlkeld, Jover Lee, Jeremy Stone, Evan McDermot, Melissa Truong, Jay Shendure, Hanna N. Oltean, Cécile Viboud, Helen Chu, Nicola F. Müller, Trevor Bedford. “Local-Scale phylodynamics reveal differential community impact of SARS-CoV-2 in metropolitan US county.” **medRxiv**, December 15, 2022. DOI: <https://doi.org/10.1101/2022.12.15.22283536>.

Non-published research/tool development

Developer for nextstrain.org

Nextstrain.org is a website that provides real-time phylogenetic inference for currently circulating viruses. During the emergence of the SARS-CoV-2 pandemic in spring of 2020, I maintained and updated the SARS-CoV-2 builds daily. These updates involved curating and cleaning new full-genome sequence data deposited in public databases, running the phylogenetics pipeline, error-checking results, and using the resulting phylogeny to infer new introduction and community transmission patterns. To ensure that data submitters were credited for their contributions and to alert them to noteworthy patterns in the data, I finished each update by tweeting relevant observations from the Nextstrain twitter account (@nextstrain) with data submitters tagged.

From 2017 to present, I built and maintain the Nextstrain builds for mumps viruses and avian influenza viruses hosted at nextstrain.org/mumps/na and nextstrain.org/flu/avian. These builds track transmission of mumps virus in North America, and global avian influenza transmission and evolution patterns of H5N1, H5Nx, H7N9, and H9N2 subtypes. These builds are updated monthly.

Fellowships, Honors, and Awards

- 2023 **Scialog Fellow – Mitigating Zoonotic Threats**, *Research Corporation for Science Advancement* (2023)
- 2019 **Life Sciences Research Foundation Post-doctoral Fellowship**, *The Life Sciences Research Foundation* (2019-2020, left early upon receipt of K99/R00)
- 2019 **Best Poster Award**, *Human Biology Division Annual Retreat*, Fred Hutchinson Cancer Research Center

- 2016 **Macrae Foundation Young Investigator Award**, *XVIII International Symposium on Respiratory Viral Infections, Lisbon, Portugal*
- 2016 **Wisconsin Distinguished Graduate Fellowship**, *University of Wisconsin-Madison*
- 2016 **Student Research Travel Grant**, *University of Wisconsin-Madison*
- 2015 **Pasteur Institute Young Investigator Award**, *1st International Meeting on Respiratory Pathogens, Singapore*
- 2012 **NIH T32 Molecular Biosciences Training Grant**, *University of Wisconsin-Madison (2012-2016)*
- 2011 **Phi Beta Kappa Honors Society**
- 2008 **Schreyer Honors College Academic Scholarship**, *The Pennsylvania State University (2008-2012)*

Invited research talks

- 2023 “Plenary event: live podcast recording: Ongoing H5Nx Outbreak Live podcast recording”
Centers of Excellence for Influenza Research and Response Annual Network Meeting, *Baltimore, MD, USA (August 28, 2023)*, **plenary panelist**
- 2023 “Nextstrain as a toolkit for tracking avian influenza evolution and transmission”
Centers of Excellence for Influenza Research and Response Annual Network Meeting, *Baltimore, MD, USA (August 28, 2023)*
- 2023 “Using multi-scale genomic approaches to disentangle H5Nx evolution and cross-species transmission”
Centers of Excellence for Influenza Research and Response Computational Modeling Core Seminar Series, *virtual (August 23, 2023)*
- 2023 “Using multi-scale genomics to disentangle respiratory virus emergence and transmission”
Colorado State University, **Genomics of Disease in Wildlife Workshop Plenary speaker**, *Fort Collins, CO, USA (June 7, 2023)*, **plenary speaker**
- 2023 “Using multi-scale genomics to disentangle respiratory virus emergence and transmission”
Princeton University Infectious Disease Group seminar, *Princeton, NJ, USA (April 5, 2023)*
- 2023 “Using multi-scale genomics to disentangle respiratory virus emergence and transmission”
University of Pennsylvania, **Institute for Infectious and Zoonotic Diseases Symposium** (invited speaker), *Philadelphia, PA, USA (March 30, 2023)*
- 2023 “Using multi-scale genomics to disentangle respiratory virus emergence and transmission”
University of Georgia Infectious Disease Seminar series, *Athens, GA, USA (February 20, 2023)*
- 2022 “Using multi-scale genomics to disentangle H5N1 emergence and transmission”
American Society for Virology Annual meeting, Satellite Symposium: “Shaking the Trees: Sequence-Based Inference in Virus Ecology and Evolution”, *Madison, WI, USA (July 16, 2022)*
- 2021 “Nextstrain as a tool kit for tracking avian influenza virus evolution and transmission”
Toward Mitigating Pandemic Influenza Risk: A regional consultation on avian influenza surveillance in Asia, *virtual (December 2, 2021)*
- 2020 “Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State”

UC Berkeley Evolution Seminar Series, virtual (December 2, 2020)

- 2020 "Harnessing viral genomics to interrogate SARS-CoV2 transmission at the community to individual scale"
Chilean Genetics Society annual meeting, Roche invited speaker, virtual (November 25, 2020)
- 2020 "Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State"
Virus Evolution Seminar Series, joint-hosted by University of Wisconsin-Madison and UC Davis, virtual (November 23, 2020)
- 2020 "Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State"
Vaccine and Infectious Disease Departmental Scientific Seminar Series, Fred Hutchinson Cancer Research Center, Seattle, WA, virtual (May 5, 2020)
- 2018 "Genomic characterization of H5N1 spillover infection in humans and poultry in Cambodia"
Institut Pasteur du Cambodge, Phnom Penh, Cambodia (September 5, 2018)

Oral research presentations (submitted abstracts)

- 2023 "Viral genotype and endemic circulation increase risk of H5Nx human infection"
Centers of Excellence for Influenza Research and Response Annual Network Meeting, Baltimore, MD, USA (August 29, 2023)
- 2018 "Genomic characterization of H5N1 spillover infection in humans and poultry in Cambodia"
Orthomyxovirus 2018 Conference, Hanoi, Vietnam (September 12-14, 2018)
- 2018 "Genomic reconstruction of a mumps virus outbreak in Washington state"
Models of Infectious Disease Agent Study network meeting, Washington D.C, USA (April 3-5, 2018)
- 2016 "Selective bottlenecks shape evolutionary pathways taken during mammalian adaptation of a 1918-like avian influenza virus"
The Macrae Foundation's XVIII International Symposium on Respiratory Viral Infections, Lisbon, Portugal (March 31-April 2, 2016)
- 2015 "Selective bottlenecks shape evolutionary pathways taken during mammalian adaptation of a 1918-like avian influenza virus"
1st International Meeting on Respiratory Pathogens, Furama Riverfront, Singapore (September 2-4, 2015)
- 2013 "A novel nonhuman primate model for influenza transmission."
Joint University of Minnesota-University of Wisconsin Virology Training Grant Symposium, University of Wisconsin-La Crosse, La-Crosse, WI, USA

Poster presentations (submitted abstracts)

- 2019 "Quantifying within-host evolution of H5N1 viruses in humans and poultry in Cambodia"
Options X for the Control of Influenza, Singapore
- 2016 "Quantifying the limits of accurate and reproducible influenza sequencing"
Options IX for the Control of Influenza, Chicago, Illinois, USA
- 2015 "Selective bottlenecks shape evolutionary pathways during mammalian adaptation of a 1918 like avian virus"

III. Professional Service

Ad-hoc peer review service

Cell Host and Microbe, Nature Communications, Nature Ecology and Evolution, eLife, PLOS Pathogens, Virus Evolution, MBio, Journal of Virology, Epidemics, Scientific Reports, Cell Reports, Cell Reports Medicine, Infection Genetics and Evolution, PLOS One, Evolution Medicine and Public Health, Communications Medicine, Ecology and Evolution, Virulence, BMC Bioinformatics, Open Forum ID, Journal of Infectious Diseases

Grant review service

Natural Sciences and Engineering Research Council of Canada Discovery Grant; Medical Research Council Career Development Award

Science communication

Podcasts

- 2023 **This Week in Virology**, live Podcast recording, Centers of Excellence for Influenza Research and Response Annual Network Meeting, August 28, 2023: <https://www.microbe.tv/twiv/>
- 2023 **The Naked Scientist, BBC** Podcast episode, “A Bird Flu Pandemic Hovering on the Horizon”, February 14, 2023: <https://www.thenakedscientists.com/podcasts/naked-scientists-podcast/bird-flu-pandemic-hovering-horizon>
- 2022 **This Week in Evolution** Podcast episode, “Viruses of a Feather Bottleneck Together”, July 29, 2022: https://www.youtube.com/watch?v=UcHmebKO_K4

Outbreak Commentary

- 2023 Commentary for **The Atlantic**, “Bird flu has never done this before.” August 8, 2023: <https://www.theatlantic.com/science/archive/2023/08/avian-flu-vaccine-wild-bird-transmission-endemic/674903/>
- 2023 Commentary for **Science News**, “Bird flu can jump to mammals. Should we worry?” March 6, 2023: <https://www.sciencenews.org/article/bird-flu-mammals-influenza-pandemic>
- 2022 Commentary for **BBC News**, “What is bird flu and how deadly is it?” November 30, 2022: <https://www.bbc.com/news/science-environment-63464065>
- 2022 **Nature News** Article, “Why is bird flu so bad right now?” October 21, 2022: <https://www.nature.com/articles/d41586-022-03322-2>
- 2020 Commentary for **Science News**, “Is the coronavirus mutating? Yes. But here’s why you don’t need to panic.” May 26, 2020: <https://www.sciencenews.org/article/coronavirus-covid19-mutations-strains-variants>
- 2020 Commentary for **KNKX radio**, “New research suggests nation's first COVID-19 case was not the source of Washington's outbreak.” May 28, 2020: <https://www.knkx.org/post/new-research-suggests-nations-first-covid-19-case-was-not-source-washingtons-outbreak>
- 2020 Commentary for **Wall Street Journal**, May 4, 2020: <https://www.wsj.com/articles/the-search-is-on-for-americas-earliest-coronavirus->

[deaths11588597831?shareToken=st53246b5625b043cb89ec5493cb64017a&reflink=article_email_share](https://www.kiro7.com/news/local/cdc-first-us-coronavirus-deaths-happened-weeks-before-first-death-kirkland/HCTCEX45XFCRVE5742JWR7ZP44/?_website=cmg-tv-10090)

2020 Commentary for **Kiro7 news**, April 22, 2020: https://www.kiro7.com/news/local/cdc-first-us-coronavirus-deaths-happened-weeks-before-first-death-kirkland/HCTCEX45XFCRVE5742JWR7ZP44/?_website=cmg-tv-10090

IV. Teaching, Mentorship and Outreach

Classroom teaching

Genomics of Disease in Wildlife Workshop, Fort Collins, CO (2023)

This workshop is an intensive, 8 day course covering computational aspects of studying diseases in wildlife. I provided 1.5 hours of lecture and 2.5 hours of computer lab instruction covering introductions to phylodynamics and Bayesian phylogenetics, and setting up and interpreting analyses with the BEAST and Nextstrain softwares. I designed each lecture and lab activity, which are publicly available on both the course website and my professional github page (<https://github.com/lmoncla/csu-genomics-disease-wildlife-workshop>).

Teaching Assistant, Biochemistry 575: Biology of Viruses (2014)

Biochemistry 575 is a course designed for undergraduate students to teach the fundamentals of virology. As a teaching assistant for this course, I provided weekly tutoring sessions, lectured, wrote exam questions, and administered and graded exams.

Mentorship

Mentored Post-docs in Moncla lab:

Lambodhar Damodaran, post-doctoral research fellow (2023-)

Mentored PhD students in Moncla lab:

Maria Maltepes, PhD student, Biology Graduate Program (2023-)

Jordan Ort, PhD student, Microbiology Virology and Parasitology Program (2023-)

Mentored rotation students in Moncla lab:

Sonja Zolnoski, PhD rotation student, Microbiology Virology and Parasitology Program (2023)

Natalie Hagan, PhD rotation student, Microbiology Virology and Parasitology Program (2023)

Thesis and advisory committees:

Andrew Marques, PhD student, Frederic Bushman lab (2023-)

Ashley Soebel-Leonard, Pediatric Infectious Disease Fellow, Scott Hensley Lab (2023-)

Olivia Pilling, PhD student, Daniel Beiting lab (2023-)

Qianzuan She, PhD student, Paul Planet lab (2023-)

Mentored students during PhD and post-doc:

Cassia Wagner, graduate student (2020-2021)

Gage Moreno, graduate student (2020-2021); *now post-doctoral researcher at the Broad Institute in the laboratory of Pardis Sabeti*

Katarina Braun, MD/PhD student (2015-2021); *now finishing medical training at University of Wisconsin*

Macy Pell, undergraduate research assistant (2015-2017); *now PhD student at Michigan State University in laboratory of Shannon Manning*

Mauricio Salvo, graduate student (2014-2017); *now research scientist at Roche*

Olivia Charlier, undergraduate research assistant (2012-2014); *now a physician's assistant*
Kelsey Florek, Microbiology Doctoral Training Program rotation student (2013); *now lead bioinformatician at the Wisconsin State Lab of Hygiene*

Outreach

Facilitator for Girls Who Code (2017-2022)

Girls who code is an outreach program targeting high-school aged girls who are interested in learning to code. During my post-doc, I have served each year as a course facilitator. As a facilitator, I volunteer with coding sessions during which participants learn fundamentals of coding in python or R, and work towards completing a coding-based project that is showcased for parents and researchers at the end of the semester. During each session, I assist in trouble shooting, answer questions, and provide general support while participants develop coding skills.

Expanding Your Horizons Outreach program (2015-2016)

Expanding Your Horizons is an outreach program intended to promote interest and confidence in middle school girls to pursue STEM fields. During my PhD, I participated as a student volunteer, where I led an activity introducing the participants to programming in python and shared my path to becoming a scientist.

Madison Science Museum Women in STEM Symposium (2016)

The Madison Science Museum Women in STEM Symposium is an event targeted to high school girls who are interested in STEM fields. The event brings in successful women working in STEM fields to speak about their career paths, the challenges they have faced and why it is important to build a diverse work environment. As a volunteer I helped register and direct participants to the talks and activities and discussed my own aspirations as a scientist with the participating young women.