Thomas Jiaxian Li

Curriculum Vitae

Education

- 2011–2015 Ph.D. Degree in Applied Mathematics, Department of Mathematics and Computer Science, University of Southern Denmark, Odense, Denmark.
 Dissertation Title: Combinatorics of shapes, topological RNA structures and RNA-RNA interactions. Supervised by Prof. Christian M. Reidys.
- 2008–2011 Master&Ph.D. Program in Discrete Mathematics, *Center for Combinatorics, Nankai University*, Tianjin, China.
- 2004–2008 Bachelor Degree in Mathematics, *Department of Mathematics, Nankai University*, Tianjin, China.

Special Class in mathematics founded by Shiing-Shen Chern

Work Experience

- 2021–present Research Scientist, *Biocomplexity Institute*, University of Virginia, Charlottesville, United States.
 - 2018–2020 Senior Research Associate, *Biocomplexity Institute*, University of Virginia, Charlottesville, United States.
 - 2015–2018 Postdoctoral Research Associate, *Virginia Bioinformatics Institute*, Virginia Tech, Blacksburg, United States.

Research Interests

Discrete mathematics Bioinformatics and computational biology RNA secondary structure, RNA pseudoknot, RNA-RNA interaction RNA sequence, structure, evolution and phylogenetic implications Topology of large data sets

Publications

- [1] Barrett, C., Bura, A., He, Q., Huang, FW, Li, T.J.X. and Reidys, C.M. (2023) Motifs in SARS-CoV-2 evolution. Available from: https://doi.org/10.1101/2023.01.27.525936. Submitted to RNA, under review.
- [2] Barrett, C., Huang, FW, Li, T.J.X., Warren, A. and Reidys, C.M. (2022) Rapid threat detection in SARS-CoV-2. Available from: https://doi.org/10.1101/2022.08.05.22278480. Submitted to PLOS ONE, under review.

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- [3] Bura, A., Dutta, N., Li, T.J.X. and Reidys, C.M. (2022) A computational framework for weighted simplicial homology. Available from: arXiv:2206.04612. Submitted to Journal of Symbolic Computation, under review.
- [4] Li, T.J.X. and Reidys, C.M. (2022) On Weighted Simplicial Homology. Available from: arXiv:2205.03435. Submitted to Rocky Mountain Journal of Mathematics, under review.
- [5] Barrett, C., Bura, A., He Q., Huang, FW, Li, T.J.X. and Reidys, C.M. (2021) Buying time: detecting VOCs in SARS-CoV-2 via co-evolutionary signals. Available from: https://doi.org/10.1101/2022.07.21.500897. bioRxiv.
- [6] Li, T.J.X. and Reidys, C.M. (2021) On the Loop Homology of a Certain Complex of RNA Structures. *Mathematics*, 9(15):1749.
- [7] Barrett, C., Bura, A., He Q., Huang, FW, Li, T.J.X., Waterman, M. and Reidys, C.M. (2021) Multiscale feedback loops in SARS-CoV-2 viral evolution. *Journal of Computational Biology*, 28(3):248–256.
- [8] Li, T.J.X. and Reidys, C.M. (2020) On an enhancement of RNA probing data using Information Theory. Algorithms for Molecular Biology, 15: 15.
- [9] Li, T.J.X., Burris, C. S., and Reidys, C.M. (2019) The block spectrum of RNA pseudoknot structures. *Journal of Mathematical Biology*, 79(3): 791–822.
- [10] Li, T.J.X. and Reidys, C.M. (2018) From unicellular fatgraphs to trees. Available from: https://doi.org/10.48550/arXiv.1806.03319. arXiv.
- [11] Li, T.J.X. and Reidys, C.M. (2018) The rainbow spectrum of RNA secondary structures. Bulletin of Mathematical Biology, 80(6):1514–1538.
- [12] Li, T.J.X. and Reidys, C.M. (2017) Statistics of topological RNA structures. Journal of Mathematical Biology, 74(7):1793–1821.
- [13] Barrett, C. L., Li, T.J.X. and Reidys, C.M. (2016) RNA secondary structures having a compatible sequence of certain nucleotide ratios. *Journal of Computational Biology*, 23(11):857–873.
- [14] Li, T.J.X. and Reidys, C.M. (2015) A combinatorial interpretation of the $\kappa_g^*(n)$ coefficients. arXiv preprint, arXiv:1406.3162.
- [15] Han, H.S.W., Li, T.J.X. and Reidys, C.M. (2014) Combinatorics of γ-structures. Journal of Computational Biology, 21:591–608.
- [16] Li, T.J.X. and Reidys, C.M. (2013) The topological filtration of γ -structures. Mathematical Biosciences, 241(1):24–33.
- [17] Li, T.J.X. and Reidys, C.M. (2012) Combinatorics of RNA-RNA interaction. Journal of Mathematical Biology, 64(3):529–556.
- [18] Li, T.J.X. and Reidys, C.M. (2011) Combinatorial analysis of interacting RNA molecules. *Mathematical Biosciences*, 233(1):47–58.

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Conferences

- 2019, Oct International Symposium on Biomathematics and Ecology Education and Research (BEER19), University of Wisconsin, La Crosse, USA, Invited Talk, Title: On an Enhancement of RNA Probing Data Using Information Theory.
- 2019, Apr Quantitative and Computational Biology Colloquium, University of Southern California, USA, Invited Talk, Title: Exploring large RNA secondary structures via information theory.
- 2017, July SIAM: SIAM Conference on Applied Algebraic Geometry (AG17), Atlanta, USA, Title: Statistics of Topological RNA Structures.
- 2016, June SIAM: SIAM Conference on Discrete Mathematics (DM16), Atlanta, USA, Title: Analyzing RNA Secondary Structures with Fixed Percentage of Bases.
- 2014,Sep Significance of Knotted Structures for Function of Proteins and Nucleic Acids, *Thematic Meeting of the Biophysical Society*, Warsaw, Poland, Poster Presentation: A combinatorial interpretation of the $\kappa_a^{\star}(n)$ coefficients.
- 2014, June The 25th International Conference on Probabilistic, Combinatorial and Asymptotic Methods for the Analysis of Algorithms (AofA 2014), Paris, France.
- 2013, July Topology Driven Methods for Complex Systems (TOPDRIM), San Benedetto del Tronto, Italy, Talk title: Bijections on planar bicellular maps.

Professional Activities

- 2015–present **Reviewer for academic journals and databases**, Computational and Mathematical Biophysics, Journal of Theoretical Biology, Mathematics, Non-Coding RNA, Entropy, Axioms, Symmetry, Mathematical Reviews, Zentralblatt MATH Open.
- 2015–present **Grant Writing**, Biocomplexity Institute, University of Virginia & Virginia Tech, I have experience in writing proposals for NSF, NIH, Simons Foundation, CDC, VDH, and DARPA.
- 2018-present **Software Developer**, Biocomplexity Institute, University of Virginia, I developed a software package RNAStructureIdentifier for identifying the target secondary structure from an RNA structure ensemble. I worked with my colleagues on implementing a Python software package WeightedSimplicialHomology for computing weighted simplicial homology over a discrete valuation ring.
 - 2017–2018 **Graduate Student Mentor**, Virginia Tech, I mentored graduate student Christina Burris on her master thesis: Analytic Combinatorics Applied to RNA Structures.
 - 2013–2015 **Project Participation**, University of Southern Denmark, I participated in the ERC project TOPDRIM (Topology Driven Methods for Complex Systems).
 - 2011–2015 **Teaching Assistant**, University of Southern Denmark, I taught the following courses: Measure and Integration Theory, Linear algebra, Rings and Number Theory, Algebra, Representation theory, Probability theory I&II, Geometry of Surfaces, Current topics in geometry, Algebraic topology, Combimatorics.

Computer Skills

Proficient at C, Maple, Mathematica, Matlab, Python, Sage, R, SPSS, LaTeX.

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