Alisa Yurovsky

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RESEARCH INTERESTS

Algorithms in Computational Biology, statistical analysis of biological data.

Analysis of single cell and bulk RNA-seq, spatial transcriptomics, genome composition.

Precision Medicine, mixture modeling/deconvolution.

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

2023	**IDEA Fellowship**. Full-time, 12-month, non tenure-track faculty position at the lecturer level. Two year support with anticipated transition to tenure-track.
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

2023–   **IDEA Fellow, Lecturer**, Stony Brook University, Dept. of Biomedical Informatics, Stony Brook, NY.

2021-23   **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.

TEACHING

2023-24   Faculty co-advisor for the Stony Brook VIP Webgen team, a long-term multi-disciplinary project for undergraduate and graduate students. Stony Brook's Vertically Integrated Projects Program is a member of the VIP Consortium.

2022-23   Developing and teaching BMI540, a graduate course in Statistical Methods in Biomedical Informatics, Stony Brook University School of Medicine, Dept. of Biomedical Informatics.

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.

2015-16   Teaching Assistant for undergraduate Algorithms and Software Engineering courses, Stony Brook University, Dept. of Computer Science.

PUBLICATIONS

Peer-Reviewed Journal Articles and Conference Proceedings

2023   Sejour R, Leatherwood J, **Yurovsky A**, Futcher B. (2023) No Ramp Needed: Spandrels, Statistics, and a Slippery Slope. eLife. 2023 Nov 13; 12:RP89656. doi: 10.7554/eLife.89656.2.

2023   Hegelmeyer NK, Parkin LA, Previti ML, Andrade J, Utama R, Sejour RJ, Gardin J, Muller S, Ketchum S, **Yurovsky A**, Futcher B, Goodwin S, Ueberheide B, Seeliger JC. Gene recoding

by synonymous mutations creates promiscuous intragenic transcription initiation in mycobacteria. mBio. 2023 Oct 31;14(5):e0084123. doi: 10.1128/mbio.00841-23. PubMed PMID: 37787543.

2023   Sweeney MD, Torre-Healy LA, Ma VL, Hall MA, Chrastecka L, **Yurovsky A**, Moffitt RA. (2023) FaStaNMF: a Fast and Stable Non-negative Matrix Factorization for Gene Expression. IEEE/ACM Trans Comput Biol Bioinform. Epub ahead of print. 2023/07/19; doi: 10.1109/TCBB.2023.3296979. PubMed PMID: 37467096.

2022   **Yurovsky A**, Gardin J, Futcher B, Skiena S. (2022) Statistical Methodology for Ribosomal Frameshift Detection. Proceedings of the 2022 ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (ACM-BCB). 12:1-10. doi: 10.1145/3535508.3545529.

2019   **Yurovsky A**, Futcher B, Skiena S. (2019) Pre-Phaser: Precise Cell-Cycle Phase Detector for scRNA-seq. Proceedings of the 2019 ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (ACM-BCB). 376-382 doi: 10.1145/3307339.3342174.

2018   **Yurovsky A**, Amin MR, Gardin J, Chen Y, Skiena S, Futcher B. (2018) Prokaryotic coding regions have little if any specific depletion of Shine-Dalgarno motifs. PLoS One. 13(8):e0202768. doi: 10.1371/journal.pone.0202768. PubMed PMID: 30138485.

2018   Amin MR, **Yurovsky A**, Chen Y, Skiena S, Futcher B. (2018) 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. doi: 10.1371/journal.pone.0202767. PubMed PMID: 30138483.

2018   Amin MR, **Yurovsky A**, Tian Y, Skiena S. (2018) DeepAnnotator: Genome Annotation with Deep Learning. Proceedings of the 2018 ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB). 2018;254-259. doi: 10.1145/3233547.3233577.

2015   Waszak SM, Delaneau O, Gschwind AR, Kilpinen H, Raghav SK, Witwicki, RM, Orioli A, Wiederkehr M, Panousis NI, **Yurovsky A**, Romano-Palumbo L, Planchon A, Bielser D, Padioleau I, Udin G, Thurnheer S, Hacker D, Hernandez N, Reymond A, Deplancke B, Dermitzakis ET. (2015) Population variation and genetic control of modular chromatin architecture in humans. Cell. 2015;162(5):1039-1050. doi: 10.1016/j.cell.2015.08.001. PubMed PMID: 26300124.

2015   Futcher B, Gorbatsevych O, Shen SH, Stauft CB, Song Y, Wang B, Leatherwood J, Gardin J, **Yurovsky A**, Mueller S, Wimmer E. (2015) Reply to Simmonds et al.: Codon pair and dinucleotide bias have not been functionally distinguished. Proceedings of the National Academy of Sciences. 2015/07/14;112(28):E3635-6. doi: 10.1073/pnas.1507710112. PubMed PMID: 26071446.

2015   Shen SH, Stauft CB, Gorbatsevych O, Song Y, Ward CB, **Yurovsky A**, Mueller S, Futcher B, Wimmer E. (2015) Large-scale recoding of an arbovirus genome to rebalance its insect versus mammalian preference. Proceedings of the National Academy of Sciences. 112(15):4749-4754. doi: 10.1073/pnas.1502864112. PubMed PMID: 25825721.

2015   Gutierrez-Arcelus M, Ongen H, Lappalainen T, Montgomery SB, Buil A, **Yurovsky A**,

Bryois J, Padioleau I, Romano L, Planchon A, Falconnet E, Bielser D, Gagnebin M, Giger T, Borel C, Letourneau A, Makrythanasis P, Guipponi M, Gehrig C, Antonarakis SE, Dermitzakis ET. Tissue-specific effects of genetic and epigenetic variation on gene regulation and splicing. PLoS Genet. 2015 Jan 29;11(1):e1004958. doi: 10.1371/journal.pgen.1004958. PMID: 25634236.

2014   Gardin J, Yeasmin R, **Yurovsky A**, Cai Y, Skiena S, Futcher B. (2014) Measurement of average decoding rates of the 61 sense codons in vivo. eLife. 2014 Oct 27:3:e03735. doi: 10.7554/eLife.03735. PubMed PMID: 25347064.

2014   Waszak SM, Kilpinen H, Gschwind AR, Orioli A, Raghav SK, Witwicki RM, Migliavacca E, **Yurovsky A**, Lappalainen T, Hernandez N, Reymond A, Dermitzakis ET, Deplancke B. (2014) Identification and removal of low-complexity sites in allele-specific analysis of ChIP-seq data. Bioinformatics. 2014 Jan 15;30(2):165-71. doi: 10.1093/bioinformatics/btt667. PubMed PMID: 24255646.

2013   Kilpinen H, Waszak SM, Gschwind AR, Raghav SK, Witwicki RM, Orioli A, Migliavacca E, Wiederkehr M, Gutierrez-Arcelus M, Panousis NI, **Yurovsky A**, Lappalainen T, Romano-Palumbo L, Planchon A, Bielser D, Bryois J, Padioleau I, Udin G, Thurnheer S, Hacker D, Core LJ, Lis JT, Hernandez N, Reymond A, Deplancke B, Dermitzakis ET. (2013) Coordinated effects of sequence variation on DNA binding, chromatin structure, and transcription. Science. 2013;342(6159):744-7. doi: 10.1126/science.1242463. PubMed PMID: 24136355.

2013   Gutierrez-Arcelus M, Lappalainen T, Montgomery SB, Buil A, Ongen H, **Yurovsky A**, Bryois J, Giger T, Romano L, Planchon A, Falconnet E, Bielser D, Gagnebin M, Padioleau I, Borel C, Letourneau A, Makrythanasis P, Guipponi M, Gehrig C, Antonarakis SE, Dermitzakis ET. (2013) Passive and active DNA methylation and the interplay with genetic variation in gene regulation. Elife. 2013 Jun 4:2:e00523. doi: 10.7554/eLife.00523. PubMed PMID: 23755361.

2011   **Yurovsky A**, Moret BME. (2011) FluReF, an automated flu virus reassortment finder based on phylogenetic trees. BMC Genomics. 2011;12 Suppl 2(Suppl 2):S3. doi: 10.1186/1471-2164-12-S2-S3. PubMed PMID: 21989112.

2010   **Yurovsky A**, Moret BME. FluRF, an automated flu virus reassortment finder based on phylogenetic trees. 2010 IEEE International Conference on Bioinformatics and 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 GSC, **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 MD, Torre-Healy LA, Ma VL, Hall MA, Chrastecka L, **Yurovsky A** and Moffitt RA. 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 MR**, Yurovsky A, Tian Y, Skiena S. DeepAnnotator: Genome Annotation with Deep Learning, presented at ACM-BCB 2018.

2010   **Yurovsky A**, Moret BME. FluRF, an automated flu virus reassortment finder based on phylogenetic trees, presented at BIBM-2010.

Refereed Conference Poster Presentations

2023   **Yurovsky A**, Moffitt RA. Sample-Specific Compartment Deconvolution. Poster Presentation at 2023 ISMB/ECCB in Lyon, France.

2017   **Yurovsky A**, Amin MR, 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 BME. FluRF. Poster presentation at the 1st European Student Council Symposium workshop at the 9th European Conference on Computational Biology (ECCB-10), September 2010.

Campus Talks and Panel Discussions

2024   Panelist for CELT AI Ethics in Teaching and Learning Panel, Stony Brook, NY, invited by Rose Tirotta-Esposito, February 20, 2024.

2023   Panelist for CSTEP Biomedical Engineering Panel, Stony Brook, NY, invited by Daniene Byrne, October 4, 2023.

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.

PROFESSIONAL SERVICE

2019-24   **Reviewer** for BMC Genomics 2024, Computational and Structural Biotechnology 2022 and Scientific Reports 2022 Journals, Bioinformatics 2019.

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**.

PROFESSIONAL MEMBERSHIPS

Member of ISCB.

MENTEES

MS Research

2023–   Eliezer Aravera

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 Michagan.

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.

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