

Sergey Nurk

CONTACT INFORMATION	Email: sergeynurk@gmail.com , sergeynurk@nih.gov Homepage: https://genomeinformatics.github.io/people/nurk/ Phone: +1-202-830-43-44
BIOGRAPHICAL DATA	DOB: March 8th, 1989 Citizenship: Russian Federation Marital status: Married
EDUCATION	<p>St. Petersburg State University Ph.D in Computational Biology and Bioinformatics</p> <ul style="list-style-type: none">• Conferred: May 2019• Thesis: “Assembling genomes of non-cultivable microorganisms from high-throughput sequencing data”• Advisor: Pavel A. Pevzner• Area of study: <i>de novo</i> genomic and metagenomic assembly <p>St. Petersburg State University, Faculty of Mathematics and Mechanics Specialist degree (equiv. of MSc) in Computer Science and Software Engineering</p> <ul style="list-style-type: none">• Period of study: 2006 – 2011• Thesis: “Development of de Bruijn graph processing algorithms for genome assembly”• Advisor: Nikolay I. Vyahhi• Diploma cum laude <p>Lyceum of Mathematics and Physics #239</p> <ul style="list-style-type: none">• Period of study: 2002 – 2006• GPA 5.0
ADDITIONAL EDUCATION	<p>Academy of Modern Software Engineering</p> <ul style="list-style-type: none">• Period of study: 2008 – 2010
EMPLOYMENT	<p>Genome Informatics Section, NHGRI, NIH</p> <ul style="list-style-type: none">• 2019 – present• Visiting Fellow• Genomic and metagenomic assembly with modern sequencing technologies• Bethesda MD, USA <p>Center for Algorithmic Biotechnology, St. Petersburg State University</p> <ul style="list-style-type: none">• 2015 – 2019• Junior Research Fellow• Computational methods for genome-resolved metagenomic analysis, in particular metagenomic assembly• St. Petersburg, Russia <p>Algorithmic Biology Laboratory, St. Petersburg Academic University</p> <ul style="list-style-type: none">• 2011 – 2015• Junior Research Fellow• Methods for (single-cell) microbial genome assembly and comparative genomics• St. Petersburg, Russia

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- 2009 – 2011
- Software Engineer (Java) in Department of Structured Web Mining
- St. Petersburg, Russia

AREAS OF
INTEREST

genome assembly
genome-resolved metagenomics
comparative genomics
algorithms and data structures for computational genomics
software development

PUBLICATIONS

- **Sergey Nurk***, Sergey Koren*, Arang Rhie*, Mikko Rautiainen* (*equal contribution), The Telomere-to-Telomere Consortium, Evan Eichler, Karen Miga, Adam Phillippy
“**The complete sequence of a human genome**”.
Submitted, bioRxiv, 2021
- Mitchell Vollger, Xavi Guitart, Philip Dishuck, Ludovica Mercuri, William Harvey, Ariel Gershman, Mark Diekhans, Arvis Sulovari, Katherine Munson, Alexandra Lewis, Kendra Hoekzema, David Porubsky, Ruiyang Li, **Sergey Nurk**, Sergey Koren, Karen Miga, Adam Phillippy, Winston Timp, Mario Ventura, Evan Eichler
“**Segmental duplications and their variation in a complete human genome**”.
Submitted, bioRxiv, 2021
- Tiago Leão, Mingxun Wang, Nathan Moss, Ricardo da Silva, Jon Sanders, **Sergey Nurk**, Alexey Gurevich, Gregory Humphrey, Raphael Reher, Qiyun Zhu, Pedro Belda-Ferre, Evgenia Glukhov, Syrena Whitner, Kelsey Alexander, Robert Rex, Pavel Pevzner, Pieter C Dorrestein, Rob Knight, Nuno Bandeira, William H Gerwick, Lena Gerwick
“**A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria**”.
Marine Drugs, Jan;19(1), 2021
- Glennis Logsdon, Mitchell Vollger, PingHsun Hsieh, Yafei Mao, Mikhail Liskovych, Sergey Koren, **Sergey Nurk**, Ludovica Mercuri, Philip Dishuck, Arang Rhie, Leonardo de Lima, David Porubsky, Andrey Bzikadze, Milinn Kremitzki, Tina Graves-Lindsay, Chirag Jain, Kendra Hoekzema, Shwetha Murali, Katherine Munson, Carl Baker, Melanie Sorenson, Alexandra Lewis, Urvashi Surti, Jennifer Gerton, Vladimir Lari-onov, Mario Ventura, Karen Miga, Adam Phillippy, Evan Eichler
“**The structure, function, and evolution of a complete human chromosome 8**”.
Nature, May;593(7857):101-107, 2021
- Christopher Quince, **Sergey Nurk**, Sebastien Raguideau, Robert James, Orkun Soyer, J Kimberley Summers, Antoine Limasset, A Murat Eren, Rayan Chikhi, Aaron Darling
“**Metagenomics Strain Resolution on Assembly Graphs**”.
In press., bioRxiv, 2020
- **Sergey Nurk**, Brian Walenz, Arang Rhie, Mitchell Vollger, Glennis Logsdon, Robert Grothe, Karen Miga, Evan Eichler, Adam Phillippy and Sergey Koren
“**HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads**”.
Genome Research, Sep;30(9):1291-1305, 2020

- Tatiana Dvorkina, Dmitry Antipov, Anton Korobeynikov and **Sergey Nurk**
“SPAligner: alignment of long diverged molecular sequences to assembly graphs”.
 BMC Bioinformatics, 21(Suppl 12), 2020
- Jon G. Sanders, **Sergey Nurk**, Rodolfo A. Salido, Jeremiah Minich, Zhenjiang Z. Xu, Qiyun Zhu, Cameron Martino, Marcus Fedarko, Timothy D. Arthur, Feng Chen, Brigid S. Boland, Greg C. Humphrey, Caitriona Brennan, Karenina Sanders, James Gaffney, Kristen Jepsen, Mahdiah Khosroheidari, Cliff Green, Marlon Liyanage, Jason W. Dang, Vanessa V. Phelan, Robert A. Quinn, Anton Bankevich, John T. Chang, Tariq M. Rana, Douglas J. Conrad, William J. Sandborn, Larry Smarr, Pieter C. Dorrestein, Pavel A. Pevzner and Rob Knight
“Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads”.
 Genome Biology, 20, 226, 2019
- Xin Fang, Jonathan Monk, **Sergey Nurk**, Margarita Akseshina, Qiyun Zhu, Christopher Gemmell, Connor Gianetto-Hill, Nelly Leung, Richard Szubin, Jon Sanders, Paul L Beck, Weizhong Li, William J Sandborn, Scott D Gray-Owen, Rob Knight, Emma Allen-Vercoe, Bernhard O Palsson, Larry Smarr
“Metagenomics-based, strain-level analysis of Escherichia coli from a time-series of microbiome samples from a Crohn’s disease patient”.
 Frontiers in Microbiology 9, 2559, 2018
- **Sergey Nurk***, Dmitry Meleshko* (*equal contribution), Anton Korobeynikov, and Pavel A. Pevzner
“metaSPAdes: a new versatile metagenomic assembler.”
 Genome Research, 27(5), 824-834, 2017
- Yu Lin, **Sergey Nurk** and Pavel A. Pevzner
“What is the difference between the breakpoint graph and the de Bruijn graph?”.
 BMC genomics, 15(6), S6, 2014
- Gabriela I Guzman, Jose Utrilla, **Sergey Nurk**, Elizabeth Brunk, Jonathan M Monk, Ali Ebrahim, Bernhard Ø Palsson, Adam M. Feist
“Model-driven discovery of underground metabolic functions in Escherichia coli”.
 Proceedings of the National Academy of Sciences, 112(3), 2015
- Andrey D. Prjibelski, Irina Vasilinetc, Anton Bankevich, Alexey Gurevich, Tatiana Krivosheeva, **Sergey Nurk**, Son Pham, Anton Korobeynikov, Alla Lapidus and Pavel A. Pevzner
“ExSPAndeR: a universal repeat resolver for DNA fragment assembly”.
 Bioinformatics, 30(12), i293-i301, 2014
- **Sergey Nurk***, Anton Bankevich* (*equal contribution), Dmitry Antipov, Alexey A. Gurevich, Anton Korobeynikov, Alla Lapidus, Andrey D. Prjibelski, Alexey Pyshkin, Alexander Sirotkin, Yakov Sirotkin, Ramunas Stepanauskas, Scott R. Clin- genpeel, Tanja Woyke, Jeffrey S. Mclean, Roger Lasken, Glenn Tesler, Max A. Alek- sejev, and Pavel A. Pevzner
“Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products”.
 Journal of Computational Biology 20(10), 2013
- Jeffrey S. McLean, Mary-Jane Lombardo, Michael G. Ziegler, Mark Novotny, Joyclyn Yee-Greenbaum, Jonathan H. Badger, Glenn Tesler, **Sergey Nurk**, Valery Lesin,

Daniel Bami, Adam P. Hall, Anna Edlund, Lisa Z. Allen, Scott Durkin, Sharon Reed, Francesca Torriani, Kenneth H. Nealson, Pavel A. Pevzner, Robert Friedman, J. Craig Venter and Roger S. Lasken

“Genome of the pathogen *Porphyromonas gingivalis* recovered from a biofilm in a hospital sink using a high-throughput single cell genomic platform”.

Genome research, 23(5), 867-877

- Anton Bankevich*, **Sergey Nurk*** (*equal contribution), Dmitry Antipov, Alexey Gurevich, Mikhail Dvorkin, Alexander Kulikov, Valery Lesin, Sergey Nikolenko, Son Pham, Andrey Prjibelski, Alexey Pyshkin, Alexander Sirotkin, Nikolay Vyahhi, Glenn Tesler, Max Alekseyev and Pavel Pevzner

“SPAdes: a New Genome Assembler and its Applications to Single Cell Sequencing”.

Journal of Computational Biology 19(5), 2012

- **Sergey Nurk**
“An $O(2^{0.4058m})$ Upper Bound for *Circuit SAT*”.
PDMI preprint 10/2009, 2009

SELECTED TALKS

- “Custom assembly pipeline for CHM13 T2T reconstruction”
[T2T/HPRC Meeting](#), 2020.
- “metaSPAdes: a New Versatile Metagenomic Assembler”
20th Conference on Research in Computational Molecular Biology (RECOMB-2016).
Los Angeles, USA, 2016.
- “Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads”
17th Conference on Research in Computational Molecular Biology (RECOMB-2013).
Beijing, China, 2013.

TEACHING EXPERIENCE

- “BIN420: Bioinformatics for functional metagenomics” course
NMBU, As, Norway, September 2017
Instructor on (metagenomic) assembly
- “Methods for genome-resolved metagenomics” workshop
BiATA Conference, August 2017
Instructor
- “Molecular sequence analysis” course
St. Petersburg Academic University, 2014 – 2015
Lecturer
- “Java programming language” course
St. Petersburg Academic University, 2012 – 2013
Teaching assistant

RELEVANT SKILLS

- C++
- Python
- Snakemake workflows
- NGS genomics stack
- Java
- R
- SQL
- \LaTeX , bash, git, vim, Snakemake

LANGUAGES

- English: fluent
- Russian: native