

	<p>MELESHKO, Dmitrii A. Assistant professor PhD</p>
<p>Research interests</p>	<ul style="list-style-type: none"> ✓ NGS data analysis ✓ Genome assembly ✓ Algorithms in bioinformatics
<p>List of the supervisor's research projects (participation/supervision)</p>	<ul style="list-style-type: none"> ✓ Quality control of genomic assemblies ✓ Genomic assembly of non-model organisms ✓ Adaptation of assembly algorithms for searching and characterizing antibiotic resistance genes ✓ Comparative genomics of non-model organisms
<p>List of potential thesis topics</p>	<ul style="list-style-type: none"> ✓ Development of algorithms for improving T2T diploid assemblies ✓ Development of algorithms and programs for assessing the quality of T2T assemblies ✓ Adaptation of the SPAdes collector to the search for AMR genes in metagenomic sequencing data ✓ Applications of pangenomics methods to improve the search for structural variations and solve problems of population genetics
<p>Publications in the last five years</p>	<p>8 (Scopus / Web of Science / RSCI)</p>
<p>Key publications</p>	<ol style="list-style-type: none"> 1. Meleshko D., Prjbelski A.D., Raiko M., Tomescu A., Tilgner H., Hajirasouliha I. CLOUDRNASPADES: isoform assembly using bulk barcoded RNA sequencing data//Bioinformatics, 2024, Vol. 40, No. 2, pp. btad781 2. Meleshko D.A., Korobeynikov A. Benchmarking state-of-the-art approaches for norovirus genome assembly in metagenome sample//Biology, 2023, Vol. 12, No. 8, pp. 1066 3. Mak L., Meleshko D., Danko D., Barakzai W., Maharjan S., Belchikov N., Hajirasouliha I. Ariadne: synthetic long read deconvolution using assembly graphs//Genome Biology, 2023, Vol. 24, No. 1, pp. 197 4. Meleshko D., Hajirasouliha I., Korobeynikov A. coronaSPAdes: from biosynthetic gene clusters to RNA viral assemblies//Bioinformatics, 2022, Vol. 38, No. 1, pp. 1-8 5. Edgar R.C., Taylor B., Lin V., Altman T., Barbera P., Meleshko D., Lohr D., Novakovsky G., Buchfink B., Al-Shayeb B., Banfield J., De La Pena M., Korobeynikov A., Chikhi

	R., Babaian A. Petabase-scale sequence alignment catalyses viral discovery//Nature, 2022, Vol. 602, No. 7895, pp. 142-147
Key IPs	<ul style="list-style-type: none"> ✓ 2023687688 (18.12.2023) ‘Program for assembling gene clusters from short reads’ (biosyntheticSPAdes) ✓ 2023687488 (14.12.2023) ‘Program for assembling a transcriptome from barcoded reads’ (cloudrnaSPAdes) ✓ 2023687489 (14.12.2023) ‘Program for automated genome assembly of coronaviruses using HMM’ (coronaSPAdes) ✓ 2023687490 (14.12.2023) ‘Program for deconvolution of Sars-Cov-2 strains using assembly graphs’ (wastewaterSPAdes)
Supervisor’s specific requirements	<ul style="list-style-type: none"> ✓ Basic knowledge of biology and genetics ✓ Ability to program in one of the popular programming languages (preferably C++/Python) ✓ Algorithmic thinking
Code of the subject area of the PhD program	1.5.7 Genetics