BIOGRAPHICAL SKETCH

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NAME: Thomas H. Hampton

eRA COMMONS USER NAME (credential, e.g., agency login): THHAMPTON

POSITION TITLE: Research Scientist

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Pennsylvania, Philadelphia, PA	B.S.	05/1978	Russian
Dartmouth College, Hanover, NH	M.S.	05/1986	Computer Inf. Science
Birmingham University, Birmingham, UK	Ph.D.	08/2017	Systems Biology

A. Personal Statement

I am a Research Scientist with ten years' experience analyzing biomedical gene expression data and teaching bioinformatics. I currently serve as Bioinformatics Training Director for two program projects at Dartmouth. I have taught bioinformatics on the Dartmouth campus through R Club, a weekly bioinformatics seminar that I founded, at Mount Desert Island Biological Laboratory in Maine, and at the University of Birmingham, UK. In many cases, courses have been designed in collaboration with students and former students, and I have had the good fortune to stay in contact with many former class participants for almost a decade. Some of those people are now helping me design and promote new versions these courses and related seminar series. Last year, in our discussions regarding a third generation of Applied Bioinformatics and Environmental Genomics courses, we agreed that that single cell RNA-seq presented an excellent opportunity for future course offerings. I am therefore excited to begin work developing a course for the Chan Zuckerberg Initiative that will develop and promote a one-week bioinformatic training in scRNA-seq for biologist at all levels, allowing them to engage effectively with data from the Human Cell Atlas. I feel well positioned to lead this effort, not only because of my experience developing bioinformatics training programs, but also because of my experience managing and directing complex technology projects.

B. Positions and Honors

Positions and Employment

1979-1986 Laboratory Technician, Dartmouth College, Hanover NH
1986-1990 Systems Analyst, Litle & Company, Salem NH
1986-1987 Manager of Operations, Litle & Company, Salem NH
1987-1995 Director of New Technology, Litle & Company, Salem NH
1995-1997 President, The Writer's Resource, Hanover NH
1997-2003 Senior Software Engineer, Vicinity Corporation/Microsoft, Sunnyvale, CA
2004-2012 Bioinformatics Specialist, Pharm/Tox Department, Dartmouth Medical School
2013-2017 Senior Bioinformatics Analyst, Microbiology and Immunology, Geisel School of Medicine
2017- Research Scientist, Microbiology and Immunology, Geisel School of Medicine

Patents

Hampton et al, "Confirming identity of telephone caller"
United States Patent 5,465,290
November 7, 1995
Assignee: Litle & Co. (Salem, NH)

Hampton, TH, "Method and system to determine the geographic location of a network user"
United States Patent 7,062,572
June 13, 2006
Assignee:Microsoft Corporation (Redmond, CA)

Short Films

In small doses: Arsenic (2009) Created by Thomas Hampton

Mercury: From source to seafood (2012) Conceived by Thomas Hampton and Nancy Serrell

C. Contribution to Science

Molecular Basis of Metal Toxicity: Exposure to toxic metals is associated with cancer, developmental abnormalities, neurological problems and contributes to a wide range of chronic diseases. My earliest laboratory experiences in 1980 included the measurement of metal-induced DNA strand breaks and DNA cross links as the basis of genotoxicity. Twenty-five years later, bioinformatic analyses I performed identified new metallothionein genes in *Daphnia,* immunotoxic arsenic effects in mice and the ability of arsenic to interfere with phenotypic plasticity.

a. Shaw JR, Colbourne JK, Davey JC, Glaholt SP, Hampton TH, Chen CY, et al. Gene response profiles for Daphnia pulex exposed to the environmental stressor cadmium reveals novel crustacean metallothioneins. BMC Genomics. 2007;8(1):477–20.
b. Kozul CD, Hampton TH, Davey JC, Gosse JA, Nomikos AP, Eisenhauer PL, et al. Chronic exposure to arsenic in the drinking water alters the expression of immune response genes in mouse lung. Environ Health Perspect. 2009 Jul;117(7):1108–15.
c. Shaw JR, Hampton TH, King BL, Whitehead A, Galvez F, Gross RH, et al. Natural selection canalizes expression variation of environmentally induced plasticity-enabling genes. Molecular Biology and Evolution. 2014 Nov;31(11):3002–15.
d. Hampton TH, Jackson C, Jung D, Chen CY, Glaholt SP, Stanton BA, et al. Arsenic Reduces Gene Expression Response to Changing Salinity in Killifish. Environ Sci Technol. 2018 Aug 7;52(15):8811–21.

Integrative Analysis of Gene Expression Data: The advent of high throughput transcriptional assays created both opportunities and challenges. I have contributed several novel approaches that allow gene expression data from multiple sources to be interpreted simultaneously and automate the process of analyzing gene expression patterns in a larger scientific context.

a. Gosse JA, Hampton TH, Davey JC, Hamilton JW. A New Approach to Analysis and Interpretation of Toxicogenomic Gene Expression Data and its Importance in Examining Biological Responses to Low, Environmentally Relevant Doses of Toxicants. Toxicogenomics. Chichester, UK: John Wiley & Sons, Ltd; 2008. 31 p.
b. Davis AP, Murphy CG, Saraceni-Richards CA, Rosenstein MC, Wiegers TC, Hampton TH, et al. GeneComps and ChemComps: a new CTD metric to identify genes and chemicals with shared toxicogenomic profiles. Bioinformation. 2009 Oct 15;4(4):173–4.
c. Hampton TH, Stanton BA. A novel approach to analyze gene expression data demonstrates that the ΔF508 mutation in CFTR downregulates the antigen presentation pathway. AJP: Lung Cellular and Molecular Physiology. American Physiological Society; 2010 Apr 1;298(4):L473–82.
d. Koeppen K, Stanton BA, Hampton TH. ScanGEO: parallel mining of high-throughput gene expression data. Bioinformatics. 2017 Jul 14;:1–2.

CF Airway Microbiome Structure as a Predictor of Disease: Advances such as inhaled antibiotics have improved CF outcomes, but microbial infections, especially those that result in pulmonary exacerbations, nonetheless occur, leading gradual decreases in lung function. My analysis of bacterial 16S data patient samples has helped establish that, although bacterial communities change in individual patients during cycles of baseline, exacerbation, treatment and recovery phases of disease, antibiotic treatment in adult patients leaves bacterial community structure fundamentally intact. This suggests that antibiotic treatment is not simply eradicating the pathogens that become more abundant during exacerbation as was previously thought and suggests that antibiotics may instead alter pathogen behavior. My analysis of bacterial communities from identical and fraternal twins suggests that environmental factors predominate of genetic factors in the development of the CF airway microbiome, suggesting a critical window of intervention.

a. Madan JC, Koestler DC, Stanton BA, Davidson L, Moulton LA, Housman ML, et al. Serial analysis of the gut and respiratory microbiome in cystic fibrosis in infancy: interaction between intestinal and respiratory tracts and impact of nutritional exposures. mBio. 2012;3(4):e00251–12–e00251–12.
b. Filkins LM, Hampton TH, Gifford AH, Gross MJ, Hogan DA, Sogin ML, Morrison HG, Paster BJ, O'Toole GA. Prevalence of streptococci and increased polymicrobial diversity associated with cystic fibrosis patient stability.J Bacteriol. 2012 Sep;194(17):4709-17. doi: 10.1128/JB.00566-12. Epub 2012 Jun 29. PubMed PMID: 22753064; PubMed Central PMCID: PMC3415522.
c. Price KE, Hampton TH, Gifford AH, Dolben EL, Hogan DA, Morrison HG, Sogin ML, O'Toole GA. Unique microbial communities persist in individual cystic fibrosis patients throughout a clinical exacerbation. Microbiome. 2013 Nov 1;1(1):27. doi: 10.1186/2049-2618-1-27. PubMed PMID: 24451123; PubMed Central PMCID: PMC3971630
d. Hampton TH, Green DM, Cutting GR, Morrison HG, Sogin ML, Gifford AH, et al. The microbiome in pediatric cystic fibrosis patients: the role of shared environment suggests a window of intervention. Microbiome. 2014;2(1):14

Complete List of Published Work
https://scholar.google.com/citations?user=Dt9YJ68AAAAJ&hl=en&oi=ao

D. Research Support
Ongoing Research Support

P30 GM106394 Stanton (PI) 09/01/13-07/31/18
NIH/NIGMS
Dartmouth Lung Biology Center for Molecular, Cellular and Translational Research
The major goal of this COBRE grant is to develop a multidisciplinary Lung Biology Center at Dartmouth.
Role: Co-Investigator: bioinformatics and biostatistics

P42 ES007373 Stanton (PI) 04/01/08-03/31/19
NIH/NIEHS
Sources and Protracted Effects of Early Life Exposure to Arsenic and Mercury
The goal is to conduct innovative, multidisciplinary research to identify the major sources of As and Hg exposure and to elucidate the protracted effects of early life exposure to As and Hg on human health.
Role: Co-Investigator: biostatistics

STANTO15R0 Stanton (PI) 07/01/15-6/30/19
Cystic Fibrosis Foundation
Translational Research in Cystic Fibrosis
The goal of this grant is to develop and support CF research at the Geisel School of Medicine at Dartmouth, primarily by recruiting and supporting faculty and providing support for infrastructure.
Role: Co-investigator: biostatistics and bioinformatics

Completed Research Support

U53-EH001110 Borsuk (PI) 03/01/2014–8/31/2015
NHDES/CDC
Arsenic in private wells in NH: A survey to estimate exposure and potential health effects from water testing and treatment rates

The major goals of this project are to assess the factors determining the rates of private well water testing and treatment in New Hampshire and estimate statewide exposure to well water arsenic and associated health risks.
Role: Co-Investigator: biostatistics