

Lenwood Scott Heath

Curriculum Vitae

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CONTACT INFORMATION

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EDUCATION

Ph.D., Computer Science, University of North Carolina, Chapel Hill, 1985

Dissertation: **Algorithms for Embedding Graphs in Books**

M.S., Mathematics, University of Chicago, 1976

B.S., Mathematics, University of North Carolina, Chapel Hill, 1975

RESEARCH INTERESTS

Algorithms, theoretical computer science, graph theory, bioinformatics, computational biology, computational epidemiology, genomics, probability, symbolic computation, computational algebra, parallel architectures, graph embeddings, topology, computational geometry

PROFESSIONAL EXPERIENCE

- 2021– Affiliated Faculty of the Center for Advanced Innovation in Agriculture (CAIA), Virginia Polytechnic Institute and State University, Blacksburg, VA
- 2020– Affiliated Faculty of the Center for Emerging, Zoonotic, and Arthropod-borne Pathogens (CeZAP), Virginia Polytechnic Institute and State University, Blacksburg, VA
- 2019–2021 Member of the Quantum Information Science and Engineering (QISE) Working Group, Virginia Polytechnic Institute and State University, Blacksburg, VA
- 2018– Member of Microbial Systems, Virginia Polytechnic Institute and State University, Blacksburg, VA
- 2014– Faculty of Health Sciences, Virginia Polytechnic Institute and State University, Blacksburg, VA
- 2011– Sanghani Center for Artificial Intelligence and Data Analytics (Formerly, the Discovery Analytics Center (DAC)), Virginia Polytechnic Institute and State University, Blacksburg, VA
- 2003– Faculty of the Genomics, Bioinformatics, and Computational Biology PhD program, Founding Faculty Member, Virginia Polytechnic Institute and State University, Blacksburg, VA
- 2003– Professor of Computer Science, Virginia Polytechnic Institute and State University, Blacksburg, VA
- 1993–2003 Associate Professor of Computer Science, Virginia Polytechnic Institute and State University, Blacksburg, VA
- 1987–1993 Assistant Professor of Computer Science, Virginia Polytechnic Institute and State University, Blacksburg, VA
- 1985–1987 Instructor of Applied Mathematics, Theoretical Computer Science Group, Department of Mathematics, Massachusetts Institute of Technology, Cambridge, MA

JOURNAL PAPERS

Published

- [1] “Investigating the Nature of Prokaryotic Genomic Island Locations Within a Genome,” Reem Aldaihani and Lenwood S. Heath. **PLOS ONE**, 2024, 14 pages.
- [2] “A Deep-Learning Approach for Identifying Prospective Chemical Hazards,” Sohaib Habiballah, Lenwood S. Heath, and Brad Reisfeld. **Toxicology** **501**, 2024, 9 pages.
- [3] “Genomic Delineation and Description of Species and Within-species Lineages in the Genus *Pantoea*,” Katherine C. Crosby, Mariah Rojas, Parul Sharma, Marcela Aguilera Johnson, Reza Mazloom, Brian H. Kvitko, Theo H. M. Smits, Stephanus N. Venter, Teresa A. Coutinho, Lenwood S. Heath, Marike Palmer, and Boris A. Vinatzer. **Frontiers in Microbiology** **14**, 2023, 23 pages.

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- [4] “ARGem: A New Metagenomics Pipeline for Antibiotic Resistance Genes: Metadata, Analysis, and Visualization,” Xiao Liang, Jingyi Zhang, Yoonjin Kim, Josh Ho, Kevin Liu, Ishi Keenum, Suraj Gupta, Benjamin Davis, Shannon L. Hepp, Liqing Zhang, Kang Xia, Katharine F. Knowlton, Jingqiu Liao, Peter J. Vikesland, Amy Pruden, and Lenwood S. Heath. **Frontiers in Genetics** **14**, 2023, 14 pages.
- [5] “Towards Understanding Paleoclimate Impacts on Primate De Novo Genes,” Xiao Liang and Lenwood S. Heath. **G3: Genes—Genomes—Genetics**, 2023, 14 pages.
- [6] “Adaptive Group Testing Strategy for Infectious Diseases using Social Contact Graph Partitions,” Jingyi Zhang and Lenwood S. Heath. **Scientific Reports** **13**, 2023, 16 pages.
- [7] “A Complete Theoretical Framework for Inferring Horizontal Gene Transfers using Partial Order Sets,” Nahla A. Belal and Lenwood S. Heath. **PLOS ONE**, 2023, 39 pages.
- [8] “A Time Evolving Online Social Network Generation Algorithm,” Pouyan Shirzadian, Blessy Antony, Akshaykumar Gattani, Nure Tasnina, and Lenwood S. Heath. **Scientific Reports** **13**, 2023, 14 pages.
- [9] “Connecting Genomic Islands across Prokaryotic and Phage Genomes via Protein Families,” Reem Aldaihani and Lenwood S. Heath. **Scientific Reports** **13**, 2023, 9 pages.
- [10] “HT-ARGfinder: A Comprehensive Pipeline for Identifying Horizontally Transferred Antibiotic Resistance Genes and Directionality in Metagenomic Sequencing Data,” Badhan Das, Muhit Islam Emon, Nazifa Ahmed Moumi, Justin Sein, Amy Pruden, Lenwood S. Heath, and Liqing Zhang. **Frontiers in Environmental Science** **10**, 2022, 9 pages.
- [11] “Investigating Plant Disease Outbreaks with Long-read Metagenomics: Sensitive Detection and Strain-level Identification of *Xylella fastidiosa*,” Marcela A. Johnson, Haijie Liu, Elizabeth Bush, Parul Sharma, Shu Yang, Reza Mazloom, Lenwood S. Heath, Mizuho Nita, Song Li, and Boris A. Vinatzer. **Microbial Genomics** **8**, 2022, 14 pages.
- [12] “Could a Focus on the “Why” of Taxonomy Help Taxonomy Better Respond to the Needs of Science and Society?” Leighton Pritchard, C. Titus Brown, Bailey Harrington, Lenwood S. Heath, N. Tessa Pierce-Ward, and Boris Vinatzer. **Frontiers in Microbiology** **13**, Evolutionary and Genomic Microbiology, 2022, 4 pages.
- [13] “Meta Analysis of the *Ralstonia solanacearum* Species Complex (RSSC) Based on Comparative Evolutionary Genomics and Reverse Ecology,” Parul Sharma, Marcela A. Johnson, Reza Mazloom, Caitilyn Allen, Lenwood S. Heath, Tiffany M. Lowe-Power, and Boris A. Vinatzer. **Microbial Genomics** **8**, 2022, 14 pages.
- [14] “Developmental gene regulatory network connections predicted by machine learning from gene expression data alone,” Jingyi Zhang, Farhan Ibrahim, Emily Najmulski, George Katholos, Doaa Altarawy, Lenwood S. Heath, and Sarah L. Tulin. **PLOS ONE** **16**, 2021, 17 pages.
- [15] “MetaMLP: A Fast Word Embedding Based Classifier to Profile Target Gene Databases in Metagenomic Samples,” Gustavo Arango-Argoty, Lenwood S. Heath, Amy Pruden, Peter Vikesland, and Liqing Zhang. **Journal of Computational Biology** **28**, 2021, 12 pages.

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- [16] “Next Generation Sequencing Approaches to Evaluate Water and Wastewater Quality,” Emily Garner Benjamin C. Davis, Erin Milligan, Matthew F. Blair, Ishi Keenum, Ayella Maile-Moskowitz, Jin Pan, Mariah Gnegy, Krista Liguori, Suraj Gupta, Aaron J. Prussin, Linsey C. Marr, Lenwood S. Heath, Peter J. Vikesland, Liqing Zhang, and Amy Pruden. **Water Research** **194**, 2021, 24 pages.
- [17] “LINflow: A Computational Pipeline that Combines an Alignment-free with an Alignment-based Method to Accelerate Generation of Accurate Similarity Matrices for Prokaryotic Genomes,” Long Tian, Reza Mazloom, Lenwood S. Heath, and Boris A. Vinatzer. **PeerJ**, 2021, 17 pages.
- [18] “AgroSeek: A System for Computational Analysis of Environmental Metagenomic Data and Associated Metadata,” Xiao Liang, Kyle Akers, Ishi Keenum, Lauren Wind, Suraj Gupta, Chaoqi Chen, Reem Aldaihani, Amy Pruden, Liqing Zhang, Katharine F. Knowlton, Kang Xia, and Lenwood S. Heath. **BMC Bioinformatics** **22**, 2021, 14 pages.
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- [20] “Computing Genomic Signatures Using de Bruijn Chains,” Lenwood S. Heath and Amrita Pati. **Advances in Computing and Engineering** **1**, 2021, 26 pages.
- [21] “Characterization of Protein-protein Interactions Between Rice Viruses and Vector Insects,” Junjie Zhu, Fatma Elzahraa Eid, Lu Tong, Wan Zhao, Wei Wang, Lenwood S. Heath, Le Kang, and Feng Cui. **Insect Science** **28**, 2021, 976–986.
- [22] “Strain-level Identification of Bacterial Tomato Pathogens Directly from Metagenomic Sequences,” Marco E. Mechan Llontop, Parul Sharma, Marcela Aguilera Flores, Shu Yang, Jill Pollock, Long Tian, Chenjie Huang, Lenwood S. Heath, Steve Rideout, Song Li, and Boris A. Vinatzer. **Phytopathology** **110**, 2020, 12 pages.
- [23] “LINbase: A Web Server for Genome-based Identification of Prokaryotes as Members of Crowdsourced Taxa,” Long Tian, Chengjie Huang, Reza Mazloom, Lenwood S. Heath, and Boris A. Vinatzer. **Nucleic Acids Research**, 2020, 9 pages.
- [24] “ARGminer: A Web Platform for Crowdsourcing-based Curation of Antibiotic Resistance Genes,” Gustavo Alonso Arango-Argoty, Giselle K. P.Guron, Emily Garner, Virginia Riquelme, Peter J. Vikesland, and Liqing Zhang. **Bioinformatics**, 2020, 8 pages.
- [25] “Comparing Time Series Transcriptome Data Between Plants Using a Network Module Finding Algorithm,” Jiyoung Lee, Lenwood S. Heath, Ruth Grene, and Song Li. **Plant Methods** **15**, 2019, 16 pages.
- [26] “NanoARG: A Web Service for Contextualizing Antimicrobial Resistance Genes Identified from Nanopore-Derived Metagenomes,” Gustavo Arango, Dongjuan Dai, Amy Pruden, Peter Vikesland, Lenwood S Heath, and Liqing Zhang. **Microbiome** **7**, 2019, 18 pages.
- [27] “Cyberbiosecurity Challenges of Pathogen Genome Databases,” Boris A. Vinatzer, Lenwood S. Heath, Hussain Almohri, Micheal J. Stuhlberg, Christopher Lowe, and Song Li. **Frontiers in Bioengineering and Biotechnology**, 2019, 11 pages.

- [28] “Effect of Antibiotic Use and Composting on Antibiotic Resistance Gene Abundance and Resistome Risks of Soils Receiving Manure-derived Amendments,” Chaoqi Chen, Christine A. Pankow, Min Oh, Lenwood S. Heath, Liqing Zhang, Pang Du, Kang Xia, and Amy Pruden. **Environment International** **128**, 2019, 233–243.
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- [35] “Beacon Editor: Capturing Signal Transduction Pathways Using the SBGN Activity Flow Language,” Haitham Elmarakeby, Mostafa Arefiyan, Elijah Myers, Song Li, Ruth Grene, and Lenwood S. Heath. **Journal of Computational Biology** **24**, 2017, 4 pages.
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- [40] “Computational Identification of Tissue-Specific Splicing Regulatory Elements in Human Genes from RNA-Seq Data,” Eman Badr and Lenwood S. Heath. **PLOS ONE** **11**, 2016, 18 pages.
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- [42] “Metagenomic Profiling of Historic Colorado Front Range Flood Impact on Distribution of Riverine Antibiotic Resistance Genes,” Emily Garner, Joshua Wallace, Gustavo Argoty, Caitlin Wilkinson, Nicole Fahrenfeld, Lenwood S. Heath, Liqing Zhang, Mazdak Arabi, Diana Aga, and Amy Pruden. **Scientific Reports** **6**, 2016, 10 pages.
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- [44] “DeNovo: Virus-Host Sequence-Based Protein-Protein Interaction Prediction,” Fatma-Elzahraa Eid, Mahmoud ElHefnawi, and Lenwood S. Heath. **Bioinformatics** **32**, 2016, pp. 1144-1150.
- [45] “Potential Targets of VIVIPAROUS1/ABI3-LIKE1 (VAL1) Repression in Developing *Arabidopsis thaliana* Embryos,” Andrew Schneider, Delasa Aghamirzaie, Haitham Elmarakeby, Arati N. Poudel, Abraham J. Koo, Lenwood S. Heath, Ruth Grene, and Eva Collakova. **The Plant Journal** **85**, 2016, pp. 305–319.
- [46] “Transcriptome-wide Functional Characterization Reveals Novel Relationships Among Differentially Expressed Transcripts in Developing Soybean Embryos,” Delasa Aghamirzaie, Dhruv Batra, Lenwood S. Heath, Andrew Schneider, Ruth Grene, and Eva Collakova. **BMC Genomics** **16**, 2015, 23 pages.
- [47] “CoSREM: A Graph Mining Algorithm for the Discovery of Combinatorial Splicing Regulatory Elements,” Eman Badr and Lenwood S. Heath. **BMC Bioinformatics** **16**, 2015, 15 pages.
- [48] “Similarity-Based Codes Sequentially Assigned to Ebolavirus Genomes are Informative of Species Membership, Associated Outbreaks, and Transmission Chains,” Alexandra J. Weisberg, Haitham A. Elmarakeby, Lenwood S. Heath, and Boris A. Vinatzer. **Open Forum Infectious Diseases** **2**, 2015, 11 pages.
- [49] “Identifying Splicing Regulatory Elements with de Bruijn Graphs,” Eman Badr and Lenwood S. Heath, **Journal of Computational Biology** **21**, 2014, pp. 880-897.
- [50] “A System to Automatically Classify and Name Any Individual Genome-Sequenced Organism Independently of Current Biological Classification and Nomenclature,” Haitham Marakeby, Eman Badr, Hanaa Torkey, Yuhyun Song, Scotland Leman, Caroline L. Monteil, Lenwood S. Heath, and Boris A. Vinatzer. **PLOS ONE** **9**, 2014, 12 pages.
- [51] “Mining Posets from Linear Orders,” Proceso L. Fernandez, Lenwood S. Heath, Naren Ramakrishnan, Michael Tan, and John Paul C. Vergara. **Discrete Mathematics, Algorithms and Applications** **5**, 2013, 15 pages.

- [52] “Changes in RNA Splicing in Developing Soybean (*Glycine max*) Embryos,” Delasa Aghamirzaie, Mahdi Nabiyouni, Yihui Fang, Curtis Klumas, Lenwood S. Heath, Ruth Grene, and Eva Collakova. **Biology** **2**, Special issue on Insights from Plant Genomes, 2013, 1311–1337.
- [53] “The Poset Cover Problem,” Lenwood S. Heath and Ajit K. Nema. **Open Journal of Discrete Mathematics** **3**, 2013, 101–111.
- [54] “Metabolic and Transcriptional Reprogramming in Developing Soybean (*Glycine max*) Embryos,” Eva Collakova, Delasa Aghamirzaie, Yihui Fang, Curtis Klumas, Farzaneh Tabataba, Akshay Kakumanu, Elijah Myers, Lenwood S. Heath, and Ruth Grene. **Metabolites** **3**, 2013, 26 pages.
- [55] “Evidence for Extensive Heterotrophic Metabolism, Antioxidant Action, and Associated Regulatory Events during Winter Hardening in Sitka Spruce,” Eva Collakova, Curtis Klumas, Haktan Suren, Elijah Myers, Lenwood S. Heath, Jason A. Holliday, and Ruth Grene. **BMC Plant Biology** **13**, 2013, 16 pages.
- [56] “Mining and Visualization of Microarray and Metabolomic Data Reveal Extensive Cell Wall Remodeling During Winter Hardening in Sitka Spruce (*Picea sitchensis*),” Ruth Grene, Curtis Klumas, Haktan Suren, Kuan Yang, Eva Collakova, Elijah Samuel Myers, Lenwood S. Heath, and Jason A. Holliday. **Frontiers in Plant Systems Biology** **3**, 2012, 14 pages.
- [57] “REGEN: Ancestral Genome Reconstruction for Bacteria,” Kuan Yang, Lenwood S. Heath, and João C. Setubal. **Genes** **3**, 2012, pp. 423–443.
- [58] “Mining for Meaning: Visualization Approaches to Deciphering Arabidopsis Stress Responses in Roots and Shoots,” Lecong Zhou, Christopher Franck, Kuan Yang, Guillaume Pilot, Lenwood S. Heath, and Ruth Grene. **OMICS: A Journal of Integrative Biology** **16**, 2012, pp. 208–228.
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- [61] “A Network of SCOP Hidden Markov Models and Its Analysis,” Liqing Zhang, Layne T. Watson, and Lenwood S. Heath. **BMC Bioinformatics** **12**, 2011, 11 pages.
- [62] “A Theoretical Model for Whole Genome Alignment,” Nahla A. Belal and Lenwood S. Heath. **Journal of Computational Biology** **18**, 2011, pp. 705–728.
- [63] “Differential Expression of Heat Shock Protein Genes in Preconditioning for Photosynthetic Acclimation in Water-Stressed Loblolly Pine,” Cecilia Vasquez-Robinet, Jonathan I. Watkinson, Allan A. Sioson, Naren Ramakrishnan, Lenwood S. Heath, and Ruth Grene. **Plant Biochemistry and Physiology** **48**, 2010, pp. 256–264.

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- [50] “A Generalized Comparison of Quadtree and Bintree Storage Requirements,” Clifford A. Shaffer, Ramana Juvvadi, and Lenwood S. Heath, Technical Report TR 89-23, Department of Computer Science, Virginia Polytechnic Institute and State University, 1989.
- [51] “An $O(n \log n)$ Algorithm for Finding Minimal Perfect Hash Functions,” Edward A. Fox, Lenwood S. Heath, and Qi Fan Chen, Technical Report TR 89-10, Department of Computer Science, Virginia Polytechnic Institute and State University, 1989.
- [52] “Optimal Embeddings of Butterfly-Like Graphs in the Hypercube,” David S. Greenberg, Lenwood S. Heath, and Arnold L. Rosenberg, COINS Technical Report 88-103, Computer and Information Science, University of Massachusetts at Amherst, 1988.
- [53] “Optimal Embeddings of the FFT Graph in the Hypercube,” David S. Greenberg, Lenwood S. Heath, and Arnold L. Rosenberg, COINS Technical Report 88-23, Computer and Information Science, University of Massachusetts at Amherst, 1988.
- [54] “A More Cost Effective Algorithm for Finding Perfect Hash Functions,” Edward A. Fox, Qi Fan Chen, Lenwood S. Heath, and Sanjeev Datta, Technical Report TR 88-30, Department of Computer Science, Virginia Polytechnic Institute and State University, 1988.
- [55] “An Optimal Mapping of the FFT Algorithm onto the Hypercube Architecture,” Lenwood S. Heath and Arnold L. Rosenberg, COINS Technical Report 87-19, Computer and Information Science, University of Massachusetts at Amherst, 1987.
- [56] “Algorithms for Embedding Graphs in Books,” Lenwood S. Heath, Doctoral Dissertation, Technical Report 85-028, University of North Carolina, Chapel Hill, 1985.
- [57] “Multi-layer Circuit Layouts,” Lenwood S. Heath, abstract in Proceedings of the First Microelectronics Center of North Carolina Semi-Annual Research Review, 1984.
- [58] “Final Technical Report, SRC Contract 82-11-003, Transfer of Software Methodology to VLSI Design,” Frederick P. Brooks, Jr., with Richard R. Gross and Lenwood S. Heath, University of North Carolina, Chapel Hill, 1984.
- [59] “Multi-Layer Channel Routing,” Lenwood S. Heath, in Course Projects on VLSI Algorithms: 1983, Microelectronics Center of North Carolina Technical Report 83-06, 1983.

FUNDING

Current

- [1] USDA NIFA: *Expanding an Established Genome-based Identification Resource to Surveillance of Fungal Pathogens*, \$650,000. 07-01-2023 - 06-30-2026. PI: Boris A. Vinatzer. Co-PIs: Lenwood S. Heath, David C. Haak. Personal share: 25%.
- [2] National Science Foundation 2125798: *NRT-HDR: Convergence at the Interfaces of Policy, Data Science, Environmental Science and Engineering to Combat the Spread of Antibiotic Resistance*, \$3,000,000. 09/01/2021 - 08/31/2026. PI: Amy Pruden. Co-PIs: Liqing Zhang, Leigh Anne Krometis, Todd Schenk, Tiffany Drape. Senior Personnel: Lenwood S. Heath et al. Personal share: 8%.

- [3] National Science Foundation 1918656: *Collaborative Research: Expeditions: Global Pervasive Computational Epidemiology*, \$10,000,000. 04/01/2020 - 03/31/2025. PI: Madhav V. Marathe. VT share: \$1,587,064. VT PI: Naren Ramakrishnan. VT co-PIs: Lenwood S. Heath et al. Personal share of VT share: 14%.
- [4] National Science Foundation DBI-2018522: *BBSRC-NSF/BIO:Collaborative Research: CIBR: genomeRxiv: A Microbial Whole-genome Database and Diagnostic Marker Design Resource for Classification, Identification, and Data Sharing*, \$653,114. 08/01/20 - 07/31/24. PI: Boris A. Vinatzer. Co-PI: Lenwood S. Heath. Personal share: 50%.
- [5] NSF 2243691: *Collaborative Research: RESEARCH-PGR: Unraveling the Origin of Vegetative Desiccation Tolerance in Vascular Plants*, \$2,000,000. 02/02/2023 – 01/31/2026. PI: Luis R Herrera-Estrella (Texas Tech University). Co-PI: John C Cushman (University of Nevada, Reno). Virginia Tech PI: Lenwood S. Heath. Virginia Tech funding share: \$370,704. Personal share: 100% of VT share.

Completed

- [6] USDA 2017-68003-26498: *Developing Computational Tools to Identify Critical Control Points for Mitigating the Spread of Antibiotic Resistance in Agro-ecosystem*, \$1,200,000. 05/16/17 - 05/15/23. PI: Amy J. Pruden-Bagchi. Co-PIs: Lenwood S. Heath, Katharine F. Knowlton, Kang Xia, Liqing Zhang. Personal share: 25%.
- [7] Water Research Foundation: *Standardizing Methods with QA/QC Standards for Investigating the Occurrence and Removal of Antibiotic Resistant Bacteria/Antibiotic Resistance Genes (ARB/ARGs) in Surface Water, Wastewater, and Recycled Water*, \$200,000. 09/01/2020 - 12/01/2022. PI: Amy Pruden. Co-PIs: Valerie J. Harwood, Lenwood S. Heath. Personal share: 20%.
- [8] Virginia Tech ICTAS EFO Seed Grant Award: *A Unified, Natural, and Computationally Efficient Genome-Based Classification System for All Microbes*, \$10,000. 10/17/2022 - 06/30/2023. PI: Lenwood S. Heath. Co-PI: Boris A. Vinatzer. Personal share: 50%.
- [9] Water Research Foundation: *The Use of Next Generation Sequencing (NGS) Technologies and Metagenomics Approaches to Evaluate Water and Wastewater Quality Monitoring and Treatment Technologies*, \$300,000. 10/01/2019 - 09/30/2021. PI: Amy Pruden. Co-PIs: Emily Garner, Peter Vikesland, Linsey Marr, Liqing Zhang. Senior personnel: Lenwood S. Heath, et al. Personal share: 10%.
- [10] USDA Animal and Plant Health Inspection Service (APHIS): *Genome-based Circumscription and Phenotyping of Regulated Microbes, Especially the Select Agent *Ralstonia solanacearum**, \$261,207. 08/01/19 - 08/01/21. PI: Kellye Eversole. Co-PIs: Caitilyn Allen, Mohammad Arif, Gwyn Beattie, Lenwood S. Heath, Michael Stulberg (USDA-APHIS), Boris A. Vinatzer (VT-SPES). VT share: \$129,210. Personal share: 50% of VT share.
- [11] IARPA: *Integrative Genomics Approach to Computational Assessment of Threats (IGACAT)*, \$12,622,546. 03/01/17 - 05/31/20. PI: Stephen Eubank. Research Scientist: Lenwood S. Heath. Personal share: 4%.

- [12] National Science Foundation 1545756: *PIRE: Halting Environmental Antimicrobial Resistance Dissemination (HEARD)*, \$3,333,000. 10/01/15 - 09/30/20. PI: Peter Vikesland. Co-PIs: Pedro Alvarez, Diana Aga, Amy Pruden, Krista Wigginton. Senior Personnel: Lenwood S. Heath, Liqing Zhang, *et al.* Personal share: 0%.
- [13] Virginia Tech Microbiology at the Nexus of Food, Energy, Water, and Health Systems (MicroFEWHS) concept area: *Continued Development and Enhancement of DeepARG, a Web Service for Accurate Annotation of Antibiotic Resistance Genes*, \$3,725. 12/01/2019 - 05/15/2020. PI: Liqing Zhang. Co-PIs: Lenwood S. Heath. Personal share: 50%.
- [14] Virginia Tech Microbiology at the Nexus of Food, Energy, Water, and Health Systems (MicroFEWHS) concept area: *Developing ARGminer, a Powerful Web Platform for Crowdsourcing-based Curation of Antibiotic Resistance Genes*, \$3,000. 12/01/2018 - 05/15/2019. PI: Liqing Zhang. Co-PIs: Lenwood S. Heath. Personal share: 50%.
- [15] Virginia Tech College of Agriculture and Life Sciences (CALs): *Identifying Select Agents Using a Nanopore Sequencing and Secure Cyberphysical System*, \$20,000. 05/15/2018 - 12/31/2018. PI: Song Li. Co-PIs: Lenwood S. Heath, Boris Vinatzer. Personal share: 25%.
- [16] National Science Foundation 1238057: *GEPR-Evolutionary Gain and Loss of Function in Parasitic Plant Genomes*, \$3,406,833. 08/01/13 - 07/31/18. PI: James H. Westwood. Co-PIs: Eva Collakova, Claude W. dePamphilis, Lenwood S. Heath, Aaron Mackey, Michael P. Timko, John I. Yoder. Personal share: 10%. VT share: \$934,389.
- [17] National Science Foundation DBI-1062472: *ABI Development: Representation, Visualization, and Modeling of Signaling Pathways in Higher Plants*, Advances in Biological Informatics (ABI), \$1,057,337. 04/15/11 - 03/31/17. PI: Lenwood S. Heath. Co-PIs: Ruth Grene, Andy Pereira. Personal share: 37%.
- [18] National Institutes of Health Grant 1 R25 GM066354-06: *VT Post Baccalaureate Research and Education*, National Institute of General Medical Sciences. First year: \$275,603; second year: \$276,635; third year: \$277,689; fourth year: \$278,793. 03/01/2009 - 01/31/2013. PI: Edward J. Smith; Research Mentor: Lenwood S. Heath, *et al.*
- [19] National Science Foundation ITR-0428344: *ITR-(NHS)-(sim): Computational Models for Gene Silencing: Elucidating a Pervasive Biological Defensive Response*, Information Technology Research (ITR), \$1,500,000. 09/01/04 - 8/31/10. PI: Lenwood S. Heath. Co-PIs: Richard F. Helm, Alexey Onufriev, Malcolm Potts, Naren Ramakrishnan.
- [20] National Institutes of Health Grant 1 R25 GM066354-01A1: *VT Post Baccalaureate Research and Education*, National Institute of General Medical Sciences. First year: \$254,871; second year: \$411,184; third year: \$413,757; fourth year: \$416,407; fifth year: \$419,135. 08/04/2003 - 07/31/2008. PI: Edward J. Smith; Research Mentor: Lenwood S. Heath, *et al.*
- [21] Department of Defense Multidisciplinary University Research Initiative (MURI), Defense Advanced Research Projects Agency Grant N00014-01-1-0852: *Dryophile Genes to Engineer Stasis-Recovery of Human Cells*, \$4,532,622: \$2,602,790 (basic 3-year) plus \$1,929,832

- (2-year option), 05/01/2001 – 05/31/2007. Principal investigator: Malcolm Potts. Senior Personnel: Lenwood S. Heath, Richard F. Helm, Naren Ramakrishnan, Thomas O. Sitz (Virginia Tech), Frederic Bloom, Paul Price (Life Technologies), and John Battista (Louisiana State University).
- [22] National Science Foundation Grant ITR-0219322: *ITR: Understanding Stress Resistance Mechanisms in Plants: Multimodal Models Integrating Experimental Data, Databases, and the Literature*, Division of Integrative Biology and Neuroscience (BIO/IBN) — ITR Small grants, \$499,973. 09/15/2002 - 08/31/2005. PI: Lenwood S. Heath; Co-PIs: Ruth G. Alscher, Boris I. Chevone, Naren Ramakrishnan, and Layne T. Watson. Supplemental funding of \$70,705 received February, 2005; expiration extended until 12/31/2006.
- [23] National Science Foundation Grant EIA-01903660: *A Microarray Experiment Management System*, \$600,000. 8/01/2001 – 8/31/2004. Principal investigators: Naren Ramakrishnan, Lenwood S. Heath, Layne T. Watson, Ruth G. Alscher, and Jennifer W. Weller (VBI).
- [24] Virginia Tobacco Settlement Foundation (VTSF): *Using Molecular Genetics to Target “High Risk” Youth Smokers*. Initial participation with the Virginia Tobacco Prevention Research Consortium, in particular, research in furthering the Espresso project and applying it to the needs of the consortium. \$96,000. 3/16/2002 – 3/15/2002. Principal investigators: Naren Ramakrishnan, Lenwood S. Heath.
- [25] National Science Foundation Grant INT-0000424: *U.S.-Brazil Cooperative Research: The Fine Algebraic Structure of Derivations and Hochschild Cohomology*. \$24,900, 9/1/00–8/31/03. Principal investigators: Daniel R. Farkas, Edward L. Green, and Lenwood S. Heath.
- [26] National Science Foundation Grant CCR-9732068: *A System for Symbolic Computation in Hopf Algebras*. \$180,000, 8/16/98–8/31/01. Principal investigators: Edward L. Green and Lenwood S. Heath.
- [27] Arts and Sciences Pilot Research Project Grant: *Experimenting With Algorithms for Difficult, Non-numeric Problems*. \$3,000, 12/96–12/98.
- [28] National Science Foundation Grant IRI-9116991: *A User-Centered Database from the Computer Science Literature (REU Supplement)*. \$8,000, 5/15/92–5/15/93. Principal investigator. Funding to pay two undergraduates to participate in research.
- [29] National Science Foundation Grant IRI-9116991: *A User-Centered Database from the Computer Science Literature*. \$443,391, 9/15/91–2/28/95. Equipment supplement \$29,941, 1992. Principal investigators: Edward A. Fox, Lenwood S. Heath, and Deborah Hix.
- [30] National Science Foundation Grant CCR-9009953: *Analyzing Parallel Architectures With Algebraic Topology*. \$40,000, 7/15/90–12/31/92. Principal investigator.

DOCTORAL STUDENTS SUPERVISED

- [1] Reem Aldaihani, “Identifying The Structure Of Genomic Islands In Prokaryotes,” 2022.
- [2] Siddharth Krishnan, “Seeing the Forest for the Trees: New Approaches to Characterizing and Forecasting Cascades,” 2018.
- [3] Hanaa A. Torkey, “Machine Learning Approaches for Identifying microRNA Targets and Conserved Protein Complexes,” 2017.
- [4] Fatma Elzahraa Sobhy Eid, “Predicting the Interactions of Viral and Human Proteins,” 2017.
- [5] Doaa Abdelsalam Ahmed Mohamed Altarawy, “DeTangle: A Framework for Interactive Prediction and Visualization of Gene Regulatory Networks,” 2017.
- [6] Haitham Abdulrahman Elmarakeby, “Deep Learning for Biological Problems,” 2017.
- [7] Andrew Scott Warren, “Methods for Analysis of Prokaryotic Genome Architecture,” 2017.
- [8] Eman Badr, “Identifying Splicing Regulatory Elements with de Bruijn Graphs,” 2015.
- [9] Kuan Yang, “Ancestral Genome Reconstruction in Bacteria,” 2012. Ph.D. in Genetics, Bioinformatics, and Computational Biology. Co-advisor with João C. Setubal of the Virginia Bioinformatics Institute.
- [10] Nahla A. Belal, “Two Problems in Computational Genomics,” 2011.
- [11] Amrita Pati, “Graph-Based Genomic Signatures,” 2008.
- [12] Allan A. Sioson, “Multimodal Networks in Biology,” 2005.
- [13] Douglas J. Slotta, “Evaluating Biological Data Using Rank Correlation Methods,” 2005.
- [14] Craig A. Struble, “Analysis and Implementation of Algorithms for Noncommutative Algebra,” 2000. Co-advisor with Edward L. Green of the Department of Mathematics.
- [15] John Paul A. Vergara, “Sorting by Bounded Rearrangements,” 1997.
- [16] Benjamin J. Keller, “Algorithms and Orders for Finding Noncommutative Gröbner Bases,” 1997. Co-advisor with Edward L. Green of the Department of Mathematics.
- [17] Ramana R. Juvvadi, “Perfect Hashing and Some Related Problems,” 1993.
- [18] Sriram V. Pemmaraju, “Exploring the Powers of Stacks and Queues via Graph Layouts,” 1992.

MASTERS THESIS STUDENTS SUPERVISED

- [1] Aarathi Raghuraman, “Predicting Mutational Pathways of Influenza A H1N1 Virus using Q-learning,” 2021.
- [2] Ashkan Nazari, “Machine Learning Application in Energy Storage System’s State Estimation: State of Health (SOH),” 2021.
- [3] Jeffrey A. Robertson, “Entropy Measurements and Ball Cover Construction for Biological Sequences,” 2018.
- [4] Yanshen Yang, “MCAT: Motif Combining and Association Tool,” 2018.
- [5] Rathna Senthil, “IDLE: A Novel Approach to Improving Overlapping Community Detection in Complex Networks,” 2016.
- [6] Ying Ni, “A Machine Learning Approach to Predict Gene Regulatory Networks in Seed Development in Arabidopsis Using Time Series Gene Expression Data,” 2016.
- [7] Deepti Aggarwal, “Inferring Signal Transduction Pathways from Gene Expression Data using Prior Knowledge,” 2015.
- [8] Nidhi Kiranbhai Parikh, “Generating Random Graphs with Tunable Clustering Coefficient,” 2011.
- [9] Amrita Pati, “Modeling and Analysis of Regulatory Elements in *Arabidopsis thaliana* from Annotated Genomes and Gene Expression Data,” 2005.
- [10] Maulik Shukla, “GeneSieve: A Probe Selection Strategy for cDNA Microarrays,” 2004.
- [11] Harsha K. Rajasimha, “PathMeld: A Methodology for The Unification of Metabolic Pathway Databases,” 2004.
- [12] Guillermo Averboch, “A System for Document Analysis, Translation, and Automatic Hypertext Linking,” 1995.
- [13] Fred L. Drake, Jr., “odb/Tools Project Report,” 1995.
- [14] Dennis J. Brueni, “Minimal PMU Placement for Graph Observability: A Decomposition Approach,” 1993.
- [15] John Paul A. Vergara, “Edge-packing by Isomorphic Subgraphs,” 1990.
- [16] Thurman W. Tunnell, “Development of New Heuristics for the Euclidean Traveling Salesman Problem,” 1989.

PROFESSIONAL ORGANIZATIONS

Association of Computing Machinery, Member

Institute of Electrical and Electronics Engineers (IEEE), Lifetime Senior Member

IEEE Computer Society, Lifetime Member

Models of Infectious Disease Agent Study (MIDAS) Network, Member

Society for Industrial and Applied Mathematics (SIAM), Lifetime Member

SIAM Activity Group on Discrete Mathematics

SIAM Activity Group on Life Sciences

PROFESSIONAL SERVICE

2021 Program Committee Member, IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 2021.

2020 Program Committee Member, IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 2020.

2017–20 Associate Editor, Mathematical Foundations of Computing (MFOC).

2017– Managing Editor, Journal of Interconnection Networks (JOIN).

2017 Guest editor-in-chief of the **Special Issue of the Proceedings of the IEEE on Bioinformatics of DNA**, March, 2017. Other guest editors are Hector Corrada Bravo, Mario Caccamo, and Michael Schatz. “Scanning the Issue: Bioinformatics of DNA,” Lenwood S. Heath, Hector Corrada Bravo, Mario Caccamo, and Michael Schatz. Guest editor introduction. Proceedings of the IEEE 105, 2017, 419–421.

2013–17 Editor, New Journal of Science.

2011–14 Editor, ISRN Computational Mathematics

2011 Member of program committee of **First IEEE Conference on Healthcare Informatics, Imaging, and Systems Biology (HISB) 2011**.

2010 Member of program committee of **33rd Annual ACM SIGIR Conference 2010**.

2005 Member of program committee of **Brazilian Symposium on Bioinformatics 2005**.

Moderator for panel on systems biology at the Biomedical Engineering Research and Science Conference, March 4, 2005. Sponsored by the Virginia Tech National Capital Region and College of Engineering and by the Wake Forest University School of Medicine.

2003–16 Editor, Journal of Interconnection Networks (JOIN).

2002 Guest editor, with Naren Ramakrishnan, of the **Special Issue of IEEE Computer on Bioinformatics Software**, July, 2002.

Member of program committee of **High Performance Computing Symposium 2002 (HPC 2002)**, accepted six papers for two tracks on Bioinformatics Applications.

1995–2000

ACM Special Interest Group on Automata and Computability Theory (SIGACT) Theory Calendar. Maintained WWW calendar of conferences and other events of interest to the theory community. Calendar also appeared as a column four times a year in **SIGACT News**.

HONORS AND AWARDS

Sigma Xi, The Scientific Research Honor Society, 1991

Department of Computer Science, Virginia Tech, Outstanding Department Contributor Award for Exemplary Faculty Service, 2019

Institute of Electrical and Electronics Engineers, Lifetime Senior Member, 2018

Institute of Electrical and Electronics Engineers, Senior Member, 1999

Board of Governor's Fellowship in Science and Technology, University of North Carolina, Chapel Hill, 1984

Archibald Henderson Prize for outstanding undergraduate in mathematics, University of North Carolina, Chapel Hill, 1975

Phi Beta Kappa, University of North Carolina, Chapel Hill, 1973

Jackson Tuition Scholarship, University of North Carolina, Chapel Hill, 1971

National Merit Scholarship, 1971

Westinghouse Science Talent Search winner, 1971

National Science Foundation Student Science Training Program, University of North Carolina, Chapel Hill, Summer 1970; first in mathematics class

Governor's School, Winston-Salem, NC, Summer, 1969