

University	Peter the Great St.Petersburg Polytechnic University
Level of English proficiency	Proficient (C2)
Educational program and field of the educational program for which the applicant will be accepted	<u>BIOLOGY & BIOTECHNOLOGY</u> <u>PHYSICAL SCIENCES & TECHNOLOGY</u> 1.5.2 Biophysics
List of research projects of the potential supervisor (participation/leadership)	<ul style="list-style-type: none"> • Inference of fitness landscape of a population of organisms from DNA data • Modeling the evolution of new variants of concern of SARS CoV-2 • Modeling the evolution of immunologically important regions of the virus and the role of vaccination in evolution
List of the topics offered for the prospective scientific research	<ul style="list-style-type: none"> • Inference of fitness landscape of a population of organisms from DNA data • Modeling the evolution of new variants of concern of SARS CoV-2 • Modeling the evolution of immunologically important regions of the virus and the role of vaccination in evolution.
 <p>Research supervisor: Igor Rouzine Ph.D., Associate Professor Organization awarding degree: A.F. Ioffe Physico-Technical Institute RAS</p>	1.07. Other natural sciences
	Supervisor's research interests Pathogens evolve rapidly to circumvent drug treatments and immune surveillance, which dramatically impacts public health. Research and treatment are complicated by high genetic diversity of some viruses within and across infected individuals, as well as their complex evolutionary mechanisms, including selection, random genetic drift, and temporal variation in a host environment. Moreover, many pathogens have a large number of linked sites approximately 102 -103 for HIV and hepatitis C virus (HCV) that evolve simultaneously and inter-dependently through two different effects, "epistasis" due to interaction between proteins and signaling network, and site linkage due to common ancestry. Our research is focused on developing mathematical tools that predict evolution of pathogens with strong linkage effects, including analytic and computational methods and estimators of evolutionary parameters from sequence data.
	Research highlights <ul style="list-style-type: none"> • Inference of fitness landscape of a population of organisms from DNA data • Modeling the evolution of new variants of concern of SARS CoV-2 • Modeling the evolution of immunologically important regions of the virus and the role of vaccination in evolution.
	Supervisor's specific requirements: Knowledge Calculus, Linear Algebra, written English B2 oral B1, programming skills in MATLAB or Python
	Supervisor's main publications Rouzine IM* and Rozhnova G* (2023) Evolutionary implications of SARS-CoV-2 vaccination for the future design of vaccine strategies, Communications Medicine, accepted for publication. Likhachev IV and Rouzine IM* (2023) Measurement of selection coefficients from genomic samples of adapting populations by computer modeling, STAR Protocols 4, 101821.

Rouzine, IM. (2022) A role for CD4 helper cells in HIV control and progression. *AIDS* 36:1501–1510. IF 4.2

Shirogane Y, Rousseau E, Voznica J, Xiao Y, Su W, Catching A, Whitfield ZJ, Rouzine IM, Bianco* S, Andino* R. (2021) Experimental and mathematical insights on the interactions between poliovirus and a defective interfering genome. *PLoS Pathogens* 17, e1009277 IF 6.2

Pedruzzi G, Rouzine* IM (2021) An evolution-based high-fidelity method of epistasis measurement: theory and application to influenza. *PLoS Pathogens* 17, e1009669. IF 6.2

Barlukova A, Rouzine* IM (2021) The evolutionary origin of the universal distribution of mutation fitness effect. *PLoS Comp. Bio.* 17, e1008822. IF 4.5

Rouzine IM (2020) An evolutionary model of progression to AIDS. *Microorganisms* 8, 1714 IF 4.2

Pedruzzi G, Rouzine IM * (2019) Epistasis detectably alters correlations between genomic sites in a narrow parameter window. *PLoS ONE* 14, e0214036.

Pedruzzi G, Barlukova A, Rouzine* IM (2018) Evolutionary footprint of epistasis. *PLoS Computational Biology* 14, e1006426. IF 4.5

Rouzine* IM, Rozhnova G (2018) Antigenic evolution of viruses in host populations. *PLoS Pathogens* 14, e1007291. IF 6.5

Results of intellectual activity

Books:

Rouzine IM. (2023) "Mathematical Models of Evolution. Volume 2: Fitness Landscape, Red Queen, Evolutionary Enigmas, and Applications to Virology", in series Mathematics and life sciences, De Gruyter, Berlin/Boston.

Rouzine IM. (2020) "Mathematical Models of Evolution. Volume 1: One-locus and multi-locus theory and recombination", in series Mathematics and life sciences, De Gruyter, Berlin/Boston.

Peer-reviewed:

Rouzine* IM, Wakeley J, Coffin JM (2003) The solitary wave of asexual evolution. *Proc Nat Acad Sci* 100: 587-592

The first accurate mathematical analysis predicting the evolution rate of a population with a large number of linked loci in the absence of recombination.

Rouzine IM, Weinberger, AD, and Weinberger*, LS (2015) An evolutionary role for HIV latency in enhancing viral transmission. *Cell* 160, 1002–12

An evolutionary role for HIV latency as a Trojan horse effect during transmission.

Rouzine* IM, Coffin JM (2001) Transition between stochastic evolution and deterministic evolution in the presence of selection: general theory and application to virology [review]. *Microbio Mol Bio Rev* 65: 151-185

The classical stochastic theory of one-locus evolution 1930-1970 reviewed and adapted to virology.

IM Rouzine (2020) An evolutionary model of progression to AIDS. *Microorganisms* 8, 1714
<https://doi.org/10.3390/microorganisms8111714>

	<p>The first closed model of progression to AIDS based on gradual adaptation of HIV to a host.</p> <p>Rouzine* IM and Rozhnova G (2018) Antigenic evolution of viruses in host populations. PLoS Pathogens 14, e1007291 A model of genetic evolution of a virus in a host population accumulating the immune memory connects epidemiology to immunology and the modern evolution theory. The predicted parameters are tested against data for influenza A.</p> <p>Batorsky R, Kearney MF, Palmer SE, Maldarelli F, Rouzine* IM, Coffin JM (2011) Estimate of effective recombination rate and average selection coefficient for HIV in chronic infection. Proc Natl Acad Sci U S A 108: 5661</p> <p>Rouzine* IM, Coffin JM (1999) Linkage disequilibrium test implies a large effective population number for HIV in vivo. Proc Nat Acad Sci 96: 10758-10763 The effective population size and the effective recombination rate of HIV are estimated correctly for the first time.</p> <p>Rouzine* IM, Coffin JM (2005) Evolution of HIV under selection and weak recombination. Genetics 170: 7-18</p> <p>Rouzine*, IM, and Coffin, JM (2010) Many-site adaptation in the presence of infrequent recombination. Theor Pop Bio 77: 189-204 Recombination is incorporated in the multi-locus evolution theory.</p> <p>Rouzine* IM, Coffin JM (1999) Search for the mechanism of evolution in the pro gene of HIV in vivo. J Virol 73: 8167-8178. The high diversity of HIV within and between infected individuals is explained as a result of compensatory mutations for the early escape mutations in CD8 T cell epitopes.</p>
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