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Professional experience

2009-present	Assistant Professor (Research), Department of Medicine, Division of Clinical Pharmacology, Center for Health Informatics and Bioinformatics, New York University School of Medicine
2009	Postdoctoral Scholar, Department of Statistics, Stanford University
2008	Postdoctoral Fellow, European Bioinformatics Institute, Hinxton, Cambridge, UK
2002 - 2008	Research Assistant, Molecular Biology Institute, Center for Genomics and Proteomics, Center for Computational Biology, UCLA, CA
Summer 2002	Research Programmer, ZyxBio, LLC., Cleveland, OH
2001 - 2002	Research Assistant, Department of Genetics, CWRU, Cleveland, OH
2001 - 2002	Head Teaching Assistant, Department of Computer Science, CWRU, Cleveland, OH

Research Interests

Microbiomics, genetics, phylogenetics, evolution, stochastic modeling of biological and chemical processes, application and development of statistical methodologies for high throughput data, mathematical modeling, algorithms in bioinformatics

Education

2008	Ph.D., Biomathematics, University of California, Los Angeles Advisors: Marc A. Suchard and Christopher J. Lee
2003	M.Sc., Biomathematics, University of California, Los Angeles Advisor: Christopher J. Lee
2002	B.Sc., Computer Science, Case Western Reserve University, Cleveland, OH Advisors: Cenk S. Sahinalp and Evan E. Eichler

Professional service

- Associate Director of Operations, Best Practices Integrative Informatics Consultation (BPIC) service, Center for Health Informatics and Bioinformatics, New York University Langone Medical Center, 2010 - present.
- Founding member: UCLA, Bioinformatics Student Advisory Board;
- Contributor: Bayesian Evolutionary Analysis Sampling Trees (BEAST) software;
- Contributor: PyGr - A Python Graph database framework for Bioinformatics;
- NESCENT Working Group meetings on Software for Bayesian Evolutionary Analysis (BEAST), 2009 - 2011.

Students Mentored

Rotation students: Qi Wang (Ph.D. student at UCLA), Lukasz Goldschmidt (Ph.D. student at UCLA)

Referee activity

Nucleic Acids Research, Trends in Genetics, RNA Journal, Bioinformatics Journal, Advances in Bioinformatics, Systematic Biology

Languages

English, Russian, Ukrainian

Awards

2006 – 2008	NIH Systems and Integrative Biology Graduate Fellowship, University of California, Los Angeles
2005	FASEB MARC Travel Fellowship
2003 – 2005	NSF IGERT Bioinformatics Graduate Fellowship, University of California, Los Angeles
2002 – 2003	Biomathematics Department Fellowship, University of California, Los Angeles
2001 – 2002	Senior Year Scholarship, Case Western Reserve Alumni Association

Publications and talks

Refereed publications

10. **Alekseyenko, AV.**, Lytkin, NI., Ai, J., Padyukov, L., Aliferis, CF., Statnikov, A. “Causal Graph-Based Predictive Modelling of Rheumatoid Arthritis from Genome-Wide Association Data”. *Biology Direct* – *in press*.
9. Deriano, L., Chaumeil, J., Multani, A., Chou Y., **Alekseyenko, AV.**, Chang, S., Skok, JA. and Roth, DB. “The RAG2 C-terminus suppresses genomic instability and lymphomagenesis in developing lymphocytes” *Nature*, 2011 Mar 3;471(7336):119-23.
8. Gray, RR., Tatem, AJ., Johnson, JA., **Alekseyenko, AV.**, Pybus, OG., Suchard, MA., Salemi, M. “Bayesian phylogenetics of bacterial genomes: inferring the pandemic spread of Methicillin resistant *Staphylococcus aureus* ST239”. *Mol Biol Evol* first published online November 26, 2010 doi:10.1093/molbev/msq319.
7. Nelson, TA., Holmes S., **Alekseyenko, AV.**, Shenoy, M., DeSantis, T., Wu, C., Anderson, GL., Sonnenburg, J., Pasricha, PJ. and Spormann, A. “PhyloChip MicroArray Analysis Reveals Altered Gastrointestinal Microbial Communities in a Rat Model of Colonic Hypersensitivity”. *Neurogastroenterology and Motility* first published online December 3, 2010 doi:10.1111/j.1365-2982.2010.01637.x
6. Sehl, M., **Alekseyenko, AV.** and Lange, KL. “Accurate Stochastic Simulation via the Step Anticipation τ -Leaping (SAL) Algorithm”. *Journal of Computational Biology*, 2009, Vol. 16, No. 9: 1195-1208; doi: 10.1089/cmb.2008.0249.
5. **Alekseyenko, AV.**, Lee, CJ., Suchard, MA. “Wagner and Dollo: a stochastic duet by composing two parsimonious solos”. *Systematic Biology* 2008 57(5): 772 - 784; doi: 10.1080/10635150802434394.
4. **Alekseyenko, AV.**, Lee, CJ. “Nested Containment List (NCList): a new algorithm for accelerating interval query of genome alignment and interval databases.” *Bioinformatics* 2007 23: 1386 - 1393; doi:10.1093/bioinformatics/btl647.
3. **Alekseyenko, AV.**, Kim, N., Lee, CJ, “Global analysis of exon creation vs. loss, and the role of alternative splicing, in 17 vertebrate genomes.” *RNA* 2007, 13:661 - 670. doi:10.1261/rna.325107
2. Kim N, **Alekseyenko, AV.**, Roy, M., Lee, CJ., “The ASAP II database: analysis and comparative genomics of alternative splicing in 15 animal species.” *Nucl. Acids Res.* 2007 Jan; 35 (Database issue): D93 - 8. Epub 2006 Nov 15. doi: 10.1093/nar/gkl884
1. Resch, A., Xing, Y., **Alekseyenko, A.**, Modrek, B., Lee, C. “Evidence for a subpopulation of conserved alternative splicing events under selection pressure for protein reading frame preservation.” *Nucl. Acids Res.* 2004, 32: 1261 - 1269. doi: 10.1093/nar/gkh284

Conference papers

3. Holmes, S., **Alekseyenko, AV.**, Timme, A., Nelson, T., Pasricha, P.J., Spormann, A. “Visualization and statistical comparisons of Microbial Communities using R packages on PhyloChip data.” Pac Symp Biocomput. 2011:142-53.
2. Blaser, M. , Methe, B., Strober, B. , Perez Perez, G., Brown, S., and **Alekseyenko, A.** “Evaluation of the cutaneous microbiome in psoriasis.” Available from Nature Precedings <<http://dx.doi.org/10.1038/npre.2010.5276.1>> (2010)
1. Lee, C.J., **Alekseyenko, AV.**, Brown, CT. “Exploring the future of bioinformatics data sharing and mining with Pygr and Worldbase” in Proceedings of the 8th Python in Science conference (SciPy 2009), G Varoquaux, S van der Walt, J Millman (Eds.), pp. 62-67.

Submitted manuscripts

2. Cho, I., Meth, BA., Nondorf, L., Li, K., **Alekseyenko, AV.**, Blaser, MJ. “Subtherapeutic antibiotics alter the colonic microbiome and early life adiposity in mice” – under review in Nature Medicine.
1. DeSantis, TZ., Keller, K., Karaoz, U., **Alekseyenko, AV.**, Singh, NNS., Brodie, E., Pei, Z., Andersen, GL., Larsen, N. “Simrank: Rapid and sensitive general-purpose k-mer search tool” – under review in BMC Ecology.

Manuscripts in preparation

6. Pei, A., Oberdorf, WE., Yang, L., Gerz, EA., Lee, P., **Alekseyenko, AV.**, Caufield, PW., Nossa, CW., Pei, Z. “Ribosomal Constraints and Superorthology among 5S rRNA Genes in Prokaryotes”
5. **Alekseyenko, AV.**, Holmes, SP., Coram, M. “Binomial Accumulation and Replication Error Model for Sequencing of PCR-Amplified Samples”
4. **Alekseyenko, AV.**, Suchard, MA., and Goldman, N. “Independence and identity by descent in analysis of sequences related by a tree”
3. **Alekseyenko, AV.** and Lange, KL. “An MM algorithm for haplotype frequency estimation from new generation sequencing data” (data analysis in progress).
2. Kim, N., Pan, C., **Alekseyenko, AV.**, and Lee, CJ. “Pygr: A Python graph framework for highly scalable comparative genomics and annotation database analysis”
1. Lee, CJ*, Pan, C., Chen, L., and **Alekseyenko, AV.** “An Asymmetric Measure of Functional Interactions between Mutations in Highly Polymorphic Sequences” (written 2007, to be re-submitted)

Invited talks

- **Alekseyenko, AV.** “A new paradigm for analysis of genome-wide association data”, Office of Clinical Pharmacology, Food and Drug Administration *May 2010*
- **Alekseyenko, AV.** “Exploring viral heterogeneity using next generation deep sequencing”, Center for Health Informatics and Bioinformatics, NYU Medical Center. *March 2009*
- **Alekseyenko, AV.** “Multi-state stochastic Dollo model for evolution of complex characters”, Bath Institute for Complex Systems and Centre for Mathematical Biology joint seminar series, University of Bath, U.K. *November 2008*
- **Alekseyenko, AV.** “Multi-state stochastic Dollo model for evolution of complex characters”, Statistics seminar series, University of Bristol, U.K. *October 2008*
- **Alekseyenko, AV.** “Multi-state stochastic Dollo model for evolution of complex characters”, Mathematical Genetics and Bioinformatics Groups seminar series, University of Oxford, U.K. *October 2008*
- **Alekseyenko, AV.** “Evolution of alternatively spliced exons via bioinformatic, algorithmic and mathematical modeling techniques”, Scripps Research Institute, La Jolla, CA. *December 2007*
- **Alekseyenko, AV.** “Computational, comparative and stochastic modeling approaches to creation and loss of alternatively spliced exons”, NCBI, NIH, Bethesda, MD. *November 2007*

Contributed conference activities

- **Alekseyenko, AV.**, Nondorf, L., Cho, I., Blaser, M.J. “Analysis of of high-throughput 16S community sequence data in R” (poster), International Human Microbiome Congress, Vancouver, B.C. *March 2011*
- **Alekseyenko, AV.**, Methe, BA., Perez-Perez, GI., Blaser, M.J. “Analysis of Human Cutaneous Microbiota Stability With Respect to Demographic Factors and Body Site in Healthy Subjects”(poster), Human Microbiome Research Conference, St. Louis, MO *September 2010*
- Strober, BE., Perez-Perez, GI., Gao, Z., De Souza, A., Blumberg, A., Bihan, M., Li, K., Venter, E., Yooseph, S., **Alekseyenko, AV.**, Methe, BA. and Blaser, MJ “The Composition of Bacterial Taxa in Psoriatic Lesions”(poster), Human Microbiome Research Conference, St. Louis, MO *September 2010*
- **Alekseyenko, AV.**, Suchard, MA. “Approximate Bayesian inference of bacterial population trees with next-generation sequencing data”, Joint Statistical Meetings, Vancouver, B.C. *August 2010*

- **Alekseyenko, AV.**, Sehl, M., Lange, K. “Improving Speed and Accuracy in Stochastic Simulation via Higher Order Leaping”(poster), Workshop for Young Researchers in Mathematical Biology, Ohio State University, Columbus, OH *August 2009*
- **Alekseyenko, AV.** “Wagner and Dollo: A stochastic duet by composing two parsimonious solos”, Bayesian Phylogeny Workshop, Budapest, Hungary *June 2008*
- **Alekseyenko, AV.** and Lange, KL. “A method for estimation of HIV genotype frequencies in the course of drug treatment”, HIV Research: The Next Generation conference, CHIPTS, UCLA, Los Angeles, CA, USA *January 2008*
- **Alekseyenko, AV.** “Ordering properties of intervals: An enabling perspective for cross-genome databases”(poster), Institute for Digital Research and Education, UCLA *November 2007*
- **Alekseyenko, AV.** “Ordering properties of intervals: An enabling perspective for cross-genome databases”(poster), Workshop for Young Researchers in Mathematical Biology, Ohio State University, Columbus, OH *March 2007*
- Xing, Y., **Alekseyenko, AV.** and Lee, CJ. “How alternative splicing helped build the genome: exon creation, locally accelerated sequence evolution, and the production of new tissue-specific functions.”, The FASEB Journal. 20:A61 *2006*.
- Kim, N., Lee, CJ., **Alekseyenko, AV.**, Parker, S. “Pygr: a Python Graph Database Framework for Bioinformatics”(poster), (Software demonstration), ISMB, Fortaleza, Brazil *August 2006*
- **Alekseyenko, AV.** “A comparative genomics approach to distinguishing exon creation and loss shows increased exon creation associated with alternative splicing”, ISMB. Detroit, MI *June 2005*
- Lee, CJ., **Alekseyenko, AV.**, Parker, S. “Pygr: a python graph database framework for sequence analysis”(poster), (Software demonstration), ISMB. Detroit, MI *June 2005*
- **Alekseyenko, AV.**, Suchard MA. “A stochastic model for creation and loss of sequence blocks”(poster), RECOMB. Boston, MA *May 2005*