

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**, Neoliner, 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 TCBB.
- 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., Stauff, 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**.

MENTEES

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.

Updated March 2023