

# Sergey Aganezov

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## Research Interest

My current research interest focuses on developing new and utilizing existing algorithmic solutions for combinatorial problems in the area of computational biology. I am particularly interested in developing efficient algorithms, that focus on graph-theoretical problem formulations with respect multi-genome comparison, genome assembly, and cancer genome evolution. I have a strong interest in investigating the problem of genome breakages and their relations to both species evolution as well as cancer development.

## Professional Experience

- 07/2018 – present **Postdoctoral Research Associate**, Department of Computer Science, Johns Hopkins University, Baltimore, MD, USA  
**Advisor:** Prof. Michael Schatz.  
Analysis of structural variants and karyotype reconstruction in cancer genomes using various sequencing technologies. Algorithms design, complexity analysis, and software development.
- 07/2017 – 07/2018 **Postdoctoral Research Associate**, Department of Computer Science, Princeton University, Princeton, NJ, USA  
**Advisor:** Prof. Benjamin J. Raphael.  
Mathematical modeling of cancer evolution. Algorithms design, complexity analysis, and software development.

## Education

- 08/2013 – 05/2017 **Ph.D**, Department of Mathematics, *The George Washington University*, Washington, DC, USA  
Thesis: *Comparative genomics meets genome assembly: from ancestral reconstruction to scaffolding*  
**Advisor:** Prof. Max A. Alekseyev.
- 09/2013 – 06/2015 **M.S.(*summa cum laude*) in Applied Mathematics and Computer Science**, *ITMO University*, St. Petersburg, Russia, **GPA: 4.0 / 4.0**  
**Thesis:** *Multi-genome scaffolding based on the analysis of gene orders and genomic repeats*  
**Advisor:** Prof. Max A. Alekseyev.
- 09/2011 – 05/2013 **Advanced Training Degree**, *St. Petersburg Academic University*, St. Petersburg, Russia.  
This training constituted 288 academic hours and involved professional training in applied computer science.
- 09/2009 – 06/2013 **B.S.(*summa cum laude*) in Applied Mathematics and Computer Science**, *ITMO University*, St. Petersburg, Russia, **GPA: 4.0 / 4.0**  
**Thesis:** *On pairwise distance and median score of three genomes under DCJ*  
**Advisor:** Dr. Max A. Alekseyev.

## Additional Training

- 5/2016 **System Biology Workshop**, *St. Petersburg, Russia*.  
Introduction to sequencing. RNA-seq & Gene expression analysis. Medical and Population Genetics. Transcriptional and epigenetic regulation. Metabolic regulation and introduction into metabolomics.
- 8/2015 **XSEDE HPC Monthly Workshop, Big Data**, *The George Washington University, USA*.  
Workshop with a “hands-on” focus on topics such as Hadoop and Spark.

- 7/2015 **J. T. Schwartz International School for Scientific Research**, *Lipari, Italy*.  
Summer school focused on Computational Dynamic Analysis of Biological Processes with topics such as Disease Dynamics, Drug Resistance, Immune System Analysis, and Emerging Mutations.
- 5/2015 **Applied Combinatorics Summer School**, *University of Saskatchewan, Canada*.  
Included exploration sessions and open problems on different applications of combinatorics in physics, chemistry and biology.
- 5/2014 **NCBI Discovery Workshops**, *NIH, USA*.  
Workshop with a focus on a more efficient usage of the NCBI Web resources, comprised of multiple hands-on sessions.
- 10/2013 **Ensembl gene annotation workshop**, *Cold Spring Harbor Laboratory, USA*.  
Sessions on how to create your own core database, including the loading of a genome assembly into a database and the running of simple analyses using the Ensembl genebuild system.

## Experience

### Research

- 08/2013 – **Graduate Research Assistant**, Computational Biology Institute, The George Washington University, Ashburn, VA, USA.  
05/2017  
Conducting research in comparative genomics and genome assembly. I also work on algorithm development, optimization, and complexity analysis.
- 01/2015 – **Assistant Editor (Problems Datasets)**, Computational Biology Institute, The George Washington University, Ashburn, VA, USA.  
01/2016  
Preparing and revising problems, datasets and their presentation for many classical algorithms in the “Data Structures and Algorithms” online course on Coursera, that was launched by the Computer Science Department of the University of California, San Diego.
- 01/2014 – **M.S. Student Project Curator**, Computational Biology Institute, The George Washington University, Ashburn, VA, USA.  
05/2014  
Leading a team project with Nadiya Sitdykova, an M.S. bioinformatics student, on the genome scaffolding problem. Our work resulted in a paper accepted for publication in *Computational Biology and Chemistry* journal.

### Teaching

- 07/2017 – **Founder and President of JetBrains Princeton**, Princeton University, Princeton, NJ, USA.  
07/2018  
Organization, design and curation of science/programming workshops and hackathons for undergraduate and graduate students. I also give regular talks on latest developments in various programming languages with respect to scientific and educational activities.
- 01/2017 – **Course Instructor**, *Algorithms in Bioinformatics*, The George Washington University, Washington, DC, USA.  
05/2017  
Teaching a recitation course for graduate students.
- 01/2016 – **Course Instructor**, *Python and Algorithms in Bioinformatics*, The George Washington University, Washington, DC, USA.  
05/2016  
Teaching a recitation course for graduate students.
- 09/2015 – **Founder and President of JetBrains GWU**, The George Washington University, Washington, DC, USA.  
05/2017  
Organization, design and curation of science/programming workshops and hackathons for undergraduate and graduate students. I also give regular talks on latest developments in various programming languages with respect to scientific and educational activities.

## Honors and Awards

- 01/2016 – **Science roadmap advancement grant**, *ITMO University/Russian Science Foundation*, St. Petersburg, Russia.  
12/2016

- 09/2015 – **VSTC Research Scholarship**, *The George Washington University*, Washington, DC, USA.  
05/2016
- 03/2015 **Marvin Green Prize**, Department of Mathematics, *The George Washington University*, Washington, DC, USA.  
For significant use of computing in research work.
- 01/2015 **Graduate Travel Grant**, Office of Graduate Student Assistantships and Fellowships, *The George Washington University*, Washington, DC, USA.
- 09/2012 – **Academic Fellowship for Young Researchers**, *Computer Science Center*, St. Petersburg,  
05/2013 Russia.
- 09/2009 – **Academic Fellowship for Distinguished Students**, *ITMO University*, St. Petersburg,  
05/2013 Russia.

## Publications

### Journals and peer-refereed conference proceedings

- **S. Aganezov** and M. A. Alekseyev. Orientation of ordered scaffolds. *Proceedings of the 15th Annual RECOMB Satellite Workshop on Comparative Genomics (RECOMB-CG 2017)*, *Lecture Notes in Computer Science* 10562 (2017), 179-196.
- **S. Aganezov** and M. A. Alekseyev. CAMSA: A Tool for Comparative Analysis and Merging of Scaffold Assemblies. *Selected articles from the 6th IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCBAS)*, *BMC Bioinformatics* 18(Suppl 15), 496 (2017).
- **S. Aganezov** and M. A. Alekseyev. Multi-genome Scaffolds Co-Assembly Based on the Analysis of Non-uniform Gene Orders and Genomic Repeats. *Proceedings of the 12th International Symposium on Bioinformatics Research and Applications (ISBRA 2016)*, *Lecture Notes in Computer Science* 9683 (2016), 237-249, doi:10.1007/978-3-319-38782-6.
- Y. Liu, S. Hsu, **S. Aganezov**, M. A. Alekseyev et al. Transcriptome Sequencing Based Annotation and Homologous Evidence Based Scaffolding of Anguilla Japonica Draft Genome. *Proceedings of the 14th Asia Pacific Bioinformatics Conference (APBC 2016)*, *BMC Genomics* 17(Suppl 1) (2016), doi:10.1186/s12864-015-2306-6.
- P. Avdeev, S. Jiang, **S. Aganezov**, F. Hu, and M. A. Alekseyev. Reconstruction of ancestral genomes in presence of gene gain and loss. *Journal of Computational Biology* 23:3 (2015), doi:10.1089/cmb.2015.01602016.
- **S. Aganezov** N. Sitdykova, AGC Consortium, M. A. Alekseyev. Scaffold assembly based on genome rearrangement analysis. *Proceedings of the 13th Asia-Pacific Bioinformatics Conference (APBC 2015)*, *Computational Biology and Chemistry* (2015), dx.doi.org/10.1016/j.compbiolchem.2015.02.005.
- D. E. Neafsey, R. M. Waterhouse, M. R. Abai, **S. Aganezov**, M. A. Alekseyev et al. Highly evolvable malaria vectors: the genomes of 16 Anopheles mosquitoes. *Science* 347(6217) (2015), doi:10.1126/science.1258522.
- **S. Aganezov** and M. A. Alekseyev. On pairwise distances and median score of three genomes under DCJ. *Proceedings of the 10th Annual RECOMB Satellite Workshop on Comparative Genomics (RECOMB-CG 2012)*, *BMC Bioinformatics* 13(Suppl 19) (2012) S1, doi:10.1186/1471-2105-13-S19-S1.

### In preparation

- R. M. Waterhouse, **S. Aganezov**, et al. Leveraging evolutionary relationships to improve Anopheles genome assemblies. (2018).
- **S. Aganezov**, and Max A. Alekseyev. FPT algorithm for the problem of orientation of ordered scaffolds. (2018).
- **S. Aganezov**, and Benjamin J. Raphael. Reconstruction of Allele and Clone specific Cancer Karyotypes. (2018).

## ■ Presentations

### Talks

- **Reconstruction of clone- and haplotype-specific cancer genomes karyotypes from tumor mixtures**, *Advances in computational biology seminar*, ITMO university, St. Petersburg, Russia, June 15, 2018.
- **On problem of orientating ordered scaffolds**, *7th IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Orlando, Florida, USA, October 20, 2017.
- **Orientation of ordered scaffolds**, *The 15th Annual RECOMB Satellite Workshop on Comparative Genomics (RECOMB-CG)*, Barcelona, Spain, October 6, 2017.
- **Comparative genomics meets genome assembly: from ancestral reconstruction to scaffolding**, *Bioinformatics Institute*, St. Petersburg, Russia, June 15, 2017.
- **Comparative genomics meets genome assembly: from ancestral reconstruction to scaffolding**, *University of California*, Los Angeles, CA, USA, April 14, 2017.
- **Comparative genomics meets genome assembly: from ancestral reconstruction to scaffolding**, *University of California*, Santa Cruz, CA, USA, April 12, 2017.
- **Comparative genomics meets genome assembly: from ancestral reconstruction to scaffolding**, *University of California*, Davis, CA, USA, April 11, 2017.
- **Comparative genomics meets genome assembly: from ancestral reconstruction to scaffolding**, *Johns Hopkins University*, Baltimore, MD, USA, April 3, 2017.
- **CAMSA: a Tool for Comparative Analysis and Merging of Scaffold Assemblies**, *University of Maryland*, College Park, MD, USA, March 13, 2017.
- **Comparative genomics meets genome assembly: from ancestral reconstruction to scaffolding**, *Princeton University*, Princeton, NJ, USA, March 9, 2017.
- **CAMSA: a Tool for Comparative Analysis and Merging of Scaffold Assemblies**, *The 14th Annual Rocky Mountain Bioinformatics Conference (ROCKY)*, Aspen, CA, USA, December 8-10, 2016.
- **CAMSA: a Tool for Comparative Analysis and Merging of Scaffold Assemblies**, *6th IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Atlanta, GA, USA, October 13-15, 2016.
- **Comparative Genomics Meets Topology: a Novel View on Genome Median and Halving Problems**, *The 14th Annual RECOMB Satellite Workshop on Comparative Genomics (RECOMB-CG)*, Montreal, QB, Canada, October 11-14, 2016.
- **Scaffold Assembly Based on the Analysis of Gene Orders and Genomic Repeats**, *Intelligent Systems for Molecular Biology (ISMB)*, Orlando, FL, USA, July 9-12, 2016.
- **CAMSA: a Tool for Comparative Analysis and Merging of Scaffold Assemblies**, *High Throughput Sequencing Algorithms and Applications (HitSeq)*, Orlando, FL, USA, July 8-9, 2016.
- **Scaffold Assembly Based on the Analysis of Gene Orders and Genomic Repeats**, *12th International Symposium on Bioinformatics Research and Applications (ISBRA)*, Minsk, Belarus, June 5-8, 2016.
- **Scaffold Assembly Based on the Analysis of Gene Orders and Genomic Repeats**, *The 13th Annual Rocky Mountain Bioinformatics Conference (ROCKY)*, Aspen, CO, USA, December 10-12, 2015.
- **Scaffold Assembly Based on the Analysis of Gene Orders and Genomic Repeats**, *5th Workshop on Computational Advances for Next Generation Sequencing (CANGS)*, Miami, FL, USA, October 15-17, 2015.
- **Scaffold assembly based on genome rearrangement analysis**, *Moscow Conference on Computational Molecular Biology (MCCMB)*, Moscow, Russia, July 16-19, 2015.
- **Scaffold assembly based on genome rearrangement analysis**, *Knots In Washington XL*, Georgetown University, Washington, DC, USA, March 9-11, 2015.

- **Scaffold assembly based on genome rearrangement analysis**, *The 13th Asia Pacific Bioinformatics Conference*, Microelectronics and Information Systems Research Center, Kuang-Fu Campus, Chiao Tung University, HsinChu, Taiwan, January 21-23, 2015.
- **On pairwise distances and median score of three genomes under DCJ**, *Computer Science Club, POMI RAS*, St. Petersburg, Russia, November 5, 2012.
- **On pairwise distances and median score of three genomes under DCJ**, *The 10th Annual RECOMB Satellite Workshop on Comparative Genomics*, Niteroi, Brazil, October 17 – 19, 2012.

#### Posters

- **Reconstruction of clone- and haplotype-specific cancer genomes karyotypes from tumor mixtures**, *The CSHL bianual meeting on Biological Data Science*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA, November 7 – 10, 2018.
- **CAMSA: a Tool for Comparative Analysis and Merging of Scaffold Assemblies**, *The 14th Annual RECOMB Satellite Workshop on Comparative Genomics*, Montreal, QB, Canada, October 11-14, 2016.
- **CAMSA: a Tool for Comparative Analysis and Merging of Scaffold Assemblies**, *Intelligent Systems for Molecular Biology (ISMB)*, Orlando, FL, USA, July 9-12, 2016.
- **Varying resolution synteny blocks in large scale phylogenetics**, *Research Days*, The George Washington University, Washington, DC, USA. April 1 – 2, 2014.
- **Varying resolution synteny blocks construction in large scale phylogenetics**, *The Advancing Computational Biology @ Howard University Symposium*, Howard University, Washington, DC, USA, March 26, 2014.
- **Varying resolution synteny blocks construction in large scale phylogenetics**, *The 9th International Conference on Bioinformatics*, Georgia Tech, Atlanta, GA, USA, April 2 – 4, 2014.
- **Varying resolution synteny blocks construction**, *The CSHL Annual Meeting on Genome Informatics*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA, October 30 – November 3, 2013.

## Professional Service

#### Reviewer for conferences:

**International Computer Science Symposium in Russia (CSR)**, 2018.

**Conference on Research in Computational Molecular Biology (RECOMB)**, 2014/2017/2018.

**Asia Pacific Bioinformatics Conference (APBC)**, 2014/2015/2016/2017/2018.

**RECOMB Satellite Workshop on Comparative Genomics (RECOMB-CG)**, 2015/2016/2017.

**Symposium on Combinatorial Pattern Matching (CPM)**, 2014.

#### Reviewer for journals:

**Frontiers :: Bioinformatics and Computational Biology** [2018] **Nucleic Acids Research** [2018], **Bioinformatics** [2015/2017/2018], **BMC Bioinformatics** [2014/2016/2017], **BMC Genomics** [2017], **GigaScience** [2015/2017], **JBCB** [2018] .

## Developed Software

**CAMSA**, <https://cblab.org/camsa>.

A cross platform tool for comparative analysis and merging of scaffold assemblies.

**Breakpoint Graph**, <https://github.com/aganezov/bg>.

A Python (2/3) library for effective usage of Breakpoint Graph data structure.

**GOS-ASM**, <https://github.com/aganezov/gos-asm>.

A cross platform multi-genome scaffolder based on the analysis of gene orders and genomic repeats.

**MGRA (web service)**, <http://mgra.cblab.org>.

A MGRA software web-based service.

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## Computer skills

**Programming languages:** Python 2.x / 3.x (+ Django / Flask), Java, Kotlin, Git, bash, HTML, CSS, JavaScript, C, C++.

**Document systems:** LaTeX / Beamer, MS Office, iWork.

**Operational systems:** Windows, Mac OS, Linux / Unix.