

# Sergey Nurk

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## CONTACT INFORMATION

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## EMPLOYMENT

- [Center for Algorithmic Biotechnology](#)  
St. Petersburg State University  
Junior research fellow  
January 2015–present
- [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

## BIOGRAPHICAL DATA

Date of birth: 8th March 1989  
Citizenship: Russia  
Marital status: Married

## EDUCATION

[St. Petersburg State University, Mathematics and Mechanics Faculty, Software Engineering Department](#)  
M.Sc. in Computer Science, 2006–2011

- 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

## AREAS OF INTEREST

- genome assembly
- metagenomics
- comparative genomics
- software design
- online courses on statistical learning and data analysis
- board games

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. Nealon, 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

##### STUDENT SCHOOLS AND WORKSHOPS

- 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

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

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

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

Java programming language course at St. Petersburg Academic University  
Teaching assistant  
2012 – 2013

#### RELEVANT SKILLS

- C++
- Java
- Python
- R
- SQL
- NGS genomics stack
- L<sup>A</sup>T<sub>E</sub>X, bash, git, vim

#### LANGUAGES

- English: fluent
- Russian: native