

Polina A. Pavlova

PERSONAL DATA

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EDUCATION

February 2021-Present	EPAM Training Center , Python Development Basics, Saint Petersburg
2020-Present	Saint Petersburg State University , Master student, Biology Faculty, Department of Invertebrate Zoology
2016-2020	Saint Petersburg State University , Bachelor student, Biology Faculty, Department of Biochemistry
2018-2019	Bioinformatics Institute , one year program “Bioinformatics for Biologists”, Saint Petersburg
2014-2016	Lyceum 18 , High school of specialty Biology and Chemistry, Novocheboksarsk, Russia

WORK EXPERIENCE

October 2020-Present	Research project “ Covid respiratory microbiome ” under the leadership of S.V.Sidorenko, PRCCID. Automated pipeline (based on dada2 R package) analysis of the Covid-19 influence on respiratory microbiome in patients with different severity of the disease.
August 2020-Present	Research project “ Local evolutionary adaptations and host-parasite relationships: multilevel analysis of a group of closely related species of littoral gastropods ” under the leadership of A.I.Granovich, SPbU. Assembling and analyzing transcriptomes of health and infected mollusks <i>L. saxatilis</i> to search for the influence of parasitic invasion on his host at transcriptomic level. Automated pipeline is creating for it.
April 2019-December 2020	Research project “ Microevolution of cryptic species of marine gastropods of the genus Littorina ” under the leadership of A.I.Granovich, SPbU. Automated proteomics and metabolomics data analysis of 5 cryptic species of mollusks of the genus <i>Littorina</i> to search for differences between species at proteomics and metabolomics level.

February-May 2019	<p>Research Project in Bioinformatics Institute, Saint Petersburg “Effect of smoking on human leukocyte epigenome”</p> <p>RBBS data were analyzed to search for differentially methylated CpG islands and regions (DMR). Two approaches were used: based on A-clustering algorithm and based on DMRcate R package.</p>
September-December 2018	<p>Research Project in Bioinformatics Institute, Saint Petersburg “Development of a library of functions for express analysis of FASTA/FASTQ files”.</p> <p>Developed a library of functions based on Biopython that allows:</p> <ul style="list-style-type: none"> - counting GC-content, quality scores, N bases in reads - filtering reads with poor quality, short length, particular motif, filtering duplicated reads - joining reads from files, finding overlapping between files, subtracting sets of reads from files.

SKILLS

Programming languages	Python, R
Bioinformatics tools	Software tools for genome data analysis and alignment (Samtools, BWA tools, VarScan, HISAT2 etc.), transcriptome assembly (Trinity), phylogenetic analysis (MrBayes, RAxML etc.), R packages dada2, limma, phyloseq, microbiome
Molecular biology	DNA and protein extraction and purification, PCR, SDS-PAGE, 2D-DIGE, sample preparation for GC-MS
Data analysis	Linear Models, Multivariate statistics
Other	Linux, Bash, Git

PUBLICATIONS

2020	Abstract “The impact of habitat conditions on the metabolome of mollusks of genus Littorina”, Student scientific session Belomorskaia, Saint Petersburg, 2020.
2019	Abstract “A library of functions for express analysis of FASTA/FASTQ files” Bioinformatics Institute 2018/2019. Saint Petersburg 2019. ISBN 978-5-6043094-2-1
2019	Abstract “Effect of smoking on human leukocyte epigenome” Bioinformatics Institute 2018/2019. Saint Petersburg 2019. ISBN 978-5-6043094-2-1

HONORS

2020	Winner in “I am professional” in biotechnology track, All-Russian student Olympiad by Yandex
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LANGUAGES

Russian: Native speaker

English: Upper-intermediate