

Dr. Olga O. Bochkareva

Address: 1030 Faculty of Life Sciences, University of Vienna,
Djerassiplatz 1, Vienna, Austria
E-mail: olga.bochkareva@univie.ac.at
Web site: <https://www.bochkareva.me/>
ORCID (incl. Publications): 0000-0003-1006-6639

The impact and importance of the main research outputs:

I'm working on the intersection of comparative genomics, algorithmic biology, and evolutionary biology to build a deep understanding of bacterial genome organization and the molecular mechanisms providing complex dynamic genotype-phenotype connections. To tackle my research goals, I created a synthesis between theory and experimentation under the confines of a single laboratory combining the computational methods developed by myself and experimental assays of engineered cultures performed in collaborations with top-ranked scientists. Mainly working on fundamental knowledge about bacterial genome complexity, I create efficient pipelines which might be used as a basis for clinical and industrial applications.

I have developed a set of the methods for analysis of structural variants (PaReBRick, BADLON) which provide a basis for holistic prediction of genotype-to-phenotype connection. The most significant result was prediction of phase variation in *S. pneumoniae* affecting a gene whose product was selected as a target for a novel vaccine. Phase variation allows for bacterial populations to generate phenotypic variants, some of which may be better adapted to particular environmental conditions. Uncovering such molecular mechanisms is important for efficient strategies of vaccine development and antibiotics therapy. In gut microbiota, I revealed phase-variation mechanisms in polysaccharide utilization loci, responsible for nutrients recognition and glycan digestion. Alteration of expression of locus-encoded transporters allows *Bacteroides* to thrive in fluctuating conditions within the human gut. Although I started my academic career as a computational scientist, I design and supervise the experiments to support and proof my predictions.

The developed methodology has a great potential to be used in other related areas, e.g. I contributed to the development of ML models for discovery of antibiotics resistance markers suggesting the training dataset selection based on phylogeny-based parallelism score which reduce the number of features in the analysis, while simultaneously increasing models' performance and allowing to discover more biologically meaningful markers.

Work experience:

2023 – present ESPRIT Principal Investigator, CUBE, Centre for Microbiology and Environmental Systems Science, University of Vienna, Austria.

2019 – 2023 postdoctoral researcher, Institute of Science and Technology (ISTA), Austria. Prof. Fyodor Kondrashov group.

2017 – 2019 junior research scientist, Department of Life Sciences, Skolkovo Institute of Science and Technology, Moscow, Russia.

(Career break) 2014 – 2017 maternity leave (twins)

2012 – 2019 junior research scientist, Kharkevich Institute for Information Transmission Problems RAS, Moscow, Russia.

Funding and Awards:

(under review) “Genetic heterogeneity of Bacteroides PULs”, total amount **664,218€**

Austrian Science Fund, Principal Investigator Project, postdoc+PhD personal costs included

2023 “Large-scale genomic features and bacterial phenotypes”, total amount – **294,015€**

Austrian Science Fund ESPRIT Programme (“Early Stage Programme: Research, Innovation and Training”)

2019 ISTplus postdoctoral fellowship. Funding from the **European Union’s Horizon 2020** research and innovation programme under the Marie Skłodowska-Curie grant agreement No 754411

Education:

2019 Ph.D., Kharkevich Institute for Information Transmission Problems RAS, PhD thesis: “*Reconstruction of evolutionary history of genome rearrangements in bacteria*”, Supervisor: *Prof. Mikhail S. Gelfand*.

2012 Master of Science (applied mathematics and physics), Department of Molecular and Biological Physics, Moscow Institute of Physics and Technology.

2010 Bachelor of Science (applied mathematics and physics), Moscow Institute of Physics and Technology.

Publications:

10 peer-reviewed publications, 3 first and 3 last authorships (* - equal contribution)

1. K Jain, R Hauschild, **OO Bochkareva**, R Roemhild, G Tkacik, CC Guet Pulsatile basal gene expression as a fitness determinant in bacteria **Proc. Natl. Acad. Sci. U.S.A.** 2025 Apr 07, 122(15) e2413709122 doi:10.1073/pnas.2413709122
2. A Yurtseven, S Buyanova, AA Agrawal, **OO Bochkareva** & OV Kalinina. Machine learning and phylogenetic analysis improves predicting antibiotic resistance in *M. tuberculosis* 2023 **BMC Microbiol** 23, 404 doi:10.1186/s12866-023-03147-7
3. M Baumgartner, R Zirnbauer, S Schlager, D Mertens, N Gasche, B Sladek, C Herbold, **OO Bochkareva**, V Emelianenko, H Vogelsang, M Lang, A Klotz, B Moik, A Makristathis, D Berry, S Dabsch, V Khare & C Gasche. Atypical enteropathogenic *E. coli* are associated with disease activity in ulcerative colitis **Gut Microbes**, 2022, Nov 22; 14(1):2143218 doi: 10.1080/19490976.2022.2143218
4. NO Dranenko, M Tutukina, MS Gelfand, F Kondrashov & **OO Bochkareva** Chromosome-encoded IpaH ubiquitin ligases indicate non-human pathogenic *Escherichia* **SciRep** 2022 Apr 27, 12:6868 doi:10.1038/s41598-022-10827-3
5. A Zabelkin, Y Yakovleva, **O Bochkareva*** & N Alexeev*. PaReBrick: PArallel REarrangements and BReaks identification toolkit. **Bioinformatics** 2021 Oct 03; 38(2):357-363 doi:0.1093/bioinformatics/btab691
6. Z Seferbekova, A Zabelkin, Y Yakovleva, R Afasizhev, N Alexeev, MS Gelfand & **OO Bochkareva**. High rates of genome rearrangements and pathogenicity of *Shigella* spp. **Frontiers Microbiology** 2021 Apr 12; 12:831. doi:10.3389/fmicb.2021.628622
7. O Sigalova, AV Chaplin, **OO Bochkareva**, PV Shelyakin, VA Filaretov, EE Akkuratov, V Burskaya & MS Gelfand. *Chlamydia* pan-genomic analysis reveals balance between host adaptation and selective pressure to genome reduction. **BMC Genomics**. 2019 Sep 12;20(1):710. doi:10.1186/s12864-019-6059-5.
8. PV Shelyakin*, **OO Bochkareva***, AA Karan & MS Gelfand. Micro-evolution of three *Streptococcus* species: selection, antigenic variation, and horizontal gene inflow. **BMC Evol. Biol.** 2019. Mar 27;19(1):83. doi:10.1186/s12862-019-1403-6.

9. **OO Bochkareva**, EV Moroz, II Davydov & MS Gelfand. Genome rearrangements and selection in multi-chromosome bacteria *Burkholderia* spp. **BMC Genomics**. 2018 Dec 27;19(1):965. doi:10.1186/s12864-018-5245-1.
10. **OO Bochkareva**, NO Dranenko, ES Ocheredko, GM Kanevsky, YN Lozinsky, VA Khalaycheva, II Artamonova & MS Gelfand. Genome rearrangements and phylogeny reconstruction in *Yersinia pestis*. **PeerJ**. 2018 Mar 27;6:e4545. doi:10.7717/peerj.4545.

Preprints and submitted papers:

- C Zioutis, M Lang, F Pereira, **O Bochkareva**, E Kolodyazhnaya, J Osvatic, KD McCoy, S Künzel, H Fokt, JF Baines, D Berry Rapid genetic diversification of *Bacteroides thetaiotaomicron* in mono-associated mice revealed through deep population-level sequencing. bioRxiv 2025.06.24.661302 doi: 10.1101/2025.06.24.661302
- M Lang, C Zioutis, A Heberlein, N Ivanovova, J Schwarz, S Köstlbacher, **O Bochkareva**, KJ Flanagan, FC Pereira, D Berry Nutrient landscape shapes the genetic diversification of the human gut commensal *Bacteroides thetaiotaomicron* bioRxiv 2025.06.24.661248 doi:10.1101/2025.06.24.661248
- NO Dranenko, AD Rodina, YV Demenchuk, MS Gelfand & **OO Bochkareva**. Evolutionary trajectories of secondary replicons in multipartite genomes bioRxiv 2023 Apr 09: 536151; doi:10.1101/2023.04.09.536151
- EV Vostokova, NO Dranenko, MS Gelfand, **OO Bochkareva**. Genome rearrangements and host adaptation in *Wolbachia* bioRxiv 2023 Oct doi:10.1101/2023.10.25.563763

Papers in preparation:

- An evolutionary-conserved mechanism of phase variation in dominant members of the mammalian gut microbiota. N Gruber, B Hekele, S Khadem, N Dranenko, E Kolodyazhnaya, R Romhild, M Hennessey, F Kondrashov, D Berry, C Guet, **O Bochkareva**
- Descent from a common ancestor restricts evolutionary exploration of protein sequence space LH Isakova, E Streltsova, **OO Bochkareva**, PK Vlasov, FA Kondrashov
- Stress-induced adaptive mutation modulated by luxS. M Hennessey-Wesen, **O Bochkareva**, J Merrin, CC Guet, B Hof

Other contributions to the research community

Invited Talks

2024 Trinity College Dublin, Ireland; 2024 Okinawa Institute of Science and Technology, Japan; 2022 Helmholtz Institute for Pharmaceutical Research Saarland (HIPS) Saarland, Germany; 2022 SMTB'22 University of Tartu, Tartu, Estonia; 2021 EMBL, Heidelberg Germany

Supervised students:

>15 term papers, 2 BS theses, 4 MS theses, 2 co-supervised PhD theses

New courses development and implementation to educational programs:

- **Semester course**, “Comparative genomics of prokaryotes” for master and PhD students.

Taught for Bioinformatics Institute (St Petersburg, Russia) in Fall 2020, final evaluation by students: 9.3 out of 10 (the highest evaluation across all courses during the term).

- **Bioinformatics workshops** for a broad audience.

Services for the scientific community and volunteering

- **Summer School of Theoretical and Molecular Biology**

design of the research project, hiring lab staff, lecturers and course instructors; design of lectures and courses; management of courses execution and labs; student supervision.

- **Bioinformatics Institute** (non-governmental non-profit Bioinformatics research and educational institution)

giving open lectures and workshops for broad audience interested in bioinformatics

- **Member of Scholars-Without-Borders programme**

supporting students and academics from Ukraine, Belarus or Russia affected by the war

- **Member of Women In Biology Initiative**

supporting the careers of female scientists at all levels

Languages: English (fluent), German (A2), Russian (native)

Contact details of referees:

Prof. Mikhail Gelfand:

mikhail.gelfand@gmail.com

<https://faculty.skoltech.ru/people/mikhailgelfand>

Prof. Fyodor Kondrashov:

Fyodor.Kondrashov@oist.jp

<https://www.oist.jp/research/fyodor-kondrashov>

Prof. Calin Guet:

Calin.Guet@ist.ac.at

<https://ist.ac.at/en/research/guet-group/>

Prof. David Berry:

david.berry@univie.ac.at

<https://dome.univie.ac.at/berry/>