

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.

Algorithms for enabling more precise survival, differential expression, and classification analyses for genomics and imaging data.

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

- 2022– 3 semesters, developing and teaching BMI540, a graduate course in Statistical Methods in Biomedical Informatics, Stony Brook University School of Medicine, Department of Biomedical Informatics
- 2023– 3 semesters, faculty co-advisor for the Stony Brook VIP Webgen team, a long-term multi-disciplinary project for undergraduate students. Stony Brook's Vertically Integrated Projects Program is a member of the VIP Consortium.
- 2024– Excellence in Teaching Program participant, nominated for the 2024-2025 cohort by the CEAS dean, offered through Stony Brook University Office of the Provost.
- 2021– Once per year lecture on RNA-seq Informatics for BMI511, a graduate Translational Bioinformatics course, Stony Brook University School of Medicine, Dept. of Biomedical Informatics.
- 2024– Once per semester lecture on Bioinformatics at the BMI Bootcamp for Stony Brook undergraduate students.
- 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.
- 2015–16 Teaching Assistant for undergraduate Algorithms and Software Engineering courses, Stony Brook University, Dept. of Computer Science.

PUBLICATIONS

Pre-prints and Manuscripts Under Review

- 2025 **Yurovsky A**, Moffitt RA. Improving Differential Expression and Survival Analyses with Sample Specific Compartment Deconvolution. Under review for ISMB 2025.
- 2024 Ganguly A, Chatterjee D, Huang W, Zhang J, **Yurovsky A**, Johnson TS, Chen C. MERGE: Multi-faceted Hierarchical Graph-based GNN for Gene Expression Prediction from Whole Slide Histopathology Images. arXiv. 2024, Dec 3. doi: 10.48550/arXiv.2412.02601. Under review for CVPR 2025.
- 2024 Huang W, Xu M, Hu X, Abousamra S, Ganguly A, Kapse S, **Yurovsky A**, Prasanna P, Kurc T, Saltz J, Miller ML, Chen C. (2024) RankByGene: Gene-Guided Histopathology Representation Learning Through Cross-Modal Ranking Consistency. arXiv. 2024, Nov 22. doi: 10.48550/arXiv.2411.15076. Under review for CVPR 2025.
- 2024 Sha C, Van Brunt T, Kudria J, Schmidt D, **Yurovsky A**, Bandovic J, Giarrizzo M, Lin J, Tsirka SA, Bialkowska AB, Wollmuth L, Speer E, Hsieh H. (2024) A graded neonatal mouse model of necrotizing enterocolitis demonstrates that mild enterocolitis is sufficient to activate microglia and increase cerebral cytokine expression. bioRxiv. 2024 May 1. doi: 10.1101/2023.08.03.551849.
- 2023 Sejour R, Leatherwood J, **Yurovsky A**, Futcher B. (2023) No Ramp Needed: Spandrels, Statistics, and a Slippery Slope. bioRxiv. 2023 Aug 19. doi: 10.1101/2022.06.27.497802.

Peer-Reviewed Journal Articles and Conference Proceedings

- 2024 Hasan M, Kim Silva A, Abousamra S, Tang S, Prasanna P, Saltz J, Gardner KL, Chen C, **Yurovsky A**. (2024) New Spatial Phenotypes from Imaging Uncover Survival Differences for Breast Cancer Patients. Proceedings of the 2024 ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (ACM-BCB). 17:1-12. doi: 10.1145/3698587.370133.
- 2024 Sejour R, Leatherwood J, **Yurovsky A**, Futcher B. (2024) Enrichment of rare codons at 5' ends of genes is a spandrel caused by evolutionary sequence turnover and does not improve translation. eLife. 2024 Jul 15. 12:RP89656. doi: 10.7554/eLife.89656.3
- 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, Chrasticka L, **Yurovsky A**, Moffitt RA. (2023) FaStaNMF: a Fast and Stable Non-negative Matrix Factorization for Gene Expression. IEEE/ACM Trans Comput Biol Bioinform. 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**, Fitcher 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, Fitcher 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, Fitcher 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 Fitcher B, Gorbatshevych O, Shen SH, Stauff 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, Stauff CB, Gorbatshevych O, Song Y, Ward CB, **Yurovsky A**, Mueller S, Fitcher 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, Fitcher 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 Fitcher 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)

- 2025 **Aggarwal P**, Sochan AJ, Kim R, Kuhia R, Zhao Z, Fiore SM, Chesler D, Egnor M, Yurovsky A, Hsieh H. Pediatric Traumatic Brain Injury: Uncovering Injury Patterns and Their Clinical Consequences. Talk accepted for ACS 2025: Feb 11-13, Las Vegas, Nevada.
- 2025 **Aggarwal P**, Kim R, Kuhia R, Zhao Z, Fiore SM, Chesler D, Egnor M, Yurovsky A, Hsieh H. Breaking Up a Bimodal Distribution: Guidelines for Pediatric Traumatic Brain Injury Research. Talk accepted for ACS 2025: Feb 11-13, Las Vegas, Nevada.

- 2024 Hasan M, Kim Silva A, Abousamra S, Tang S, Prasanna P, Saltz J, Gardner KL, Chen C, **Yurovsky A**. New Spatial Phenotypes from Imaging Uncover Survival Differences for Breast Cancer Patients. Presented at ACM-BCB 2024.
- 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

- 2024 **Dutta P**, Sathian R, Obusan M, Surana P, Chao M, Papineni N, Yurovsky A, Davuluri RV. Prediction of Cancer Somatic Mutations that impact Gene Regulatory Elements by application of DNABERT fine-tuned models on Whole Genome Sequencing Data. Poster presentation at 2024 CSHL Biological Data Science Meeting in Cold Spring Harbor, NY.
- 2024 **Yurovsky A**, Moffitt RA. Improving Differential Expression and Survival Analyses with Sample-Specific Compartment Deconvolution (SSCD). Poster presentation at 2024 ISMB in Montreal, Canada.
- 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.

Invited Talks and Panel Discussions

- 2024 Invited speaker, "Improving Differential Expression and Survival analyses", 2024 Stony Brook Cancer Center GI Symposium, Port Jefferson, NY, invited by Georgios Georgakis, May 31, 2024.
- 2024 Panelist for CSTEP Engineering Panel, Stony Brook, NY, invited by Daniene Byrne, March 20, 2024.
- 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 Invited speaker, "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

Conferences and Journals

2023-24 **Program Committee** Member for ACM-BCB 2024, 2023.

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

2022-24 **Session Chair** for ACM-BCB 2024, 2022.

University Service

2024-24 Stony Brook University College of Engineering and Applied Sciences, DEI climate survey committee member.

2018-20 Stony Brook University Computer Science, **WPhD Vice President**.

2019-19 Stony Brook University Computer Science, **WPhD Acting President**.

PROFESSIONAL MEMBERSHIPS

ISCB member since 2023. ACM and ACM-W member since 2024.

MENTEES

Undergraduate Research

2024- Aaron Das

2024- Ilirjana Gocaj

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

2024- Shriya Jaddu: Simons Summer Research student

2024- Thomas Li: Simons Summer Research student

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 January 2025