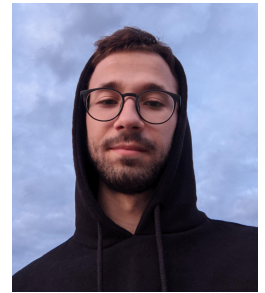


Andrey A. Tomarovsky

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Education

- Sep 2021 - Jun 2026 **PhD in Genetics.** Novosibirsk State University, Novosibirsk, Russia. PhD thesis: Consequences of interspecific hybridization and phylogenetic relationships in the genus *Martes* (fam. Mustelidae).
GPA: 5.0 (max 5.0)
Supervisors: Dr. [Sergei F. Kliver](#) & Dr. [Alexander S. Graphodatsky](#)
- Sep 2019 - Jun 2021 **MS in Bioinformatics.** Saint-Petersburg State University, St. Petersburg, Russia. MS thesis: Assembly and annotation of sable (*Martes zibellina*) and pine marten (*Martes martes*) genomes. GPA: 4.5 (max 5.0)
Supervisor: Dr. [Sergei F. Kliver](#)
- Sep 2015 - Jun 2019 **BS in Biotechnologies.** Belgorod State National Research University, Belgorod, Russia.
GPA: 4.6 (max 5.0)
Supervisor: Nadezhda I. Zhivina

Work experience

- May 2023 - Present **Junior Researcher | Bioinformatician**
Institute of Molecular and Cellular Biology SB RAS, Novosibirsk, Russia
[Laboratory of Diversity and Evolution of Genomes](#) · Full-time

Comparative genomics of Mustelidae family species.
- Apr 2021 - Nov 2023 **Junior System Administrator**
Moscow State University, Moscow, Russia
[Faculty of bioengineering and bioinformatics](#) · Part-time

Administration of "Makarich" computational cluster.
- Feb 2022 - May 2023 **Junior Researcher | Bioinformatician**
Institute of Molecular and Cellular Biology SB RAS, Novosibirsk, Russia
Laboratory of Animal Cytogenetics, Department of Diversity and Evolution of Genomes · Part-time

Comparative genomics of Mustelidae family species.
- Mar 2021 - Dec 2022 **Research Programmer | Bioinformatician**
ITMO University, St. Petersburg, Russia
Research Center for Genomic Diversity, [International Laboratory "Computer Technologies"](#) · Contract

Genomics of *Martes* species (fam. Mustelidae).

Feb 2021 - present

Blastim's online courses · Part-time

Visiting lecturer:

- [Introduction to Linux for Bioinformatics](#)
- [Snakemake for Bioinformatics](#)

Technical and software support, cluster administration:

- [Python for data analysis in science](#)
- [Analyzing NGS data](#)
- [Analyzing RNA-seq data](#)
- [Statistics, R and data analysis](#)

Skills

Languages:	Russian – native, English – full professional proficiency
OS:	Linux, Windows
Shell:	Bash. Shell tools: vim, grep, awk, sed, etc.
Programming:	Python, R
Python libraries:	Biopython, Matplotlib, Numpy, Pandas, Etc3
R libraries:	ggplot2, dplyr, readxl
Workflow managers:	Snakemake
Workload managers:	Slurm, PBS
Container platforms:	Apptainer/Singularity, Docker
Package managers:	Conda/Mamba, pip, cran
Version control systems:	git
HPC:	ResOps experience with computations on HPC clusters
Others:	SQL, Circos, Tcl.

Areas of expertise

Genome assembly:	<i>De novo</i> chromosome-level genome assembly of mammalian species using both short- and long-read sequencing technologies.
Genome annotation:	Structural and functional genome annotation; <i>De novo</i> assembly and annotation of repetitive elements and transposable elements.
Comparative genomics:	Comparative analysis of chromosomal rearrangements.
Population genomics:	Assessment of genome-wide genetic diversity; Identification of runs of homozygosity and inbreeding estimation; Population structure analysis and ancestry inference; Reconstruction of population history.
Phylogenomics:	Phylogenetic and phylogenomic analysis; Species tree inference and assessment of incomplete lineage sorting.
Conservation biology:	Assessment of genomic consequences of population decline and isolation.

On the Side

Supervision of master students:

- Pavel Ponomarev (2025, ITMO University). MS thesis: Optimization and Quality Assurance of a Pipeline for Phylogeny Reconstruction Based on Single-Copy Conserved BUSCO Orthologs.

Software development:

- [BuscoClade](#). Snakemake-based pipeline to construct species phylogenies using universal single-copy orthologs BUSCOs. Phylogenetic tree reconstruction using IQtree, MrBayes, RaxML-NG, RapidNJ and Astral III. Visualization using Ete3.
- [ITSPipe](#). Snakemake-based pipeline for the analysis of ITS sequences from the ribosomal cluster. Coverage visualization using Matplotlib and variant calling using Gatk, Pscs, and Bcftools is performed.
- [Biocrutch](#). Python package for genome data processing and plotting.
- [Bashare](#). Bash scripts for NGS automation and batch HPC workflows.

Side projects:

- [UlkaVPN](#). Co-founder and developer of a VPN service (200+ active users). Designed and maintained the backend infrastructure: server deployment, traffic routing, monitoring, and user management.

Grants

- 2022 - 2023 Russian Scientific Foundation, grant № [22-24-01076](#) “Comparative genomics: analysis of evolutionary changes in syntenic chromosome blocks (Canidae and Cetartiodactyla) based on Hi-C maps”.
- 2022 - 2023 Russian Scientific Foundation, grant № [19-14-00034-P](#) “Autosomes, sexual and additive chromosomes of vertebrates. Organization and Evolution”.
- 2020 - 2022 Russian Foundation for Basic Research, grant № [20-04-00808 A](#), “Genomes and genetic diversity of mustelids (fam. Mustelidae) of Russia and South-Eastern Asia”.

Publications

1. Tomarovsky, A.A., Totikov, A.A., Bulyonkova, T.M., Perelman, P.L., Abramov, A.V., Serdyukova, N.A., Yakupova, A.R., Prokopov, D., Beklemisheva, V.R., Sinding, M.-H., Davletshina, G., Pobedintseva, M., Krashenninnikova, K., Foerster, D., Mukhacheva, A.S., Mironova, A., Sidorov, M., Nie, W., Wang, J., Romanenko, S.A., Proskurykova, A., Ferguson-Smith, M., Yang, F., Cherkasov, N., Balanovska, E., Gilbert, T.P., Okhlopkov, I.M., Zhuk, A., Graphodatsky, A.S., Powell, R., Koepfli, K.-P., Kliver, S. Genomics of sable (*Martes zibellina*) × pine marten (*Martes martes*) hybridization. *Genome Biology and Evolution*, 2026; Volume 18, Issue 3, evag018. <https://doi.org/10.1093/gbe/evag018>, Q1, IF=3.3, Scopus, WoS, RSCI.
2. Totikov, A.A., Tomarovsky, A.A., Perelman, P.L., Bulyonkova, T.M., Serdyukova, N.A., Yakupova, A.R., Mohr, D., Foerster, D.W., Grau Jipoulou, J.H., Beklemisheva, V.R., Sidorov, M., Miranda, I., Farelo, L., Abramov, A.V., Krashenninnikova, K., Mukhacheva, A.S., Panov, V.V., Balanovska, E., Cherkasov, N., Zub, K., Scott, A.F., Melo-Ferreira, J., Okhlopkov, I.M., Zhuk, A., Koepfli, K.-P., Graphodatsky, A.S., Kliver, S. Comparative genomics and phylogenomics of the Mustelinae lineage (Mustelidae, Carnivora). *Genome Biology and Evolution*, 2026; ; Volume 18, Issue 3, evag014. <https://doi.org/10.1093/gbe/evag014>, Q1, IF=3.3, Scopus, WoS, RSCI.
3. Kusliy, M.A., Malikov, D.G., Klementiev, A.M., Samarina, S.A., Modina, S.A., Tishakova, K.V., Lemskaya, N.A., Serdyukova, N.A., Budenchuk, E.V., Yakovlev, A.V., Cheklyuev, P.A., Yurlova, A.A., Tomarovsky, A.A., Totikov, A.A., Nushtaev, Y.Y., Popova, K.O., Pavlov, I.S., Pavlova, N.I., Protopopov, A.V., Graphodatsky, A.S., Vorobieva, N.V., Molodtseva, A.S. New genetic data on the Pleistocene Ovodon horses of Siberia. *Quaternary Science Reviews*, 2026; Vol. 372. P. 109696. <https://doi.org/10.1016/j.quascirev.2025.109696>, Q1, IF=3.3, Scopus, WoS, RSCI.
4. Tomarovsky, A.A., Khan, R., Dudchenko, O., Beklemisheva, V.R., Perelman, P.L., Totikov, A.A., Serdyukova, N.A., Bulyonkova, T.M., Pobedintseva, M., Abramov, A.V., Weisz, D., Yakupova, A., Zhuk, A., Graphodatsky, A.S., Powell, R., Aiden, E., Koepfli, K.-P., Kliver, S. Novel Chromosome-Length Genome Assemblies of Three Distinct Subspecies of Pine Marten, Sable, and Yellow-Throated Marten (Genus *Martes*, Family Mustelidae). *Journal of Heredity*, 2025; esaf101. <https://doi.org/10.1093/jhered/esaf101>, Q1, IF=2.5, Scopus, WoS, RSCI.

5. Tomarovsky, A.A., Khan, R., Dudchenko, O., Totikov, A.A., Serdyukova, N.A., Weisz, D., Vorobieva, N.V., Bulyonkova, T., Abramov, A.V., Nie, W., Wang, J., Romanenko, S.A., Proskuryakova, A.A., Cherkasov, N., Ferguson-Smith, M.A., Yang, F., Balanovskaya, E., Gilbert, M.T.P., Graphodatsky, A.S., Aiden, E.L., Powell, R., Koepfli, K.-P., Perelman, P.L., Kliver, S. Chromosome length genome assembly of the stone marten (*Martes foina*, Mustelidae): a new view on one of the cornerstones in carnivore cytogenetics. *Journal of Heredity*, 2025; esaf001. <https://doi.org/10.1093/jhered/esaf001>, Q1, IF=2.5, Scopus, WoS, RSCI.
6. Tomarovsky, A., Totikov, A.A., Yakupova, A.R., Graphodatsky, A.S., Kliver, S. Review of heterozygosity visualization approaches in the context of conservation research. *Ecological genetics*, 2023. Vol. 21. N. 4. P. 383-400, (ru). <https://doi.org/10.17816/ecogen609552>, Q4, IF=0.2, Scopus, RSCI.
7. Kliver, S., Houck, M.L., Perelman, P.L., Totikov, A.A., Tomarovsky, A., Dudchenko, O., Omer, A.D., Colaric, Z., Weisz, D., Aiden, E.L., Chan, S., Hastie, A., Komissarov, A., Ryder, O.A., Graphodatsky, A.S., Johnson, W.E., Maldonado, J.E., Pukazhenthi, B.S., Marinari, P.E., Wildt, D.E., Koepfli, K.-P. Chromosome-length genome assembly and karyotype of the endangered black-footed ferret (*Mustela nigripes*). *Journal of Heredity*, 2023; esad035, <https://doi.org/10.1093/jhered/esad035>, Q1, IF=2.5, Scopus, WoS, RSCI.
8. Totikov, A.A., Tomarovsky, A.A., Yakupova, A.R., Graphodatsky, A.S., Kliver, S. Review of population history reconstruction methods in conservation biology. *Ecological genetics*, 2023. Vol. 21. N. 1. P. 85-102, (ru). <https://doi.org/10.17816/ecogen120078>, Q4, IF=0.2, Scopus, RSCI.
9. Yakupova, A., Tomarovsky, A., Totikov, A.A., Beklemisheva, V., Logacheva, M., Perelman, P.L., Komissarov, A., Dobrynin, P., Krashenninnikova, K., Tamazian, G., Serdyukova, N.A., Rayko, M., Bulyonkova, T., Cherkasov, N., Pylev, V., Peterfeld, V., Penin, A., Balanovska, E., Lapidus, A., DNA Zoo Consortium, O'Brien, S.J., Graphodatsky, A., Koepfli, K.-P., Kliver, S. Chromosome-Length Assembly of the Baikal Seal (*Pusa sibirica*) Genome Reveals a Historically Large Population Prior to Isolation in Lake Baikal. *Genes*, 2023. 14(3), 619, <https://doi.org/10.3390/genes14030619>, Q2, IF=2.8, Scopus, WoS, RSCI.
10. Derežanin, L., Blažytė, A., Dobrynin, P., Duchêne, D.A., Grau, J.H., Jeon, S., Kliver, S., Koepfli, K.-P., Meneghini, D., Preick, M., Tomarovsky, A., Totikov, A.A., Fickel, J., Förster, D.W. Multiple types of genomic variation contribute to adaptive traits in the mustelid subfamily Guloninae. *Molecular Ecology*, 2022, 31, 2898-2919. <https://doi.org/10.1111/mec.16443>, Q1, IF=3.9, Scopus, WoS, RSCI.
11. Totikov, A.A., Tomarovsky, A., Prokopov, D., Yakupova, A., Bulyonkova, T., Derežanin, L., Rasskazov, D., Wolfsberger, W.W., Koepfli, K.-P., Oleksyk, T.K., Kliver, S. Chromosome-Level Genome Assemblies Expand Capabilities of Genomics for Conservation Biology. *Genes*, 2021, 12(9), 1336. <https://doi.org/10.3390/genes12091336>, Q2, IF=2.8, Scopus, WoS, RSCI.

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1. Totikov, A., Tomarovsky, A., Perelman, P., Bulyonkova, T., Panov, V., DNA Zoo Consortium, Graphodatsky, A., Kliver, S. Chromosome-level genome assembly of the Least Weasel (*Mustela nivalis*). 14th International Multiconference Bioinformatics of Genome Regulation and Structure / Systems Biology (BGRSSB-2024). August 5–10, 2024, Novosibirsk, Russia. <https://doi.org/10.18699/bgrs2024-abstracts>.
2. Tomarovsky, A., Totikov, A., Perelman, P., Beklemisheva, V., Serdyukova, N., Bulyonkova, T., Sidorov, M., Mamaev, N., Okhlopkov, I., Mukhacheva, A., Koniaeva, K., Abramov, A., Graphodatsky, A., Kliver, S. Whole-genome data confirm the presence of crossover in hybrids of sable (*M. zibellina*) and pine marten (*M. martes*). 14th International Multiconference Bioinformatics of Genome Regulation and Structure / Systems Biology (BGRSSB-2024). August 5–10, 2024, Novosibirsk, Russia. <https://doi.org/10.18699/bgrs2024-abstracts>.
3. Totikov, A., Tomarovsky, A., Perelman, P., Beklemisheva, V., Serdyukova, N., Bulyonkova, T., Panov, V., Mukhacheva, A., Abramov, A., Graphodatsky, A., Kliver, S. Assessment of heterozygosity levels of the *Mustela* species. International Conference “Chromosome-2023”, Novosibirsk, (ru). <https://doi.org/10.25205/978-5-4437-1514-8>.

4. Tomarovsky, A., Totikov, A., Perelman, P., Beklemisheva, V., Serdyokova, N., Bulyonkova, T., Sidorov, M., Mamaev, N., Okhlopkov, I., Mukhacheva, A., Koniaeva, K., Abramov, A., Graphodatsky, A., Kliver, S. Assessment of heterozygosity levels of the sable (*Martes zibellina*), the pine marten (*Martes martes*), and their hybrids. International Conference “Chromosome-2023”, Novosibirsk, (ru). <https://doi.org/10.25205/978-5-4437-1514-8>.
5. Totikov, A.; Tomarovsky, A.; Perelman, P.; Serdyokova, N.; Beklemisheva, V.; Bulyonkova, T.; Zub, K.; Panov, V.; Mukhacheva, A.; Abramov, A.; Koepfli, K.; Graphodatsky, A.; Melo-Ferreira, J.; Kliver, S. Reconstruction of the demographic history for three populations of the least weasel *Mustela nivalis*. 10th Moscow Conference on Computational Molecular Biology (MCCMB-2021). July 30th – August 2nd, 2021, Moscow, Russia. ISBN: 978-5-901158-32-6, (175).
6. Tomarovsky, A.; Totikov, A.; Beklemisheva, V.; Perelman, P.; Serdyokova, N.; Bulyonkova, T.; Koniaeva, K.; Abramov, A.; Graphodatsky, A.; Koepfli K.; Powell R.; Kliver S. Assembly and annotation of sable (*Martes zibellina*) and pine marten (*Martes martes*) genomes. 10th Moscow Conference on Computational Molecular Biology (MCCMB-2021). ISBN: 978-5-901158-32-6, (176).