BIOGRAPHICAL SKETCH

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NAME: Pritykin, Yury

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

POSITION TITLE: Assistant Professor, Computer Science and Genomics

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
Lomonosov Moscow State University, Moscow	Specialist (MSc)	07/2007	Mathematics
Lomonosov Moscow State University, Moscow	Candidate of Sciences (PhD)	10/2009	Mathematics
Princeton University, Princeton, New Jersey	PhD	09/2014	Computer Science
Memorial Sloan Kettering Cancer Center, New York, NY	Postdoctoral Fellow	01/2021	Postdoctoral Research Associate, Computational and Systems Biology Program

A. Personal Statement

My main interest and expertise are in using applied statistics, machine learning, and efficient algorithms to address fundamental problems in biology and medicine by integrative analysis of multi-dimensional data.

My initial training and research were in mathematics and theoretical computer science. Fascinated with life sciences, I transitioned to computational biology during my PhD and then received postdoctoral training in computational systems biology. I have gained versatile experience in computational method development and analysis of bulk and single-cell transcriptional, post-transcriptional and epigenetic regulatory genomics data (ATAC-seq, DNase-seq, RNA-seq, ChIP-seq, CUT&RUN, Hi-C, CLIP-seq) in collaboration with multiple immunologists and cancer biologists. I have studied systems biology of immune cell differentiation and function across tissues and mouse models; developed a new tool for better design and analysis of guide RNAs for CRISPR-based genome editing experiments; studied protein roles in the functional organization of the cell; studied the biological function of non-coding RNA and RNA-binding proteins.

My independent lab at the Lewis-Sigler Institute for Integrative Genomics and the Computer Science Department at Princeton University opened in January 2021. The lab currently includes three PhD students, one postdoctoral research associate, one Lewis-Sigler scholar, and one undergraduate researcher, and we are actively recruiting at multiple levels. I am fully committed to training the next generation of biomedical research workforce and promoting inclusive, safe and supportive research environment in my interdisciplinary lab. Research in the lab has two major directions: we develop computational methods for design and analysis of high-throughput functional genomic assays and perturbations, with a focus on multi-modal single-cell and spatial technologies; and we apply these methods to study regulatory genomics of cell function and cell-cell interactions *in vivo* in close collaboration with experimental biologists, with a focus on immunology and cancer.

Ongoing and recently completed projects that I would like to highlight include:

National Institute of Allergy and Infectious Diseases DP2 New Innovator Award (1DP2AI171161-01)
Pritykin (PI)
07/19/22-06/30/27
Regulatory genomics of T cells in mouse and human

Ludwig Cancer Research Princeton Branch

Pritykin (PI, subaward) / Rabinowitz (PI)
01/01/22-12/31/22
Metabolic analysis of T cell function via computational genomics

Rutgers Cancer Institute of New Jersey New Investigator Award
Pritykin (PI, subaward) / Libutti (PI)
Cancer Center Support Grant (5P30CA072720-22)
06/28/21-02/28/23

Princeton Biocondensate Program
Pritykin, Levine (Co-PIs, subaward) / Brangwynne (PI)
10/01/21-09/30/23
Biocondensate composition and chromatin architecture in T cell functional differentiation

AACR Bristol-Myers Squibb Immuno-oncology Research Fellowship (19-40-15-PRIT)
Pritykin (PI)
07/01/19-01/15/21
Systems biology of the T cell immune response in cancer and infection

Memorial Sloan Kettering–Parker Institute for Cancer Immunotherapy–Cycle for Survival Fund Award
Pritykin (PI)
10/08/18-01/15/21
Systems biology of the T cell immune response in cancer

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointments

2021 -	Assistant Professor, Princeton University, Lewis-Sigler Institute for Integrative Genomics, Computer Science Department, Princeton, NJ
2021 -	Associate Member, Rutgers Cancer Institute of New Jersey, New Brunswick, NJ
2014 - 2021	Research Associate, Memorial Sloan Kettering Cancer Center, Computational and Systems Biology Program, New York, NY

Honors

2022	NIAID DP2 New Innovator Award
2022	Ludwig Cancer Research Princeton Branch funding award
2021	New Investigator Award, Rutgers Cancer Institute of New Jersey
2021	Princeton Biocondensate Program Award, Bioengineering Initiative, Princeton University
2020	Selected for oral presentation, 32nd annual meeting on The Biology of Genomes (virtual)
2019	AACR Bristol-Myers Squibb Immuno-oncology Research Fellowship, AACR
2019	The People's Choice Award for the best poster, 2nd Annual Single Cell Research Initiative Symposium, Memorial Sloan Kettering Cancer Center
2018	Memorial Sloan Kettering–Parker Institute for Cancer Immunotherapy–Cycle for Survival Fund Award, MSKCC
2017	Selected for oral presentation, RECOMB/ISCB Conference on Regulatory & Systems Genomics
2014	Selected for participation (top 70 out of 600 applications), Winter School “Future Biotech”, Moscow, Russia
2013	Selected for oral presentation, Cold Spring Harbor Laboratory meeting on Systems Biology: Networks
2012	NSF Student Travel Grant, 16th Annual International Conference on Research in Computational Molecular Biology (RECOMB)

2009	Best Student Paper Award, 4th International Computer Science Symposium in Russia (CSR)
2007	Diploma with Honors, Lomonosov Moscow State University
2007	Appreciation (=4th place), All-Russian Euler Contest of student research papers in mathematics
2007	Short visit, Department of Mathematics and Statistics, University of Turku, Finland
2007	Short visit grant, AutoMathA program of European Science Foundation, Palermo, Italy
2007	Finalist (top 6) and special prize for the best talk, 11th All-Russian Mobius Contest of student research papers in mathematics
2006	2nd prize, 10th All-Russian Mobius Contest of student research papers in mathematics
2006	Short visit, Laboratoire d'Informatique Fondamentale de Marseille, France
2005 - 2007	Kolmogorov Scholarship for excellence in research, Division of Mathematical Logic and Theory of Algorithms, Department of Mechanics and Mathematics, Lomonosov Moscow State University

C. Contribution to Science

1. **Computational genomics for immunology.** My major interest is in using multi-modal functional genomic assays, especially at a single-cell and spatial level, for studying immune cell activation, differentiation and function across tissues and conditions in mouse models and humans. At the same time, immunology mouse models provide unique opportunities for uncovering general principles of gene expression regulation *in vivo*. By integrative analysis of bulk and single-cell genomic data (ATAC-seq, RNA-seq, DNase-seq, CUT&RUN), I have characterized epigenetic and transcriptional regulatory programs of CD8 T cell functional states in mouse models of cancer and infection (*Mol Cell 2021*), and self-tolerance (*in preparation*). By integrative analysis of genomic data (ChIP-seq, ATAC-seq, RNA-seq), I explored the function of the transcription factor Foxp3 and its interaction with a highly expressed closely related factor Foxp1 in regulatory CD4 T cells (*Nat Immunol 2019*). In numerous collaborations with immunologists, I have brought my expertise in computational analysis of data from genomic assays to study function of T cells, innate and innate-like lymphocytes, dendritic cells across tissues and models (*Cell 2016*, *Cell 2017*, *Nat Immunol 2018*, *Cell Reports 2018*, *Cell 2019*, *PNAS 2020*, *Sci Transl Med 2021*, *Nat Immunol 2022, Immunity 2022*).

    a. Zhang M, Zhao Z, **Pritykin Y**, Hannum M, Scott AC, Kuo F, Sanghvi V, Chan TA, Seshan V, Wendel HG, Schietinger A, Sadelain M, Huse M. Ectopic activation of the miR-200c-EpCAM axis enhances antitumor T cell responses in models of adoptive cell therapy. Sci Transl Med. 2021 Sep 15;13(611):eabg4328. PubMed PMID: 34524864.

    b. van der Veeken J, Campbell C, **Pritykin Y**, Schizas M, Verter J, Hu W, Wang ZM, Matheis F, Mucida D, Charbonnier LM, Chatila TA, Rudensky AY. Genetic tracing reveals transcription factor Foxp3-dependent and Foxp3-independent functionality of peripherally induced Treg cells. Immunity. 2022 Jul 12;55(7):1173-1184.e7. PMID: 35700740

    c. **Pritykin Y***, van der Veeken J*, Pine AR, Zhong Y, Sahin M, Mazutis L, Pe'er D, Rudensky AY, Leslie CS. A unified atlas of CD8 T cell dysfunctional states in cancer and infection. Mol Cell. 2021 Jun 3;81(11):2477-2493.e10. PubMed PMID: 33891860; NIHMSID: NIHMS1692683.

    d. Konopacki C*, **Pritykin Y***, Rubtsov Y, Leslie CS, Rudensky AY. Transcription factor Foxp1 regulates Foxp3 chromatin binding and coordinates regulatory T cell function. Nat Immunol. 2019 Feb;20(2):232-242. PubMed Central PMCID: PMC7534899.

2. **Development of GuideScan, a comprehensive and customizable CRISPR guide RNA design and analysis tool.** CRISPR technology enables high-throughput editing of mammalian genomes. To facilitate the design of CRISPR libraries and extend their use to the noncoding genome, we developed GuideScan, a fully customizable guide RNA (gRNA) design software and companion website (*Nat Biotechnol 2017*). GuideScan outperforms other tools in the identification of potential off-targets, generates high-density gRNA databases, and enables batch design of single- and paired-gRNA vectors for genome-wide screens. We now continue working on tools for design and analysis of CRISPR-based genome perturbations and their combinations with single-cell functional genomic assays, and recently released GuideScan2 software and preprint (*bioRxiv 2022*).

a. Perez AR*, **Pritykin Y***, Vidigal JA*, Chhangawala S, Zamparo L, Leslie CS, Ventura A. GuideScan software for improved single and paired CRISPR guide RNA design. Nat Biotechnol. 2017 Apr;35(4):347-349. PubMed Central PMCID: PMC5607865.

3. **Computational genomics to study non-coding RNA and RNA-binding proteins.** I have developed and applied computational genomics methods to study non-coding RNA biology and post-transcriptional regulation of gene expression by RNA-binding proteins. I developed a new algorithm and software CLIPanalyze for analysis of CLIP-seq and CLIP-like data. I used this algorithm for comprehensive analysis of data from the new assay HEAP (Halo-Enhanced Ago2 Pull-down) to study microRNA targets *in vivo* in mouse embryonic stem cells, developing embryos, adult tissues and multiple cancer models (*Mol Cell 2020*). During my PhD, I performed integrative analysis of genomic data from Drosophila embryo development to study different components of the piRNA pathway. In particular, we characterized the role of the protein Cutoff in regulation of non-coding and protein-coding RNA expression (*RNA 2017*).

   a. Li X*, **Pritykin Y***, Concepcion CP*, Lu Y, La Rocca G, Zhang M, King B, Cook PJ, Au YW, Popow O, Paulo JA, Otis HG, Mastroleo C, Ogrodowski P, Schreiner R, Haigis KM, Betel D, Leslie CS, Ventura A. High-Resolution In Vivo Identification of miRNA Targets by Halo-Enhanced Ago2 Pull-Down. Mol Cell. 2020 Jul 2;79(1):167-179.e11. PubMed Central PMCID: PMC7446397.
   b. **Pritykin Y**, Brito T, Schupbach T, Singh M, Pane A. Integrative analysis unveils new functions for the *Drosophila* Cutoff protein in noncoding RNA biogenesis and gene regulation. RNA. 2017 Jul;23(7):1097-1109. PubMed Central PMCID: PMC5473144.
   c. **Pritykin Y***, Lu Y*, Lianoglou S, Leslie C. CLIPanalyze: detect and analyze peaks in CLIP-seq data. ENCODE Consortium Meeting; 2016 June; San Diego, California, USA.

4. **Integrative systems biology analysis of cell function across organisms.** The availability of large-scale protein-protein interaction networks for numerous organisms provided us an opportunity to comprehensively analyze the roles proteins play in the functional organization of the cell. I analyzed the protein interaction networks across five organisms and confirmed significant and consistent functional and structural differences between two classes of hub proteins, intramodular and intermodular (*PLOS Comput Biol 2013*). I also studied the role of multifunctional genes on a genome scale (*PLOS Comput Biol 2015*).

   a. **Pritykin Y**, Ghersi D, Singh M. Genome-Wide Detection and Analysis of Multifunctional Genes. PLoS Comput Biol. 2015 Oct;11(10):e1004467. PubMed Central PMCID: PMC4593560.
   b. **Pritykin Y**, Singh M. Simple topological features reflect dynamics and modularity in protein interaction networks. PLoS Comput Biol. 2013;9(10):e1003243. PubMed Central PMCID: PMC3794914.

5. **Theoretical computer science, mathematical logic and foundations of mathematics.** I did research in pure mathematics and theoretical computer science, studying problems at intersection of mathematical logic and foundations of mathematics, formal languages and automata theory, combinatorics, and symbolic dynamics. This resulted in a number of peer-reviewed publications in journals and conferences, as well as multiple awards.

   a. **Pritykin Y**. Almost periodicity, finite automata mappings, and related effectiveness issues. Russian Mathematics. 2010; 54(1):59–69. DOI: 10.3103/S1066369X1001007X
   b. Nicolas F^, **Pritykin Y^**. On uniformly recurrent morphic sequences. International Journal of Foundations of Computer Science. 2009; 20(5):919-940. DOI: 10.1142/S0129054109006966
   c. **Pritykin Y^**, Ulyashkina J^. Aperiodicity measure for infinite sequences. Computer Science - Theory and Applications, Lecture Notes in Computer Science. 2009; 5675:274-285. DOI: 10.1007/978-3-642-03351-3_26
   d. Muchnik A^, **Pritykin Y^**, Semenov A^. Sequences close to periodic. Russian Mathematical Surveys. 2009; 64(5):805. DOI: 10.1070/RM2009v064n05ABEH004641

* equal contribution

^ alphabetical order