Andrey A. Tomarovsky

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Education

Sep 2021 - Jul 2025 **PhD student 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 - Jul 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 - Jul 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 | Bioinformatican**
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 | Bioinformatican**
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 | Bioinformatican**
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, Ete3
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:	*De novo* chromosome-level genome assembly of mammalian species using both short- and long-read sequencing technologies.
Genome annotation:	Structural and functional genome annotation; *De novo* 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, Pisces, and Bcftools is performed.
- Biocrutch. Python package for genome data processing and plotting.
- Bashare. Bash scripts for NGS automation and batch HPC workflows.

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. 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 Ovodov 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.
2. 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.
3. 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., Krasheninnikova, 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. https://doi.org/10.1093/gbe/evag018, Q1, IF=3.3, Scopus, WoS, RSCI.
4. 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.
5. 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., Krasheninnikova, 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. https://doi.org/10.1093/gbe/evag014, Q1, IF=3.3, 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., Krasheninnikova, 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., Derezanin, 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.

Conferences

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., Serdyokova, 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).