

# ALEXANDER G. LUCACI, PH.D.

Email ◇ agl4001@med.cornell.edu

Website ◇ aglucaci.github.io

## EDUCATION

---

<b>Temple University</b> Ph.D. in Bioinformatics	2023
<b>New York University</b> M.S. in Biology	2018
<b>Stony Brook University</b> B.S. in Biochemistry	2011

## RESEARCH POSITIONS

---

<b>Weill Cornell Medical College</b> <i>Postdoctoral Associate</i>	July 2023 to Present <i>Advisors: Dr. Christopher E. Mason and Dr. Ari Melnick</i>
---	---

- Conducting interdisciplinary research at the interface of evolutionary biology, metagenomics, and immuno-oncology. Applying molecular sequence analysis and evolutionary theory to study genomic and transcriptomic data from cancer and microbial systems. Focus areas include selection pressure analysis, tumor-immune interactions, and the role of the virome in cancer progression. Contributing to collaborative projects spanning spaceflight microbiome studies, lymphoma evolution, and computational tool development for large-scale sequence data interpretation

<b>Temple University</b> <i>Graduate Research Assistant</i>	Spring 2020 to Spring 2023 <i>Advisor: Dr. Sergei L. Kosakovsky Pond</i>
--	---

- Design and implementation of computational and statistical approaches for quantifying the evolutionary impact of multinucleotide substitutions on molecular adaptation.

## OTHER POSITIONS

---

<b>NIH - Human Virome Program</b> <i>Co-Chair - Bioinformatics Working Group</i>	January 2025 to Present
---	-------------------------

Lead coordination of bioinformatics strategy for a global initiative focused on characterizing the human virome across diverse populations and environments. Guide the development of standardized pipelines for metagenomic and virome analysis, integration of multi-omic datasets, and computational methods for viral discovery, classification, and host interaction profiling. Facilitate cross-disciplinary collaboration among researchers, promote open data practices, and contribute to roadmap planning for scalable, reproducible viral bioinformatics infrastructure.

<b>The MetaSUB International Consortium</b> <i>Director of Bioinformatics</i>	June 2024 to Present
--	----------------------

Oversee the design, implementation, and management of global bioinformatics workflows for the study of urban microbiomes and metagenomes across more than 100 cities. Lead the development of scalable pipelines for taxonomic classification, functional annotation, antimicrobial resistance profiling, and viral discovery from metagenomic and metatranscriptomic datasets. Coordinate data harmonization across international collaborators, mentor junior scientists, and contribute to high-impact publications and public data releases. Drive innovation in computational approaches for environmental and public health microbiology.

## PREPRINTS

---

1. Gao Z\*, Wu J\*, **Lucaci AG\***, Ouyang J, Wang L, Ryon K, Elhaik E, Probst AJ, Rod X, Velavan TN, Chasapi A, Ouzounis CA, Oliveira M, Dias-Neto E, Osuolale OO, Poulsen M, Meleshko D, Bhattacharyya M, Ugalde JA, Sierra MA, Tierney BT, Prithiviraj B, Sharma NK, Munteanu V, Mangul S, Ushio M, abaj PP, Toscan R, Subramanian B, Frolova A, Burkhart J, Deng Y, Udekwu KI, Schriml LM, Hazrin-Chong NH, Suzuki H, Lee PKH, Wang LF, Mason CE, Shi T. Diversity and Distinctive Traits of the Global RNA Virome in Urban Environments. *SSRN*. 2024. doi: 10.2139/ssrn.4871972.
2. **Lucaci AG**, Pond SL. AOC: Analysis of Orthologous CollectionsAn Application for the Characterization of Natural Selection in Protein-Coding Sequences. *arXiv*. 2024. arXiv:2406.09522. arxiv.org/abs/2406.09522.
3. Mak L, Tierney B, **Lucaci AG**, Ronkowski C, Toomey M, Martinez JSA, Zimmerman S, Fu C, Kopbayeva M, Noyvert A, Farthing B, Tang S, Mason C, Hajirasouliha I. A Modular Metagenomics Analysis System for Integrated Multi-Step Data Exploration. *bioRxiv*. 2023. doi: 10.1101/2023.04.09.536171.
4. Munteanu V, Saldana M, Ciorba D, Bostan V, Su JM, Kasianchuk N, Sharma NK, Knyazev S, Gordeev V, Amann E, Lobiuc A, Covasa M, Crandall KA, Ouyang WO, Wu NC, Mason C, Tierney BT, **Lucaci AG**, Zelikovsky A, Mangul S. SARS-CoV-2 Wastewater Genomic Surveillance: Approaches, Challenges, and Opportunities. *arXiv*. 2024. arXiv:2309.13326. doi.org/10.48550/arXiv.2309.13326.

## PUBLICATIONS

---

1. Lei H, Du S, Tong X, Chan WL, Leung MHY, Bifot KO, Bezdan D, Butler DJ, Danko DC, Green DC, Hernandez MT, Kelly FJ, **Lucaci AG**, Meydan C, Nieto-Caballero M, Ryon K, Tierney B, Udekwu KI, Young BG, Mason CE, Dybwad M, Lee PKH. Global biogeography of airborne viruses in public transit systems and their host interactions. *Microbiome*. 2025 Aug 29;13(1):193. doi: 10.1186/s40168-025-02173-z. PMID: 40883783; PMCID: PMC12395665.
2. Amirali, A., Sharkey, M. E., Choudhary, S., Babler, K. M., Beaver, C. C., Biswas, P., Bowie, K. R., Burke, T., Currall, B. B., Grills, G. S., Healy, H. G., **Lucaci, A. G.**, Mason, C. E., McGuire, M., Ramos, R., Ruedaflores, M., Solle, N. S., Schrer, S. C., Shukla, B. S., Solo-Gabriele, H. M. (2025). Long term assessment of SARS-CoV-2 in wastewater and the transition to evaluate additional viral targets. *Science of The Total Environment*, 995, 180096. <https://doi.org/10.1016/J.SCITOTENV.2025.180096>
3. Selberg Avery, Clark Nathan L, Sackton Timothy B, Muse Spencer V, **Lucaci Alexander G**, Weaver Steven, Nekrutenko Anton, Chikina Maria, Pond Sergei L Kosakovsky (2025) Minus the Error: Testing for Positive Selection in the Presence of Residual Alignment Errors *eLife* 14:RP106921 <https://doi.org/10.7554/eLife.106921.1>
4. Melendez-Vazquez F, **Lucaci AG**, Selberg A, Clavel J, Rincon-Sandoval M, Santaquiteria A, White WT, Drabeck D, Carnevale G, Duarte-Ribeiro E, Miya M, Westneat MW, Baldwin CC, Hughes LC, Ort G, Kosakovsky Pond SL, Betancur-R R, Arcila D. Ecological interactions and genomic innovation fueled the evolution of ray-finned fish endothermy. *Sci Adv*. 2025 Jun 27;11(26):eads8488. doi: 10.1126/sciadv.ads8488. Epub 2025 Jun 25. PMID: 40561012.
5. Gordeev V, Hlzer M, Desir D, Goraichuk IV, Knyazev S, Solo-Gabriele H, Skums P, Karthikeyan S, Evans A, Agrawal S, **Lucaci AG**, et al. Leveraging wastewater sequencing to strengthen global public health surveillance. *BMC Glob Public Health*. 2025;3(1):23. doi:10.1186/s44263-025-00138-w.
6. Zlenko OB, Kit MY, Bondarenko O, Gincu AE, **Lucaci AG**. Spatially-distributed viral evolutionary analysis of Influenza A Virus (IAV). *Biopolym Cell*. 2024;40(3):217.

7. Tierney BT, Foox J, Ryon KA, et al., **Lucaci AG**, Mason CE. Towards geospatially-resolved public-health surveillance via wastewater sequencing. *Nat Commun.* 2024;15(1):8386. doi:10.1038/s41467-024-52427-x.
8. Overbey EG, Kim J, Tierney BT, et al., **Lucaci AG**, Mason CE. The Space Omics and Medical Atlas (SOMA) and international astronaut biobank. *Nature.* 2024. doi:10.1038/s41586-024-07639-y.
9. Mason CE, Green J, Adamopoulos KI, et al., **Lucaci AG**. A Second Space Age Spanning Omics, Platforms, and Medicine Across Orbits. *Nature.* 2024. doi:10.1038/s41586-024-07586-8.
10. **Lucaci AG**, Brew WE, Lamanna J, et al. The evolution of mammalian Rem2: unraveling the impact of purifying selection and coevolution. *Front Bioinform.* 2024. doi:10.3389/fbinf.2024.1381540.
11. Garcia-Medina JS, Sienkiewicz K, Narayanan SA, et al., **Lucaci AG**, Mason CE. Genome and clonal hematopoiesis stability during spaceflight. *Precis Clin Med.* 2024;7(1):pbae007. doi:10.1093/pccmedi/pbae007.
12. **Lucaci AG**. The Role of Complex Evolutionary Dynamics in Molecular Sequence Analysis. Ph.D. dissertation. Temple University, 2023. Available from: ProQuest.
13. **Lucaci AG**, Zehr JD, Enard D, Thornton JW, Kosakovsky Pond SL. Evolutionary shortcuts via multinucleotide substitutions. *Mol Biol Evol.* 2023;40(7):msad150. doi:10.1093/molbev/msad150.
14. Zehr JD, Kosakovsky Pond SL, Millet JK, et al., **Lucaci AG**. Natural selection in feline coronavirus phenotypes. *Virus Evol.* 2023;9(1):vead019. doi:10.1093/ve/vead019.
15. Silva SR, Miranda VF, Michael TP, et al., **Lucaci AG**. Organellar genome dynamics in carnivorous plants. *Mol Phylogenet Evol.* 2023. doi:10.1016/j.ympev.2023.107711.
16. Tegally H, Moir M, Everatt J, et al., **NGS-SA consortium**. Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5. *Nat Med.* 2022;28(9):17851790. doi:10.1038/s41591-022-01911-2.
17. **Lucaci AG**, Notaras MJ, Kosakovsky Pond SL, Colak D. Evolution of BDNF under purifying selection and coevolution. *Transl Psychiatry.* 2022;12(1):258. doi:10.1038/s41398-022-02021-w.
18. Benndorf R, Velazquez R, Zehr JD, Pond SLK, Martin JL, **Lucaci AG**. Human small heat shock proteins in vertebrate evolution. *Cell Stress Chaperones.* 2022;27(4):309323. doi:10.1007/s12192-022-01268-y.
19. Viana R, Moyo S, Amoako DG, et al., **Lucaci AG**. Rapid epidemic expansion of Omicron in Southern Africa. *Nature.* 2022;603(7902):679686. doi:10.1038/s41586-022-04411-y.
20. **Lucaci AG**, Zehr JD, Shank SD, et al. RASCL: Rapid Assessment of Selection in Clades. *PLoS One.* 2022;17(11):e0275623. doi:10.1371/journal.pone.0275623.
21. Martin DP, Lytras S, **Lucaci AG**, et al. Unusual mutational clusters in Omicron BA.1. *Mol Biol Evol.* 2022;39(4):msac061. doi:10.1093/molbev/msac061.
22. Martin DP, Weaver S, Tegally H, et al., **Lucaci AG**. Ongoing convergent evolution of SARS-CoV-2 N501Y lineages. *Cell.* 2021;184(20):51895200.e7. doi:10.1016/j.cell.2021.09.003.
23. **Lucaci AG**, Wisotsky SR, Shank SD, et al. Instantaneous multiple-nucleotide changes. *PLoS One.* 2021;16(3):e0248337. doi:10.1371/journal.pone.0248337.
24. Yao C, Vanderpool KG, Delfiner M, et al., **Lucaci AG**, Pereda AE. Electrical synaptic transmission in zebrafish. *J Neurophysiol.* 2014;112(9):21022113. doi:10.1152/jn.00397.2014.

## TEACHING EXPERIENCE

---

### International Workshops and Summer Schools

- **Instructor, VEME 2024 & 2023 (International Workshop on Virus Evolution and Molecular Epidemiology)** Taught a half-day module on Molecular Adaptation to global researchers in bioinformatics and public health.
- **Instructor, EEBG 2024 (Eastern European Bioinformatics and Computational Genomics School)** Delivered a half-day module on Molecular Adaptation to participants in bioinformatics and genomics.

### Temple University Bioinformatics Studio *Co-Founder*

Spring 2018 to 2023

- Co-founded a student-led initiative providing inclusive, hands-on training in bioinformatics for learners at all levels.
- Organized and led workshops, tutorials, and peer mentoring in computational biology.

### Temple University Genomics in Medicine (Graduate TA)

Fall 2019 to 2021

- Supported 100 to 160 students per semester in a cross-listed graduate/undergraduate course.
- Led office hours, guided assignments, explained primary research articles, and advised on classroom projects.

### Temple University Laboratory Instruction (Graduate TA)

2018 to 2019

- **Intro to Organismal Biology (Spring 2019)** Led two lab sections, instructed hands-on exercises, and provided feedback to 40 students.
- **General Biology I (Fall 2018)** Directed lab sessions for 40 students, demonstrated experimental protocols, and evaluated lab work.

### New York University Adjunct Professor

2017 to 2018

- **Fundamentals of Bioinformatics (Spring 2018)** Instructed 20 students in weekly recitations, offering guidance on bioinformatics software and theory.
- **Molecules of Life (Fall 2017)** Led two laboratory sections for 40 students in total, reinforcing lecture topics with hands-on practice.
- **Principles of Biology Lab (Spring 2017)** Taught two laboratory sections, reviewing core concepts and experimental methods.

## FELLOWSHIPS, AWARDS, AND HONORS

---

- **2024** NIH LRP Award, *National Cancer Institute (NCI)*, **\$100,000**
- **2023** The Evolution of Animal Genomes, *EMBO*, **350**
- **2023** SMBE Satellite Meeting Travel Award, *Princeton University*, **\$300**
- **2023** Metascience Conference Travel Award, *Center for Open Science*, **\$300**
- **2023** Young Investigators Travel Award, *SMBE*, **\$3,500**
- **2023** Opening Influenza Research Fellowship, *Center for Open Science*, **\$2,000**
- **2022** CST Outstanding Research Award, *Temple University*, **\$500**
- **2020** Young Investigators Travel Award, *SMBE*, **\$1,500**

## PROFESSIONAL SERVICE

---

- **2025** Journal reviewer for *Bioinformatics Advances*
- **2024** Journal reviewer for *Molecular Biology and Evolution (MBE)*
- **2023** Journal reviewer for *Virus Evolution*
- **2021** Journal reviewer for *Genomics*

## PRESENTATIONS

---

- **2025, RdRp Summit** The global RNA virome in urban environments
- **2025, Clarkson University (Invited Speaker)** Challenges in examining the global urban microbiome
- **2025, AGBT 2025** Diversity and distinctive traits of the global RNA virome in urban environments
- **2025, CAMERA 2025** Challenges in examining the global urban microbiome
- **2024, MetaSUB Consortium** Quantifying Natural Selection in Urban Environments
- **2023, 30th Dynamics and Evolution** Selection analyses identify broad evolutionary features across viral families
- **2023, Temple University** The role of complex evolutionary dynamics in molecular sequence analysis
- **2022, Weill Cornell Medical College** Advances in quantifying natural selection in coding sequences
- **2022, 29th Dynamics and Evolution of Human Viruses** RASCL: Rapid Assessment of Selection in Clades through molecular sequence analysis
- **2021, EMBO** Widespread empirical support for instantaneous multiple-nucleotide changes
- **2021, Mid-Atlantic Bioinformatics Conference** Rapid assessment of selection in SARS-CoV-2 variants
- **2021, 28th Dynamics and Evolution of Human Viruses** Rapid assessment of selection in SARS-CoV-2 variants
- **2020, Cold Spring Harbor Laboratory** Widespread empirical support for instantaneous multiple-nucleotide changes
- **2020, Human Genetics in NYC** Widespread empirical support for instantaneous multiple-nucleotide changes
- **2020, SMC** Evaluating the impact of multiple simultaneous mutations on evolutionary rate inference
- **2020, Binghamton University** Evaluating the impact of multiple simultaneous mutations on evolutionary rate inference
- **2019, Temple University, BGSS Retreat** Evaluating the impact of multiple simultaneous mutations on evolutionary rate inference
- **2019, MABC** Evaluating the impact of multiple simultaneous mutations on evolutionary rate inference
- **2019, EPiC** Evaluating the impact of multiple simultaneous mutations on evolutionary rate inference