Borislav Hristov

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Research Interests

Artificial Intelligence for Genomics, Computational Biology, Machine Learning, Biomedical Informatics, Probabilistic Algorithms

Education

Ph.D Computer Science, Princeton University 09/2019
Thesis: Deciphering disease genomes in a network context
Advisor: Prof. Mona Singh

Sc.M Computer Science, Princeton University 05/2014

B.Sc *magna cum laude*, Mathematics and Computer Science, Brown University 05/2010
Thesis: Max-likelihood algorithms for reconstruction of human segmental duplications
Advisor: Prof. Benjamin Raphael

Research & Professional Experience

Postdoctoral Scholar, University of Washington 2019 - present
  • Designed a scalable AI framework for integrating millions of single cell measurements from disjoint experiments with Prof. William Noble. Developed probabilistic models to robustly assess the role of inter-chromosomal interactions and investigated lncRNA-DNA bindings in the malaria parasite

Graduate Research Assistant, Princeton University 2013 - 2019
  • Investigated heterogenous disease genomes through the lens of machine learning algorithms and probabilistic models over large protein-protein interaction networks with Prof. Mona Singh

Software Engineer, Oracle Inc. 2010 - 2013
  • Participated in the design and development of Oracle's first multitenant database, introduced in 12c. Explored and solved the problems arising from consolidating pluggable databases and implemented algorithms for efficient caching of internal sql queries

Research Assistant, Brown University 2009 - 2010
  • Studied stochastic algorithms and developed statistical models to help reconstruct the evolutionary history of human genome segmental duplications with Prof. Ben Raphael

Publications

1. **Borislav Hristov**, WS Noble, A Bertero. Systematic identification of inter-chromosomal interaction networks supports the existence of RNA factories. *In revision, Genome Research*

2. Hollin Thomas, Abel Steven, **Borislav Hristov**, et al. Proteome-wide identification of RNA-dependent proteins: an emerging role for RNAs in Plasmodium falciparum protein complexes. *Accepted, Nature Communications*

3. Anupama Jha, **Borislav Hristov**, et al. Predicting trans Hi-C contacts from DNA sequence with TwinC. *Submitted to ISMB*

4. Fang T, ... **Borislav Hristov**, et al. Enhancing Hi-C contact matrices for loop detection with Capricorn, a multi-view diffusion model. *Submitted to RECOMB*

5. Batugedara G, Xueqing M. Lu, **Borislav Hristov**, et al. Novel insights into the role of long non-coding RNA in the human malaria parasite, Plasmodium falciparum. *Nature Communications 14, 2023, 5086*

6. **Borislav Hristov**, Jeffrey A. Bilmes, and William Stafford Noble. Linking cells across single-cell modalities by synergistic matching of neighborhood structure. *Bioinformatics 38, 2022, 148-154*

7. **Borislav Hristov**, B. Chazelle, and Mona Singh. uKIN Combines New and Prior Information with Guided Network Propagation to Accurately Identify Disease Genes. *Cell Systems 10.6, 2020, 470-479*

8. KB Cook, **Borislav Hristov**, et al. Measuring significant changes in chromatin conformation with ACCOST. *Nucleic acids research 48.5, 2020, 2303-2311*

9. **Borislav Hristov**, B. Chazelle, and Mona Singh A guided network propagation approach to identify disease genes that combines prior and new information. *Research in Computational Molecular Biology, RECOMB Proceedings 24, 2020*

10. **Borislav Hristov**. Deciphering Disease Genomes in a Network Context. *Doctoral Thesis, Princeton University, 2019*

11. **Borislav Hristov** and Mona Singh. Network-based coverage of mutational profiles reveals cancer genes. *Cell Systems, volume 5, 2017, 221-229*

12. Dao P, ... **Borislav Hristov**, et al. Algorithmic Advances and Applications from RECOMB 2017 *Cell Systems, volume 5, 2017, 176-186*

13. C.L. Kahn, **Borislav Hristov**, and B.J. Raphael. Parsimony and likelihood reconstruction of human segmental duplications. *Bioinformatics (Proceedings of the 9th European Conference on Computational Biology (ECCB))* 26(18):i446-52

Teaching Experience

Assistant Instructor, Princeton University   2014 - 2017
    • Taught weekly precepts for *COS551: Introduction to Genomics and Computational Molecular Biology, COS234: An Integrated, Quantitative Introduction to the Natural Sciences* and *COS126: Introduction to Computer Science*
    • Oversaw students' semester-long projects (*COS551*)
    • Designed and graded exams, held office hours (*COS234, COS126*)

Head Teaching Assistant, Brown University   2009 - 2010
    • Supervised the work of undergraduate teaching assistants
    • Proposed new class projects
    • Created and graded exams
CS149: Combinatorial Optimizations; *CS155: Probabilistic Algorithms*; *CS16: Data Structures*

Teaching Assistant, Brown University   2007 - 2008
    • Graded assignments, held office hours
MATH18: Advanced Calculus, CS16: Data Structures, CS155: Probabilistic Algorithms

Grants

- Contributed to R01-CA208148 *Interaction-based computational methods for analyzing cancer genomes*
  PI: Mona Singh; my contribution: preliminary data analysis and writing for one aim
- Contributed to R01-HG011466 *Deep tensor genomic imputation*
  PI: William Noble; my contribution: preliminary data analysis and writing for one aim

Awards & Honors

UW Data Science Postdoctoral Award for emerging interdisciplinary scientist with impactful research in the area of data science	2020 - 2023
Princeton Gordon Wu Fellowship for outstanding doctoral studies	2013 - 2018
Senior Prize for exceptional teaching service, Brown University	2010
Sidney E. Frank Scholar, recipient of dedicated financial assistance for students in need, Brown University	2006 - 2010
UTRA - Undergraduate Teaching and Research Award, Brown University	2009

Selected Talks

- Computational Biology Seminar, Department of Genome Sciences, University of Washington — 2023
  "Computational identification of inter-chromosomal interaction networks"
- European Conference on Computational Biology (**ECCB**), Barcelona, Spain — 2022
  "Linking cells across modalities by synergistic matching of neighborhood structure"
- Biomathematics Seminar, Institute of Mathematics and Informatics, Sofia, Bulgaria — 2021
  "Application of supermodular optimization to single cell genomics"
- Research in Computational Molecular Biology (**RECOMB**) Conference, Padova, Italy — 2020
  "Combining new and prior information with guided network propagation to accurately identify disease genes"
- Big Data Series, eScience Institute, University of Washington — 2020
  "Finding needle in a haystack of mutations: detecting rare cancer-driving variants"
- National Institutes of Health (**NIH**) Computational Biology Seminar, Bethesda, MD — 2019
  "Network algorithms for interrogating cancer genomes"
- Computational Genomics Seminar, School of Medicine, UC San Diego — 2019
  "Deciphering disease genomes through the lens of protein interaction networks"
- Society for Industrial and Applied Mathematics (**SIAM**) Conference, Denver, CO — 2018
  "Detecting low frequency disease-causing variants via random walks"
- Research in Computational Molecular Biology (**RECOMB**) Conference, Hong Kong, HK — 2017
  "Network-based coverage of mutational profiles reveals cancer genes"

Service

Conference reviewer
- International Conference on Machine Learning (ICML 2021, 2023)
- Machine Learning in Computational Biology (MLCB 2022, 2023)
- Intelligent Systems For Molecular Biology (ISMB 2020)
- Research in Computational Molecular Biology (RECOMB 2019, 2020, 2021, 2022, 2023)
- Machine-learning Methods for Single-cell Analysis Workshop (ACM-BCB 2021)

Journal reviewer
- Bioinformatics, Algorithms for Molecular Biology, PLOS Computational Biology, Journal of Computational Biology, Frontiers in Genetics, Nucleic Acids Research, Briefings in Bioinformatics

College Admission Interviewer, Brown University   2011 - 2021

Science Outreach Advocate, summer bridge research program for students from underprivileged communities, Princeton University   2014 - 2016

References

William Noble, *Professor*, Department of Computer Science and Department of Genome Sciences, University of Washington, Seattle, Washington
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Mona Singh, *Professor*, Department of Computer Science and Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, New Jersey
mona@cs.princeton.edu   +1 609-258-2087

Alessandro Bertero, *Associate Professor*, Department of Molecular Biotechnology and Health Sciences, University of Turin, Italy
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Jeffrey Bilmes, *Professor*, Department of Electrical Engineering, University of Washington, Seattle, Washington
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