

# Alisa Yurovsky

29 Mount Road  
Stony Brook, New York 11790

Email: alisa.yurovsky@gmail.com  
Phone: +1 631 461 1280

## RESEARCH INTERESTS

Algorithms in Computational Biology, statistical analysis of biological data.

Analysis of RNA-seq data, genome composition, and phylogenetics.

Precision Medicine, mixture modeling.

## EDUCATION

- Ph.D. Computer Science, **Stony Brook University**, December 2020  
Specialization: Computational Biology  
Advised by: Steven Skiena  
Dissertation: *Understanding Mechanisms of Translation and Transcription*
- M.S. Computer Science, **EPFL**, December 2010  
Specialization: Computational Biology  
Advised by: Bernard Moret  
Dissertation: *A Study of Flu Virus Reassortment*
- B.S. Computer Science, **Carnegie Mellon University**, May 2001  
Minor: Mathematics

## FELLOWSHIPS, GRANTS, AWARDS

- 2020 **NSF/CRA/CCC Computing Innovation Postdoctoral Fellow 2020 (CIFellows 2020)**.  
Full financial support for two years of postdoctoral research, with 9 months extension.
- 2017 CEWIT 2017 Best Poster Award: one of three Best Poster Awards based on technical merit, potential impact, clarity, poster aesthetics, and quality of presentation.
- 2016 **NSF Graduate Research Fellowship Program (GRFP)**. Full financial support for three years of graduate study.
- 2015 Computer Science Department Chair Fellowship for first year PhD students.
- 2015 Pieper Merit Award for first year PhD students.
- 2010 Prix Annaheim - Mattille for high quality Master's Thesis devoted to bringing together life sciences and information technology.
- 2007 Organizational Level Award awarded by Cadence Design Systems, Inc. for work on semiconductor process constraints.

## EMPLOYMENT

- 2021– **Postdoctoral Fellow**, Stony Brook University School of Medicine, Dept. of Biomedical Informatics, Stony Brook, NY.
- 2016-20 **Research Assistant**, Stony Brook University, Dept. of Computer Science, Stony Brook, NY.
- 2015-16 **Teaching Assistant**, Stony Brook University, Dept. of Computer Science, Stony Brook, NY.
- 2013-15 **Data Manager/Statistician**, Stony Brook University, Dept. of Microbiology and Immunology, Stony Brook, NY.
- 2011-12 **Bioinformatician**, University of Geneva Medical School, Functional Population Genomics and Genetics of Complex Traits Lab, Geneva, Switzerland.
- 2004-08 **Senior Member of Technical Staff**, Cadence Design System, Inc., Pittsburgh, PA.
- 2001-04 **Software Engineer**, Neolinear, Inc., Pittsburgh, PA.
- 2000-01 **Research Programmer**, Medical Robotics and Assisted Surgery, Inc., Pittsburgh, PA.
- 1998-99 **Summer Research Programmer**, Carnegie Mellon University, Language Technologies Institute, Pittsburgh, PA.

## PUBLICATIONS

### Preprints and Under Review

- 2023 Sweeney, M.D., Torre-Healy, L.A., Ma, V.L., Hall, M.A., Chrastecka, L., **Yurovsky, A.** and Moffitt, R.A, “FaStaNMF: a Fast and Stable Non-negative Matrix Factorization for Gene Expression”, under review in TCB.
- 2023 Hegelmeyer, N.K, Previti, M.L,... **Yurovsky, A.**, et al. “Gene recoding by synonymous mutations creates promiscuous intragenic transcription initiation in mycobacteria”, bioRxiv. Preprint. <https://doi.org/10.1101/2023.03.17.532606>; under review in PLoS Biology.

### Peer-Reviewed Journal Articles and Conference Proceedings

- 2022 **Yurovsky, A.**, Gardin, J., Futcher, B., Skiena, S. “Statistical Methodology for Ribosomal Frameshift Detection”, Proceedings of the 2022 ACM International Conference on Bioinformatics, Computational Biology and Health Informatics, (ACM-BCB 2022)
- 2019 **Yurovsky, A.**, Futcher, B., Skiena, S. “Pre-Phaser: Precise Cell-Cycle Phase Detector for scRNA-seq”, Proceedings of the 2019 ACM International Conference on Bioinformatics, Computational Biology and Health Informatics, 376-382 (ACM-BCB 2019)
- 2018 **Yurovsky, A.**, Amin, M.R., Gardin, J., Chen, Y., Skiena, S., et al. “Prokaryotic coding regions have little if any specific depletion of Shine-Dalgarno motifs”, PLOS ONE 13(8): e0202768.
- 2018 Amin, M.R., **Yurovsky, A.**, Chen Y., Skiena, S., Futcher, B. “Re-annotation of 12,495 prokaryotic 16S rRNA 3' ends and analysis of Shine-Dalgarno and anti-Shine-Dalgarno sequences”, PLOS ONE 13(8): e0202767.
- 2018 Amin, M.R., **Yurovsky, A.**, Tian, Y., Skiena, S. “DeepAnnotator: Genome Annotation with Deep Learning”, Proceedings of the 2018 ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics, 254-259 (ACM-BCB 2018)

- 2015 Waszak, S.M., Delaneau, O., ... **Yurovsky, A.**, et al. "Population variation and genetic control of modular chromatin architecture in humans", Cell 2015, 162 (5), 1039-1050.
- 2015 Futcher, B., Gorbatshevych, O., ... **Yurovsky, A.**, et al. "Reply to Simmonds et al.: Codon pair and dinucleotide bias have not been functionally distinguished", Proceedings of the National Academy of Sciences 2015, 112 (28), E3635-E3636.
- 2015 Shen, S.H., Stauft, C.B., ... **Yurovsky, A.**, et al. "Large-scale recoding of an arbovirus genome to rebalance its insect versus mammalian preference", Proceedings of the National Academy of Sciences 2015, 112(15), 4749-4754.
- 2015 Gutierrez-Arcelus, M., Ongen, A., ... **Yurovsky, A.**, et al. "Tissue-specific effects of genetic and epigenetic variation on gene regulation and splicing", PLoS genetics 2015, 11 (1), e1004958.
- 2014 Gardin, J., Yeasmin, R., **Yurovsky, A.**, Cai, Y., Skiena, S., Futcher, B., "Measurement of average decoding rates of the 61 sense codons in vivo", eLife 2014; 10.7554/eLife.03735
- 2014 Waszak, S.M., Kilpinen, H., ... **Yurovsky, A.**, et al. "Identification and removal of low-complexity sites in allele-specific analysis of ChIP-seq data", Bioinformatics 2014; 30 (2), 165-171
- 2013 Kilpinen, H., Waszak, S.M., ... **Yurovsky, A.**, et al. "Coordinated effects of sequence variation on DNA binding, chromatin structure, and transcription", Science 2013; 342 (6159), 744-747
- 2013 Gutierrez-Arcelus, M., Lappalainen, T., Montgomery, S.B., Buil, A., Ongen H., **Yurovsky, A.**, et al. "Passive and active DNA methylation and the interplay with genetic variation in gene regulation", eLife 2013;2:e00523
- 2011 **Yurovsky, A.**, Moret, B.M.E. "FluReF, an automated flu virus reassortment finder based on phylogenetic trees", BMC Genomics 2011, 12(Suppl 2):S3
- 2010 **Yurovsky, A.**, Moret, B.M.E. "FluRF, an automated flu virus reassortment finder based on phylogenetic trees", 2010 IEEE International Conference on Bioinformatics & Biomedicine (BIBM-2010)
- 2005 **Yurovsky, A.**, Gopalakrishnan, P. "A new Cell-Planning based automatic placement technique for optimization of Analog, RF, and mixed-signal circuit layouts", Cadence Technical Conference, May 2005.

### **US Patents**

- 2019 Futcher, B., Gardin, J., Skiena, S., **Yurovsky, A.**, Wimmer, E., Mueller, S. "Modified protein encoding sequences having increased rare hexamer content". US Patent App. 15/773,685.
- 2011 Colwell, R., Lamant, G. S. C., **Yurovsky, A.**, Rosek, T. "Registry for Electronic Design Automation of Integrated Circuits". Assignee: Cadence Design Systems. Issued on 05/17/2011.
- 2010 Gopalakrishnan, P., **Yurovsky, A.** "Optimizing Circuit Layouts by Configuring Rooms for Placing Devices" Assignee: Cadence Design Systems. Issued on 02/16/2010.

## TALKS AND PRESENTATIONS

### Refereed Conference Talks (presenter name is in bold)

- 2022 Sweeney, M.D., Torre-Healy, L.A., Ma, V.L., Hall, M.A., Chrastecka, L., **Yurovsky, A.** and Moffitt, R.A, "FaStaNMF: a Fast and Stable Non-negative Matrix Factorization for Gene Expression", presented at APBC 2022.
- 2022 **Yurovsky, A.**, Gardin, J., Futcher, B., Skiena, S. "Statistical Methodology for Ribosomal Frameshift Detection", presented at ACM-BCB 2022.
- 2019 **Yurovsky, A.**, Futcher, B., Skiena, S. "Pre-Phaser: Precise Cell-Cycle Phase Detector for scRNA-seq", presented at ACM-BCB 2019.
- 2018 **Amin, M.R.**, Yurovsky, A., Tian, Y., Skiena, S. "DeepAnnotator: Genome Annotation with Deep Learning", presented at ACM-BCB 2018.
- 2010 **Yurovsky, A.**, Moret, B.M.E. "FluRF, an automated flu virus reassortment finder based on phylogenetic trees", presented at BIBM-2010.

### Campus Talks

- 2022 "Compartment Deconvolution for Precision Medicine", Pathology Cancer Center Grand Rounds Seminar, Stony Brook University School of Medicine, Stony Brook, NY, invited by Kenneth R. Shroyer, December 13, 2022.

### Refereed Conference Poster Presentations

- 2017 **Yurovsky, A.**, Amin, M.R., Skiena, S. "Word Embeddings for Genome Annotation with Deep Learning", Poster presentation at the 13th International Conference on Emerging Technologies for a Smarter World (CEWIT2017), November 2017.
- 2010 **Yurovsky, A.**, Moret, B.M.E. "FluRF", Poster presentation at the 1st European Student Council Symposium workshop at the 9th European Conference on Computational Biology (ECCB-10), September 2010.

## TEACHING

- 2023-23 Developing and teaching BMI530, a graduate course in Software Development in Biomedical Informatics, Stony Brook University School of Medicine, Dept. of Biomedical Informatics.
- 2021-23 Lectures on RNA-seq Informatics for BMI511, a graduate Translational Bioinformatics course, Stony Brook University School of Medicine, Dept. of Biomedical Informatics.
- 2022-22 Developing and teaching BMI540, a graduate course in Statistical Methods in Biomedical Informatics, Stony Brook University School of Medicine, Dept. of Biomedical Informatics.
- 2015-16 Teaching Assistant for undergraduate Algorithms and Software Engineering courses, Stony Brook University, Dept. of Computer Science.

## **PROFESSIONAL SERVICE**

- 2019-22 **Reviewer** for Bioinformatics, Computational and Structural Biotechnology, and Scientific Reports Journals.
- 2022-22 **Session Chair** for ACM-BCB 2022.
- 2018-20 Stony Brook University Computer Science, **WPhD Vice President**.
- 2019-19 Stony Brook University Computer Science, **WPhD Acting President**.

## **MENDEES**

### **Undergraduate Research**

- 2021-22 Michael D. Sweeney: resulted in coauthored paper with student as the first author  
Next position: graduate student research assistant at the University of Michigan.

### **High School Research**

- 2021-22 Ashley Hsu: joint work resulted in a winning entry for the bioinformatics category at the 2022 International Science and Engineering Fair, while representing New York.  
Next position: undergraduate student at Duke University.

## **SKILLS AND METHODS**

### **Statistical and Computational Methods**

Algorithms development, embeddings and deep learning, mixture modeling, statistics.  
RNA-seq analysis, genomics and phylogenetic analysis.

### **Programming Languages**

Python, R, C++, C, Perl, SQL, Tcl/Tk, Unix Shell, UML, HTML, Java.

### **Natural Languages**

Fluent in English and Russian, limited working proficiency in Spanish and French.

## **REFERENCES**

Upon request.