

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

2025– **Professor Emeritus of Computer Science**, Virginia Polytechnic Institute and State University, Blacksburg, VA

2021– Affiliated Faculty of the Center for Advanced Innovation in Agriculture (CAIA), Virginia Polytechnic Institute and State University, Blacksburg, VA

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- 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
- 2014– Faculty of Health Sciences, Virginia Polytechnic Institute and State University, Blacksburg, VA
- 2011– Faculty of 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 (GBCB) PhD program, Founding Faculty Member, Virginia Polytechnic Institute and State University, Blacksburg, VA
- 2003–2025 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
- 1984–1985 Research Assistant, Duke University, Durham, NC; VLSI theory
- 1983 Instructor, University of North Carolina, Chapel Hill; computer organization
- 1982–1983 Research Assistant, University of North Carolina, Chapel Hill; transfer of software engineering technology to VLSI design
- 1981–1982 Teaching Assistant, University of North Carolina, Chapel Hill; NMOS and CMOS VLSI, language and automata theory
- 1977–1982 Software Engineer, Telex Terminal Communications, Raleigh, NC; application of microprocessors to communications
- 1976–1977 President and Engineer, Micronics, Inc., Greenville, NC; microcomputer products
- 1973–1975 Programmer, Burroughs-Wellcome Co., Greenville, NC; scientific and business programming; summer employment

JOURNAL PAPERS

Published

- [1] “Variant Evolution Graph: Can We Infer How SARS-CoV-2 Variants are Evolving?,” Badhan Das and Lenwood S. Heath. **PLOS ONE** **20**, 2025, 25 pages.
- [2] “Genotypic and Phenotypic Analyses Show *Ralstonia solanacearum* Cool Virulence is a Quantitative Trait Not Restricted to ‘Race 3 biovar 2’,” Ronnie J. Dewberry, Parul Sharma, Jessica L. Prom, Noah A. Kinscherf, Tiffany Lowe-Power, Reza Mazloom, Xuemei Zhang, Mohammad Arif, Michael Stulberg, Lenwood S. Heath, Kellye Eversole, Gwyn A. Beattie, Boris Vinatzer, and Caitilyn Allen. **Phytopathology**, 2024, 13 pages.
- [3] “LINGroups as a Robust Principled Approach to Compare and Integrate Multiple Bacterial Taxonomies,” Reza Mazloom, N. Tessa Pierce-Ward, Parul Sharma, Leighton Pritchard, C. Titus Brown, Boris A. Vinatzer, and Lenwood S. Heath. **IEEE/ACM Transactions on Computational Biology and Bioinformatics**, 2024, 2304–2314.
- [4] “Investigating the Nature of Prokaryotic Genomic Island Locations Within a Genome,” Reem Aldaihani and Lenwood S. Heath. **PLOS ONE**, 2024, 14 pages.
- [5] “A Deep-Learning Approach for Identifying Prospective Chemical Hazards,” Sohaib Habiballah, Lenwood S. Heath, and Brad Reisfeld. **Toxicology** **501**, 2024, 9 pages.
- [6] “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.
- [7] “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.
- [8] “Towards Understanding Paleoclimate Impacts on Primate De Novo Genes,” Xiao Liang and Lenwood S. Heath. **G3: Genes—Genomes—Genetics**, 2023, 14 pages.
- [9] “Adaptive Group Testing Strategy for Infectious Diseases using Social Contact Graph Partitions,” Jingyi Zhang and Lenwood S. Heath. **Scientific Reports** **13**, 2023, 16 pages.
- [10] “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.
- [11] “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.
- [12] “Connecting Genomic Islands across Prokaryotic and Phage Genomes via Protein Families,” Reem Aldaihani and Lenwood S. Heath. **Scientific Reports** **13**, 2023, 9 pages.

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- [13] “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 Mouni, Justin Sein, Amy Pruden, Lenwood S. Heath, and Liqing Zhang. **Frontiers in Environmental Science** **10**, 2022, 9 pages.
- [14] “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.
- [15] “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.
- [16] “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.
- [17] “Developmental Gene Regulatory Network Connections Predicted by Machine Learning from Gene Expression Data Alone,” Jingyi Zhang, Farhan Ibrahim, Emily Najmowski, George Katholos, Doaa Altarawy, Lenwood S. Heath, and Sarah L. Tulin. **PLOS ONE** **16**, 2021, 17 pages.
- [18] “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.
- [19] “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.
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- [21] “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.
- [22] “Systematic Auditing is Essential to Debiasing Machine Learning in Biology,” Fatma-Elzahraa Eid, Haitham Elmarakeby, Yujia Alina Chan, Nadine Fornelos, Mahmoud ElHefnawi, Eli Van Allen, Lenwood S. Heath, and Kasper Lage. **Communications Biology** **4**, 2021, 9 pages.

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- [23] “Computing Genomic Signatures Using de Bruijn Chains,” Lenwood S. Heath and Amrita Pati. **Advances in Computing and Engineering** **1**, 2021, 26 pages.
- [24] “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.
- [25] “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.
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- [27] “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.
- [28] “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.
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- [31] “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.
- [32] “MCAT: Motif Combining and Association Tool,” Yanshen Yang, Jeffrey A. Robertson, Zhen Guo, Jake Martinez, Christy Coghlan, and Lenwood S. Heath. **Journal of Computational Biology** **26**, 2018, 15 pages.
- [33] “MetaCompare: A Computational Pipeline for Prioritizing Environmental Resistome Risk,” Min Oh, Amy Pruden, Lenwood S. Heath, Kang Xia, and Liqing Zhang. **FEMS Microbiology Ecology** **94**, 2018, 9 pages.
- [34] “DeepARG: A Deep Learning Approach for Predicting Antibiotic Resistance Genes from Metagenomic Data,” Gustavo Arango-Argoty, Emily Garner, Amy Pruden, Lenwood S. Heath, Peter Vikesland, and Liqing Zhang. **Microbiome** **6**, 2018, 15 pages.
- [35] “Identification of Regulatory Modules in Genome Scale Transcription Regulatory Networks,” Qi A. Song, Ruth Grene, Lenwood S. Heath, and Song Li. **BMC Systems Biology** **18**, 2017, 18 pages.

- [36] “PEAK: Integrating Curated and Noisy Prior Knowledge in Gene Regulatory Network Inference,” Doaa Altarawy, Fatma-Elzahraa Eid, and Lenwood S. Heath. **Journal of Computational Biology** **24**, 2017, 863–873.
- [37] “MicroTarget: MicroRNA Target Gene Prediction Approach with Application to Breast Cancer,” Hanaa Torkey, Lenwood S. Heath, and Mahmoud Elhefnawi. **Journal of Bioinformatics and Computational Biology** **15**, 2017, 17 pages.
- [38] “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.
- [39] “Expresso: A Database and Web Server for Exploring the Interaction of Transcription Factors and Their Target Genes in *Arabidopsis thaliana* Using ChIP-Seq Data,” Delasa Aghamirzaie, Karthik Raja Velmurugan, Shuchi Wu, Doaa Altarawy, Lenwood S. Heath, and Ruth Grene. **F1000Research** **6**, 2017, 5 pages.
- [40] “A Proposal for a Portal to Make Earth’s Microbial Diversity Easily Accessible and Searchable,” Boris A. Vinatzer, Long Tian, and Lenwood S. Heath. **Antonie van Leeuwenhoek** **110**, 2017, 1271–1279.
- [41] “A Proposal for a Precise Genome Similarity-based Taxonomy for Plant Pathogenic Bacteria that is Sufficiently Precise to Reflect Phylogeny, Host Range, and Outbreak Affiliation Applied to *Pseudomonas syringae sensu lato* as a Proof of Concept,” Boris A. Vinatzer, Alexandra J. Weisberg, Caroline L. Monteil, Haitham A. Elmarakeby, Samuel K. Sheppard, and Lenwood S. Heath. **Phytopathology** **107**, 2017, pp. 18–28.
- [42] “Labeled Cuts in Graphs,” Tridib Dutta, Lenwood S. Heath, V. S. Anil Kumar, and Madhav V. Marathe. **Theoretical Computer Science** **648**, 2016, pp. 34–39.
- [43] “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.
- [44] “A Machine Learning Approach to Predict Gene Regulatory Networks in Seed Development in Arabidopsis,” Ying Ni, Delasa Aghamirzaie, Haitham Elmarakeby, Eva Collakova, Song Li, Ruth Grene, and Lenwood S. Heath. **Frontiers in Plant Science** **7**, 2016, 13 pages.
- [45] “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.
- [46] “MetaStorm: A Public Resource for Customizable Metagenomics Annotation,” Gustavo Arango-Argoty, Gargi Singh, Lenwood S. Heath, Amy Pruden, Weidong Xiao, and Liqing Zhang. **PLOS ONE** **11**, 2016, 13 pages.
- [47] “DeNovo: Virus-Host Sequence-Based Protein-Protein Interaction Prediction,” Fatma-Elzahraa Eid, Mahmoud Elhefnawi, and Lenwood S. Heath. **Bioinformatics** **32**, 2016, pp. 1144–1150.

- [48] “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.
- [49] “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.
- [50] “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.
- [51] “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.
- [52] “Identifying Splicing Regulatory Elements with de Bruijn Graphs,” Eman Badr and Lenwood S. Heath, **Journal of Computational Biology** **21**, 2014, pp. 880-897.
- [53] “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.
- [54] “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.
- [55] “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.
- [56] “The Poset Cover Problem,” Lenwood S. Heath and Ajit K. Nema. **Open Journal of Discrete Mathematics** **3**, 2013, 101–111.
- [57] “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.
- [58] “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.

- [59] “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.
- [60] “REGEN: Ancestral Genome Reconstruction for Bacteria,” Kuan Yang, Lenwood S. Heath, and João C. Setubal. **Genes** **3**, 2012, pp. 423–443.
- [61] “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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- [63] “Generating Random Graphs with Tunable Clustering Coefficient,” Lenwood S. Heath and Nidhi Parikh. **Physica A** **390**, 2011, pp. 4577–4587.
- [64] “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.
- [65] “A Theoretical Model for Whole Genome Alignment,” Nahla A. Belal and Lenwood S. Heath. **Journal of Computational Biology** **18**, 2011, pp. 705–728.
- [66] “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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- [69] “Molecular and Physiological Adaptation to Prolonged Drought Stress in the Leaves of two Andean Potato Genotypes,” Srinivasrao P. Mane, Cecilia Vasquez Robinet, Alexander Ulanov, Roland Schafleitner, Luz Tincopa, Amelie Gaudin, Giannina Nomberto, Carlos Alvarado, Christian Solis, Luis Avila Bolivar, Raul Blas, Oscar Ortega, Julio Solis, Ana Panta, Cristina Rivera, Ilanit Samolski, Doris H. Carbajulca, Meredith Bonierbale, Amrita Pati, Lenwood S. Heath, Hans J. Bohnert and Ruth Grene, **Functional Plant Biology** **35**, 2008, pp. 669–688.
- [70] “Tuber Development Phenotypes in Adapted and Acclimated, Drought-stressed *Solanum tuberosum* ssp. andigena Have Distinct Expression Profiles of Genes Associated with Carbon Metabolism,” Jonathan I. Watkinson, Lori Hendricks, Allan A. Sioson, Lenwood S.

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- [75] “Response Diversity of *Arabidopsis thaliana* Ecotypes in Elevated [Co₂] in the Field,” P. H. Li, A. Sioson, S. P. Mane, A. Ulanov, G. Grothaus, L. S. Heath, T. M. Murali, H. J. Bohnert, and R. Grene, **Plant Molecular Biology** **62**, 2006, pp. 593–609.
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WORKSHOPS

- [1] **Gordon Conference on Plant Molecular Biology**, poster presenter, Holderness School, Plymouth, New Hampshire, July 16–21, 2000.
- [2] **Computational Challenges of the Post Genomic Age**, participant, San Francisco, California, May 11–13, 2000.
- [3] **DIMACS Workshop on Combinatorial Structures in Molecular Biology**, participant, Rutgers, New Brunswick, New Jersey, November 4, 1994.
- [4] **DIMACS Workshop on Graph Embeddings and Parallel Architectures**, invited participant, Rutgers, New Brunswick, New Jersey, January 13–15, 1992.

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- [3] “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,” Liguori, K., I. Keenum, B. Davis, E. Milligan, L. S. Heath, A. Pruden, J. Calarco, and V. J. Harwood. Project 5052. Denver, CO: The Water Research Foundation. 2023, 239 pages.
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- [60] “Multi-layer Circuit Layouts,” Lenwood S. Heath, abstract in Proceedings of the First Microelectronics Center of North Carolina Semi-Annual Research Review, 1984.
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PRESENTATIONS

- [1] “Networks in Bioinformatics,” Keynote Speaker, **International Symposium on Parallel Architectures, Algorithms, and Networks (I-SPAN 2002)**, Makati City, Metro Manila, Philippines, May 23, 2002.
- [2] “Functional Genomics and Bioinformatics Applied to Understanding Oxidative Stress Resistance in Plants,” with Ruth Grene, Department of Computer Science at the University of Maryland, College Park, Maryland, December 14, 2001,

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- [3] “Some Biology that Computer Scientists Need for Bioinformatics,” Department of Computer Science at the University of Maryland, College Park, Maryland, December 14, 2001.
 - [4] “Functional Genomics and Bioinformatics Applied to Understanding Oxidative Stress Resistance in Plants,” with Ruth Grene and Naren Ramakrishnan, National Science Foundation, December 6, 2001.
 - [5] “Opportunities in Bioinformatics for Computer Science,” Department of Computer Science at the University of Iowa, November 16, 2001,
 - [6] “Expresso: A System for Microarray Design, Management, and Data Analysis,” Bioinformatics Research Center, the Medical College of Wisconsin, November 15, 2001,
 - [7] “Modeling and Understanding Stress Response Mechanisms with Expresso,” with Ruth Grene, National Science Foundation site visit for the NSF Pine Genome award. North Carolina State University, Raleigh, North Carolina, July 12, 2001.
 - [8] “Modeling and Understanding Stress Response Mechanisms with Expresso,” with Ruth Grene and Naren Ramakrishnan, **ORNL (Oak Ridge National Laboratories) Workshop on Genomics**, Duke University, Durham, North Carolina, May 1, 2001.
 - [9] “Towards an Understanding of Stress Response Mechanisms in Loblolly Pine: A First Generation Stress Chip,” with Ruth Grene, **Interdepartmental Plant Physiology Seminar Series**, Blacksburg, Virginia, March 1, 2001.
 - [10] “Biology and Theoretical Computer Science,” **Bioinformatics’99**, Blacksburg, Virginia, October 8, 1999.
 - [11] “Efficient Algorithms for Finding Conway Polynomials,” **Tenth Annual ACM-SIAM Symposium on Discrete Algorithms**, Baltimore, Maryland, January 18, 1999.
 - [12] “New Algorithms for Generating Conway Polynomials over Finite Fields,” invited presentation, University of Iowa, Iowa City, Iowa, June 29, 1998.
 - [13] “Recognizing Undirected and Directed Leveled-Planar Graphs,” **903rd Meeting of the American Mathematical Society**, Boston, Massachusetts, October 7, 1995.
 - [14] “Recognizing Leveled-Planar Dags in Linear Time,” **Graph Drawing ’95**, Passau, Germany, September 21, 1995.
 - [15] “SWAN—A Data Structure Visualization System,” **Graph Drawing ’95**, Passau, Germany, September 20, 1995. Paper presentation and system demonstration.
 - [16] “Open Problems in Stack and Queue Layouts,” **Seventh SIAM Conference on Discrete Mathematics**, Albuquerque, New Mexico, June 22, 1994. Also, organizer of **Minisymposium on Stack and Queue Layouts of Directed Graphs**, of which this presentation was a part.
 - [17] “The PMU Placement Problem,” **Seventh SIAM Conference on Discrete Mathematics**, Albuquerque, New Mexico, June 23, 1994.

- [18] “Graph Embeddings and Simplicial Maps,” **Seventh SIAM Conference on Discrete Mathematics**, Albuquerque, New Mexico, June 24, 1994.
- [19] “Graph Embeddings and Simplicial Maps,” invited presentation, University of Iowa, Iowa City, Iowa, April 29, 1994.
- [20] “Lower Bounds for Graph Embeddings Via Algebraic Topology,” **Fifth Annual ACM Symposium on Parallel Algorithms and Architectures**, Velen, Germany, July 2, 1993.
- [21] “Edge Coloring Planar Graphs with Two Outerplanar Subgraphs,” **Second ACM-SIAM Symposium on Discrete Algorithms**, San Francisco, California, January 29, 1991.
- [22] “Polyhedra: Faces are Better than Vertices,” **Second Canadian Conference in Computational Geometry**, Ottawa, Ontario, Canada, August 8, 1990.
- [23] “Improved Algorithms for the Minimum Weight Triangulation Problem,” **Fifth SIAM Conference on Discrete Mathematics**, Atlanta, Georgia, June 11, 1990. Also, session chair.
- [24] “Algorithms for Embedding Graphs in Books,” Minisymposium on Book Embeddings, **Third SIAM Conference on Discrete Mathematics**, Clemson, South Carolina, May 15, 1986.
- [25] “Algorithms for Embedding Graphs in Books,” invited presentation, Wesleyan University, Middletown, Connecticut, December 13, 1985.
- [26] “Embedding Planar Graphs in Seven Pages,” **25th Annual IEEE Symposium on Foundations of Computer Science**, Singer Island, Florida, October 24, 1984.
- [27] “Multi-Layer Circuit Layouts,” Lenwood S. Heath, **First Microelectronics Center of North Carolina Semi-Annual Research Review**, Research Triangle Park, North Carolina, October 23, 1984.

FUNDING

Current

- [1] USDA NIFA 1030077: *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] NSF 2243691: *Collaborative Research: RESEARCH-PGR: Unraveling the Origin of Vegetative Desiccation Tolerance in Vascular Plants*, \$2,000,000. 03/01/2023 – 02/28/2027. 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.

- [3] 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%.
- [4] National Science Foundation 1918656: *Collaborative Research: Expeditions: Global Pervasive Computational Epidemiology*, \$10,000,000. 04/01/2020 - 03/31/2026. 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%.

Declined

- [5] USDA: *Genome Similarity-based Classification of Xylella fastidiosa for Improved Detection of Emerging and Exotic Strains*, \$120,006. 08-01-2023 - 07-31-2024. PI: Boris A. Vinatzer. Co-PIs: Lenwood S. Heath, Elizabeth A. Bush. Personal share: 30%.
- [6] NSF: *EDGE FGT: ARGnet: Developing a Comprehensive Resource for Identification, Curation, and Surveillance of Novel Antibiotic Resistance Genes*, \$1,344,979. 10/01/23 - 09/30/26. PI: Liqing Zhang. Co-PIs: Anne Brown, Amy Pruden, Peter Vikesland, Lenwood S. Heath. Personal share: 10%.
- [7] NSF: *Collaborative Research: IntBIO: A Predictive, Biologically-aware Framework for Horizontal Gene Transfer Dynamics in Wastewater Microbiomes*, \$1,030,092. 08/16/23 - 08/15/26. Lead PI: Allison Lopatkin, University of Rochester. VT PI: Lenwood S. Heath. Co-PIs: Amy Pruden, Peter Vikesland, Liqing Zhang. Personal share: 40%.
- [8] NSF: *PIPP Phase I: Predictive Intelligence for Atmospheric Incursions of Plant Pandemics*, \$1,000,000. 04/15/22 - 10/14/23. PI: David Schmale. Co-PIs: Boris A. Vinatzer, Shane David Ross. Senior Personnel: Lenwood S. Heath et al. Personal share: 1%.
- [9] USDA: *Cattle CARTS: A Coordinated, Auditable, Robust, Traceability System for Beef Industry Data*, \$650,000. 06/01/2022 - 05/30/2026. PI: Robin White. Co-PIs: Vitor Mercadante, Thang Hoang, and Lenwood S. Heath. Personal share: 10%.
- [10] NSF: *URoL-EN: Structure-function-metabolism of Microbial N-cycle Communities and Networks in Engineered Wastewater Treatment Plants*, \$3,000,000. 01/01/2023 - 12/31/2028. PI: Kartik Chandra (Columbia University). Co-PIs: Allison Lopatkin (Barnard University) and Lenwood S. Heath. VT share: \$704,169. Personal share of subcontract: 100%.
- [11] NSF: *Collaborative Research: IntBIO: Predicting Resistomes: Machine Learning-enabled Mechanism Discovery of Plasmid Prevalence in Microbial Communities in Drinking Water*, \$1,560,611. 08/16/22 - 08/15/25. Lead PI: Allison Lopatkin, Barnard College. VT PI: Lenwood S. Heath. Co-PIs: Amy Pruden, Marc A. Edwards, Liqing Zhang. Personal share: 40%.
- [12] National Science Foundation: *EDGE FGT: ARGnet: Developing a Comprehensive Data and Tool Resource for Identification of Novel and Rare Antibiotic Resistance Genes*, \$1,288,785. 10/01/2021 - 09/30/2024. PI: Liqing Zhang. Co-PIs: Anne M. Brown, Lenwood S. Heath, Amy Pruden, and Peter J. Vikesland. Personal share: 20%. Declined.

- [13] National Science Foundation: *Collaborative Research: MIM: Predicting Resistomes: Incorporating Horizontal Gene Transfer into Microbiome Theory using Phylogenetic Networks*, \$2,198,275 (VT share). 10/01/2021 - 09/30/2026. PI: Lenwood S. Heath. Co-PIs: Amy Pruden, Liqing Zhang, and Allison Lopatkin (Barnard College). Personal share: 40%. Declined.
- [14] National Institutes of Health: *Viral Genome Comparison, Identification, Naming, and Transmission Paths for Epidemiology*, \$400,778. 04/01/2021 - 03/31/2023. PI: Lenwood S. Heath. Co-PI: Boris Vinatzer. Personal share: 50%. Declined.
- [15] National Science Foundation: *Collaborative Research: MTM 2: Predicting Resistomes: Incorporating Horizontal Gene Transfer into Microbiome Theory using Phylogenetic Networks*, \$2,021,134 (VT share). 11/01/2020 - 10/31/2025. PI: Lenwood S. Heath. Co-PIs: Amy Pruden, Liqing Zhang, and Allison Lopatkin (Barnard College). Personal share: 40%. Declined.
- [16] National Science Foundation: *AI Institute: Precision Agriculture for Animal Welfare*, \$20,000,000. 08/02/20 - 07/31/25. PI: Prasenjit Mitra, Penn State. VT PI: Naren Ramakrishnan. VT Co-PIs: Erica N. Feuerbacher, Lenwood S. Heath, Bert Huang, Leonie Jacobs, Brian B. Mayer, Srijan Sengupta, Robin White. VT share: \$5,996,818. Personal share: 10%. Declined.
- [17] NSF: *TRTech-PGR Transcovery: Identifying Conserved Stress-Responsive Genes and Cis-regulatory Modules in Plants*, \$2,197,403. 09/01/2019 - 08/31/2023. PI: Song Li. Co-PIs: Christopher Franck, Takeshi Fukao, Lenwood S. Heath, Sushma Naithani. Personal share: 20%. Declined.
- [18] VT ICTAS Targeted Opportunity for Proposals: *Connecting Genomes to Taxonomy, the Literature, and Online Media*, \$75,000. 07/01/2019 - 06/30/2020. PI: Lenwood S. Heath. Co-PIs: Naren Ramakrishnan, Boris A. Vinatzer. Declined.
- [19] VT: *Prokaryotic Networks from DNA Sequencing for the Benefit of Human Well-being*, \$30,000. 01/01/2019 - 06/30/2019. A proposal submitted in response to the 2018 Request for Concepts of the Data and Decisions Destination Area of Virginia Tech. PI: Lenwood S. Heath. Co-PIs: Frank Aylward, Liqing Zhang. Declined.
- [20] NSF: *Reconciling the Tree of Life and Web of Life with Evolutionary Networks*. Two-page NSF Convergence research idea submitted 2018. PIs: Frank Aylward, Lenwood S. Heath, Liqing Zhang. Declined.
- [21] NSF EAGER: *Collaborative Research: GenomeRxiv, a Preprint Server for Genomes*, \$199,521. 08/01/2018 - 07/31/2020. PI: Boris A. Vinatzer. Co-PI: Lenwood S. Heath. Personal share: 50%. Declined.
- [22] IARPA: *Cryptic and Apparent Genetic Engineering in Mosquitoes and Prokaryotes*, \$13,566,152. 02/01/2018 - 07/31/2021. PI: Madhav V. Marathe. Research scientist: Lenwood S. Heath. Personal share: 8%. Declined.
- [23] National Science Foundation: *ECA-PGR: Inference, Comparison and Visualization of Stress Response Transcriptome and Regulatory Networks Across Plant Species*, \$1,128,233. 06/01/18 - 05/31/22. PI: Song Li. Co-PIs: Ruth Grene, Lenwood S. Heath. Personal share: 25%. Declined.

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- [24] National Science Foundation: *TRIPODS: Institute for Data, Models, and Algorithms Across Scales*, \$1,498,424. 10/01/17 - 09/30/20. PI: Mark Embree. Research Scientist: Lenwood S. Heath. Personal share: 6%. Declined.
- [25] ICTAS: *Maternal Influence on Colostrum Composition: Novel Use of Machine Learning Tools to Integrate “-omics” Technology*, \$79,341. 07/01/17 - 06/30/19. PI: Rebecca Cockrum. Co-PI: Lenwood S. Heath. Personal share: 20%. Declined.
- [26] Worldwide Cancer Research: *Understanding Checkpoint Failures that Lead to Cancer*, \$257,456. 01/01/17 - 12/31/19. PI: Silke Hauf. Co-PI: Lenwood S. Heath. Personal share: 17%. Withdrawn.
- [27] National Institutes of Health: *The Mitotic Checkpoint: Linking Gene Expression Control to Function*, \$1,912,212. 09/01/16 - 08/31/21. PI: Silke Hauf. Co-PI: Lenwood S. Heath. Personal share: 13%. Declined.
- [28] Qatar National Research Fund: *Predicting Novel Molecular Biomarkers for Cancer*, \$300,000 (subcontract). 05/16/16 - 05/15/18. PI: Lenwood S. Heath. Personal share: 100%. Declined.
- [29] National Science Foundation: *RAPID: Evolution of Ebola Genomes: Identification, Naming, and Transmission Paths*, \$200,000. 08/10/15 - 08/09/16. PI: Lenwood S. Heath. Co-PI: Boris A. Vinatzer. Personal share: 60%. Withdrawn.
- [30] National Science Foundation: *ABI Development: MetaStorm: A System for the Metagenomics of Built Environment/National Environment Interfaces*, \$1,364,244. 05/16/16 - 05/15/20. PI: Lenwood S. Heath. Co-PIs: Amy J. Pruden-Bagchi, Liqing Zhang. Personal share: 40%. Declined.
- [31] National Science Foundation: *Preliminary Proposal: A Genome-Similarity Based Framework for the Phylogenetic Description of Bacterial Diversity*, amount TBD. PI: Boris A. Vinatzer. Co-PIs: Lenwood S. Heath, Jeff Newman. Personal share: 30%. Declined.
- [32] National Science Foundation: *III: Small: New Algorithmic Tools for Information Cartography*, \$500,000. PI: Naren Ramakrishnan. Co-PIs: Lenwood S. Heath, Bert Huang. Personal share: 30%. Declined.
- [33] Qatar National Research Fund: *Predicting Novel Molecular Biomarkers for Cancer*, \$315,000. LPI: Lenwood S. Heath. Co-LPI: Jihad Mohamad Jaam (Qatar University). Personal share: 100%. Declined.
- [34] DARPA: *Scaling Up the Assembly and Comprehension of Complex Mechanisms Using Causal Mechanistic Models*, \$8,353,225. PI: Naren Ramakrishnan. Co-PIs: Lenwood S. Heath, T. M. Murali, John J. Tyson. Personal share: 10%. Declined.
- [35] Department of Energy: *Genomic Networks Underlying Intraspecific Adaptation to Drought in Poplar: A Systems Biology Approach*, \$1,495,769. PI: Jason A. Holliday. Co-PIs: Dhruv Batra, Ruth Grene, Lenwood S. Heath, Erik T. Nilsen. Personal share: 20%. Declined.

Completed

- [36] 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%.
- [37] 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%.
- [38] 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%.
- [39] 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%.
- [40] 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%.
- [41] 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.
- [42] IARPA: *Integrative Genomics Approach to Computational Assessment of Threats (IGA-CAT)*, \$12,622,546. 03/01/17 - 05/31/20. PI: Stephen Eubank. Research Scientist: Lenwood S. Heath. Personal share: 4%.
- [43] 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%.
- [44] 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%.

- [45] 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%.
- [46] 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%.
- [47] 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.
- [48] 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%.
- [49] 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.*
- [50] 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.
- [51] 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.*
- [52] 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).
- [53] 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.

- [54] 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).
- [55] 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.
- [56] 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.
- [57] 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.
- [58] Arts and Sciences Pilot Research Project Grant: *Experimenting With Algorithms for Difficult, Non-numeric Problems*. \$3,000, 12/96–12/98.
- [59] 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.
- [60] 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.
- [61] 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] Xiao Liang, “Computational Insights into Evolutionary Dynamics of Human and Primate Genes,” 2024.
- [2] Parul Sharma, “Bacterial Plant Pathogen Identification using Genomics and Metagenomics,” 2023.
- [3] Reem Aldaihani, “Identifying The Structure Of Genomic Islands In Prokaryotes,” 2022.
- [4] Siddharth Krishnan, “Seeing the Forest for the Trees: New Approaches to Characterizing and Forecasting Cascades,” 2018.
- [5] Hanaa A. Torkey, “Machine Learning Approaches for Identifying microRNA Targets and Conserved Protein Complexes,” 2017.
- [6] Fatma Elzahraa Sobhy Eid, “Predicting the Interactions of Viral and Human Proteins,” 2017.

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- [7] Doaa Abdelsalam Ahmed Mohamed Altarawy, “DeTangle: A Framework for Interactive Prediction and Visualization of Gene Regulatory Networks,” 2017.
 - [8] Haitham Abdulrahman Elmarakeby, “Deep Learning for Biological Problems,” 2017.
 - [9] Andrew Scott Warren, “Methods for Analysis of Prokaryotic Genome Architecture,” 2017.
 - [10] Eman Badr, “Identifying Splicing Regulatory Elements with de Bruijn Graphs,” 2015.
 - [11] 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.
 - [12] Nahla A. Belal, “Two Problems in Computational Genomics,” 2011.
 - [13] Amrita Pati, “Graph-Based Genomic Signatures,” 2008.
 - [14] Allan A. Sioson, “Multimodal Networks in Biology,” 2005.
 - [15] Douglas J. Slotta, “Evaluating Biological Data Using Rank Correlation Methods,” 2005.
 - [16] Craig A. Struble, “Analysis and Implementation of Algorithms for Noncommutative Algebra,” 2000. Co-advisor with Edward L. Green of the Department of Mathematics.
 - [17] John Paul A. Vergara, “Sorting by Bounded Rearrangements,” 1997.
 - [18] Benjamin J. Keller, “Algorithms and Orders for Finding Noncommutative Gröbner Bases,” 1997. Co-advisor with Edward L. Green of the Department of Mathematics.
 - [19] Ramana R. Juvvadi, “Perfect Hashing and Some Related Problems,” 1993.
 - [20] Sriram V. Pemmaraju, “Exploring the Powers of Stacks and Queues via Graph Layouts,” 1992.

MASTERS THESIS STUDENTS SUPERVISED

- [1] Atul Bharadwaj, “COVID-19 Variant Analyzer through Genomic Sequences and Jaccard Similarities,” 2025.
- [2] Chandra Sekhar Nerella, “Comparative Analysis of Genomic Similarity Tools in Species Identification,” 2024.
- [3] Sahar Heidari, “Studying Co-occurrences of Eukaryotic Linear Motifs and Point Mutations to Identify Cases of Viral Mimicry in SARs-CoV-2,” co-supervisor, University of Bologna, Italy, 2022.
- [4] Aarathi Raghuraman, “Predicting Mutational Pathways of Influenza A H1N1 Virus using Q-learning,” 2021.
- [5] Ashkan Nazari, “Machine Learning Application in Energy Storage System’s State Estimation: State of Health (SOH),” 2021.

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

PROFESSIONAL ORGANIZATIONS

Association of Computing Machinery, Member

ACM Special Interest Group on Algorithms and Computation Theory

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

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).

2017–25 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**.

REVIEWER

ACM Computing Surveys
ACM Transactions on Algorithms (TALG)
ACM Transactions on Information Systems
ACM Transactions on Modeling and Computer Simulation
ACM-SIAM Symposium on Discrete Algorithms (SODA)
Algorithmica
Algorithms
Algorithms for Molecular Biology
American Mathematical Monthly
Applied Mathematics Letters
Artificial Intelligence in Medicine
Bioinformatics
BMC Bioinformatics
BMC Genomics
Canadian Foundation for Innovation
Chemometrics
Cogen Mathematics and Statistics
Combinatorica
Communications in Algebra
Communications of the ACM
Computers in Biology and Medicine
Conference on Information and Knowledge Management
Digital Libraries '94
Discrete and Computational Geometry
Discrete Applied Mathematics
Discrete Mathematics

Electronic Journal of Combinatorics

Foundations of Software Technology & Theoretical Computer Science

Frontiers in Genetics

Frontiers in Molecular Biosciences

Fund for Scientific Research (F.R.S.-FNRS), Belgium

Genetics

IEEE Access

IEEE/ACM Transactions on Computational Biology and Bioinformatics

IEEE Computer

IEEE Transactions on Computers

IEEE Transactions on Knowledge and Data Engineering

IEEE Transactions on Parallel and Distributed Systems

IEICE

Information and Computation

Information and Control

Information Sciences

International Journal of Computational Geometry and Applications

International Journal of Computer Science and Applications

International Parallel Processing Symposium and Symposium on Parallel and Distributed Processing

Information Processing Letters

ISRN Computational Mathematics

Joint Summer Research Conferences

Journal of Algorithms

Journal of the ACM

Journal of Combinatorial Optimization

Journal of Combinatorial Theory

Journal of Complexity

Journal of Computational Biology
Journal of Computer and System Sciences
Journal of Computer Science & Systems Biology
Journal of Graph Algorithms and Applications
Journal of Graph Theory
Journal of Interconnection Networks (JOIN)
Journal of Parallel and Distributed Computing
Journal of Supercomputing
Journal of Universal Computer Science
Management Science
Mathematical Systems Theory
Mathematics of Operations Research
National Institutes of Health
National Science Foundation
Netherlands Organization for Scientific Research (NWO)
NETWORKS
Parallel Processing Letters
Philippine Journal of Science
PLOS Computational Biology
PLOS ONE
SIAM Journal on Computing
SIAM Journal on Discrete Mathematics
SIAM Journal on Mathematics of Data Science
SIGIR Conference
Symposium on Applied Computing
Theoretical Computer Science
Transactions on Algorithms
United States Department of Agriculture
University of Queensland, Australia

HONORS AND AWARDS

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

Sigma Xi, The Scientific Research Honor Society, 1991

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