

Sergey Nurk

CONTACT INFORMATION	Email: sergeynurk@gmail.com Homepage: http://cab.spbu.ru/employees/sergey-nurk/ Phone: +1-416-824-24-12
BIOGRAPHICAL DATA	Date of birth: 8th March 1989 Citizenship: Russia Marital status: Married
EDUCATION	Saint-Petersburg State University Ph.D candidate <ul style="list-style-type: none">• Expected degree: PhD in Bioinformatics• Thesis: “Assembling genomes of non-cultivable microorganisms from high-throughput sequencing data”• Advisor: Pavel A. Pevzner• Area of study: <i>de novo</i> microbial (single-cell) and metagenomic assembly• Expected defense date: May 2019 St. Petersburg State University, Mathematics and Mechanics Faculty, Software Engineering Department M.Sc. in Computer Science, 2006–2011 <ul style="list-style-type: none">• Thesis: “Development of de Bruijn graph processing algorithms for genome assembly problem” (Advisor: Nikolay I. Vyahhi)• Diploma cum laude Lyceum of Mathematics and Physics #239, GPA 5.0 (2002–2006)
ADDITIONAL EDUCATION	Academy of Modern Software Engineering Student 2008–2010
EMPLOYMENT	<ul style="list-style-type: none">• Center for Algorithmic Biotechnology St. Petersburg State University Junior research fellow January 2015–November 2018• Algorithmic Biology Laboratory St. Petersburg Academic University Junior research fellow February 2011–January 2015• Yandex company Search engine company in Russia, developing various Internet-based services Structured Web Mining Department Software Engineer (Java) 2009–2011• Digital SPomics Co-founder January 2014–present
AREAS OF INTEREST	

- genome assembly
- metagenomics
- 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

- CAMI+M3 Workshop.
College Park, USA. May 2017
- 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 “Past, present and future of metaSPAdes metagenomic assembler”
CAMI+M3 Workshop.
College Park, USA, 2017
- **Talk “metaSPAdes: a New Versatile Metagenomic Assembler”**
20th 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”**
17th 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
- L^AT_EX, bash, git, vim

LANGUAGES

- English: fluent
- Russian: native