

Veronika Dubinkina

Gladstone Institutes
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Education

University of Illinois Urbana-Champaign Jan 2017 — Aug 2022

• Ph.D, Bioengineering

Thesis: “Mechanistic modeling of complex microbial communities.”

Advisor: Prof. Sergei Maslov

Moscow Institute of Physics and Technology Sep 2013 — Jun 2015

• M.Sc. (summa cum laude) in Applied Mathematics and Physics

Thesis: “Development of a method to evaluate the diversity of metagenomes from the human intestinal microbiome on the basis of a k-mer approach.”

Advisors: Prof. Dmitry Alexeev, Dr. Alexander Tyakht

Sep 2009 — Jun 2013

• B.Sc. (summa cum laude) in Applied Mathematics and Physics

Thesis: “Computer modeling of structure and dynamics of lipid bilayer simulating bacterial membrane.”

Advisor: Prof. Roman Efremov

Research interests

Computational biology, bioinformatics, human microbiome, bacterial genome structure and functions, statistical methods for analysis of genomic data, ecology and evolution of microbial communities.

Research experience

Bioinformatics Fellow 2022 — present

Gladstone Institutes, San Francisco, US

I work in Prof. Pollard lab on development of bioinformatic pipelines for metagenome-wide association studies (MWAS). I also study eco-evolutionary forces that shape human gut microbiome via strain level analysis of taxonomic and functional structure of the community.

Research Affiliate 2022 — present

Institute for Sustainability, Energy, and Environment,

Urbana-Champaign, US

As a continuation of my work for CABBI, I perform bioinformatic analysis of multi-omics data for novel yeast species with an aim of discovering genes involved in low pH tolerance and antimicrobial drug resistance.

Research assistant 2017 — 2022

Carl R. Woese Institute for Genomic Biology, Urbana-Champaign, US

I worked in Prof. Maslov’s group. Main focus of my studies were consumer-resource dynamic models of bacterial ecosystems. We developed several models for microbes exhibiting diauxic growth and for environments with multiple limiting resources. I was also involved in a project on predicting cancer drug responses using machine learning methods in collaboration with Argonne National Lab. My role was to identify features important for the prediction of various algorithms and evaluate the quality of the models. From 2019 I started to work on the reconstruction of gene regulatory networks for novel yeast species by bioinformatic analysis of genomic and transcriptomic data for the Center of Advanced Bioenergy and Bioproducts Innovation (CABBI).

Research assistant 2013 — 2016

Scientific Research Institute of Physical-Chemical Medicine FMBA of

Russia, Moscow, Russia

During my master's program, I have started to work in a laboratory of bioinformatics. My master’s thesis included developing and testing alignment-free tools of comparison metagenomic whole genome sequencing (WGS) data using frequencies of short oligonucleotides (k-mers) and de-novo assembly. These methods allow for a fast high-throughput reference-free comparison of metagenomic data for the bacterial communities from poorly studied environments.

Moscow Institute of Physics and Technology, Dolgoprudny, Russia

I worked as a part of a team carrying out several metagenomic research projects. My research was focused on investigating the associations of gut bacteria with different diseases including irritable bowel syndrome, alcoholic liver cirrhosis, and alcohol dependence syndrome. Since our lab was a part of the Russian Metagenomic Project we worked in close connection with medical research centers all over the country, and I had an opportunity to participate in every step of large cohort studies. I used plenty of tools and pipelines for sequence alignment, quality assessment, de novo assembly, and functional and taxonomic profiling of metagenomes, and analysis of bacterial phylogeny. Also on a constant basis, I wrote programs for data processing on UNIX shell, and for statistical analysis and visualization in R.

Research assistant**The M.M. Shemyakin–Yu.A. Ovchinnikov Institute of Bioorganic****Chemistry of the Russian Academy of Sciences, Moscow, Russia**

I became involved with IBCH laboratory of biomolecular modeling during my undergraduate program at MIPT as a part of the educational process. My research project consisted of modeling the lipid bilayer which simulated the membrane of gram-negative bacteria. The goal was to understand how does the mixture ratio of various phospholipids determines properties of the membrane surface, that may be essential for a living cell.

Publications

*denotes equal contribution

1. Nambiar, A., **Dubinkina, V.**, Liu, S., & Maslov, S. (2022) FUN-PROSE: A Deep Learning Approach to Predict Condition-Specific Gene Expression in Fungi. *bioRxiv*
2. Bhogale, S.*, **Dubinkina, V.***, Hsieh, PH.*, Dibaeinia P., Nambiar, A., Yoshikuni, Y., Sinha, S., & Maslov, S. (2022) A transcriptomic atlas of low pH stress response in multiple *Issatchenkia orientalis* strains. *in preparation*
3. **Dubinkina, V.***, Goyal, A.*, Pandey, P. P.*, Fridman, Y.*, & Maslov, S. (2022). Competition-driven strategies for controlling multistable microbial communities, *in preparation*
4. Rashid, F.*, **Dubinkina, V.***, Maslov, S., & Irudayaraj, J. (2021) Effect of subacute exposure to PFOS and GenX on gut microbiota-host metabolome homeostasis in male mice. *Scientific reports (under review)*
5. Nande, A.*, **Dubinkina, V.***, Zhang, G.*, Ravasio, R.*, & Berman, G. (2022). Bottlenecks, Modularity, and the Neural Control of Behavior. *Frontiers in Behavioral Neuroscience*, 16, 1662-5153
6. Xia, F., Allen, J., Balaprakash, P., Brettin, T., Garcia-Cardona, C., Clyde, A., Cohn, J., Doroshov, J., Duan, X., **Dubinkina, V.**, ... & Stevens, R. (2021) A cross-study analysis of drug response prediction in cancer cell lines. *Briefings in Bioinformatics*, 23(1), bbab356.
7. Wang, Z., Goyal, A., **Dubinkina, V.**, George, A. B., Wang, T., Fridman, Y., & Maslov, S. (2021). Complementary resource preferences spontaneously emerge in diauxic microbial communities. *Nat Commun* 12, 6661.
8. Goyal, A., Wang, T., **Dubinkina, V.**, Maslov, S. (2021) Ecology-guided prediction of cross-feeding interactions in the human gut microbiome. *Nat Commun* 12, 1335.
9. Wang, T., Goyal, A., **Dubinkina, V.**, Maslov, S. (2019) Evidence for a multi-level trophic organization of the human gut microbiome. *PLOS Computational Biology*, 15(12): e1007524.
10. **Dubinkina, V.***, Fridman, Y.*, Pandey, P. P.*, & Maslov, S. (2019). Multistability and regime shifts in microbial communities explained by competition for essential nutrients. *eLife*, 8.
11. **Dubinkina, V.***, Fridman, Y.*, Pandey, P.*, & Maslov, S. (2018). Alternative stable states in a model of microbial community limited by multiple essential nutrients. *bioRxiv*, 439547.
12. Goyal, A.*, **Dubinkina, V.***, & Maslov, S. (2018). Multiple stable states in microbial communities explained by the stable marriage problem. *The ISME journal*, 12(12), 2823.
13. **Dubinkina, V. B.***, Tyakht, A. V.*, Odintsova, V. Y., Yarygin, K. S., Kovarsky, B. A., Pavlenko, A. V., ... & Nasyrova, R. F. (2017). Links of gut microbiota composition with alcohol dependence syndrome and alcoholic liver disease. *Microbiome*, 5(1), 141.
14. Tyakht, A. V., **Dubinkina, V. B.**, Odintsova, V. Y., Yarygin, K. S., Kovarsky, B. A., Pavlenko, A. V., ... & Nasyrova, R. F. (2017). Data on gut metagenomes of the patients with alcoholic dependence syndrome and alcoholic liver cirrhosis. *Data in Brief*, 11, 98-102.
15. Danilova, N, Markelova, M., Boulygina, E., Vasilyev, I., Abdulkhakov, S., Grigoryeva, T., **Dubinkina V.**, ... & Abdulkhakov, R. (2017). Abundance of key intestinal dysbiosis markers in gut metagenomes of patients with ulcerative colitis and Crohn's disease. *HELICOBACTER* (Vol. 22).
16. Danilova, N., Abdulkhakov, S., Grigoryeva, T., **Dubinkina, V.**, Odintsova, V., Tyakht, A., ... & Govorun, V. (2017). P794 Alterations of intestinal microbiota in ulcerative colitis. *Journal of Crohn's and Colitis*, 11(suppl_1), S486-S486.

17. Ulyantsev, V. I., Kazakov S.V., **Dubinkina, V. B.**, Tyakht, A. V., & Alexeev, D. G. (2016). MetaFast: fast reference free graph-based comparison of shotgun metagenomic data. *Bioinformatics*, 1-9.
18. **Dubinkina, V. B.**, Ischenko, D. S., Ulyantsev, V. I., Tyakht, A. V., & Alexeev, D. G. (2016). Assessment of k-mer spectrum applicability for metagenomic dissimilarity analysis. *BMC bioinformatics*, 17(1), 1.
19. **Dubinkina, V. B.**, Tyakht, A. V., Ilina, E. N., Ischenko, D. S., Kovarsky, B. A., Yarygin, K. S., ... & Nasyrova, R. F. (2016). Metagenomic analysis of taxonomic and functional changes in gut microbiota of patients with the alcohol dependence syndrome. *Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry*, 10(2), 184-190.
20. Shalikiani, N. V., Bakulin, I. G., **Dubinkina, V. B.**, Ishchenko, D. S., Alekseev, D. G., Tyakht, A. V., ... & Skorodumova, L. O. (2014). [Specific features of the enteric microbiota composition in patients with alcoholic liver cirrhosis]. *Terapevticheskii arkhiv*, 87(12), 59-65.

Selected talks and conference presentations

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| 1. KITP program: The Ecology and Evolution of Microbial Communities, Santa Barbara | Aug 2021 |
| 2. Invited Talk: IGB fellows Symposium, Urbana | May 2021 |
| 3. Talk: Microbial Systems Initiative Symposium, Urbana | Mar 2021 |
| 4. Poster: BSSD PI meeting 2021, online | Feb 2021 |
| 5. Talk: APS March Meeting 2020, Denver | Mar 2020 |
| 6. Invited Talk: Institute of gene biology RAS, seminar, Moscow | Feb 2020 |
| 7. Poster: Boulder School 2019: Theoretical Biophysics, Boulder | Aug 2019 |
| 8. Talk: CPLC/CBQB Graduate/Postdoc Symposium, Urbana-Champaign | Nov 2018 |
| 9. Talk: APS March Meeting 2018, Los Angeles | Mar 2018 |
| 10. Poster: Moscow Conference on Computational Molecular Biology (MCCMB'15), Moscow | Jul 2015 |
| 11. Poster: 23rd Annual International Conference on Intelligent Systems for Molecular Biology and the 14th European Conference on Computational Biology, Dublin | Jul 2015 |
| 12. Poster: The 4th International Conference on Science and Applied Research "Post-Genome Methods of Analysis in Biology and Laboratory and Clinical Medicine", Kazan | Oct 2014 |
| 13. Poster: The German Conference on Bioinformatics (GCB), Bielefeld | Sep 2014 |
| 14. Talk: The 57th MIPT Scientific Conference, Dolgoprudny | Nov 2014 |
| 15. Workshop: Summer bioinformatics school, Saint-Petersburg | Jul 2014 |
| 16. Workshop: Modern biology & biotechnology of the future, Puschino | Jan 2013 |

Community services and outreach

- Workshop:** "Modeling Microbial Ecology at Multiple Scales",
tutorial on consumer-resource models (<https://modelmems.github.io/>) Apr 2021
- Workshop:** "NGS data analysis",
tutorial on WGS metagenomic data analysis May 2016
- Mentoring students** on "Science" career track through Phystech Union mentorship program 2019 — 2020

Reviewed manuscripts for *Journal of Gastroenterology and Hepatology*, *Bioinformatics*, *PLOS Computational Biology*, *Journal of Oral Microbiology*, *Physical Review E*, *Current Genetics*, *Nature Communications*.

Scholarships and awards

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| Bioengineering department fellowship | 2017 |
| Government Academic Scholarship for excellence in studies | 2013 |

Technical skills

Proficiency in R, knowledge of Python, C/C++, MATLAB, basic knowledge of UNIX systems, HPC, bash, Git, SVN, experience working with gromacs, NAMD, VMD, PyMOL, and various bioinformatic pipelines and libraries for raw sequence data processing (16S rRNA, WGS, RNA-seq) and statistical analysis

References

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