

## Sergey Nurk

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CONTACT INFORMATION	Email: <a href="mailto:sergeynurk@gmail.com">sergeynurk@gmail.com</a> Homepage: <a href="http://bioinf.spbau.ru/members/sergey-nurk">http://bioinf.spbau.ru/members/sergey-nurk</a> Phone: +7-950-043-44-06
PRESENT POSITION	<ul style="list-style-type: none"><li>• <a href="#">Algorithmic Biology Laboratory</a> <a href="#">St. Petersburg Academic University</a> Junior research fellow February 2011–present</li><li>• <a href="#">Digital SPomics</a> Co-founder January 2014–present</li></ul>
BIOGRAPHICAL DATA	Date of birth: 8th March 1989 Citizenship: Russia Marital status: Single
EDUCATION	<a href="#">Saint-Petersburg Academic University</a> Ph.D. student since 2011. <ul style="list-style-type: none"><li>• Expected degree: Ph.D. in Computational Biology</li><li>• Advisor: <a href="#">Pavel A. Pevzner</a></li><li>• Area of study: computational genomics</li><li>• Expected defense date: Fall 2015</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
AREAS OF INTEREST	<ul style="list-style-type: none"><li>• bioinformatics</li><li>• computational genomics</li><li>• algorithms design</li><li>• software design</li></ul>
RESEARCH PAPERS	<ul style="list-style-type: none"><li>• <b>Sergey Nurk</b>, Pavel A. Pevzner “SPArcle: Identifying Microbial Genome Variations with Colored de Bruijn Graphs”. Manuscript in preparation</li></ul>

- 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”.  
Accepted to PNAS
- Andrey D. Prjibelski, Irina Vasilinetc, Anton Bankevich, Alexey Gurevich, Tatiana Krivosheeva, **Sergey Nurk**, Son Pham, Anton Korobeynikov, Alla Lapidus and Pavel A. Pevzner  
“ExSPAnde: 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. 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
- **Sergey Nurk\***, Anton Bankevich\* (\* equal contribution), Dmitry Antipov, Alexey A. Gurevich, Anton Korobeynikov, Alla Lapidus, Andrey Prjibelski, Alexey Pyshkin, Alexander Sirotkin, Yakov Sirotkin, Ramunas Stepanauskas, Jeffrey McLean, Roger Lasken, Scott R. Clingenpeel, Tanja Woyke, Glenn Tesler, Max A. Alekseyev, and Pavel A. Pevzner  
“Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads”.  
Proceedings of the 17th Annual International Conference on Research in Computational Molecular Biology, Lecture Notes in Computer Science 7821 (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

ATTENDED  
CONFERENCES  
AND STUDENT  
SCHOOLS

- Systems Biology Workshop.  
Saint-Petersburg, Russia, 2014
- Microsoft School on Algorithms for Massive Data (ALMADA).  
Moscow, Russia, 2013

- 17<sup>th</sup> Conference on Research in Computational Molecular Biology.  
Beijing, China, 2013.
- 16<sup>th</sup> Conference on Research in Computational Molecular Biology.  
Barcelona, Spain, 2012.
- 10<sup>th</sup> European Conference on Computational Biology.  
Vienna, Austria, 2011.
- 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 AND POSTERS

- Poster “New Frontiers of Genome Assembly with SPAdes 3.1”  
ISMB 2014, joint work with Irina Vasilinetc, Andrey Prjibelski, Anton Bankevich, Alexey Gurevich, Yana Safonova, Dmitry Antipov, Anton Korobeynikov, Alla Lapidus and Pavel Pevzner  
Boston, USA, 2014.
- Poster “New Frontiers of Genome Assembly with SPAdes 3.0”  
JGI User Meeting, joint work with Alla Lapidus, Dmitry Antipov, Anton Bankevich, Alexey Gurevich, Anton Korobeynikov, Andrey D. Prjibelski, Yana Safonova, Irina Vasilinetc and Pavel Pevzner  
Walnut Creek, USA, 2014.
- Talk “Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads”  
17<sup>th</sup> Conference on Research in Computational Molecular Biology.  
Beijing, China, 2013.
- Poster “Expandable de novo genome assembler for short-read sequence data.”  
ISMB/ECCB, joint work with Nikolay Vyahhi, Anton Bankevich, Max Alekseyev and Pavel Pevzner  
Vienna, Austria, 2011
- 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

#### INDUSTRIAL EXPERIENCE

- [Yandex company](#) (Yandex is the largest search engine in Russia and develops a number of Internet-based services and products)  
Structured Web Mining Department
- Software Engineer (Java)  
2009–2011
  - Software Engineering intern  
Summer 2009

TEACHING  
EXPERIENCE

“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

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

LANGUAGES

- Russian: native
- English: fluent