BIOGRAPHICAL SKETCH

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NAME: Maslov, Sergei

eRA COMMONS USER NAME (credential, e.g., agency login): maslov

POSITION TITLE: Professor of Bioengineering and Physics, Bliss Faculty Scholar

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
Moscow Institute for Physics and Technology, Moscow	Master of Science	06/1992	Theoretical physics and applied mathematics
Stony Brook University, Stony Brook, NY	Doctor of Philosophy	06/1996	Theoretical statistical physics
Brookhaven National Laboratory, Upton, NY	Postdoctoral Fellow	06/1998	Theoretical physics

A. Personal Statement

I have a broad expertise in computational modeling of complex biological systems with particular emphasis on dynamics of microbial ecosystems, evolution of bacterial genomes, and complex biomolecular networks (PPI, regulatory, metabolic, food webs). I am a member of Argonne National Laboratory/National Cancer Institute joint project where I am applying machine learning techniques to personalized prediction of cancer drug combinations and Center for Advanced Bioenergy and Bioproducts Innovation (CABBI). Here our task is predicting transcriptional regulatory networks and machine learning of gene expression in non-model yeast species. For five years, I was the Associate Chief Science Officer and one of the four co-PIs of the DOE Systems Biology Knowledgebase (KBase) – a large computational biology project funded by the Office of Biological and Environmental Research of US Department of Energy. In KBase I managed a team of scientists from Brookhaven National Laboratory, Cold Spring Harbor Laboratory and Yale University working on networks and –omics analysis in plants and other eukaryotes. My experience on this and other projects taught me how to organize the activity of a distributed team of scientists, and how to carry out proposed research on time and on budget. In short, I have both scientific and technical expertise as well as leadership skills necessary to carry out the proposed work.

1. Wang, Z., Goyal, A., Dubinkina, V., George, A. B., Wang, T., Fridman, Y. & Maslov, S. Complementary resource preferences spontaneously emerge in diauxic microbial communities. Nature Communications 2021 Nov; 12:6661-6612, doi:10.1038/s41467-021-27023-y
2. Wang T, Goyal A, Dubinkina V, Maslov S. Evidence for a multi-level trophic organization of the human gut microbiome. PLoS Comput Biol. 2019 Dec;15(12):e1007524. PubMed Central PMCID: PMC6922320.

3. Dubinkina V, Fridman Y, Pandey P, Maslov S. Multistability and regime shifts in microbial communities explained by competition for essential nutrients. eLife. 2019 November 22; 8:-. Available from: https://elifesciences.org/articles/49720 DOI: 10.7554/eLife.49720
4. Arkin A, Cottingham R, Henry C, Harris N, Stevens R, Maslov S, Dehal P, Ware D, Perez F, Canon S, Sneddon M, Henderson M, Riehl W, Murphy-Olson D, Chan S, Kamimura R, Kumari S, Drake M, Brettin T, Glass E, Chivian D, Gunter D, Weston D, Allen B, Baumohl J, Best A, Bowen B, Brenner S, Bun C, Chandonia J, Chia J, Colasanti R, Conrad N, Davis J, Davison B, DeJongh M, Devoid S, Dietrich E, Dubchak I, Edirisinghe J, Fang G, Faria J, Frybarger P, Gerlach W, Gerstein M, Greiner A, Gurtowski J, Haun H, He F, Jain R, Joachimiak M, Keegan K, Kondo S, Kumar V, Land M, Meyer F, Mills M, Novichkov P, Oh T, Olsen G, Olson R, Parrello B, Pasternak S, Pearson E, Poon S, Price G, Ramakrishnan S, Ranjan P, Ronald P, Schatz M, Seaver S, Shukla M, Sutormin R, Syed M, Thomason J, Tintle N, Wang D, Xia F, Yoo H, Yoo S, Yu D. KBase: The United States Department of Energy Systems Biology Knowledgebase. Nature Biotechnology. 2018; 36(7):566-569. Available from: http://www.nature.com/articles/nbt.4163 DOI: 10.1038/nbt.4163

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointments

2015 -	Professor of Bioengineering and Physics, Bliss Faculty Scholar, University of Illinois at Urbana-Champaign (UIUC), Urbana, IL
2015 -	Affiliate Faculty, Carl R. Woese Institute for Genomic Biology, UIUC
2015 -	Faculty, National Center for Supercomputing Applications (NCSA), UIUC
2016 -	Joint appointment at the Computing, Environment, and Life Sciences (CELS) directorate, Argonne National Laboratory, Lemont IL
2011 - 2015	Tenured biophysicist, Computational Biology Group Leader, Brookhaven National Laboratory, Department of Biological Environmental and Climate Sciences, Upton, NY
2002 - 2011	Physicist (with tenure since 2004), Department of Condensed Matter Physics and Material Sciences, Brookhaven National Laboratory, Upton, NY
2000 - 2002	Associate Physicist, Department of Condensed Matter Physics and Material Sciences, Brookhaven National Laboratory, Upton, NY
1998 - 2000	Assistant Physicist, Department of Physics, Brookhaven National Laboratory, Upton, NY

Honors

2021	Presidential Award and Medallion, University of Illinois. For modeling COVID-19 Pandemic Response at the University of Illinois and the State of Illinois
2021	Fellow, American Institute for Medical and Biological Engineering (AIMBE) Citation: “For his contributions to computational biology including microbiome dynamics, microbial and viral ecology, genomics, and studies of complex biological networks”
2020	Fellow, American Physical Society. Citation: “For seminal discoveries and contributions to the dynamics and statistical physics of networks, with wide-ranging applications in physics, self-organizing systems, information networks, and complex biological systems”
2015	Bliss Faculty Scholar, University of Illinois at Urbana-Champaign
2004	Presidential Early Career Award for Scientists and Engineers (PECASE), White House

C. Contribution to Science

1. In (Nat Comm 2021a Nov, Nat Comm 2021 Feb, PLoS Comp Bio 2019, ISME 2018, eLife 2019, PRL 2018) we computationally modeled microbial communities competing for nutrients and/or cross-feeding each other with metabolic byproducts. We introduced the stable matching problem to understand multiple stable states in microbial communities (ISME 2018, eLife 2019, mSystems 2019). We studied population dynamics of phages and their bacterial hosts with the focus on co-evolution of CRISPR immunity (Nat Ecol Evol 2020), sudden population collapses (Sci Rep 2015, PLoS Comp Bio 2015, Sci Rep. 2017) and spatial dynamics of phage epidemics in chemotaxing bacteria (ISME J 2019).

    a. Wang Z, Goyal A, Dubinkina V, George AB, Wang T, Fridman Y, Maslov S. Complementary resource preferences spontaneously emerge in diauxic microbial communities. Nature Communications. 2021 Nov 18; 12:6661:1-12. doi: 10.1038/s41467-021-27023-y. PubMed Central PMCID: PMC8602314.

    b. Goyal A, Wang T, Dubinkina V, Maslov S. Ecology-guided prediction of cross-feeding interactions in the human gut microbiome. Nat Commun. 2021 Feb 26;12(1):1335. PubMed Central PMCID: PMC7910475.

    c. Dubinkina V, Fridman Y, Pandey P, Maslov S. Multistability and regime shifts in microbial communities explained by competition for essential nutrients. eLife. 2019 November 22; 8:-. Available from: https://elifesciences.org/articles/49720 DOI: 10.7554/eLife.49720

    d. Goyal A, Dubinkina V, Maslov S. Multiple stable states in microbial communities explained by the stable marriage problem. The ISME Journal. 2018; 12(12):2823-2834. Available from: http://www.nature.com/articles/s41396-018-0222-x DOI: 10.1038/s41396-018-0222-x

2. I participated in a number of machine learning and knowledgebase development projects. In (Xia et al. 2018) and (Xia et al. 2022) we compared the performance of multiple deep learning algorithms in predicting tumor cell line response to drug pairs. In (Nambiar et al. 2020) we developed Protein RoBERTa - a transformer neural network algorithm fine-tuned to solve two different protein prediction tasks: protein family classification and protein interaction prediction. In (Arkin et al 2018) we designed the v1.0 of the DOE Systems Biology Knowledgebase (KBase), an open-source software and data platform that enables data sharing, integration, and analysis of microbes, plants, and their communities.

    a. Xia F, Allen J, Balaprakash P, Brettin T, Garcia-Cardona C, Clyde A, Cohn J, Doroshow J, Duan X, Dubinkina V, Evrard Y, Fan YJ, Gans J, He S, Lu P, Maslov S, Partin A, Shukla M, Stahlberg E, Wozniak JM, Yoo H, Zaki G, Zhu Y, Stevens R. A cross-study analysis of drug response prediction in cancer cell lines. Brief Bioinform. 2022;23(1):bbab356. http://doi.org/10.1093/bib/bbab356

    b. Nambiar A, Heflin M, Liu S, Maslov S, Hopkins M, Ritz A. Transforming the Language of Life. Proceedings of the 11th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics. BCB '20: 11th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics; 21 0 20; Virtual Event USA. New York, NY, USA: ACM; 2020. Available from: https://dl.acm.org/doi/10.1145/3388440.3412467 DOI: 10.1145/3388440.3412467

    c. Xia F, Shukla M, Brettin T, Garcia-Cardona C, Cohn J, Allen J, Maslov S, Holbeck S, Doroshow J, Evrard Y, Stahlberg E, Stevens R. Predicting tumor cell line response to drug pairs with deep learning. BMC Bioinformatics. 2018 December 21; 19(S18):-. Available

from: https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-018-2509-3 DOI: 10.1186/s12859-018-2509-3

d. Arkin A, Cottingham R, Henry C, Harris N, Stevens R, Maslov S, Dehal P, Ware D, Perez F, Canon S, Sneddon M, Henderson M, Riehl W, Murphy-Olson D, Chan S, Kamimura R, Kumari S, Drake M, Brettin T, Glass E, Chivian D, Gunter D, Weston D, Allen B, Baumohl J, Best A, Bowen B, Brenner S, Bun C, Chandonia J, Chia J, Colasanti R, Conrad N, Davis J, Davison B, DeJongh M, Devoid S, Dietrich E, Dubchak I, Edirisinghe J, Fang G, Faria J, Frybarger P, Gerlach W, Gerstein M, Greiner A, Gurtowski J, Haun H, He F, Jain R, Joachimiak M, Keegan K, Kondo S, Kumar V, Land M, Meyer F, Mills M, Novichkov P, Oh T, Olsen G, Olson R, Parrello B, Pasternak S, Pearson E, Poon S, Price G, Ramakrishnan S, Ranjan P, Ronald P, Schatz M, Seaver S, Shukla M, Sutormin R, Syed M, Thomason J, Tintle N, Wang D, Xia F, Yoo H, Yoo S, Yu D. KBase: The United States Department of Energy Systems Biology Knowledgebase. Nature Biotechnology. 2018; 36(7):566-569. Available from: http://www.nature.com/articles/nbt.4163 DOI: 10.1038/nbt.4163

3. In (PNAS 2021, eLife 2021) we developed a new type of epidemiological model with stochastic social activity and applied it to describe successive waves of COVID-19 epidemic in US during Summer 2020-Winter 2021. Mark Lipsitch, who was the editor of (eLife 2021) in his evaluation of this work printed alongside the article stated: “This is an excellent and elegant example of what theory can do at its best in epidemiology. … This should stimulate much further work in the field.”. In (PRX 2020) we calibrated the age-of-infection model to multiple data streams (cases, hospitalizations, deaths) to describe the COVID-19 epidemic dynamics in Illinois. This work was done while I served as one of the founding members of the COVID-19 modeling team for the Governor of Illinois.

    a. Tkachenko AV, Maslov S (co-corresponding author), Elbanna A, Wong GN, Weiner ZJ, Goldenfeld N. Time-dependent heterogeneity leads to transient suppression of the COVID-19 epidemic, not herd immunity. Proc Natl Acad Sci U S A. (2021);118(17). Epub 2021/04/10. doi: 10.1073/pnas.2015972118.

    b. Tkachenko AV, Maslov S (co-corresponding author), Wang T, Elbana A, Wong GN, Goldenfeld N. Stochastic social behavior coupled to COVID-19 dynamics leads to waves, plateaus, and an endemic state. Elife. (2021);10:e68341. Epub 2021/11/09. doi: 10.7554/eLife.68341.

    c. Wong GN, Weiner ZJ, Tkachenko AV, Elbanna A, Maslov S (co-corresponding author), Goldenfeld N. Modeling COVID-19 Dynamics in Illinois under Nonpharmaceutical Interventions. Physical Review X. (2020);10(4). doi: 10.1103/PhysRevX.10.041033.

4. In (JMB 2009, PNAS 2015) we developed scalable computational algorithms to estimate core and pan-genomes of bacterial species and to analyze Single-Nucleotide Polymorphisms (SNP) within this core genome. Our algorithm separates vertically inherited, clonal, segments from recombined (horizontally transferred) ones. For closely related pairs of E. coli strains, we identified a patchwork of long recombined segments interspersed among clonally inherited genomic segments. Once sequence divergence between strains exceeds ~1.3%, clonal segments virtually disappear. Our results implicate generalized transducing phages in horizontal transfer of genomic segments between strains. In (Genetics 2017) we modeled the evolutionary dynamics based on these observations and applied the model to define stability and boundaries of 12 bacterial species. Biomedical applications of our findings include

understanding the emergence and spread of pathogenic bacterial strains (e.g. E. coli) and of antibiotic resistance in bacterial populations.

a. Dixit PD, Pang TY, Maslov S. Recombination-Driven Genome Evolution and Stability of Bacterial Species. Genetics. 2017 Sep;207(1):281-295. PubMed Central PMCID: PMC5586378.
b. Dixit PD, Pang TY, Studier FW, Maslov S. Recombinant transfer in the basic genome of Escherichia coli. Proc Natl Acad Sci U S A. 2015 Jul 21;112(29):9070-5. PubMed Central PMCID: PMC4517234.
c. Studier FW, Daegelen P, Lenski RE, Maslov S, Kim JF. Understanding the differences between genome sequences of Escherichia coli B strains REL606 and BL21(DE3) and comparison of the E. coli B and K-12 genomes. J Mol Biol. 2009 Dec 11;394(4):653-80. PubMed PMID: 19765592.

5. In (PNAS 2009) we proposed the “toolbox” model of co-evolution of metabolic and regulatory networks by Horizontal Gene Transfer in bacterial and archaeal genomes. Our model explained a number of trends in properties of these networks with genome size. These insights into modular properties of bacterial genomes and networks are important for bioengineering and biomedical applications. In (PLoS Com Bio 2011) we extended our toolbox model to include anabolic (biosynthetic) pathways. To this end we came up with a computational algorithm predicting the minimal biosynthetic pathway to add to the existing metabolic network of an organism so that it can synthesize a desired target metabolite. Algorithms proposed in this paper are relevant for synthetic biology applications. In (NAR 2017; NAR 2011; PNAS 2013) we identified functional and evolutionary determinants of sizes of gene families and the frequency with which they are encoded in bacterial genomes.

a. De Lazzari E, Grilli J, Maslov S, Cosentino Lagomarsino M. Family-specific scaling laws in bacterial genomes. Nucleic Acids Res. 2017 Jul 27;45(13):7615-7622. PubMed Central PMCID: PMC5737699.
b. Pang T, Maslov S. Universal distribution of component frequencies in biological and technological systems. Proceedings of the National Academy of Sciences. 2013 March 25; 110(15):6235-6239. Available from: http://www.pnas.org/cgi/doi/10.1073/pnas.1217795110 DOI: 10.1073/pnas.1217795110
c. Pang TY, Maslov S. A toolbox model of evolution of metabolic pathways on networks of arbitrary topology. PLoS Comput Biol. 2011 May;7(5):e1001137. PubMed Central PMCID: PMC3098196.
d. Maslov S, Krishna S, Pang T, Sneppen K. Toolbox model of evolution of prokaryotic metabolic networks and their regulation. Proceedings of the National Academy of Sciences. 2009 May 29; 106(24):9743-9748. Available from: http://www.pnas.org/cgi/doi/10.1073/pnas.0903206106 DOI: 10.1073/pnas.0903206106

The full list of my publications is available at:
http://www.ncbi.nlm.nih.gov/myncbi/browse/collection/45132040/?sort=date&direction=descending