

## Sergey Nurk

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CONTACT INFORMATION	Email: <a href="mailto:sergeynurk@gmail.com">sergeynurk@gmail.com</a> Homepage: <a href="http://cab.spbu.ru/employees/sergey-nurk/">http://cab.spbu.ru/employees/sergey-nurk/</a> Phone: +1-416-824-24-12
BIOGRAPHICAL DATA	Date of birth: 8th March 1989 Citizenship: Russia Marital status: Married
EDUCATION	<a href="#">Saint-Petersburg State University</a> Ph.D candidate <ul style="list-style-type: none"><li>• Expected degree: Ph.D. in Bioinformatics</li><li>• Advisor: <a href="#">Pavel A. Pevzner</a></li><li>• Area of study: <i>de novo</i> microbial (single-cell) and metagenomic assembly</li><li>• Expected defense date: Fall 2018</li></ul> <a href="#">St. Petersburg State University, Mathematics and Mechanics Faculty, Software Engineering Department</a> M.Sc. in Computer Science, 2006–2011 <ul style="list-style-type: none"><li>• Thesis: “Development of de Bruijn graph processing algorithms for genome assembly problem” (Advisor: <a href="#">Nikolay I. Vyahhi</a>)</li><li>• Diploma cum laude</li></ul> Lyceum of Mathematics and Physics #239, GPA 5.0 (2002–2006)
ADDITIONAL EDUCATION	<a href="#">Academy of Modern Software Engineering</a> Student 2008–2010
EMPLOYMENT	<ul style="list-style-type: none"><li>• <a href="#">Center for Algorithmic Biotechnology</a> St. Petersburg State University Junior research fellow January 2015–present</li><li>• <a href="#">Algorithmic Biology Laboratory</a> St. Petersburg Academic University Junior research fellow February 2011–January 2015</li><li>• <a href="#">Yandex company</a> Search engine company in Russia, developing various Internet-based services Structured Web Mining Department Software Engineer (Java) 2009–2011</li><li>• <a href="#">Digital SPomics</a> Co-founder January 2014–present</li></ul>
AREAS OF INTEREST	<ul style="list-style-type: none"><li>• genome assembly</li><li>• metagenomics</li></ul>

- comparative genomics
- software design
- data analysis

## RESEARCH PAPERS

1. **Sergey Nurk**, Yury Gorshkov and Pavel A. Pevzner  
**“Reconstructing individual genomes from multiple metagenomic samples with MTS pipeline.”**  
 Manuscript in preparation
2. **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
3. 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
4. Gabriela I Guzman, Jose Utrilla, **Sergey Nurk**, Elizabeth Brunk, Jonathan M Monk, Ali Ebrahim, Bernhard Palsson, Adam M. Feist  
**“Model-driven discovery of underground metabolic functions in Escherichia coli”**.  
 Proceedings of the National Academy of Sciences, 112(3), 2015
5. 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
6. **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. Clingenpeel, Tanja Woyke, Jeffrey S. Mclean, Roger Lasken, Glenn Tesler, Max A. Alekseyev, and Pavel A. Pevzner  
**“Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products”**.  
 Journal of Computational Biology 20(10), 2013
7. 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
8. 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

9. **Sergey Nurk**

**“An  $O(2^{0.4058m})$  Upper Bound for *Circuit SAT*”.**

PDMI preprint 10/2009, 2009

ATTENDED

WORKSHOPS AND  
STUDENT SCHOOLS

- Systems Biology Workshop.  
Saint-Petersburg, Russia, 2015
- Systems Biology Workshop.  
Saint-Petersburg, Russia, 2014
- Microsoft School on Algorithms for Massive Data (ALMADA).  
Moscow, Russia, 2013
- Russian Summer School in Information Retrieval (RuSSIR).  
Voronezh, Russia, 2010
- Microsoft Data Structures and Algorithms School (MIDAS).  
Saint-Petersburg, Russia, 2010
- NoNA Summer School on Complexity Theory.  
Saint-Petersburg, Russia, 2009
- Joint Advanced Student School (JASS).  
Saint-Petersburg, Russia, 2009.  
Topic: Propositional Proof Complexity

TALKS

- **Talk “metaSPAdes: a New Versatile Metagenomic Assembler”**  
20<sup>th</sup> Conference on Research in Computational Molecular Biology (RECOMB-2016).  
Los Angeles, USA, 2016.
- Talk “Probabilistic models in molecular sequence analysis”  
Bioinformatics summer school  
St. Petersburg, Russia, 2014
- Talk “De Bruijn graphs and genome assembly algorithms”  
Bioinformatics summer school  
Moscow, Russia, 2013
- **Talk “Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads”**  
17<sup>th</sup> Conference on Research in Computational Molecular Biology (RECOMB-2013).  
Beijing, China, 2013.
- Talk about a web-harvesting tool developed by my department at Yandex  
Yet Another Conference (YaC’2010)  
Moscow, Russia, 2010
- Talk “Upper bound for Circuit SAT”  
Estonian Theory Days 2009  
Palmse, Estonia, 2009
- Talk “Lower bounds for  $k - DNF$  resolution on random  $3 - CNFs$ ”  
Joint Advanced Student School (JASS’2009)  
St. Petersburg, Russia, 2009

TEACHING  
EXPERIENCE

“BIN420: Bioinformatics for functional metagenomics” course  
Instructor on (metagenomic) assembly  
NMBU, s, Norway, September 2017

“Methods for genome-resolved metagenomics” workshop  
Instructor  
BiATA Conference, August 2017

“Molecular sequence analysis” course  
Lecturer  
St. Petersburg Academic University, Spring 2015

“Comparative genomics” student seminar  
Supervisor  
St. Petersburg Academic University, Spring 2014

“Molecular sequence analysis” course  
Lecturer  
St. Petersburg Academic University, Spring 2014

“Java programming language” course  
Teaching assistant  
St. Petersburg Academic University, 2012 – 2013

#### RELEVANT SKILLS

- C++
- Java
- Python
- R
- SQL
- NGS genomics stack
- $\text{\LaTeX}$ , bash, git, vim

#### LANGUAGES

- English: fluent
- Russian: native