

# 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

- 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 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.
- 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**, Fitcher 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**, Fitcher 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*. 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, Gorbatsvych 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, Gorbatsvych 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**,

- Bryoïs 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, Bryoïs 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**, Bryoïs 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)

- 2022 Sweeney MD, Torre-Healy LA, Ma VL, Hall MA, Chrasticka 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, Futch B, Skiena S. Statistical Methodology for Ribosomal Frameshift Detection, presented at ACM-BCB 2022.
- 2019 **Yurovsky A**, Futch 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. (2023) 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

- 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

- 2023-23 **Program Committee Member** for ACM-BCB 2023.
- 2019-22 **Reviewer** for Bioinformatics 2019, Computational and Structural Biotechnology 2022, and Scientific Reports Journals 2022.
- 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 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.

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