Alexandru M. Bologa

- DATE OF BIRTH: 07/09/1995
- GENDER: Male
- NATIONALITY: Romanian

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SKILLS

- Genetics
- Genomics
- Bioinformatics
- Molecular Biology
- Computational Biology
- Linux programming
- R programming
- Data Analysis

LANGUAGE

- MOTHER TONGUE: Romanian
- English
  - Listening: C2
  - Reading: C2
  - Spoken production: C2
  - Spoken interaction: C2
  - Writing: C2

ABOUT ME

I am a Ph.D. student who is dedicated and motivated to gain knowledge in the fields of genetics, genomics and bioinformatics. I am passionate about science and looking to build a career in biological research.

EDUCATION AND TRAINING

Ph.D. student in Biology 2019 - CURRENT

Faculty of Biology I University of Bucharest

Certificate of Achievement OCTOBER 2023

Bioinformatics for biologists: analysing and interpreting genomics datasets | WELLCOME CONNECTING SCIENCE

Certificate of Achievement MARCH 2021

Bioinformatics for biologists: an introduction to Linux, Bash scripting and R I WELLCOME CONNECTING SCIENCE

Certificate of Attendance at The 4th Romanian Bioinformatics Seminar on NGS technologies FEBRUARY 2019

Romanian Society of Bioinformatics I Bucharest

During the seminar, I learned how the data generated from DNA and RNA sequencing experiments can be processed and manipulated, using different types of bioinformatics tools, but in particular the command line of the UNIX system. I learned about the principles underlying the latest sequencing techniques and I performed the stages of the genome assembly process both theoretically and practically.

Master Degree in Microbiology and Immunology 2017 - 2019

Faculty of Biology I University of Bucharest

Bachelor's Degree in Biology 2014 - 2017

Faculty of Biology I University of Bucharest

WORK EXPERIENCE

Research Assistant 2018 - CURRENT

Faculty of Biology I University of Bucharest

Since August, 2018 I have participated in the scientific research activity in the fields of genetics, genomics and bioinformatics, in the Drosophila genetics laboratory of the Department of Genetics of the Faculty of Biology, University of Bucharest. Using *Drosophila melanogaster* as an experimental model, I have performed multiple tasks regarding the research activity in the laboratory, such as:

- preparation of the culture media,
- maintenance and monitoring of *D. melanogaster* strains,
- anesthetizing and examining the fruitflies,
- performing genetic crosses and using balancer chromosomes.

I have performed transposon insertional mutagenesis experiments and molecular techniques such as DNA isolation, agarose gel electrophoresis, PCR and Inverse PCR techniques.

I have also participated in bioinformatics analyses of nucleic acid sequences using online applications, but especially in the Bash command line (UNIX systems: Ubuntu, Linux Mint, BioLinux) and R programming language.

During my activity in this laboratory, I wrote my Master's thesis called "Analysis of microarray data obtained following experimental infection of *Drosophila melanogaster* males with *Pseudomonas aeruginosa*", benefiting from the opportunity to use experimental microarray data obtained during a research project carried out in collaboration with the FlyChip Laboratory, Cambridge, UK. These efforts resulted in the publication of a scientific article in the IJMS journal called: “Mutations of γCOP Gene Disturb *Drosophila melanogaster* Innate Immune Response to *Pseudomonas aeruginosa*” (https://doi.org/10.3390/ijms23126499).

In addition to this, I analyzed the distribution of P{lacW} and P{EP} artificial transposons in the genome of *D. melanogaster*, concluding that the distributions of both transposons within chromosomal divisions are significantly correlated and may have a periodic behavior. Our results are presented in the article called "Insertions of P{lacW} and P{EP} artificial transposons on the chromosomal divisions of *Drosophila melanogaster* are not randomly distributed", published in the bioRxiv database, with the following DOI: https://doi.org/10.1101/770172. Besides this analysis, I also participated as a co-author in another investigation that led to another pre-print paper called “A bioinformatics pipeline for the assessment of the evolutionary relationship of some *Drosophila* species based on class II transposons mapping”, having the following DOI: https://doi.org/10.1101/2022.09.13.507812.

Considering the topic of my doctoral thesis, in my first year as a Ph.D. student, I managed to participate in the sequencing of the whole genome of a local population of *D. melanogaster*, in order to identify and characterize the transposable elements in this genome (especially P element). We used Oxford Nanopore MinION technology to sequence twice the fruitfly genome and ONT reads data have been uploaded to the National Center for Biotechnology Information (https://www.ncbi.nlm.nih.gov) under bioproject “**WGS sequencing of a local Drosophila melanogaster strain from Horezu, Romania**“ with the accessing number **PRJNA629549**.

We managed to perform the sequencing in the Drosophila laboratory from the Genetics Department of the Faculty of Biology, University of Bucharest. Also, in 2016 in this laboratory was developed a bioinformatics tool called Genome ARTIST, dedicated to the analysis of transposons. In November 2020, I was a co-author in a paper published in the IJMS journal called "Genome ARTIST_v2—An Autonomous Bioinformatics Tool for Annotation of Natural Transposons in Sequenced Genomes" (https://doi.org/10.3390/ijms232012686), in which the updates brought to this tool and the new performances are presented.

University Teaching Assistant 2019 - CURRENT

Faculty of Biology I University of Bucharest

With my admission to the doctoral program, I assisted the professors with whom I collaborated in various courses, laboratories and seminars. After a short time, I was engaged in some of the practical genetics laboratories targeting topics such as the genetics of *D. melanogaster*, visualizing and identifying genetic markers associated with balancer chromosomes, in the reproduction of experiments initiated by Thomas Morgan, complementation test crosses, mutagenesis experiments with artificial transposons. In addition to the Genetics field, I held practical bioinformatics seminars, covering topics such as introduction to bash programming, BLAST, analysis and processing of NGS data, and analysis and interpretation of Microarray data.

PUBLICATIONS

Insects 25.05.2023

The Landscape of the DNA Transposons in the Genome of the Horezu_LaPeri Strain of *Drosophila melanogaster* - https://doi.org/10.3390/insects14060494

International Journal of Molecular Sciences 28.11.2022

ONT-Based Alternative Assemblies Impact on the Annotations of Unique versus Repetitive Features in the Genome of a Romanian Strain of *Drosophila melanogaster* - https://doi.org/10.3390/ijms232314892

International Journal of Molecular Sciences 21.10.2022

Genome ARTIST_v2—An Autonomous Bioinformatics Tool for Annotation of Natural Transposons in Sequenced Genomes - https://doi.org/10.3390/ijms232012686

International Journal of Molecular Sciences 10.06.2022

Mutations of γCOP Gene Disturb *Drosophila melanogaster* Innate Immune Response to *Pseudomonas aeruginosa* - https://doi.org/10.3390/ijms23126499

bioRxiv 15.09.2022

A bioinformatics pipeline for the assessment of the evolutionary relationship of some Drosophila species based on class II transposons mapping - https://doi.org/10.1101/2022.09.13.507812

bioRxiv 16.09.2019

Insertions of P{lacW} and P{EP} artificial transposons on the chromosomal divisions of *Drosophila melanogaster* are not randomly distributed - https://doi.org/10.1101/770172