

Andrey O. Kislyuk

CONTACT INFORMATION	DNAnexus, Inc. 1975 W El Camino Real, Suite 101 Mountain View, CA 94040 U.S.	Tel: +1 (925) 683-0172 kislyuk@gmail.com http://topaz.gatech.edu/~kislyuk
OBJECTIVE	Director, bioinformatics or computational biology.	
OVERVIEW	Technical leader in software engineering and genomics. Bioinformatics specialist with expertise in genome sequence analysis, machine learning, high performance computing, scalable distributed systems architecture, API design, Linux systems, development operations, and cloud security.	
SPECIALTIES AND AREAS OF EXPERTISE	NGS data analysis, annotation, variant calling and interpretation, distributed systems and data stores, Amazon Web Services EC2, S3, GCE, high availability, release engineering, configuration management, IT automation, probabilistic graphical models, sequencing technology R&D, metagenomics, DNA methylation and epigenomics, single molecule sequencing.	
EDUCATION	Georgia Institute of Technology , Atlanta, Georgia Ph.D. 2010, Bioinformatics	Advisor: Joshua S. Weitz
	University of California, Berkeley B.A. 2004, Computer Science, Mathematics, and Statistics	Advisor: Inna Dubchak
EMPLOYMENT	DNAnexus, Inc. , 2011 – Manager, developer relations and technical strategy: Architecture and development of AWS-based bioinformatics solutions. Supervisor: Andreas Sundquist, CEO	
	Pacific Biosciences of California , 2010 – 2011 Scientist, bioinformatics: Research, development, and support of various bioinformatics projects. Supervisor: Stephen Turner, CTO	
PROJECTS	Technical lead on the full stack of the DNAnexus Platform (2011 –).	
	Published two popular Python modules (argcomplete and ensure) (2012 –).	
	Researched and developed a DNA modification detection pipeline. (Pacific Biosciences, 2010 –; 2 publications.)	
	Researched, developed, and evaluated an unsupervised metagenomic binner application. (Georgia Tech, 2008 – 2009; 1 publication.)	
	Researched, developed, and evaluated a prokaryotic frameshift finder application for genome sequencing quality control. (Georgia Tech/DOE JGI, 2007 – 2008; 1 publication.)	
	Developed and integrated a set of algorithms for gene finding, genome assembly, annotation and error correction in the Georgia Tech Neisseria Base. Supported deployment of a pipeline containing these components. (Georgia Tech/CDC, 2008 – 2009; 3 publications.)	
	Implemented components of the Berkeley Genome Pipeline. (LBL/UC Berkeley, 2004 – 2005; 1 publication.)	

Programming languages: Python, Javascript/Coffeescript, C, C++, Java, Perl, Ruby, R, MATLAB, Bash.

Tools and platforms used: Extensive knowledge of bioinformatics tools, algorithms, and frameworks for local and whole-genome sequence alignment, assembly, base calling, genome finishing, variant calling, repeat masking, genome browsing, genome data mining, profile alignment, secondary structure prediction, cluster and cloud computing.

Applications: Diverse aspects of Linux infrastructure, instrumentation and provisioning toolkits (Gentoo Linux developer), bioinformatics tools (repository maintainer), DBMS (PostgreSQL, MySQL), development tools (Eclipse IDE, Visual Studio), system administration and server management tools, Apache web server; mathematics, science and engineering suites (R, ggplot, matplotlib, NumPy, BioPython); authoring and content tools (LATEX, BibTex, MediaWiki).

Hardware: Scientific and cluster computing, wide HPC deployments, datacenters, network administration and infrastructure development.

PUBLICATIONS

D. A. Rasko, D. R. Webster, J. W. Sahl, A. Bashir, N. Boisen, F. Scheutz, E. E. Paxinos, R. Sebra, C.-S. Chin, D. Iliopoulos, A. Klammer, P. Peluso, L. Lee, **A.O. Kislyuk**, J. Bullard, A. Kasarskis, S. Wang, J. Eid, D. Rank, J. C. Redman, S. R. Steyert, J. Frimodt-Møller, C. Struve, A. M. Petersen, K. A. Krogfelt, J. P. Nataro, E. E. Schadt, and M. K. Waldor, "Origins of the E. coli Strain Causing an Outbreak of Hemolytic-Uremic Syndrome in Germany." *NEJM*, doi:10.1056/NEJMoa1106920, 2011.

L. S. Katz, J. C. Humphrey, A. B. Conley, V. Nelakuditi, **A.O. Kislyuk**, S. Agrawal, P. Jayaraman, B. H. Harcourt, M. A. Olsen-Rasmussen, M. Frace, N. V. Sharma, L. W. Mayer, and I. K. Jordan, "Neisseria Base: a comparative genomics database for Neisseria meningitidis." *Database*, doi:10.1093/database/bar035, 2011.

A.O. Kislyuk, B. Haegeman, N. H. Bergman, and J. S. Weitz, "Genomic fluidity: an integrative view of gene diversity within microbial populations." *BMC Genomics*, doi:10.1186/1471-2164-12-32, 2011.

A.O. Kislyuk, L. S. Katz, S. Agrawal, M. S. Hagen, A. B. Conley, P. Jayaraman, V. Nelakuditi, J. C. Humphrey, S. A. Sammons, D. Govil, R. D. Mair, K. M. Tatti, M. L. Tondella, B. H. Harcourt, L. W. Mayer, and I. K. Jordan, "A computational genomics pipeline for prokaryotic sequencing projects," *Bioinformatics*, doi:10.1093/bioinformatics/btq284, 2010.

A.O. Kislyuk, A. Lomsadze, A.L. Lapidus, and M. Borodovsky. "Frameshift detection in prokaryotic genomic sequences." *International Journal of Bioinformatics Research and Applications*, vol. 5, no. 4, pp. 458-477, 2009.

A.O. Kislyuk, S. Bhatnagar, J. Dushoff, and J.S. Weitz. "Unsupervised Statistical Clustering of Environmental Shotgun Sequences." *BMC Bioinformatics*, doi:10.1186/1471-2105-10-316, 2009.

L.S. Katz, C. Bolen, B. Harcourt, S. Schmink, X. Wang, **A.O. Kislyuk**, R. Taylor, L. Mayer, and I.K. Jordan. "Meningococcus Genome Informatics Platform: a System for Analyzing Multilocus Sequence Typing Data." *Nucleic Acids Research*, vol. 37, pp. W606-W611, 2009.

I. Dubchak, A. Poliakov, **A.O. Kislyuk**, and M. Brudno. "Multiple whole genome alignments without a reference organism." *Genome Research*, vol. 19, pp. 682-689, 2009.

D. Papatsenko, **A.O. Kislyuk**, M. Levine, and I. Dubchak. "Conservation patterns in different functional sequence categories of divergent drosophila species." *Genomics*, vol. 88, no. 4, pp. 431-442, 2006.

ACADEMIC EXPERIENCE

- 2008 – 2010 Georgia Institute of Technology (Advisor: Joshua S. Weitz)
Research assistant: Research, development, and support of various bioinformatics projects.
- 2005 – 2008 Georgia Institute of Technology (Advisor: Mark Borodovsky)
Research assistant: Research, development, and support of various bioinformatics projects.
- 2004 – 2005 Lawrence Berkeley National Laboratory (Advisor: Inna Dubchak)
Research assistant: Tools for genome sequence alignment and comparative analysis.
- 2003 – 2004 Northern Arizona University Mathematics REU Program (Advisor: Nikolay Sirakov)
Research assistant: Computer vision, image contour and support tracing and comparison.
- 2003 UC Berkeley Space Sciences Laboratory (Advisor: Stephen Mende)
Lab assistant: Software and hardware solutions for a CCD IR telescope performing gravity wave observations.

POSTERS AND PRESENTATIONS

- A.O. Kislyuk**, J.S. Weitz, and I.K. Jordan. "Comparative Sequence Analysis for Predictive Assembly Gap Closure." Sequencing, Finishing, and Analysis in the Future 2009, Santa Fe, NM.
- A.O. Kislyuk**, S. Bhatnagar, J. Dushoff, and J.S. Weitz. "Unsupervised Statistical Clustering of Environmental Shotgun Sequences." Metagenomics 2008, La Jolla, CA.
- A.O. Kislyuk** and J.S. Weitz. "Working with metagenomic data." DARPA Fundamental Laws of Biology 2008, San Francisco, CA.
- A.O. Kislyuk**, A. Lomsadze, A. Lapidus, and M. Borodovsky. "Frameshift detection in prokaryotic genomic sequences." Finishing in the Future 2008, Santa Fe, NM.
- A.O. Kislyuk**, A. Lomsadze, A. Lapidus, and M. Borodovsky. "Frameshift detection in prokaryotic genomic sequences." Microbial Genomics (IMMG) 2007, College Park, MD.
- A.O. Kislyuk** and M. Borodovsky. "Frameshift detection in prokaryotic genomic sequences." 6th Georgia Tech-ORNL International Conference on Bioinformatics, in silico Biology 2007, Atlanta, GA.

TEACHING EXPERIENCE

Teaching Assistantships at Georgia Institute of Technology

- Spring 2008 **Theoretical Ecology** (BIOL 4422/6422).
- Fall 2007 **Bioinformatics** (BIOL 7023). Developed a new set of laboratory manuals.
- Fall 2006 **Biological Principles** (BIOL 1502).
- Summer 2006 **Applied Combinatorics** (MATH 3012).
- Spring 2006 **Calculus II and Linear Algebra** (MATH 1510).
 Fall 2005 *Guest Lectures at Georgia Institute of Technology*
- Spring 2009 Special Topics/**Computational Genomics** (BIOL 8803): 3 guest lectures.

PROFESSIONAL
EXPERIENCE

Supervised one undergraduate and three graduate research assistants. (Georgia Tech, 2008 – 2009.)

President of ABiS (Association of Bioinformatics Students), a professional student society. (Georgia Tech, 2008 – 2009.)

Developer, Gentoo Linux. Science project lead, Google Summer of Code mentor. (2008 –)

Procured, administered and upgraded a multi-user HPC cluster environment. (2008 –)

Judge, Siemens Westinghouse Science and Technology Competition regional finals. (2007)

Intern, Department of Energy Joint Genome Institute. (2007)

Programmer, Web data mining applications for economics research (part-time). (2005 – 2008)

Software Engineer, Versant Corporation. Performance instrumentation for object relational database management systems. (2005)

AWARDS

Bioinformatics Research Excellence Award (Georgia Tech, 2009).

CDC and ATSDR Honor Award, Partners in Public Health Improvement Category (Centers for Disease Control and Prevention, 2009).

Pacific Biosciences Rock Star Award (2011).

CITIZENSHIP

US citizen.

PERSONAL

Languages: English (fluent), Russian (native).

Interests: Running, cycling, martial arts, photography, aviation, robotics.

REFERENCES

Available upon request.