

# Dmitry Penzar

## Bioinformatician, ML enthusiast, teacher

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The online version is available at

<https://dmitrypenzar1996.github.io/resume>

### Residence

Moscow

### Github

[github](#)

### Email

[dmitrypenzar1996@gmail.com](mailto:dmitrypenzar1996@gmail.com)

Python	+++++	R	+++++	C/C++	+++	Golang	++	Statistics	+++++	Classical ML	+++++
Deep learning	++++	Algorithms	+++++	Molecular biology	+++	Bioinformatics	+++	English (speaking)	+++	English (technical literature)	+++++

ML enthusiast

## Professional Experience

### Department of Computational Systems Biology, VIGG RAN

June 2017 - Current

Advisor: Dr. Ivan Kulakovskiy.

Classical ML and Deep Neural Networks application for the regulatory mutations effect

ML biology healthcare

### Belozersky Institute of Physico-Chemical Biology, Department of Mathematical Methods in Biology

September 2016 - June 2017

Advisor: S.A. Spirin

We developed a novel program, named PQ, for reconstructing protein and nucleic acid phylogenies following a new character-based principle.

C/C++ phylogeny software development

### Internship in Netherlands, LUMC, Molecular Epidemiology, Department of Medical Statistics and Bioinformatics

July 2016

Advisor: Dr. Szymon Kielbasa

R-Shiny based NGS data quality control and outliers detection toolkit Zeeuw

R NGS software development

### Technosphere, Mail.Ru Group

October 2016 - December 2017

Intense two-year program by a leading Russian IT company.

Within the program, I participated in different ML Kaggle competitions, acquired a huge experience in ML and software development, deepened knowledge of C/C++.

I quitted from the third semester of the program due to job offer from Insilico Medicine company

R NGS software development

Developer in startup curated by AIAR Labs Inc, department of machine learning

August 2017 - October 2017

NDA

ML DNN software development

Developer in InSilico Medicine, department of machine learning

November 2017 - August 2018

I've been working on generating new drugs using deep neural networks

ML DNN drug design software development

## Education

Lomonosov Moscow State University, Faculty of Bioengineering and Bioinformatics. 2013 - 2019. specialist degree, GPA - 5/5

VIGG, Department of Computational Systems Biology, 2019-2023, phd degree

## Publications

Insights gained from a comprehensive all-against-all transcription factor binding motif benchmarking study

The species Severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2

H3K4me3, H3K9ac, H3K27ac, H3K27me3 and H3K9me3 Histone Tags Suggest Distinct Regulatory Evolution of Open and Condensed Chromatin Landmarks

Integration of Multiple Epigenomic Marks Improves Prediction of Variant Impact in Saturation Mutagenesis Reporter Assayheader:

Retroelement—Linked Transcription Factor Binding Patterns Point to Quickly Developing Molecular Pathways in Human Evolution

What Do Neighbors Tell About You: The Local Context of Cis-Regulatory Modules Complicates Prediction of Regulatory Variants

PQ, a new program for phylogeny reconstruction

Profiling of Human Molecular Pathways Affected by Retrotransposons at the Level of Regulation by Transcription Factor Proteins

# Additional Experience

## Additional courses

I've attend a huge variety of additional courses, including: 1. Categorical grammar 2. Neuroscience and neuromarketing 3. Macromolecular modeling 4. Pattern recognition 5. Mathematical models in biology 6. Mathematical linguistics

economics linguistics mathematics

## Teacher

I've been trying to take part in teaching since I was a third-year student. Firstly, I've started as an teacher assistant, then – as one of the course authors, now I'm continue to teach different courses, including those led by me.

Short list of courses I'm taking part in:

1. Algorithms
2. Machine learning in biology (the course led by me)
3. Introduction to Python
4. Advanced Python
5. Deep learning in science

teaching communication team leader