

Research interests

Computational biology, Phylogenetics, Algorithm design, Discrete mathematics, Graph theory, Computational theory

Education

- Spring 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

- Research assistant *ISU, Fall 2016 & Summer 2017 – present.*
Focusing on Algorithm Design and evaluation for computational problems in evolutionary biology; Investigating properties of popular distance measurements on phylogenetic tree/network spaces;
- Teaching assistant *ISU, Three different courses*, including both theory and applied 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. Award in the amount of **\$2,000**
 - *NSF travel grants for students* for presenting at the ISBRA'16 and ACM-BCB'16 computational biology conferences. In the amounts of **\$1000** and **\$900** respectively
 - *Higher School of Economics Scholarship*, 2012. Award in the amount of **\$2,500**
 - *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.**, Anderson, T.K., Vadali, V.K.S.T. and Eulenstein, O., 2019. *Robinson-Foulds Reticulation Networks*. In Proceedings of ACM-BCB'2019. [bioRxiv preprint](#).
Introduces a novel applied method, RF-Net, for inference of phylogenetic networks from trees.
- **Markin, A.**, 2019. *On the Extremal Maximum Agreement Subtree Problem*. [arXiv preprint](#). Under review in Discrete Applied Mathematics, Elsevier.
The paper solves problem NC3 from Mike Steel's list of [mathematic challenges in phylogenetic](#).
- Górecki, P., **Markin, A.** and Eulenstein, O., 2018. *Cophenetic Distances: A Near-Linear Time Algorithmic Framework*. In proceedings of COCOON'2018. Paper invited to Algorithmica.

- **Markin, A.** and Eulenstein, O., 2018. *Cophenetic Median Trees*. IEEE/ACM Transactions on Computational Biology and Bioinformatics. Invited and extended paper from ACM-BCB'17.

Conference presentations

- 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

- 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).

Developed software (research-based)

- Designed algorithms and in collaboration with V. Vadali implemented *RF-Net* Java package for computation of phylogenetic networks. The method was shown to be applicable to much larger datasets than counterparts.
- Fully developed *PDC-Median* Java package that incorporates complex, dynamic programming powered algorithms for large-scale phylogenetic inference; based on three IEEE/ACM TCBB publications – see below.

Major Collaborators

Computer Science	Dr. Oliver Eulenstein (major advisor) Dr. Pawel Gorecki (University of Warsaw, Poland).
Biology	Dr. Tavis Anderson (Agricultural Research Service, USDA)

Full List of publications

- Under review: **Markin, A.**, 2018. *On the Extremal Maximum Agreement Subtree Problem*. [arXiv preprint](#). Discrete Applied Mathematics, Elsevier.
- Under review: Górecki, P., **Markin, A.** and Eulenstein, O., 2019. *Cophenetic Distances in Near-linear Time*. Journal of the ACM, JACM (extended paper from COCOON'2018).
- Under review: 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. [bioRxiv preprint](#).

- **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 software projects

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

- 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 scientific publications with web-based as well as desktop GUI (bachelor 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
Python
C/C++

C#
R
SQL

JavaScript
F#

Tools and frameworks

Java EE, Hibernate
Flask (Python framework), SQLAlchemy
Version control (Git, SVN)

Hadoop, Spark, Apache Pig
Android
OpenCV (computer vision library)