

Mikhail Kolmogorov

Tenure-Track Standtman Investigator
Cancer Data Science Laboratory
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Research Interests

The focus of my research is *computational biology* - algorithms, mathematical models and tools aimed to answer fundamental questions about living systems through the analysis of large-scale biological data. Specifically, I have extensive experience in computational genomics and proteomics, with a focus on the design and development of efficient algorithmic approaches that bridge theoretical models and real experimental data.

Research Positions

- **Tenure-Track Standtman Investigator** *Jan 2022 - now*
National Cancer Institute, Bethesda, MD, USA
- **Postdoctoral Fellow** *Jan 2021 - Dec 2021*
University of California, Santa Cruz, USA
Advisors: Benedict Paten
- **Postdoctoral Fellow** *Oct 2019 - Dec 2020*
University of California, San Diego, USA
Advisors: Rob Knight and Pavel Pevner

Education

- **PhD, Computer Science** *Sep 2014 - Sep 2019*
Department of Computer Science and Engineering,
University of California, San Diego, USA
Thesis: Algorithms for long-read assembly
Advisor: Pavel Pevzner
- **MSc, Bioinformatics** *Sep 2012 – Jul 2014*
St. Petersburg Academic University, Russia
Thesis: Genome assembly using multiple references
Advisor: Son Pham
- **BSc, Applied Mathematics and Informatics** *Sep 2008 - Jul 2012*
Department of Mathematics, ITMO University,
St.Petersburg, Russia
Thesis: Variational method for the minimum energy path calculation
Advisor: Igor Popov

Journal Publications

- Derek M. Bickhart*, **Mikhail Kolmogorov***, Elizabeth Tseng, Daniel Portik, Anton Korobeynikov, Ivan Tolstoganov, Gherman Uritskiy, (9 authors) & Tim Smith "Generation of lineage-resolved complete metagenome-assembled genomes by precision phasing." *Nature Biotechnology*, in press (2021) doi: <https://doi.org/10.1101/2021.05.04.442591>
- Dmitry Antipov, Mikhail Rayko, **Mikhail Kolmogorov** & Pavel Pevzner. "Assembling viruses and identifying their hosts from long-read metagenomics data". *Genome Research*, in press (2021)
- Shafin, K., Pesout, T., Chang, P.C., Nattestad, M., Kolesnikov, A., Goel, S., Baid, G., **Kolmogorov, M.**, Eizenga, J.M., Miga, K.H. and Carnevali, P.. "Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads". *Nature Methods* 18 1322–1332 (2021)
- Meyer, F., Fritz, A., Deng, Z. L., Koslicki, D., Gurevich, A., Robertson, G., (28 authors), **Kolmogorov M.**, (64 authors), McHardy, A. C. "Critical Assessment of Metagenome Interpretation-the second round of challenges". *bioRxiv* (2021) <https://doi.org/10.1101/2021.07.12.451567>
- Nurk, S., Koren, S., Rhie, A., Rautiainen, M., Bzikadze, A. V., Mikheenko, A., (40 authors), **Kolmogorov, M.**, (51 authors), Phillippy, A. M. "The complete sequence of a human genome". *bioRxiv* (2021) <https://doi.org/10.1101/2021.05.26.445798>
- A Bankevich, A Bzikadze, **M Kolmogorov**, D. Antipov & PA Pevzner. "Assembling Long Accurate Reads Using de Bruijn Graphs". *bioRxiv* (2021) doi: <https://doi.org/10.1101/2020.12.10.420448>
- **Mikhail Kolmogorov**, Derek M. Bickhart, Bahar Behsaz, Alexey Gurevich, Mikhail Rayko, Sung Bong Shin, Kristen Kuhn, Jeffrey Yuan, Evgeny Polevikov, Timothy P. L. Smith and Pavel A. Pevzner. "metaFlye: scalable and accurate long-read metagenome assembler". *Nature Methods* (2020) doi: 10.1038/s41592-020-00971-x
- **Mikhail Kolmogorov**, Jeffrey Yuan, Yu Lin and Pavel Pevzner. "Assembly of long error-prone reads using repeat graphs". *Nature Biotechnology* 37 540–546 (2019)
- Alla Mikheenko and **Mikhail Kolmogorov**. "Assembly Graph Browser: interactive visualization of assembly graphs". *Bioinformatics* 35 3476–3478 (2019)
- **Mikhail Kolmogorov**, Joel Armstrong, Brian J. Raney, Ian Streeter, Matthew Dunn, Fengtang Yang, Duncan Odom, Paul Flicek, Thomas Keane, David Thybert, Benedict Paten and Son Pham. "Chromosome assembly of large and complex genomes using multiple references". *Genome Research* 28 (11), 1720–1732 (2018)
- Alex Bishara, Eli L Moss, **Mikhail Kolmogorov**, Alma Parada, Ziming Weng, Arend Sidow, Anne E Dekas, Serafim Batzoglou, Ami S Bhatt. "High-quality genome sequences of uncultured microbes by assembly of read clouds". *Nature Biotechnology* 36, 1067–1075 (2018)
- Jingtao Lilue, Anthony G Doran, Ian T Fiddes, Monica Abrudan, Joel Armstrong, (22 authors), **Mikhail Kolmogorov**, (29 authors), Benedict Paten, Thomas M Keane. "Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel

functional loci". *Nature Genetics* 50, 1574–158 (2018)

- David Thybert, Maša Roller, Fábio CP Navarro, Ian Fiddes, Ian Streeter, Christine Feig, David Martin-Galvez, **Mikhail Kolmogorov**, (33 authors), Benedict Paten, Son Pham, Thomas M Keane, Duncan T Odom, Paul Flicek. "Repeat associated mechanisms of genome evolution and function revealed by the *Mus caroli* and *Mus pahari* genomes". *Genome Research* 28 (4), 448-459 (2018)
- **Mikhail Kolmogorov**, Eamonn Kennedy, Zhuxin Dong, Gregory Timp and Pavel Pevzner. "Single-Molecule Protein Identification by Sub-Nanopore Sensors". *PLoS Computational Biology* 13 (5), e1005356 (2017)
- Yu Lin*, Jeffrey Yuan*, **Mikhail Kolmogorov***, Max Shen and Pavel Pevzner. "Assembly of long error-prone reads using de Bruijn graphs". *PNAS* 113 (52), E8396-E8405 (2016), *equal contribution
- **Mikhail Kolmogorov**, Xiaowen Liu and Pavel Pevzner. "SpectroGene: a tool for proteogenomic annotations using top-down spectra". *Journal of Proteome Research* 15 (1), 144-151 (2015)

Refereed Conference Proceedings

- Evgeny Plevnikov and **Mikhail Kolmogorov**. "Synteny paths for assembly graphs comparison". *Workshop on Algorithms in Bioinformatics 2019, Niagara Falls, NY*
- **Mikhail Kolmogorov**, Jeffrey Yuan, Yu Lin and Pavel Pevzner. "Assembly of long error-prone reads using repeat graphs". *RECOMB 2018, Paris, France* (journal version in *Nature Biotech.* 2019)
- Yu Lin*, Jeffrey Yuan*, **Mikhail Kolmogorov***, Max Shen and Pavel Pevzner. "Assembly of long error-prone reads using de Bruijn graphs". *RECOMB 2016, Santa Monica, CA* (journal version in *PNAS* 2016), *equal contribution
- **Mikhail Kolmogorov**, Eamonn Kennedy, Zhuxin Dong, Gregory Timp and Pavel Pevzner. "Single-Molecule Protein Identification by Sub-Nanopore Sensors". *RECOMB-SEQ 2016, Santa Monica, CA* (journal version in *PLoS Comp. Biol* 2017)
- **Mikhail Kolmogorov**, Brian Raney, Benedict Paten, Son Pham. "Ragout - a reference-assisted assembly tool for bacterial genomes". *ISMB 2014, Boston, MA*
- Ilya Minkin, Anand Patel, **Mikhail Kolmogorov**, Nikolay Vyahhi, Son Pham. "Sibelia: a scalable and comprehensive synteny block generation tool for closely related microbial genomes". *Workshop on Algorithms in Bioinformatics 2013, Antibes, France*

Invited Talks

- "Assembly of long error-prone reads using repeat graphs". *PAG 2018, San Diego, CA*
- "Assembly of long error-prone reads using repeat graphs". *Center for Microbiome Innovation at UCSD, 2019*
- "Assembly of long error-prone reads using repeat graphs". *Australian National University, Long-read, long-range workshop, 2019*

- “Completing human genome and microbiome: algorithms for long-read assembly”, *NYU Center for Human Genetics and Genomics symposium*, 2020
- “Long-read assembly: are metagenomes easier than diploid genomes?”. *PAG 2020*, San Diego, CA
- “Metagenomic assembly using long reads”, Bioinformatics seminar series, *ITMO University, St. Petersburg, Russia*, 2020
- “Metagenomic assembly using long reads”, Metagenomic seminar series, *Universidad Miguel Hernandez*, 2020
- “Long read genome and metagenome assembly using repeat graphs”. *Oxford Nanopore Community Meeting (virtual)*, 2020
- “Completing human genome and microbiome: algorithms for long-read assembly”, *Cornell Computational Biology symposium*, 2020
- “Long read genome and metagenome assembly using repeat graphs”. *Annual Conference of the Russian-American Science Association (virtual)*, 2020
- “Generation of lineage-resolved complete metagenome-assembled genomes in complex microbial communities”. *PacBio SMRT Science Journal Club Seminar (virtual)*, 2021

Conference Contributed Talks

- “metaFlye: Scalable long-read metagenome assembly using repeat graphs”. *Genome Informatics 2019*, Cold Spring Harbor, NY (selected abstract)
- “Synteny paths for assembly graphs comparison”. *Workshop on Algorithms in Bioinformatics 2019*, Niagara Falls, NY (proceedings author)
- “Assembly of long error-prone reads using repeat graphs”. *AGBT 2019*, Marco Island, FL (selected abstract)
- “Single-Molecule Protein Identification by Sub-Nanopore Sensors”. *HUPO 2018*, Orlando, FL (selected abstract)
- “Assembly of long error-prone reads using repeat graphs”. *RECOMB 2018*, Paris, France (proceedings author)
- “Single-Molecule Protein Identification by Sub-Nanopore Sensors”. *RECOMB-SEQ 2016*, Santa Monica, CA (proceedings author)
- “SpectroGene: a tool for proteogenomic annotations using top-down spectra”. *ASMS 2015*, St. Louis, MO (selected abstract)
- “Ragout - a reference-assisted assembly tool for bacterial genomes”. *ISMB 2014*, Boston, MA (proceedings author)

Mentoring and Advising

- Ekaterina Kazantseva, “Combining Genome Graphs and Phasing Information to Generate Complete Bacterial Haplotypes”. Master thesis, ITMO University, St. Petersburg, Russia, 2021-2022
- Mentor in the Science Mentors program for Russian-speaking students (<https://sites.google.com/view/thescience Mentors/en>), 2020-2021
- Evgeny Polevikov. “Synteny paths for assembly graphs comparison” Master thesis, ITMO University, St. Petersburg, Russia, 2018-2019
- Alla Mikheenko. “Assembly Graph Browser: interactive visualization of assembly graphs” Research project, St. Petersburg Center for Algorithmic Bioinformatics, Russia, 2018-2019

Teaching

- Teaching assistant *Winter 2016*
Algorithms in Molecular Biology. UC San Diego
- Teaching assistant *Spring 2013*
Bioinformatics Seminar. St. Petersburg Academic University
- Lecturer, Bioinformatics Summer School 2016
Moscow, Russia
- Lecturer, Bioinformatics Summer School 2014
St. Petersburg, Russia

Fellowships

- CSE Doctoral Fellow Award (UCSD) *Sep 2014 - Aug 2016*

Open Source Projects

- **Flye** – De novo assembler for single molecule sequencing reads (*main developer*)
<https://github.com/fenderglass/Flye>
- **HapDup** - Generating phased diploid assembly using long reads only (*main developer*)
<https://github.com/fenderglass/HapDup>
- **Ragout** – Chromosome-level scaffolding using multiple references (*main developer*)
<https://github.com/fenderglass/Ragout>
- **Nano-Align** – Protein identification using a nanopore (*main developer*)
<https://github.com/fenderglass/Nano-Align>
- **SpectroGene** – Gene prediction using top-down mass-spectrometry (*main developer*)
<https://github.com/fenderglass/SpectroGene>

Industry Experience

- Research Intern
Illumina, San Diego, CA, USA
Mentors: Dorna Kashef and Serafim Batzoglou

Summer 2017