

Biographical Sketch

Name: Lenwood S. Heath	Title: Professor
Email: heath@vt.edu	Department: Computer Science

Education/Training:

Institution/Location	Degree/Postdoc	Year(s)	Field of Study
University of North Carolina, Chapel Hill	PhD	1985	Computer Science
University of Chicago	MS	1976	Mathematics
University of North Carolina	BS	1975	Mathematics

Personal Statement:

After my PhD, my primary research interests were algorithms, theoretical computer science, and graph theory. In the 1990's, I became interested in computational biology and worked on algorithms for genome rearrangements. Since 2000, I have been interested in computational biology and bioinformatics and was part of the committee that founded the Genetics, Bioinformatics, and Computational Biology (GBCB) PhD program. I have collaborated with biologists and others on analyzing biological data, including microarray, genomic, and RNA-Seq data. I have a keen interest in algorithms for computational genomics and biological networks. Most recently, I am working on projects revolving around algorithms for genome comparison and systems for metagenomic analysis. I have students working on machine learning projects related to predicting drug interactions, protein-protein interactions in virus-host systems, and microRNA-mRNA interactions, as well as motif finding in DNA sequences and comparing biological networks for similarity.

Selected Publications:

(5-10 recent publications in the area of systems biology; with hotlinks to the journal article or pubmed, please.)

[DeNovo: Virus-Host Sequence-Based Protein-Protein Interaction Prediction](#), Fatma-Elzahraa Eid, Mahmoud ElHefnawi, and Lenwood S. Heath. *Bioinformatics* 32, 2016, pp. 1144-1150.

[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.

[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.

[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.

[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.

[Identifying Splicing Regulatory Elements with de Bruijn Graphs](#), Eman Badr and Lenwood S. Heath, *Journal of Computational Biology* 21, 2014, pp. 880-897.

[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.

[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.

[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.

[A Theoretical Model for Whole Genome Alignment](#), Nahla A. Belal and Lenwood S. Heath. Journal of Computational Biology 18, 2011, pp. 705–728.

Current and/or Recently Completed Research Grants: (as applicable)

NSF	DBI-1062472	Lenwood S. Heath	04/15/11 - 03/31/17
Title: ABI Development: Representation, Visualization, and Modeling of Signaling Pathways in Higher Plants			
This is the Beacon project, which is a software development project for capturing, representing, visualizing, inferring, and simulating signal transduction pathways in plants. The project has developed the Beacon editor for drawing pathways in the standard Systems Biology Graphical Notation (SBGN) Activity Flow language. It has also created a database of pathways accessed through the Beacon Web site. We have developed the Beacon Inference Engine for inferring new edges in pathways from gene expression data sets. We are working on the Beacon Simulation Engine for simulating pathways represented in SBGN.			
NSF	1545756	Peter Vikesland	10/01/15 - 09/30/20
Title: PIRE: Halting Environmental Antimicrobial Resistance Dissemination (HEARD)			
The HEARD project investigates the occurrence of antibiotic resistant bacteria (ARBs) and antibiotic resistance genes (ARGs) in the environment of water treatment plants. As part of this project, environmental samples are being collected from water treatment plants at a number of locations around the world. These samples will be tested in the lab and also subjected to metagenomics DNA sequencing. A key part of the project is the computational analysis of the DNA sequencing reads to establish the presence and prevalence of ARBs and ARGs in the samples.			