KIRILL GRIGOREV / КИРИЛЛ ГРИГОРЬЕВ

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COMPUTATIONAL GENETICS, EPIGENOMICS, GENOME ASSEMBLY, GENOMICS ALGORITHMS, GENOMICS DATABASES, DATA SCIENCE

PHD CANDIDATE

Weill Cornell Medicine, New York, NY
Mason Lab, Institute for Computational Biomedicine

NASA GeneLab Multi-Omics Analysis Working Group and Visualization Working Group

M.S. in Biology, University of Puerto Rico
B.S. in Biotechnology, Saint Petersburg Chemical and Pharmaceutical Academy

PRINCIPAL AREAS OF ACADEMIC INTEREST

Genomics algorithms
Translational and personalized genomics
Epigenomics and epitranscriptomics
Space genetics

PRINCIPAL SKILLSET

Genomic data analysis
Graph and numerical algorithms
Advanced Python (SciPy stack, Numba, Dask)
Lua/LuaJIT, R, essential C and Perl

RESEARCH SUMMARY

2017 – … **Weill Cornell Medicine, Institute for Computational Biomedicine, Mason Lab**
Assembly algorithms, telomere bioinformatics, sequencing data analysis

Developed frameworks for identification of novel telomeric motifs and haplotype inference [1], studied the effects of prolonged spaceflight on dynamics of telomeres [4] and cell-free DNA [5], carried out sequence analyses in translational [3] and theoretical [9] applications.

2018 – … **NASA GeneLab**. Cross-dataset data analysis platform

Developed an API for transparent programmatic, as well as browsable, access to the space flight biological data stored in the GeneLab repository [2, 6, 7, 14, 15], powering data visualization and enabling a range of downstream applications.

2018 **New York Genome Center**. Epigenetic evolution of cancers, phylogenetics algorithms

Developed a computationally faster, scalable algorithm for the calculation of the four-gamete test [8].

2015 – 2017 **University of Puerto Rico, Caribbean Genome Center**
Methods of genome assembly, conservation genetics, Genome 10K

Carried out *de novo* whole-genome and mitogenome assemblies for a number of endangered Caribbean species, contributing to the understanding of conservation status and strategies [10, 11, 13].

2014 – 2017 **Dobzhansky Center for Genome Bioinformatics**
Methods of genome assembly, GWAS visualization tools, human epigenetics

Studied epigenomics of early childhood development [12], processed data for visualization in the Genome-Wide Association Tracks Chromosome Highway [17].

2013 – 2014 **iBinom inc.** Medical genome analysis, cloud SaaS

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PUBLIC SPEAKING & OTHER ACADEMIC EXPERIENCE

talk, 2020	**GeneLab sequencing data analysis and visualization**. Virtual (USRA / NASA Ames Research Center)
talk, 2019	**Comparative circadian transcriptomics: novel and conserved features of the mammalian pineal gland**. OU Genomics Symposium, Oakland University, MI
workshop, 2019	**GeneLab Visualization Working Group meeting**. 35th Annual Meeting of ASGSR, Denver, CO
workshop, 2019	**GeneLab visualization workshop**. Broad Institute, Cambridge, MA
workshop, 2017	**Development of robust bioinformatics pipelines** Fifth annual Bioinformatics Summer School, Moscow, Russia
talk, 2017	**Genomics and conservation of the Hispaniolan Solenodon** IX Caribbean Biodiversity Congress, Santo Domingo, Dominican Republic
TA, 2016	**Bioinformatics pipelines**. Recent Advances in Conservation Genetics, Tihany, Hungary
workshop, 2015	**Linux toolset for bioinformatics**. 3rd annual Bioinformatics Summer School, Moscow, Russia
instructor, 2015	**Introduction to genetics**. Biotechnology Stepik.org online course [16]

PUBLICATIONS

1. K Grigorev, J Foox *et al*. **Haplotype diversity and sequence heterogeneity of human telomeres**. Genome Research 31 (7), 1269. doi:10.1101/gr.274639.120
2. D Berrios *et al*. **NASA GeneLab: interfaces for the exploration of space omics data**. Nucleic Acids Research 49 (D1), D1515. doi:10.1093/nar/gkaa887
3. N Ivanov *et al*. **Sex-specific transcriptional differences and loss of gene imprinting in pancreatic neuroendocrine tumors**. medRxiv (2021). doi:10.1101/2021.06.09.21258573
4. J Luxton *et al*. **Temporal Telomere and DNA Damage Responses in the Space Radiation Environment**. Cell Reports 33 (10), 108435. doi:10.1016/j.celrep.2020.108435
5. D Bezdan *et al*. **Cell-free DNA (cfDNA) and exosome profiling from a year-long human spaceflight reveals circulating biomarkers**. IScience 23 (12), 101844. doi:10.1016/j.isci.2020.101844
6. R Scott *et al*. **Advancing the Integration of Biosciences Data Sharing to Further Enable Space Exploration**. Cell Reports 33 (10), 108441. doi:10.1016/j.celrep.2020.108441
7. D Berrios *et al*. **Visualizing Omics Data from Spaceflight Samples using the NASA GeneLab Platform**. In Proceedings of the 12th International Conference on Bioinformatics and Computational Biology (Vol. 70, pp. 89-98). doi:10.29007/rh7n
8. F Gaiti, R Chaligne, H Gu *et al*. **Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia**. Nature 569 (7757), 576. doi:10.1038/s41586-019-1198-z
9. ABR McIntyre *et al*. **Single-molecule sequencing detection of N6-methyladenine in microbial reference materials**. Nature Communications 10 (1), 579. doi:10.1038/s41467-019-08289-9
10. S Kolchanova, S Kliver *et al*. **Genomes of three closely related Caribbean amazons provide insight for species history and conservation**. Genes 10 (1), 54. doi:10.3390/genes10010054
11. K Grigorev, S Kliver *et al*. **Innovative assembly strategy contributes to understanding the evolution and conservation genetics of the endangered *Solenodon paradoxus* from the island of Hispaniola**. GigaScience 7 (6), giy025. doi:10.1093/gigascience/giy025
12. OY Naumova *et al*. **Developmental dynamics of the epigenome: a longitudinal study of three toddlers**. Neurotoxicology and teratology 66, 125-131. doi:10.1016/j.ntt.2017.12.006
13. AL Brandt, K Grigorev *et al*. **Mitogenomic sequences support a north–south subspecies subdivision within *Solenodon paradoxus***. Mitochondrial DNA Part A 28 (5), 662-670. doi:10.3109/24701394.2016.1167891

RESOURCES

14. genefab3 API: github.com/LankyCyril/genefab3, in testing stage
15. GeneLab Data Visualization portal: genelab-visualization.usra.edu, legacy genefab API
16. Stepik Biotechnology: stepik.org/course/94
17. Genome-Wide Association Tracks Chromosome Highway: gen-watch.org