Nataliya Timoshevskaya

CONTACT INFORMATION

University of Kentucky

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EDUCATION

2019 – current ***Postdoctoral Scholar, Department of Biology***
University of Kentucky, Lexington, KY, USA
Advisor: Dr. Jeramiah Smith

2001 – 2007 ***Ph.D. in Technical Sciences,*** May 2007
Specialization 05.13.01 – System analysis, control and information processing
(in the fields of informatics, computer technology and automation)
Department of Applied Mathematics and Cybernetics
Tomsk State University, Russia
Dissertation Title: "Design and Analysis of Parallel Combinatorial Algorithms"
Advisor: Professor Gennadiy P. Agibalov

1995 – 2001 ***Bachelor and Master of Science in Applied Mathematics (magma cum laude)***
Department of Applied Mathematics and Cybernetics,
Tomsk State University, Russia
Thesis Title: "Development and investigation of a parallel algorithm for the traversal of a searching tree"
Advisor: Dr. Victor A. Belyaev

EMPLOYMENT

2019 – present Postdoctoral scholar, Dept. of Biology, University of Kentucky, Lexington, KY

2015 – 2018 Research assistant (technical/paraprofessional), Dept. of Biology, University of Kentucky, Lexington, KY

2013* – 2014 Research associate, Synergy Lab., Dept. of Computer Science, Virginia Polytechnic Institute and State University, Blacksburg, VA

2005 – 2010 Senior teacher, Department of Applied Mathematics and Cybernetics, Tomsk State University, Russia

2002 – 2004 Teaching assistant, Department of Applied Mathematics and Cybernetics, Tomsk State University, Russia

2001 – 2003 Teacher, Higher College of Informatics Electronics and Management, Tomsk State University of Control Systems and Radio Electronics, Tomsk, Russia

* 2011 – 2012 time off for parental leave

RESEARCH INTEREST AND EXPERIENCE

My main expertise is in **computational analyses of genomic data**. With a background in discrete mathematics and computer science, I am captivated by the intricacies of biological systems, which require powerful algorithms and significant computational resources for analysis. Over the past eight years at the University of Kentucky in my roles of postdoc (2019-present) and research assistant, I have been actively involved in various projects, both in the lab and through collaborations, focused on studying complex genomes.

Notable projects I have been working on include: (1) characterizing the genomes of lamprey species, with a specific emphasis on programmed DNA loss; (2) assembling the salamander genome and assessing polymorphism variations across the genome and among different laboratory strains; (3) discovering highly repetitive motifs in lamprey and hagfish genomes that aid in defining eliminated chromosomes and mechanisms of DNA loss; (4) identifying miniscule differences between sex chromosomes in the giant *A. mexicanum* genome.

These projects relied on developing diverse data analysis pipelines encompassing quality control of sequencing data, *de novo* assembly, gene annotation, discovery of structural variants, evaluation of repetitive content, and gene expression while working with various browsers and databases. To address the computational challenges of processing big data sets, I have effectively utilized **high-performance computing** resources, such as local multiprocessor servers, computational clusters and clouds.

While my primary education is in mathematics and computer sciences, I have extensively educated myself on various areas within the biological sciences mainly as part of my professional work and daily interactions with colleagues. My work requires insightful and meaningful analyses of genomic data and for that, I have attended a university course on advanced genetics, as well as numerous workshops, webinars, and seminars from the Biology Department. I have presented results from my research in local, national, and international scientific meetings focused on biological systems. I co-authored 17 publications in top-notch biological journals with two of them as a first author. My contributions to collaborative projects attest to my computational expertise in diverse bioinformatics studies.

In summary, this extensive work has provided me with an **in-depth knowledge and hands-on expertise in bioinformatics**. This, combined with my analytical and computational skills, qualifies me to make impactful contributions to the advancement of biological sciences.

PUBLICATIONS

27. Marlétaz F, **Timoshevskaya N**, Timoshevskiy VA, Parey E, Simakov O, Gavriouchkina D, Suzuki M, Kubokawa K, Brenner S, Smith JJ, Rokhsar DS. *The hagfish genome and the evolution of vertebrates.* Nature. 2024 Jan 23. doi: 10.1038/s41586-024-07070-3. Epub ahead of print. PMID: 38262590.

26. Kabangu, M.; Cecil, R.; Strohl, L., II; **Timoshevskaya, N**.; Smith, J.J.; Voss, S.R. *Leukocyte Tyrosine Kinase (Ltk) Is the Mendelian Determinant of the Axolotl Melanoid Color Variant.* Genes 2023, 14, 904.

25. **Timoshevskaya N,** Eşkut KI, Timoshevskiy VA, Robb SMC, Holt C, Hess JE, Parker HJ, Baker CF, Miller AK, Saraceno C, Yandell M, Krumlauf R, Narum SR, Lampman RT, Gemmell NJ, Mountcastle J, Haase B, Balacco JR, Formenti G, Pelan S, Sims Y, Howe K, Fedrigo O, Jarvis ED, Smith JJ. *An improved germline genome assembly for the sea lamprey Petromyzon marinus illuminates the evolution of germline-specific chromosomes.* Cell Rep. 2023 Mar 28;42(3):112263.

24. Miller AK, **Timoshevskaya N**, Smith JJ, Gillum J, Sharif S, Clarke S, Baker C, Kitson J, Gemmell NJ, Alexander A. *Population Genomics of New Zealand Pouched Lamprey (kanakana; piharau; Geotria australis).* J Hered. 2022 Jul 23;113(4):380-397.

23. Gatto KP, **Timoshevskaya N**, Smith JJ, Lourenço LB. *Sequencing of laser captured Z and W chromosomes of the tocantins paradoxical frog (Pseudis tocantins) provides insights on repeatome and chromosomal homology.* J Evol Biol. 2022 Dec;35(12):1659-1674.

22. Voss SR, Smith JJ, Cecil RF, Kabangu M, Duerr TJ, Monaghan JR, **Timoshevskaya N**, Ponomareva LV, Thorson JS, Veliz-Cuba A, Murrugarra D. *HDAC Inhibitor Titration of Transcription and Axolotl Tail Regeneration.* Front Cell Dev Biol. 2021 Dec 31;9:767377.

21. Al Haj Baddar Nour, **Timoshevskaya Nataliya**, Smith Jeramiah J., Guo Houfu, Voss S. Randal. *Novel Expansion of Matrix Metalloproteases in the Laboratory Axolotl (Ambystoma mexicanum) and Other Salamander Species.* Frontiers in Ecology and Evolution v.9. 2021.

20. Schloissnig S, Kawaguchi A, Nowoshilow S, Falcon F, Otsuki L, Tardivo P, **Timoshevskaya N**, Keinath MC, Smith JJ, Voss SR, Tanaka EM (2021) *The giant axolotl genome uncovers the evolution, scaling and transcriptional control of complex gene loci.* PNAS, 118:e2017176118.

19. **Timoshevskaya N**, Voss SR, Labianca CN, High CR, Smith JJ. *Large-scale variation in single nucleotide polymorphism density within the laboratory axolotl (Ambystoma mexicanum).* Dev Dyn. 2021 Jun;250(6):822-837.

18. Keinath, MC; Davidian, A; Timoshevskiy, V; **Timoshevskaya, N**; Gall, JG (2021) *Characterization of axolotl lampbrush chromosomes by fluorescence in situ hybridization and immunostaining.* Experimental Cell Research, 401(2):112523

17. Hickner PV, **Timoshevskaya N**, Nowling RJ, Labbé F, Nguyen AD, McDowell MA, Spiegel CN, Syed Z. *Molecular signatures of sexual communication in the phlebotomine sand flies.* PLoS Negl Trop Dis. 2020 Dec 28;14(12):e0008967.

16. Hess, JE, Smith, JJ, **Timoshevskaya, N**, et al. (2020) *Genomic islands of divergence infer a phenotypic landscape in Pacific lamprey. Mol Ecol.* 2020; 29: 3841–3856.

15. Timoshevskiy, V.A.; **Timoshevskaya, N.Y.**; Smith, J.J. (2019) *Germline-Specific Repetitive Elements in Programmatically Eliminated Chromosomes of the Sea Lamprey (Petromyzon marinus).* Genes 2019, *10*, 832.

14. Smith JJ, **Timoshevskaya N**, Timoshevskiy VA, Keinath MC, Hardy D, Voss SR (2019) *A chromosome-scale assembly of the axolotl genome.* **Genome Research**, 29: 317-324.

13. Keinath MC, **Timoshevskaya N**, Timoshevskiy VA, Voss SR, Smith JJ (2018) *Miniscule differences between sex chromosomes in the giant genome of a salamander.* Scientific Reports, 8(1):17882

12. J.J. Smith, **N. Timoshevskaya**, C. Ye, C. Holt, M.C. Keinath, H.J. Parker, M.E. Cook, J.E. Hess, S.R. Narum, F. Lamanna, H. Kaessmann, V.A. Timoshevskiy, C.K.M. Waterbury, C. Saraceno, L.M. Wiedemann, S.M.C. Robb, C. Baker, E.E. Eichler, D. Hockman, T. Sauka-Spengler, M. Yandell, R. Krumlauf, G. Elgar, C.T. Amemiya. *The sea lamprey germline genome provides insights into programmed genome rearrangement and vertebrate evolution.* Nat. Genet., 50 (2018), pp. 270-277

11. Woodcock, MR, Vaughn-Wolfe J, Elias A, Kump DK, Kendall, KD, **Timoshevskaya N**, Timoshevskiy V, Perry DW, Smith JJ, Spiewak JE, Parichy DM, Voss SR, *Identification of Mutant Genes and Introgressed Tiger Salamander DNA in the Laboratory Axolotl, Ambystoma mexicanum.* Scientific Reports *7*, 1 (2017): 6.

10. Keinath MC, **Timoshevskaya NY**, Timoshevskiy VA, Tsonis PA, Voss SR, Smith JJ* (2015) *Initial characterization of the large genome of the salamander Ambystoma mexicanum using shotgun and laser capture chromosome sequencing.* Scientific Reports, 5:16413.

9. **Nataliya Timoshevskaya**, Wu-chun Feng. *SAIS-OPT: On the Characterization and Optimization of the SA-IS Algorithm for Suffix Array Construction.* In Proceedings of the 4th IEEE International Conference on Computational Advanced in Bio and Medical Sciences, Miami Beach, Florida, June 2014.

8. Mohamed, N.; Maji, N.; Jing Zhang; **Timoshevskaya, N.**; Wu-chun Feng, *Aeromancer: A Workflow Manager for Large-Scale MapReduce-Based Scientific Workflows,* Trust, Security and Privacy in Computing and Communications (TrustCom), 2014 IEEE 3th International Conference on Big Data Science and Engineering, vol., no., pp.739,746, 24-26 Sept. 2014

7. **Timoshevskaya N.** *Разработка и исследование параллельных комбинаторных алгоритмов* [Design and Research of the Parallel Combinatorial Algorithms.] *Prikl. Diskr. Mat.*, 2009, No. 2, 96–103.

6. Ww **Timoshevskaya N.** *Оценки числа покрытий линеариационных множеств заданной мощности* [Estimates for the Number of Covers with Linearization Sets of a Given Cardinality]. *Vestn. Tomsk. Gos. Univ. Appendix.* 2007. 23: 60-64.

5. **Timoshevskaya N.** *Элементы комбинаторики и комбинаторные алгоритмы: учебно-методический комплекс* [Elements of combinatorics and combinatorial algorithms: **course tutorial**], published by Tomsk State University, 2007, http://vital.lib.tsu.ru/vital/access/manager/Repository/vtls:000243999

4. **Timoshevskaya N.** *Параллельное перечисление разбиений множества методом нумерации* [Parallel Enumeration of Set Partitions by Numbering]. *Vestn. Tomsk. Gos. Univ. Appendix.* 2006. 17: 260-264.

3. **Timoshevskaya N.** *Задача о кратчайшем линеаризационном множестве* [The Shortest Linearization Set Problem]. *Vestn. Tomsk. Gos. Univ. Appendix.* 2005. 14: 79-83.

2. **Timoshevskaya N.** *Параллельные методы обхода дерева* [Parallel Methods for Tree Traverse]. *Mathematical modeling.* 2004. 16(1): 105–114.

1. **Timoshevskaya N.** *Параллельные вычисления в решении систем логических уравнений методом линеаризации* [Solving of the System of Logical Equations by Linearization Method in Parallel]. *Proceedings of the XV international seminar «Design*

and complexity of control systems» (Novosibirsk, Russia, 2004). – Novosibirsk: Institute of Mathematics, 2004: 97 – 102.

PARTICIPATION IN SPONSORED PROJECTS

2018 – present: Functional Analysis of Programmed Genome Rearrangement. NIH grant R35. Role – postdoctoral scholar.

2018 – 2022: Reconstructing the Biology of Ancestral Vertebrate Genomes. NSF MCB. Role – postdoctoral scholar.

2015 – 2020: Research Resources for Model Amphibians. NIH grant R24. Role – participant/postdoctoral scholar.

2015 – 2019: Programmed Genome Rearrangement and the Genetics of Somatic Recombination. NIH grant R01. Role – participant.

2013 – 2014: Genomes galore – Core techniques, libraries, and domain specific languages for high-throughput DNA sequencing. NSF IIS-1247693 via the NSF BIGDATA program. Role – research associate.

2005 – 2006: Parallel Algorithms in Cipher Cryptanalysis. Grant № 38025, Program of Ministry of Education and Science of the Russian Federation «Development of Higher Education». Role – senior investigator.

2003: Design and Analysis of Algorithms for Construction of the Shortest Acceptable Set Partitions, Grant of Russian Foundation for Basic Research (01-01-00774). Role – participant.

2001 – 2002: Investigation and Design of Math-based and Software Environment for Synthesis of Secure Information Systems. Grant № T00-3.1-2851, program of Ministry of Education and Science of the Russian Federation in fundamental investigations in technical sciences. Role – participant.

PRESENTATIONS

Presentations in biological scientific meetings

1. The Plant & Animal Genome Conference [poster]. **Programmed DNA Loss in Lampreys and Hagfish** (Jan. 13 - 18, 2023, San Diego, CA)
2. International Lamprey Genomics Workshop [roundtable]. **Search of a sex determination region in Pacific Lamprey** (Oct. 8-10, 2019, University of Manitoba, Winnipeg, Canada)
3. The Biology of Genomes [poster]. **DifCover – A computational pipeline for identifying structural variants in complex vertebrate genomes** (May 7 - 11, 2019, Cold Springs Harbor Laboratories, NY)

4. The Biology of Genomes [poster]. **Improving and using a chromosome-scale assembly of the enormous (32 Gb) axolotl genome** (May 7 - 11, 2019, Cold Springs Harbor Laboratories, NY)

5. Population, Evolutionary and Quantitative Genetics Conference [poster]. **Integrative Cytogenetics of the Sea Lamprey Chromosome Elimination** (May 13–16, 2018, Madison, WI)

6. Systems Biology and Omics Integration Journal Club [oral presentation: co-presenter]. **Bioinformatic approaches to characterizing salamander sex chromosomes** (April 3, 2017, Lexington, KY)

7. Biology of Genomes Meeting [poster]. **Characterization of a large vertebrate genome and sex chromosomes using shotgun and laser capture chromosome sequencing** (May 10, 2016. Cold Spring Harbor Laboratories, NY)

Selected presentations at computer science and mathematics conferences

1. 1st Annual Commonwealth Computational Summit [poster]. **Discovery of sex-specific regions in a salamander genome** (October 17, 2017, Lexington, KY)

2. 4th IEEE International Conference on Computational Advanced in Bio and Medical Sciences [talk]. **SAIS-OPT: On the Characterization and Optimization of the SA-IS Algorithm for Suffix Array Construction** (June 2014, Miami Beach, Fl)

3. Третья Сибирская школа-семинар по параллельным вычислениям [Third Siberian seminar on parallel computations] [talk]. **О методах разработки параллельных комбинаторных алгоритмов** [Methods for design of parallel combinatorial algorythms] (December, 2005, Tomsk, Russia)

4. Проблемы теоретической кибернетики. XIV Международная конференция [Problems of Theoretical Cybernetics. XIV International Conference] [talk]. *О линеаризационных множествах* [About linearization sets] (May 23–28, 2005, Penza, Russia)

5. XV международная школа-семинар "Синтез и сложность управляющих систем" [XV international seminar "Synthesis and complexity of control systems"] [talk]. *Параллельные вычисления в решении систем логических уравнений методом линеаризации* [Parallel computations in the solving of logical equations by linearization method] (Oct. 18–23, 2004, Novosibirsk, Russia)

6. Международный научно-практический семинар "Высокопроизводительные параллельные вычисления на кластерных системах" [*International theoretical and practical workshop «High-Performance parallel computing on the cluster systems»*] [talk]. *Распараллеливание обхода дерева поиска для решения задачи о рюкзаке на кластерной системе* [Parallelization of tree traversal in the knapsack problem on the cluster systems] (Nov. 20-24, 2002, Nizhny Novgorod)

BIOINFORMATICS SOFTWARE AND RESOURCES

DifCover – computational pipeline designed to retrieve sample-specific sequences by comparing resequencing data and employing the "stretching" windows technique to accommodate repetitive content and genomic regions with low coverage.

github.com/timnat/DifCover, doi:10.5281/zenodo.7574262

This pipeline became a valuable tool for numerous coverage-based analyses and has been used in many lab projects as well as in several published research works by various scientific groups.

1) Raiyemo, D.A., Bobadilla, L.K. & Tranel, P.J. Genomic profiling of dioecious Amaranthus species provides novel insights into species relatedness and sex genes. BMC Biol 21, 37 (2023).

2) Yasmin, T., Grayson, P., Docker, M.F. et al. Pervasive male-biased expression throughout the germline-specific regions of the sea lamprey genome supports key roles in sex differentiation and spermatogenesis. Commun. Biol. 5, 434 (2022).

3) Phil Grayson, Alison Wright, Colin J. Garroway, Margaret F. Docker, SexFindR: A computational workflow to identify young and old sex chromosomes. bioRxiv 2022.02.21.481346

4) Hickner PV, Timoshevskaya N, Nowling RJ, Labbé F, Nguyen AD, McDowell MA, Spiegel CN, Syed Z. *Molecular signatures of sexual communication in the phlebotomine sand flies.* PLoS Negl Trop Dis. 2020 Dec 28;14(12):e0008967.

SparseGenotyping - program allows to resolve a consensus genotype for scaffolds based on low-coverage SNP calls by accumulating an adequate number of reads that support one or another genotype across the length of a scaffold.

github.com/timnat/SparseGenotyping

This program was specifically written and played a crucial role in the assembling of the first chromosome-scale genome of axolotl.

Smith JJ, **Timoshevskaya N**, Timoshevskiy VA, Keinath MC, Hardy D, Voss SR (2019) *A chromosome-scale assembly of the axolotl genome.* **Genome Research**, 29: 317-324.

Assembly hub and online blast service for Ambystoma mexicanum genome - these services provide genome resources for the salamander community and are publicly accessible from the Sal-Site website. The assembly hub for UCSC browser hub tracks encompass gene annotations, transcriptomes, variants, epigenetics studies, RNA-seq alignments from 12 various projects, and more.

Sal-site: https://ambystoma.uky.edu/genome-resources

COMPUTATIONAL AND ANALYTICAL SKILLS

- I was trained at Tomsk State University, Russia, as a mathematician and computational scientist. I studied and taught various courses on the development of complex combinatorial algorithms (detailed in the Teaching Experience section) with the focus of my doctorate work on the design and adaptation of combinatorial algorithms for computational systems with distributed memory [21-27].

- Over the years I worked in various computing software and hardware environments. I have been administering a local Dell server under CentOS 7 with an additional 80Tb data

storage system. The weeks-long analyses were performed on clusters or virtual machines in the OpenStack cloud platform.

- I am proficient in working in Unix, installing and configuring various bioinformatics tools and packages, sketching bash scripts, one-liner complex commands, editing/adjusting or designing, if necessary, programs on bash, awk, Perl, Python, C, R or MySQL.

TEACHING EXPERIENCE

1. Design and Analysis of Algorithms (lectures, TSU, Tomsk, Russia, 2007-2010),
2. Parallel computing (lectures and computer labs, TSU, 2008-2009),
3. Complexity theory (seminars, TSU, 2005 - 2008),
4. Combinatorics (lectures and seminars, TSU, 2005-2008),
5. Combinatorial algorithms (Lectures and computer labs, TSU, 2004-2008),
6. Programming in C (computer labs, TSU, 2002 - 2004).
7. Introduction to discrete mathematics (seminars, Higher College of Informatics Electronics and Management, Tomsk, 2001 – 2003),
8. Programming in Pascal (lectures and labs, Higher College of Informatics Electronics and Management, 2001 - 2003).

MENTORING

University of Kentucky:
Graduate Students: Kaan Eşkut (current), Cody Saraceno (Graduated Ph.D. 2023), Melissa Keinath (Graduated Ph.D., 2017). Kaleb Pretto Gatto (visiting student from Brazil, 2016), Tyler Spear (Scientist 1 (current)).

Virginia Tech University:
Master Students: Nabanita Maji, Jing Zhang

Tomsk State University:
Master students: Ivan Hudyashov, Sergei Giss, Maxim Naumov, Victor Semenov, Alla Kuznetsova

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AWARDS

Winner (second place) of the Postdoc Poster Session. Poster title: "Programmed DNA loss in lampreys and hagfish". 2023 SOPS Research & Career Symposium, September 21t, 2023. Hosted by the University of Kentucky.

Winner (second place) of the One-Minute Pitch Competition. Fascinating Mysteries of the Lamprey Genome. 2020 SOPS Research & Career Symposium, September 25th, 2020. Online. Hosted by the University of Kentucky.

SERVICES

Reviewer for the 59th annual Oswald Research and Creativity Competition, category Biological Sciences. University of Kentucky, November, 2023.

Reviewer: Molecular Ecology Resources (2020), Prikladnaya Diskretnaya Matematika (2008-2009)

PROFESSIONAL REFERENCES

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B443 Biomedical Biological Sciences Research Building (BBSRB)
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Dr. Jon Hess (collaborator)
Senior Fisheries Geneticist
Columbia River Inter-Tribal Fish Commission,
Fishery Science Department
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