

Research interests

Computational biology, Phylogenetics, Epidemiology, Algorithms

Education

- 2020 **Ph.D. in Computer Science**, *Iowa State University (ISU)*, GPA: 4.0/4.0.
Advisor: Prof. Oliver Eulenstein
- 2015 **B.S. in CS**, *National Research University Higher School of Economics, Moscow, Russia*.
Advisor: Prof. Boris Mirkin
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Professional appointments

- Postdoctoral *USDA Agricultural Research Service and ISU Veterinary Diagnostic Lab*
Researcher *(joint appointment) October 2020 – present.*
Working with swine influenza experts, I develop tools that help analyze the evolution of influenza A viruses in swine and potentially assist in pandemic prevention.
- Research assistant *ISU, Fall 2016 – Summer 2020.*
Designed algorithms and tools for computational problems in evolutionary biology. Was actively involved in multi-disciplinary and multi-institutional collaborations.
- Teaching assistant *ISU, Three different courses.*
Conducted recitations, labs, office hours, and substitute lectures; performed grading; Developed software to assist the instructor in grading.
- PhD Intern *Google, Summer 2018, Software Engineering.*
Worked on an open-ended and research-oriented augmented reality project.
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Awards and scholarships

- *Research excellence and Teaching excellence Awards* from ISU, Dept. of Computer Science, 2017.
 - *Robert Stewart Early Research Recognition Award* from ISU, Dept. of Computer Science, 2016.
 - *NSF travel grants for students* for presenting at the ISBRA'16, ACM-BCB'16, and ACM-BCB'19 computational biology conferences.
 - *Higher School of Economics Scholarship*, 2012.
 - *State Academic Scholarship for students*. Awarded for excellent academic performance while studying at the Higher School of Economics, 2011-2015.
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Selected publications

- **Markin, A.**, Wagle, S., Anderson, T.K. and Eulenstein, O., 2021. *RF-Net 2: Fast Inference of Virus Reassortment and Hybridization Networks*. Submitted to Bioinformatics. [bioRxiv preprint](#).
- **Markin, A.** and Eulenstein, O., 2021. *Quartet-based inference is statistically consistent under the unified duplication-loss-coalescence model*. Bioinformatics.
- **Markin, A.** and Eulenstein, O., 2018. *Cophenetic Median Trees*. IEEE/ACM Transactions on Computational Biology and Bioinformatics.

Conference presentations

- Invited talk: Allen D. Leman Swine Conference. St Paul, Minnesota. September 2021.
- Centers of Excellence for Influenza Research and Surveillance (CEIRS) 13th annual meeting (2021). Virtual poster.
- Workshop on Algorithms in Bioinformatics (WABI'2019). “*Consensus Clusters in Robinson-Foulds Reticulation Networks*”. September 2019.
- ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB'19). “*Robinson-Foulds Reticulation Networks*”. September 2019.
- ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB'17). “*Cophenetic Median Trees Under the Manhattan Distance*”. August 2017.
- ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB'16). “*Manhattan path-difference median tree*”. October 2016.
- 12th International Symposium on Bioinformatics Research and Applications (ISBRA'16). “*Path-difference median trees*”. June 2016.

Reviewing experience (peer-review contributions)

- Reviewer for a Systematic Biology submission (2021).
- Sub-reviewer for WABI'21.
- Reviewer for a submission to SIAM Journal on Discrete Mathematics (2021).
- Sub-reviewer for RECOMB 2020.
- Sub-reviewer for RECOMB Comparative Genomics 2019 (RECOMB-CG'19).
- Reviewer for BMC Bioinformatics Special Issue of ISBRA'19 and ISBRA'18 invited papers.
- Sub-reviewer for International Symposium on Bioinformatics Research and Applications 2018 (ISBRA'18).
- Sub-reviewer for International Conference on Bioinformatics and Computational Biology 2018 (BICOB'18).
- Sub-reviewer for IEEE International Conference on Computational Advances in Bio and Medical Sciences 2017 (ICCABS'17, ICCABS'19).

Developed bioinformatics software

- *RF-Net*: Java package for inference of entangled evolutionary histories of segmented viruses and species undergoing hybridization. Developed in collaboration with V. Vadali.
- *PDC-Median*: Java package that incorporates complex, dynamic programming algorithms for large-scale phylogenomic inference.

Major Collaborators

Computer Science	Dr. Oliver Eulenstein (Iowa State University) Dr. Pawel Gorecki (University of Warsaw, Poland).
Biology	Dr. Tavis Anderson (Agricultural Research Service, USDA) Dr. Amy Vincent (Agricultural Research Service, USDA)

Full List of publications

- **Markin, A.**, Wagle, S., Anderson, T.K. and Eulenstein, O., 2021. *RF-Net 2: Fast Inference of Virus Reassortment and Hybridization Networks*. Submitted to Bioinformatics. [bioRxiv preprint](#).
- **Markin, A.** and Eulenstein, O., 2021. *Quartet-based inference is statistically consistent under the unified duplication-loss-coalescence model*. Bioinformatics.

- Paszek, J., **Markin, A.**, Górecki, P. and Eulenstein, O., 2021. *Taming the Duplication-Loss-Coalescence Model with Integer Linear Programming*. Journal of Computational Biology.
- 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).
- Ansarifar, J., **Markin, A.**, Górecki, P. and Eulenstein, O., 2020. *Integer Linear Programming Formulation for the Unified Duplication-Loss-Coalescence Model*. In International Symposium on Bioinformatics Research and Applications (pp. 229-242). Springer, Cham.
- **Markin, A.**, 2020. *On the Extremal Maximum Agreement Subtree Problem*. Discrete Applied Mathematics, Elsevier.
- Górecki, P., **Markin, A.** and Eulenstein, O., 2019. *Exact Median-tree Inference for Unrooted Reconciliation Costs*. BMC Evolutionary Biology, 20(1), pp.1-15.
- 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 (invited paper).
- **Markin, A.**, Anderson, T.K., Vadali, V.K.S.T. and Eulenstein, O., 2019. *Robinson-Foulds Reticulation Networks*. In proceedings of ACM-BCB'2019.
- **Markin, A.** and Eulenstein, O., 2019. *Consensus Clusters in Robinson-Foulds Reticulation Networks*. 19th International Workshop on Algorithms in Bioinformatics (WABI'2019). Schloss Dagstuhl-Leibniz-Zentrum fuer Informatik.
- Górecki, P., **Markin, A.** and Eulenstein, O., 2019. *Feasibility Algorithms for the Duplication-Loss Cost*. COCOON'2019.
- Górecki, P., **Markin, A.** and Eulenstein, O., 2018. *Cophenetic Distances: A Near-Linear Time Algorithmic Framework*. COCOON'2018. The extended version of this manuscript was invited for submission to *Algorithmica* and is under review.
- **Markin, A.**, Vadali, V.S.K.T. and Eulenstein, O., 2018. *Solving the Gene Duplication Feasibility Problem in Linear Time*. COCOON'2018.
- **Markin, A.** and Eulenstein, O., 2018. *Cophenetic Median Trees*. IEEE/ACM transactions on computational biology and bioinformatics, preprint. Invited and extended paper from ACM-BCB'17.
- **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, preprint. Invited and extended paper from ACM-BCB'16.
- **Markin, A.** and Eulenstein, O., 2017. *Efficient Local Search for Euclidean Path-Difference Median Trees*. IEEE/ACM transactions on computational biology and bioinformatics, preprint. Invited and extended paper from ISBRA'16.
- **Markin, A.** and Eulenstein, O., 2017. *Cophenetic median trees under the manhattan distance*. In Proceedings of the 8th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (pp. 194-202). ACM.
- 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 (pp. 234-245). Springer, Cham.
- **Markin, A.** and Eulenstein, O., 2016. *Manhattan path-difference median trees*. In Proceedings of the 7th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (pp. 404-413). ACM.
- **Markin, A.** and Eulenstein, O., 2016. *Path-difference median trees*. In International Symposium on Bioinformatics Research and Applications (pp. 211-223). Springer, Cham.

- **Markin, A.**, 2015. *Bicluster Analysis over Unstructured Text Data from the Internet*. Thesis work for B.S. Available [here](#) (in Russian). Project advisor: Prof. Boris G. Mirkin.

Other professional experience

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

Other major software projects

Distributed web service for processing of biological data (junior year, bachelors)

- Optimized a sequence alignment tool for Hadoop, enabled it to handle a whole human genome assembly
- Developed a web-interface for a user to submit custom sequence alignment jobs (Python Flask, JQuery)
- Part of a larger team effort to build a large-scale distributed Big Data service

Cluster analysis of unstructured texts with web-based as well as desktop GUI (bachelors thesis work)

- The program enabled smarter 2-dimensional analysis of collections of texts, such as paper abstracts
- Developed a web crawler of topic-based scientific abstracts
- Implemented iterative bi-clustering methods, Natural Language Processing techniques
- Developed a novel method for interactive visualization of results for desktop as well as for web

Programming skills

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

Tools and frameworks

Java EE, Hibernate	Hadoop, Spark, Apache Pig
Flask (Python framework), SQLAlchemy	Android
Version control (Git, SVN)	OpenCV (computer vision library)