ALEXEY MARKIN

amarkin@iastate.edu ◇ Google Scholar

EDUCATION

2020	**Ph.D in Computer Science,** Iowa State University (ISU) Dissertation: Phylogenetic metrics and their application towards the large-scale inference of evolutionary histories
2015	**B.Sc. in Computer Science** National Research University Higher School of Economics, Moscow, Russia

PROFESSIONAL APPOINTMENTS

2024 – present	**Computational Research Biologist, National Animal Disease Center, USDA-ARS** Staff Scientist at USDA. I develop combinatorial and machine learning algorithms to analyze massive genomic datasets for infectious disease research and pandemic prevention.
2025 – present	**Affiliated Faculty Member, Computer Science, Iowa State University** I mentor CS Ph.D. and Masters students and serve on graduate committees.
2020 – 2024	**Postdoc Research Associate, National Animal Disease Center, USDA-ARS** Developed (i) methods to parse massive genomic datasets using phylogenetics and (ii) phylogenomic and machine learning tools to identify influenza A viruses with pandemic potential.
2018 – 2020	**Research Assistant, Iowa State University** Developed combinatorial algorithms and theory for large-scale phylogenomic inference.
2018	**PhD Intern, Google,** Mountain View, California Developed augmented reality communication protocols with machine learning.
2015 – 2018	**Graduate Research & Teaching Assistant, Iowa State University**

AWARDS AND SCHOLARSHIPS

2023	**Postdoctoral Research Excellence Award,** Iowa State University.
2022	Travel Fellowship, ISMB 2022, International Society for Computational Biology.
2022	Travel Fellowship, Evolution 2022, Society of Systematic Biologists.
2019	NSF Travel Fellowship, ACM Conference on Bioinformatics and Computational Biology
2017	**Research excellence Award,** Iowa State University.
2017	**Teaching excellence Award,** Iowa State University.
2016	**Robert Stewart Early Research Recognition Award,** Iowa State University.
2016	NSF Travel Fellowship, ACM Conference on Bioinformatics and Computational Biology.
2012	Higher School of Economics Scholarship.
2011 – 2015	State Academic Scholarship for students. Awarded for excellent academic performance.

PEER-REVIEWED PUBLICATIONS

* *indicates co-first authors*
† *In Computer Science peer-reviewed full-length conference proceedings are equivalent to journal publications*

(P29) **Markin, A.**, Macken, C.A., Baker, A.L. and Anderson, T.K., 2025. Revealing reassortment in influenza A viruses with TreeSort. *Molecular Biology and Evolution*, 42(8), p.msaf133.

(P28) Vijendran, S., Anderson, T.K., **Markin, A.** and Eulenstein, O., 2025. Phylo-rs: an extensible phylogenetic analysis library in Rust. *BMC Bioinformatics*, 26(1), p.197.

(P27) Zanella, G.C., **Markin, A.**, Thomas, M.N., Snyder, C., Souza, C.K., Arruda, B., Anderson, T. and Baker, A., 2024. Transmission and pathologic findings of divergent human seasonal H1N1pdm09 influenza A viruses following spillover into pigs in the United States. *Influenza and Other Respiratory Viruses.*

(P26) Górecki, P., **Markin, A.**, Vijendran, S. and Eulenstein, O., 2025. Computing generalized cophenetic distances under all L_P norms: A near-linear time algorithmic framework. *PLOS Computational Biology*, 21(6), p.e1013069.

(P25) Nguyen, T.Q., Hutter, C., **Markin, A.**, Thomas, et al., 2025. Emergence and interstate spread of highly pathogenic avian influenza A(H5N1) in dairy cattle. *Science.*

(P24) Baker, A.L., Arruda, B., Palmer, M.V., Boggiatto, P., Sarlo Davila, K., Buckley, A., Ciacci Zanella, G., Snyder, C.A., Anderson, T.K., Hutter, C.R., Nguyen, T.Q., 2025, **Markin, A.** et al. 2024. Dairy cows inoculated with highly pathogenic avian influenza virus H5N1. *Nature*, 637(8047), pp.913-920.

(P23) Wagle, S., **Markin, A.**, Górecki, P., Anderson, T.K. and Eulenstein, O., 2024. Asymmetric Cluster-Based Measures for Comparative Phylogenetics. *Journal of Computational Biology*, 31(4), pp.312-327.

(P22) **Markin, A.**, Zanella, G.C., Arendsee, Z.W., Zhang, J., Krueger, K.M., Gauger, P.C., Vincent Baker, A.L. and Anderson, T.K., 2023. Reverse-zoonoses of 2009 H1N1 pandemic influenza A viruses and evolution in United States swine results in viruses with zoonotic potential. *PLOS Pathogens 19(7), pp. e1011476.* [press release]

(P21) Grover, S., **Markin, A.**, Anderson, T.K. and Eulenstein, O., 2023. Phylogenetic Diversity Statistics for All Clades in a Phylogeny. In proceedings of the International Conference on Intelligent Systems for Molecular Biology (ISMB) 2023. *Bioinformatics 39(Supplement 1), pp.i177-i184.*

(P20) **Markin, A.**, Wagle, S., Grover, S., Vincent Baker, A.L., Eulenstein, O. and Anderson, T.K., 2023. PARNAS: Objectively Selecting the Most Representative Taxa on a Phylogeny. *Systematic Biology, 72(5), pp.1052-1063.*

(P19) † Wagle, S., **Markin, A.**, Gorecki, P., Anderson, T.K. and Eulenstein, O., 2023. The Asymmetric Cluster Affinity Cost. *In RECOMB International Workshop on Comparative Genomics (pp. 131-145).* Lecture Notes in Bioinformatics.

(P18) **Markin, A.**, Wagle, S., Anderson, T.K. and Eulenstein, O., 2022. RF-Net 2: Fast Inference of Virus Reassortment and Hybridization Networks. *Bioinformatics 38(8), pp.2144-2152.*

(P17) † Kulkarni, A., Sabetpour, N., **Markin, A.**, Eulenstein, O. and Li, Q., 2022. CPTAM: Constituency Parse Tree Aggregation Method. *In Proceedings of the 2022 SIAM International Conference on Data Mining (SDM) (pp. 630-638).* Society for Industrial and Applied Mathematics.

(P16) Arendsee, Z.W., Chang, J., Hufnagel, D.E., **Markin, A.**, Janas-Martindale, A., Vincent, A.L., and Anderson, T.K., 2021. octoFLUshow: an interactive tool describing spatial and temporal trends in the genetic diversity of influenza A virus in U.S. swine. *Microbiology Resource Announcements, 10(50), pp.e01081-21.*

(P15) **Markin, A.** and Eulenstein, O., 2021. Quartet-based inference is statistically consistent under the unified duplication-loss-coalescence model. *Bioinformatics, 37(22), pp.4064-4074.* [Faculty Opinions recommended (Siavash Mirarab)]

(P14) Paszek, J.*, **Markin, A.***, Górecki, P. and Eulenstein, O., 2021. Taming the Duplication-Loss-Coalescence Model with Integer Linear Programming. *Journal of Computational Biology, 28(8), pp.758-773.*

(P13) Nguyen, H.N., **Markin, A.**, Friedberg, I. and Eulenstein, O., 2020. Finding orthologous gene blocks in bacteria: the computational hardness of the problem and novel methods to address it. *Bioinformatics, 36(Supplement 2), pp.i668-i674.*

(P12) **Markin, A.**, 2020. On the Extremal Maximum Agreement Subtree Problem. *Discrete Applied Mathematics, 285, pp.612-620.*

(P11) Górecki, P., **Markin, A.** and Eulenstein, O., 2019. Exact Median-tree Inference for Unrooted Reconciliation Costs. *BMC Evolutionary Biology, 20(1), pp.1-15.*

(P10) Tabaszewski, P., Górecki, P., **Markin, A.**, Anderson, T.K. and Eulenstein, O., 2019. Consensus of all Solutions for Intractable Phylogenetic Tree Inference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics, 18(1), pp.149-161.* (Invited paper.)

(P9) † **Markin, A.**, Anderson, T.K., Vadali, V.K.S.T. and Eulenstein, O., 2019. Robinson-Foulds Reticulation Networks. *In proceedings of the 10th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (pp. 77-86).*

(P8) † **Markin, A.** and Eulenstein, O., 2019.Consensus Clusters in Robinson-Foulds Reticulation Networks. *In 19th International Workshop on Algorithms in Bioinformatics (WABI'2019).* Schloss Dagstuhl-Leibniz-Zentrum fuer Informatik.

(P7) † Górecki, P., **Markin, A.** and Eulenstein, O., 2019.Feasibility Algorithms for the Duplication-Loss Cost. *In International Computing and Combinatorics Conference (COCOON'19) (pp. 206-218).*

(P6) † Górecki, P., **Markin, A.** and Eulenstein, O., 2018. Cophenetic Distances: A Near-Linear Time Algorithmic Framework. *In International Computing and Combinatorics Conference (COCOON'18) (pp. 168-179).*

(P5) † **Markin, A.**, Vadali, V.S.K.T. and Eulenstein, O., 2018. Solving the Gene Duplication Feasibility Problem in Linear Time. *In International Computing and Combinatorics Conference (COCOON'18) (pp. 378-390).*

(P4) **Markin, A.** and Eulenstein, O., 2018. Cophenetic Median Trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics, 16(5), pp.1459-1470.* (Invited paper.)

(P3) **Markin, A.** and Eulenstein, O., 2017. Computing Manhattan Path-Difference Median Trees: a Practical Local Search Approach. *IEEE/ACM Transactions on Computational Biology and Bioinformatics, 16(4), pp.1063-1076.* (Invited paper.)

(P2) **Markin, A.** and Eulenstein, O., 2017. Efficient Local Search for Euclidean Path-Difference Median Trees. *IEEE/ACM transactions on computational biology and bioinformatics, 16(4), pp.1374-1385.* (Invited paper.)

(P1) † Górecki, P., **Markin, A.**, Mykowiecka, A., Paszek, J. and Eulenstein, O., 2017. *Phylogenetic Tree Reconciliation: Mean Values for Fixed Gene Trees. In International Symposium on Bioinformatics Research and Applications (ISBRA'17) (pp. 234-245).*

MANUSCRIPTS IN PREPARATION

- **Markin, A.**, Vijendran, S. and Eulenstein, O., 2025. Bounds on the Treewidth of Level-k Rooted Phylogenetic Networks. Preprint, in preparation to submit to *Bulletin of Mathematical Biology.*
- **Markin, A.**, Anderson, T.K., 2026. Splicer: Phylogenetic Placement in Sub-Linear Time. In preparation to submit to *ISMB 2026.*
- **Markin, A.**, Anderson, T.K., 2026. Ordered Leaf Attachment (OLA) Vectors can Identify Reticulation Events even in Multifurcated Trees. Preprint, in preparation to submit to *Bioinformatics.*

RESEARCH TALKS

2025-05	Centers of Excellence for Influenza Research and Response (NIH-CEIRR 2025) annual meeting. "Fast placement of novel H5N1 influenza genomes onto phylogenetic trees for real-time genomic epidemiology."
2024-11	**Invited lecture.** ICERM semester program on Theory, Methods, and Applications of Quantitative Phylogenomics at Brown. "Curbing the complexity of phylogenetic network inference and analysis."
2024-07	Centers of Excellence for Influenza Research and Response (NIH-CEIRR 2024) annual meeting. "Inferring influenza reassortment with TreeSort."
2024-06	American Society for Virology annual meeting (ASV 2024). "Inferring Reassortment Patterns for Influenza A Viruses in Different Hosts with TreeSort."
2024-04	**Invited seminar.** University of Maryland School of Medicine. "Real-time tracking of genomic and antigenic evolution of zoonotic influenza A viruses."
2023-10	**Invited talk.** SIAM-NPP Mathematics of Evolution Minisymposium, New Jersey Institute of Technology.
2023-9	**Invited talk.** Allen D. Leman Swine Conference (Leman 2023). "New insights to control and understand influenza and other respiratory diseases".

2023-8	Tutorial. Centers of Excellence for Influenza Research and Response (NIH-CEIRR 2023) annual meeting. “PARNAS: an objective way to select strains for your analysis”.
2023-07	Intelligent Systems in Molecular Biology (ISMB 2023). “Phylogenetic Diversity Statistics for All Clades in a Phylogeny”
2023-06	American Society for Virology (ASV 2023) annual meeting. Evolution, Ecology and Reservoirs.
2022-08	Centers of Excellence for Influenza Research and Response (NIH-CEIRR) annual meeting. Topic: Viruses with pandemic potential resulting from reverse-zoonoses of the 2009 H1N1 pandemic influenza A viruses and rapid evolution in United States swine.
2022-07	Intelligent Systems in Molecular Biology (ISMB 2022). Evolution & Comparative Genomics track. [video recording]
2022-06	**Invited talk.** Evolution 2022, Towards the Phylogenetic Network of Life symposium.
2021-09	**Invited talk.** Allen D. Leman Swine Conference (Leman 2021). [video recording]
2020-05	**Seminar talk.** Cold Spring Harbor Laboratory, Adam Siepel lab.
2019-09	Workshop on Algorithms in Bioinformatics (WABI 2019).
2019-09	ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB 2019). Topic: Robinson-Foulds Reticulation Networks.
2017-08	ACM-BCB 2017. Topic: Manhattan Path-Difference Median Trees.
2016-10	ACM-BCB 2016. Topic: Cophenetic Median Trees under the Manhattan Distance.
2016-06	International Symposium on Bioinformatics Research and Applications (ISBRA 2016).

OUTREACH AND SERVICE

2023 – present	Program Committee member – Intelligent Systems for Molecular Biology (ISMB)
2023 – present	Webinar organizer for the Evolution & Comparative Genomics community of the International Society for Computational Biology (ISCB).
2021 – present	I mentor several Computer Science PhD and Master’s students at Iowa State University.
2023	Contributed to a Natural Science Foundation scoping session “LIFE: Leveraging Innovations from Evolution” to identify the priority research directions in inter-disciplinary research focused on Evolution.
2020 – present	I contribute bioinformatics analyses to bi-annual assessment of zoonotic influenza diversity reports presented at WHO vaccine consultation meetings (see Government Reports).

GOVERNMENT REPORTS

- Snyder, C., **Markin, A.**, Hufnagel, D.E., Janzen, G., Janas-Martindale, A., Inderski, B., Brown, I., Coggon, A., James, J., Banyard, A., Lewis T., World Organization for Animal Health/Food and Agriculture Organization (WOAH/FAO/OFFLU) Swine Influenza Working Group, Lewis, N.,Anderson, T.K., Vincent Baker, A.L., 2023. OFFLU animal influenza report: July 2022 to December 2022. World Health Organization. p. 62.
- Janzen, G., **Markin, A.**, Hufnagel, D.E., Snyder, C., Janas-Martindale, A., Inderski, B., Brown, I., Coggon, A., James, J., Lewis T., Banyard, A., World Organization for Animal Health/Food and Agriculture Organization (WOAH/FAO/OFFLU) Swine Influenza Working Group, Lewis, N.,Anderson, T.K., Vincent Baker, A.L. (2022). OFFLU animal influenza report: January 2022 to June 2022. World Health Organization. p. 62.
- **Markin, A.**, Hufnagel, D., Arendsee, Z.W., Snyder, C., Janas-Martindale, A., World Organization for Animal Health/Food and Agriculture Organization (OIE/FAO/OFFLU) Swine Influenza Working Group, Brown, I., Lewis, N., Anderson, T.K., Vincent, A.L., 2022. OFFLU animal influenza report: July 2021 to December 2021. World Health Organization. p. 63.
- Hufnagel, D., **Markin, A.**, Arendsee, Z.W., Essen, S., Janas-Martindale, A., et al. Mollet, B., World Organization for Animal Health/Food and Agriculture Organization (OIE/FAO/OFFLU) Swine Influenza Working Group, Brown, I., Lewis, N., Anderson, T.K., Vincent, A.L., 2021. OFFLU animal influenza report: January 2021 to June 2021. World Health Organization. p. 79.
- Arendsee, Z.W., Young, K., Hufnagel, D., **Markin, A.**, Kimble, B., et al. Souza, C.K., Essen, S., Collins, S., Whittard, E., Torchetti, M.K., Tell, R., Janas-Martindale, A., World Organization for Animal Health/Food and Agriculture Organization (OIE/FAO/OFFLU) Swine Influenza Working Group, Brown, I., Lewis, N., Anderson,

T.K., Vincent, A.L., 2021. OFFLU animal influenza report: July 2020 to December 2020. World Health Organization. p. 58.

DEVELOPED BIOINFORMATICS SOFTWARE

- **TreeSort**: Real-time detection of influenza reassortment with a rigorous hypothesis testing framework. `https://github.com/flu-crew/TreeSort`.
- **PARNAS**: Fast tool for sampling most representative taxa and virus strains on very large genomic datasets. Developed in collaboration with S. Wagle and S. Grover. `https://github.com/flu-crew/parnas`.
- **RF-Net**: Software for large-scale inference of entangled evolutionary histories of segmented viruses and species undergoing hybridization. Developed in collaboration with V. Vadali. `https://github.com/flu-crew/rf-net-2`.
- **PDC-Median:** Large-scale phylogenomic inference using supertrees. (link)

REVIEWING SERVICE

Journals

Nature
PLOS Computational Biology
Bulletin of Mathematical Biology
IEEE/ACM Transactions on Computational Biology and Bioinformatics
Scientific Reports
Bioinformatics Advances
SIAM Journal on Discrete Mathematics
Briefings in Bioinformatics
Systematic Biology
Virus Evolution (x3)
Influenza and Other Respiratory Diseases
Transboundary and Emerging Diseases
BMC Bioinformatics (x2)

Conferences

Intelligent Systems for Molecular Biology (ISMB) 2024, 2025 – PC memeber
Research in Computational Molecular Biology - Comparative Genomics (RECOMB-CG) 2022 & 2019
Workshop on Algorithms in Bioinformatics (WABI) 2021
Research in Computational Molecular Biology (RECOMB) 2020
International Symposium on Bioinformatics Research and Applications (ISBRA) 2023 & 2019 & 2018
International Conference on Computational Advances in Bio and medical Sciences (ICCABS) 2025 & 2019 & 2017
International Conference on Bioinformatics and Computational Biology (BICOB) 2018

OTHER PROFESSIONAL EXPERIENCE

- Junior Java developer, half-time position | October 2013 – July 2014 | FORS, Moscow, Russia
- Software Engineering Intern | Summer 2014 | ROSA company, Moscow, Russia
- Software Engineering Intern | Summer 2013 | PMSOFT, Moscow, Russia
- Software Engineering Intern | Summer 2012 | ROSA company, Moscow, Russia

PROGRAMMING SKILLS

Java ◇ Python ◇ R ◇ C/C++ ◇ SQL ◇ C# ◇ JavaScript