

# ALEXANDER G. LUCACI, PH.D.

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## EDUCATION

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<b>Temple University</b> Ph.D. in Bioinformatics Dissertation mentored by Dr. Sergei L Kosakovsky Pond <i>"The Role of Complex Evolutionary Dynamics in Molecular Sequence Analysis"</i>	2018 - 2023
<b>New York University</b> M.S. in Biology	2016 - 2018
<b>SUNY Stony Brook University</b> B.S. in Biochemistry	2011

## RESEARCH POSITIONS HELD

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<b>Weill Cornell Medical College</b> <i>Postdoctoral Associate</i>	July 2023 - Present
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- My research centers on leveraging evolutionary theory and molecular sequence analysis to advance research in virology and immuno-oncology. This interdisciplinary approach combines the principles of evolutionary biology with cutting-edge molecular techniques to unravel the complexities of viral evolution and host immune responses.

<b>Temple University</b> <i>Graduate Research Assistant</i>	Spring 2020-Spring 2023
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- Conducting research in molecular evolution evaluating the effect of multinucleotide mutational events on the inference of parameters of gene adaptation. This work involves the use and development of statistical models and computational software. Our current implementation is available as an extension in the Hypothesis testing in Phylogenies (HyPhy) suite of analyses.

## PREPRINTS

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1. Selberg A, Chikina M, Sackton TB, Muse S, **Lucaci A.G.**, Weaver S, et al. Minus the Error: Estimating dN/dS and Testing for Natural Selection in the Presence of Residual Alignment Errors [Internet]. bioRxiv; 2024 [cited 2024 Nov 18]. p. 2024.11.13.620707. Available from: <https://www.biorxiv.org/content/10.1101/2024.11.13.620707v1>
2. Gao, Zihao and Wu, Jun and **Lucaci, Alexander G.** and Ouyang, Jian and Wang, Lan and Ryon, Krista and Elhaik, Eran and Probst, Alexander J. and Rod, Xavier and Velavan, Thirumalaisamy and Chasapi, Anastasia and Ouzounis, Christos A. and Oliveira, Manuela and Dias-Neto, Emmanuel and Osuolale, Olayinka O. and Poulsen, Michael and Meleshko, Dmitry and Bhattacharyya, Malay and Ugalde, Juan A. and Sierra, Maria A. and Tierney, Braden T. and Prithiviraj, Bharath and Sharma, Nitesh Kumar and Munteanu, Viorel and Mangul, Serghei and Ushio, Masayuki and abaj, Pawe P. and Toscan, Rodolfo and Subramanian, Balakrishnan and Frolova, Alina and Burkhart, Joshua and Deng, Youping and Udekwu, Klas I. and Schriml, Lynn M. and Hazrin-Chong, Nur Hazlin and Suzuki, Haruo and Lee, Patrick K. H. and Wang, Lin Fa and Mason, Christopher E. and Shi, Tielu, Diveristy and Distinctive Traits of the Global RNA Virome in Urban Environments. Available at SSRN: <https://ssrn.com/abstract=4871972> or <http://dx.doi.org/10.2139/ssrn.4871972>

3. **Lucaci AG**, Pond S. AOC: Analysis of Orthologous Collections – an application for the characterization of natural selection in protein-coding sequences [Internet]. arXiv; 2024 [cited 2024 Jun 17]. Available from: <http://arxiv.org/abs/2406.09522>
4. 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 [Preprint]. 2023 Apr 9:2023.04.09.536171. doi: 10.1101/2023.04.09.536171. PMID: 37066359; PMCID: PMC10104186.
5. Munteanu, V., Saldana, M., Ciorba, D., Bostan, V., Su, J. M., Kasianchuk, N., Sharma, N. K., Knyazev, S., Gordeev, V., Amann, E., Lobiuc, A., Covasa, M., Crandall, K. A., Ouyang, W. O., Wu, N. C., Mason, C., Tierney, B. T., **Lucaci, A. G.**, Zelikovsky, A., Mangul, S. (2024). SARS-CoV-2 Wastewater Genomic Surveillance: Approaches, Challenges, and Opportunities (arXiv:2309.13326). arXiv. <https://doi.org/10.48550/arXiv.2309.13326>

## PUBLICATIONS

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1. 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):217217.
2. Tierney BT, Foox J, Ryon KA, Butler D, Damle N, Young BG, Mozsary C, Babler KM, Yin X, Carattini Y, Andrews D, **Lucaci AG**, Solle NS, Kumar N, Shukla B, Vidovic D, Currall B, Williams SL, Schrer SC, Stevenson M, Amirali A, Beaver CC, Kobetz E, Boone MM, Reding B, Laine J, Comerford S, Lamar WE, Tallon JJ, Hirschberg JW, Proszynski J, Sharkey ME, Church GM, Grills GS, Solo-Gabriele HM, Mason CE. Geospatially-resolved public-health surveillance via wastewater sequencing. medRxiv [Preprint]. 2023 Jun 1:2023.05.31.23290781. doi: 10.1101/2023.05.31.23290781. PMID: 37398062; PMCID: PMC10312847.  
[Accepted at Nature Communications]
3. Overbey EG, Kim J, Tierney BT, Park J, Houerbi N, **Lucaci AG**, Medina SG, Damle N, Najjar D, Grigorev K, Afshin EE, Ryon KA, Sienkiewicz K, Patras L, Klotz R, Ortiz V, MacKay M, Schweickart A, Chin CR, Sierra MA, Valenzuela MF, Dantas E, Nelson TM, Cekanaviciute E, Deards G, Foox J, Narayanan SA, Schmidt CM, Schmidt MA, Schmidt JC, Mullane S, Tigchelaar SS, Levitte S, Westover C, Bhattacharya C, Lucotti S, Hirschberg JW, Proszynski J, Burke M, Kleinman A, Butler DJ, Loy C, Mzava O, Lenz J, Paul D, Mozsary C, Sanders LM, Taylor LE, Patel CO, Khan SA, Suhail M, Byhaqui SG, Aslam B, Gajadhar AS, Williamson L, Tandel P, Yang Q, Chu J, Benz RW, Siddiqui A, Hornburg D, Blease K, Moreno J, Boddicker A, Zhao J, Lajoie B, Scott RT, Gilbert RR, Polo SL, Altomare A, Kruglyak S, Levy S, Ariyapala I, Beer J, Zhang B, Hudson BM, Rininger A, Church SE, Beheshti A, Church GM, Smith SM, Crucian BE, Zwart SR, Matei I, Lyden DC, Garrett-Bakelman F, Krumsiek J, Chen Q, Miller D, Shuga J, Williams S, Nemecek C, Trudel G, Pelchat M, Laneuville O, De Vlaminck I, Gross S, Bolton KL, Bailey SM, Granstein R, Furman D, Melnick AM, Costes SV, Shirah B, Yu M, Menon AS, Mateus J, Meydan C, Mason CE. The Space Omics and Medical Atlas (SOMA) and international astronaut biobank. *Nature*. 2024 Jun 11. doi: 10.1038/s41586-024-07639-y. Epub ahead of print. PMID: 38862028.
4. Mason CE, Green J, Adamopoulos KI, Afshin EE, Baechle JJ, Basner M, Bailey SM, Bielski L, Borg J, Borg J, Broddrick JT, Burke M, Caicedo A, Castaeda V, Chatterjee S, Chin C, Church G, Costes SV, De Vlaminck I, Desai RI, Dhir R, Diaz JE, Etlin SM, Feinstein Z, Furman D, Garcia-Medina JS, Garrett-Bakelman F, Giacomello S, Gupta A, Hassanin A, Houerbi N, Irby I, Javorsky E, Jirak P, Jones CW, Kamal KY, Kangas BD, Karouia F, Kim J, Kim JH, Kleinman A, Lam T, Lawler JM, Lee JA, Limoli CL, **Lucaci AG**, MacKay M, McDonald JT, Melnick AM, Meydan C, Mieczkowski J, Muratani M, Najjar D, Othman MA, Overbey EG, Paar V, Park J, Paul AM, Perdyan A, Proszynski J, Reynolds RJ, Ronca AE, Rubins K, Ryon KA, Sanders LM, Glowe PS, Shevde Y, Schmidt MA, Scott RT, Shirah B, Sienkiewicz K, Sierra M, Siew K, Theriot

- CA, Tierney BT, Venkateswaran K, Hirschberg JW, Walsh SB, Walter C, Winer DA, Yu M, Zea L, Mateus J, Beheshti A. A Second Space Age Spanning Omics, Platforms, and Medicine Across Orbits. *Nature*. 2024 Jun 11. doi: 10.1038/s41586-024-07586-8. Epub ahead of print. PMID: 38862027.
5. **Lucaci AG**, Brew WE, Lamanna J, Selberg A, Carnevale V, Moore AR, et al. The evolution of mammalian Rem2: unraveling the impact of purifying selection and coevolution on protein function, and implications for human disorders. *Front Bioinform [Internet]*. 2024 Jun 24 [cited 2024 Jun 26];4. Available from: <https://www.frontiersin.org/journals/bioinformatics/articles/10.3389/fbinf.2024.1381540/full>
  6. Garcia-Medina JS, Sienkiewicz K, Narayanan SA, Overbey EG, Grigorev K, Ryon KA, Burke M, Proszynski J, Tierney B, Schmidt CM, Mencia-Trinchant N, Klotz R, Ortiz V, Foox J, Chin C, Najjar D, Matei I, Chan I, Cruchaga C, Kleinman A, Kim J, **Lucaci AG**, Loy C, Mzava O, De Vlaminc I, Singaraju A, Taylor LE, Schmidt JC, Schmidt MA, Blease K, Moreno J, Boddicker A, Zhao J, Lajoie B, Altomare A, Kruglyak S, Levy S, Yu M, Hassane DC, Bailey SM, Bolton K, Mateus J, Mason CE. Genome and clonal hematopoiesis stability contrasts with immune, cfDNA, mitochondrial, and telomere length changes during short duration spaceflight. *Precis Clin Med*. 2024 Apr 8;7(1):pbae007. doi: 10.1093/pcmedi/pbae007. PMID: 38634106; PMCID: PMC11022651.
  7. **Lucaci AG**, Zehr JD, Enard D, Thornton JW, Kosakovsky Pond SL. Evolutionary Shortcuts via Multinucleotide Substitutions and Their Impact on Natural Selection Analyses. *Mol Biol Evol*. 2023 Jul 5;40(7):msad150. doi: 10.1093/molbev/msad150. PMID: 37395787; PMCID: PMC10336034.
  8. Zehr JD, Kosakovsky Pond SL, Millet JK, Olarte-Castillo XA, **Lucaci AG**, Shank SD, Ceres KM, Choi A, Whittaker GR, Goodman LB, Stanhope MJ. Natural selection differences detected in key protein domains between non-pathogenic and pathogenic feline coronavirus phenotypes. *Virus Evol*. 2023 Mar 15;9(1):vead019. doi: 10.1093/ve/vead019. PMID: 37038392; PMCID: PMC10082545.
  9. Silva SR, F O Miranda V, Michael TP, Pachno BJ, Matos RG, Adamec L, L K Pond S, **Lucaci AG**, Pinheiro DG, Varani AM. The phylogenomics and evolutionary dynamics of the organellar genomes in carnivorous Utricularia and Genlisea species (Lentibulariaceae). *Mol Phylogenet Evol*. 2023 Jan 21:107711. doi: 10.1016/j.ympev.2023.107711. Epub ahead of print. PMID: 36693533.
  10. Tegally H, Moir M, Everatt J, Giovanetti M, Scheepers C, Wilkinson E, Subramoney K, Makatini Z, Moyo S, Amoako DG, Baxter C, Althaus CL, Anyaneji UJ, Kekana D, Viana R, Giandhari J, Lessells RJ, Maponga T, Maruapula D, Choga W, Matshaba M, Mbulawa MB, Msomi N; **NGS-SA consortium**, Naidoo Y, Pillay S, Sanko TJ, San JE, Scott L, Singh L, Magini NA, Smith-Lawrence P, Stevens W, Dor G, Tshiabuila D, Wolter N, Preiser W, Treurnicht FK, Venter M, Chiloane G, McIntyre C, O'Toole A, Ruis C, Peacock TP, Roemer C, Kosakovsky Pond SL, Williamson C, Pybus OG, Bhiman JN, Glass A, Martin DP, Jackson B, Rambaut A, Laguda-Akingba O, Gaseitsiwe S, von Gottberg A, de Oliveira T. Emergence of SARS-CoV-2 Omicron lineages BA.4 and BA.5 in South Africa. *Nat Med*. 2022 Sep;28(9):1785-1790. doi: 10.1038/s41591-022-01911-2. Epub 2022 Jun 27. PMID: 35760080; PMCID: PMC9499863.
  11. **Lucaci AG**, Notaras MJ, Kosakovsky Pond SL, Colak D. The evolution of BDNF is defined by strict purifying selection and prodomain spatial coevolution, but what does it mean for human brain disease? *Transl Psychiatry*. 2022 Jun 22;12(1):258. doi: 10.1038/s41398-022-02021-w. PMID: 35732627; PMCID: PMC9217794.
  12. Benndorf R, Velazquez R, Zehr JD, Pond SLK, Martin JL, **Lucaci AG**. Human HspB1, HspB3, HspB5 and HspB8: Shaping these disease factors during vertebrate evolution. *Cell Stress Chaperones*. 2022 Jul;27(4):309-323. doi: 10.1007/s12192-022-01268-y. Epub 2022 Jun 9. PMID:

35678958; PMID: PMC9346038.

13. Viana R, Moyo S, Amoako DG, Tegally H, Scheepers C, Althaus CL, Anyaneji UJ, Bester PA, Boni MF, Chand M, Choga WT, Colquhoun R, Davids M, Deforche K, Doolabh D, du Plessis L, Engelbrecht S, Everatt J, Giandhari J, Giovanetti M, Hardie D, Hill V, Hsiao NY, Iranzadeh A, Ismail A, Joseph C, Joseph R, Koopile L, Kosakovsky Pond SL, Kraemer MUG, Kuate-Lere L, Laguda-Akingba O, Lesetedi-Mafoko O, Lessells RJ, Lockman S, **Lucaci AG**, Maharaj A, Mahlangu B, Maponga T, Mahlakwane K, Makatini Z, Marais G, Maruapula D, Masupu K, Matshaba M, Mayaphi S, Mbhele N, Mbulawa MB, Mendes A, Mlisana K, Mnguni A, Mohale T, Moir M, Moruisi K, Mosepele M, Motsatsi G, Motswaledi MS, Mphoyakgosi T, Msomi N, Mwangi PN, Naidoo Y, Ntuli N, Nyaga M, Olubayo L, Pillay S, Radibe B, Ramphal Y, Ramphal U, San JE, Scott L, Shapiro R, Singh L, Smith-Lawrence P, Stevens W, Strydom A, Subramoney K, Tebeila N, Tshiabuila D, Tsui J, van Wyk S, Weaver S, Wibmer CK, Wilkinson E, Wolter N, Zarebski AE, Zuze B, Goedhals D, Preiser W, Treurnicht F, Venter M, Williamson C, Pybus OG, Bhiman J, Glass A, Martin DP, Rambaut A, Gaseitsiwe S, von Gottberg A, de Oliveira T. Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. *Nature*. 2022 Mar;603(7902):679-686. doi: 10.1038/s41586-022-04411-y. Epub 2022 Jan 7. PMID: 35042229; PMID: PMC8942855.
14. **Lucaci AG**, Zehr JD, Shank SD, Bouvier D, Ostrovsky A, Mei H, Nekrutenko A, Martin DP, Kosakovsky Pond SL. RASCL: Rapid Assessment of Selection in CLades through molecular sequence analysis. *PLoS One*. 2022 Nov 2;17(11):e0275623. doi: 10.1371/journal.pone.0275623. PMID: 36322581; PMID: PMC9629619.
15. Martin DP, Lytras S, **Lucaci AG**, Maier W, Grning B, Shank SD, Weaver S, MacLean OA, Orton RJ, Lemey P, Boni MF, Tegally H, Harkins GW, Scheepers C, Bhiman JN, Everatt J, Amoako DG, San JE, Giandhari J, Sigal A; NGS-SA, Williamson C, Hsiao NY, von Gottberg A, De Klerk A, Shafer RW, Robertson DL, Wilkinson RJ, Sewell BT, Lessells R, Nekrutenko A, Greaney AJ, Starr TN, Bloom JD, Murrell B, Wilkinson E, Gupta RK, de Oliveira T, Kosakovsky Pond SL. Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. *Mol Biol Evol*. 2022 Apr 11;39(4):msac061. doi: 10.1093/molbev/msac061. PMID: 35325204; PMID: PMC9037384.
16. Martin DP, Weaver S, Tegally H, San JE, Shank SD, Wilkinson E, **Lucaci AG**, Giandhari J, Naidoo S, Pillay Y, Singh L, Lessells RJ; NGS-SA; COVID-19 Genomics UK (COG-UK), Gupta RK, Wertheim JO, Nekrutenko A, Murrell B, Harkins GW, Lemey P, MacLean OA, Robertson DL, de Oliveira T, Kosakovsky Pond SL. The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. *Cell*. 2021 Sep 30;184(20):5189-5200.e7. doi: 10.1016/j.cell.2021.09.003. Epub 2021 Sep 7. PMID: 34537136; PMID: PMC8421097.
17. **Lucaci AG**, Wisotsky SR, Shank SD, Weaver S, Kosakovsky Pond SL. Extra base hits: Widespread empirical support for instantaneous multiple-nucleotide changes. *PLoS One*. 2021 Mar 12;16(3):e0248337. doi: 10.1371/journal.pone.0248337. PMID: 33711070; PMID: PMC7954308.
18. Yao C, Vanderpool KG, Delfiner M, Eddy V, **Lucaci AG**, Soto-Riveros C, Yasumura T, Rash JE, Pereda AE. Electrical synaptic transmission in developing zebrafish: properties and molecular composition of gap junctions at a central auditory synapse. *J Neurophysiol*. 2014 Nov 1;112(9):2102-13. doi: 10.1152/jn.00397.2014. Epub 2014 Jul 30. PMID: 25080573; PMID: PMC4274921.

## TEACHING EXPERIENCE

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**28th International Workshop on Virus Evolution and Molecular Epidemiology (VEME)**

August 2024

*Instructor*

- Responsible for teaching a half-day module on Molecular Adaptation at the VEME workshop to an international audience of researchers in bioinformatics and public health.

**The 3rd Eastern European Bioinformatics and Computational Genomics School (EEBG)**  
July 2024

*Instructor*

- Responsible for teaching a half-day module on Molecular Adaptation at the EEBG workshop to an international audience of researchers in bioinformatics and genomics.

**Bioinformatics Studio at Temple University**

Spring 2018 - Present

*Co-Founder*

- The Bioinformatics Studio is an inclusive and hands-on environment for learning, training, sharing, and most importantly doing bioinformatics at Temple University.
- A student run organization that provides guided hands-on training at every level of research and computational expertise in an open studio format.

**27th International Workshop on Virus Evolution and Molecular Epidemiology (VEME)**

August 2023

*Instructor*

- Responsible for teaching a half-day module on Molecular Adaptation at the VEME workshop to an international audience of researchers in bioinformatics and public health.

**Temple University**

Fall 2021

*Graduate Teaching Assistant*

*Genomics in Medicine*

- Directed over one hundred and fifty students in a cross-listed (Graduate and Undergraduate) course.
- Responsible for holding office hours and communicating with students.
- Provide guidance on assignments, help with interpreting primary research articles and offered guidance on classroom projects.

**Temple University**

Fall 2020

*Graduate Teaching Assistant*

*Genomics in Medicine*

- Directed over one hundred and sixty students in a cross-listed (Graduate and Undergraduate) course in a virtual format.
- Responsible for holding office hours and communicating with students.
- Provide guidance on assignments, help with interpreting primary research articles and offered guidance on classroom projects.

**Temple University**

Fall 2019

*Graduate Teaching Assistant*

*Genomics in Medicine*

- Directed over one hundred students in a cross-listed (Graduate and Undergraduate) course.
- Responsible for holding office hours and communicating with students. Additionally, provided guidance on assignments, helped with interpreting primary research articles and offered guidance on classroom projects.

**Temple University**

Spring 2019

*Graduate Teaching Assistant*

*Introduction to Organismal Biology*

- Directed forty students over two sections of the Introduction to Organismal Biology Laboratory course.
- Instructed students on laboratory exercises, provided feedback, and demonstrated proper techniques.

**Temple University***Graduate Teaching Assistant*

Fall 2018

*General Biology*

- Directed forty students over two sections of the "General Biology I" Laboratory course
- Instructed students on laboratory exercises, provided feedback, and demonstrated proper techniques.

**New York University***Adjunct Professor*

Spring 2018

*Fundamentals of Bioinformatics*

- Directed twenty students in a weekly recitation section.
- Reviewed theory and topics discussed in lecture and provided guidance and hands-on support in the use of bioinformatics software and analysis.

**New York University***Adjunct Professor*

Fall 2017

*Molecules of Life*

- Directed forty students over two sections in a weekly laboratory course.
- Reviewed theory and topics discussed in lecture and provided guidance and hands-on support in the use of standard laboratory techniques.

**New York University***Adjunct Professor*

Spring 2017

*Principles of Biology Laboratory*

- Directed forty students over two sections in a weekly laboratory course.
- Reviewed theory and topics discussed in lecture and provided guidance and hands-on support in the use of standard laboratory techniques.

**FELLOWSHIPS, AWARDS, AND HONORS**


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2024	NIH LRP Award	NCI	100k USD
2023	The Evolution of Animal Genomes	EMBO	350 Euros
2023	SMBE Satellite Meeting	Princeton University	300 USD
2023	Metascience Conference Travel Award	Center for Open Science	300 USD
2023	Young Investigators Travel Award	SMBE	3,500 USD
2023	Opening Influenza Research Fellowship	Center for Open Science	2,000 USD
2022	CST Outstanding Research Award	Temple University	500 USD
2020	Young Investigators Travel Award	SMBE	1,500 USD

**PROFESSIONAL SERVICE**

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2024 Journal reviewer for Molecular Biology and Evolution (MBE)

2023 Journal reviewer for Virus Evolution

2021 Journal reviewer for Genomics

## **PRESENTATIONS**

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2024	MetaSub	Quantifying Natural Selection in Cities
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	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	CSHL	Widespread empirical support for instantaneous multiple-nucleotide changes
2020	Human Genetics in NYC	Widespread empirical support for instantaneous multiple-nucleotide changes
2020	SMBE	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.