Sergey Nurk

CONTACT INFORMATION	Email: sergeynurk@gmail.com Homepage: http://cab.spbu.ru/employees/sergey-nurk/ Phone: +7-950-043-44-06

BIOGRAPHICAL DATA

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

EDUCATION

St. Petersburg State University
Ph.D in Mathematical biology and Bioinformatics
- Conferred: May 2019
- Thesis: "Assembling genomes of non-cultivable microorganisms from high-throughput sequencing data"
- Advisor: Pavel A. Pevzner
- Area of study: genomic and metagenomic assembly

St. Petersburg State University, Faculty of Mathematics and Mechanics
Specialist degree (equiv. of MSc) in Computer Science and Software Engineering
- Period of study: 2006 – 2011
- Thesis: "Development of de Bruijn graph processing algorithms for genome assembly"
- Advisor: Nikolay I. Vyahhi
- Diploma cum laude

Lyceum of Mathematics and Physics #239
- Period of study: 2002 – 2006
- GPA 5.0

ADDITIONAL EDUCATION

Academy of Modern Software Engineering
- Period of study: 2008 – 2010

EMPLOYMENT

Center for Algorithmic Biotechnology, St. Petersburg State University
- 2015 – 2019
- Junior Research Fellow
- Development of computational methods for genome-resolved metagenomic analysis, in particular metagenomic assembly
- St. Petersburg, Russia

Algorithmic Biology Laboratory, St. Petersburg Academic University
- 2011 – 2015
- Junior Research Fellow
- Development of methods for (single-cell) microbial genome assembly and comparative genomics
- St. Petersburg, Russia

Yandex search engine company
- 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

1. Tatiana Dvorkina, Dmitry Antipov, Anton Korobeynikov and **Sergey Nurk**
   "SPAligner: alignment of long diverged molecular sequences to assembly graphs".
   Manuscript in preparation

2. **Sergey Nurk**, Yury Gorshkov and Pavel A. Pevzner
   "Reconstructing individual genomes from multiple metagenomic samples with MTS pipeline".
   Manuscript in preparation

3. 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 Crohns disease patient".
   Frontiers in Microbiology 9, 2559, 2018

4. **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

5. 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

6. 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

7. 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

8. **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

9. Jeffrey S. McLean, Mary-Jane Lombardo, Michael G. Ziegler, Mark Novotny, Joyclyn Yee-Greenbaum, Jonathan H. Badger, Glenn Tesler, **Sergey Nurk**, Valery

Lesin, Daniel Brami, 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

10. 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

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

ATTENDED
WORKSHOPS AND   • CAMI+M3 Workshop.
STUDENT SCHOOLS   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. Petersbrug, 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 $3 - CNF$s"
Joint Advanced Student School (JASS'2009)
St. Petersburg, Russia, 2009

TEACHING
EXPERIENCE

"BIN420: Bioinformatics for functional metagenomics" course
Instructor on (metagenomic) assembly
NMBU, As, 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
- LaTeX, bash, git, vim

LANGUAGES

- English: fluent
- Russian: native