

Lavrentii G. DANILOV

PERSONAL DATA

PLACE AND DATE OF BIRTH: Saint-Petersburg, Russia | 9 April 1997
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EDUCATION

2020 - present	PhD student Department of Genetics and Breeding, Faculty of Biology, Saint-Petersburg State University , Saint-Petersburg.
2018 - 2020	Graduate student of specialty in Master of Science in Biology Degree, Department of Genetics and Breeding, Faculty of Biology, Saint-Petersburg State University , Saint-Petersburg.
2014-2018	Graduate student of specialty in Bachelor of Science in Biology Degree, Department of Genetics and Breeding, Faculty of Biology, Saint-Petersburg State University , Saint-Petersburg.
2016-2017	One year program Bioinformatics Institute , Biological faculty, Saint-Petersburg.
2012-2014	High school of specialty Biology, Academic Gymnasium , Saint-Petersburg State University, Saint-Petersburg.

RESEARCH TECHNIQUES AND LABORATORY SKILLS

Methods of yeast genetics	Base methods (e.g., strain construction via hybridization, transformation etc.)
Methods of bacterial genetics	Base methods such as transformation, DNA and protein extraction and purification
Methods of molecular biology	Restriction analysis, gel electrophoresis, ligation, site-directed mutagenesis, PCR in various modifications (such as RT-PCR, PCR), sequencing library preparation
Protein biochemistry methods	SDS-PAGE, SDD-AGE, Coomassie and Ponceau staining, Western blot analysis, proteins purification, 2D protein electrophoresis
Bioinformatics tools	Software tools for genome data analysis, programs for genomes assembling and annotation, Software tools for Transcriptomic analysis (Trinity), packets of programs for phylogenetics analysis (such as FigTree, PartitionFinder, MrBayers and etc.)
Programming languages	Python, R (statistical analysis)

WORKING AND TEACHING EXPERIENCE

September 2019 - present	Lecturer in the course "Statistics and Data Analysis in R" and "Introduction in Machine Learning" at the Bioinformatics Institute.
April 2019 - June 2019	Taking part in development and testing course "Introduction in Data Science and Machine learning".
October 2018 - present	Junior Business Analyst at EPAM company.
May 2018 - December 2018	Taking part in development and testing list of courses "Easy about Statistic" (https://ru.coursera.org/specializations/prosto-o-statistike).

RESEARCH EXPERIENCE

2017 - 2020

Graduate research work at the Laboratory of Physiological Genetics, Department of Genetics and Biotechnology, Saint-Petersburg State University

Screening of proteins, which are able to coaggregate with known pathological human amyloids

Within the scope of the project we make wide scale bioinformatical screening using different algorithms, and aimed on identification proteins interacting with known human amyloids. Coaggregation of these proteins with known human amyloids may accelerate development of the disease. For the identification of such proteins we focused on proteins physically interacting with amyloids according to the BioGrid database. Such proteins were analyzed with ArchCandy and IUPred programs to identify amyloidogenic and unstructured regions. The unique feature of ArchCandy is the ability to predict special structural motifs, called beta-arches, that are found in almost all amyloids. In our analysis certain protein was assumed to be amyloidogenic if at least one predicted beta-arch was located into unstructured region. In this analysis we detected one potential human amyloid Nupl1, which demonstrated amyloidogenic properties in C-DAG bacterial system, yeast cells and *in vitro*.

2019 - PRESENT

Research work at the group "Microevolution of cryptic species of marine gastropods of the genus Littorina" under the leadership of A.I.Granovich, Saint-Petersburg State University

Ecological and molecular background of speciation: the model of parallel speciation in the complex of cryptic species of intertidal molluscs

At the moment, the project is assembling and analyzing transcriptomes of 3 cryptic species of mollusks of the genus Littorea to search for differences between species at the transcriptomic level

2014 - 2018

Graduate research work at the Laboratory of Physiological Genetics, Department of Genetics and Biotechnology, Saint-Petersburg State University

Testing the amyloid properties of the human protein HNRNPD in yeast test system

During this project we investigate amyloidogenic internals of HNRNPD, a human RNA-binding protein. We have shown that the first isoform of this protein form aggregates in the yeast test system.

2013 - 2017

Research work at the Laboratory of Physiological Genetics, Department of Genetics and Biotechnology, Saint-Petersburg State University

Influence of mutation 33-34(QA-KK) at N-domain of Sup35 protein on propagation and stability of the yeast prion [PSI⁺]

During this project we have been studying stability and propagation of yeast prion [PSI⁺] on background of one mutant alleles of SUP35. Position of corresponding mutation was predicted by model of parallel superpleated beta-structure. This mutation leads to strong inhibitory effect on [PSI⁺] propagation.

FEBRUARY-MAY
2017

Research project in Bioinformatic Institute, Saint-Petersburg

Development and improvement search strategies in the GeneQuery system

Developed pipeline that downloads a set of samples, quantifies it using ultra-fast methods of quantifying transcriptional experiments, and then removes volumetric data. Optimization methods of clustering in the GeneQuery system for transcriptomic analysis

SEPTEMBER-
DECEMBER 2016

Research project in Bioinformatic Institute, Saint-Petersburg

Human genome variations analysis

In this study we analyzed raw sequences obtained from 11 patients belonging to three families. To analyze the data we build pipeline, which include all operations mentioned below, using Bash programming. After tuning running parameters we reimplemented pipeline using Python pipeline engine SciLuigi.

ARTICLES AND ABSTRACTS (NATIONAL AND INTERNATIONAL MEETINGS)

2019	S Article "Design of a new $[PSI^+]$ -no-more mutation in <i>SUP35</i> with strong inhibitory effect on the $[PSI^+]$ prion propagation", Frontiers in Molecular Neuroscience; doi - 10.3389/fnmol.2019.00274
2019	Indexing abstract "Biochemical and biophysical properties of the human nucleoporin aggregates." Abstracts international meetings «FEBS 2019»
2018	Indexing abstract "Human nucleoporin Nup1 forms amyloid-like aggregates." Abstracts international meetings «FEBS 2018»
2018	Abstract "Bioinformatical prediction of proteins that can co-aggregate with HTT protein." Abstracts international meetings «Prion 2017»
2017	Abstract "Development and improvement search strategies in the GeneQuery system" Bioinformatics Institute 2016/2017 Saint-Petersburg 2017 ISBN 978-5-906931-29-0
2017	"Mutation in previously uncharacterized oligopeptide repeat of Sup35p efficiently eliminates $[PSI^+]$ prion". Abstracts international meetings «Prion 2017»
2016	Abstract "Human genome variation analysis" Bioinformatics Institute 2016/2017 Saint-Petersburg 2017 ISBN 978-5-906931-29-0
2015	"New $[PSI^+]$ -no-more mutation in <i>SUP35</i> with strong inhibitory effect on $[PSI^+]$ propagation". Abstracts international meetings "Prion 2015"

AWARDS AND HONORS

2020-present	Grant from Russian Foundation for Basic Research, supervisor S.A.Bondarev, co-executor.
2018-present	Grant from Russian Foundation for Basic Research, supervisor Y.A.Barbitoff co-executor.
2017-2019	Grant from Russian Science Foundation, supervisor S.A.Bondarev, co-executor.
2017	Diploma of 2-nd place of Moscow International Universiade (Biology) in personal competition.
2015-2017	Grant from president of RF, supervisor S.G. Inge-Vechtomov, co-executor
2014-2016	Grant from Russian Foundation for Basic Research, supervisor G.A. Zhouravleva, co-executor.

LANGUAGES

RUSSIAN: Native speaker

ENGLISH: Speaking and reading with dictionary (B2-C1 level)

INTERESTS AND ACTIVITIES

Volunteer work. I am participating as volunteer in school biological Olympic movements in Saint-Petersburg and Saint-Petersburg Biological Olympiad from 2014 till present.

Science. Programming, Statistic analysis, Machine learning, Molecular modeling.

Sport. Swimming, basketball.