CURRICULUM VITAE

Date: Decemeber 8, 2021

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Date & Place of Birth: January 4, 1962 Kingston, PA, USA

Education:

1983	Physics	B.S.	California Institute of Technology, Pasadena, CA
1984	Physics	M.S.	University of California, Los Angeles, CA
1990	Theoretical Particle Physics	Ph.D.	University of California, Los Angeles, CA

Postdoctoral Training:

1990-1992 Postdoctoral Fellow, Experimental Particle Physics, University of California, Los Angeles, CA

1992-1994 Staff Scientist, Molecular Genetics and Genomics, The Salk Institute for Biological Studies, La Jolla, CA

1994-1996 Research Associate, Genomics and Bioinformatics, Stanford Human Genome Center, Palo Alto, CA

Academic Appointments:

2018- present Henry Pickering Walcott Professor of Computational Biology and Bioinformatics; Chair, Department of Biostatistics; Director, Harvard Health Data Science Center, Harvard TH Chan School of Public Health
Research Activities: Development of methods in network medicine and systems biology aimed at understanding the multifactorial drivers of human health and disease, identifying disease subtypes and new

therapeutic interventions, and exploring differences between the sexes in disease etiology and response to therapy; development of open-source software tools supporting research and clinical applications.
Activities: Founding Director/Co-Director, SM Program in Computational Biology and Quantitative Genetics (CBQG); Director, BD2K T32 Training Grant; Director T32 Cancer Training Grant; Founding Co-Director and Executive Committee, Joint Biostatistics and Bioinformatics T32 Training Grant; Director, Harvard Quantitative Biomedical Research Center.

2005- present Professor of Biostatistics and Computational Biology,
Department of Data Science, Division of Computational Biology, Dana-Farber Cancer Institute;
Professor of Cancer Biology, Department of Cancer Biology, Dana-Farber Cancer Institute
Research Activities: Application of genomic technologies and integrative computational analysis to model cellular systems with an emphasis on understanding of human cancers and other diseases; development of open-source software tools supporting research and clinical applications.

2005- 2018 Professor of Computational Biology and Bioinformatics,
Department of Biostatistics, Harvard TH Chan School of Public Health
Research Activities: Application of genomic technologies and integrative computational analysis to model cellular systems with an emphasis on understanding of human cancers and other diseases; development of open-source software tools supporting research and clinical applications.
Activities: Founding Director, SM Program in Computational Biology and Quantitative Genetics (CBQG); Director, BD2K T32 Training Grant; Founding Co-Director and Executive Committee, Joint Biostatistics and Bioinformatics T32 Training Grant.

2008- 2018 Director, Canter for Cancer Computational Biology,
Dana-Farber Cancer Institute
Research Activities: Integrative approaches to data analysis focused on clinical and translational applications and linking clinical and laboratory data in support of basic research; creation of software tools and systems to support research; overall analytical support for investigative research activities for all Dana-Farber Investigators.

2007 – present Adjunct Professor of Bioinformatics, Boston University
Activities: Mentoring PhD student thesis research.

2003- 2005 Professor, Chemical Engineering, University of Maryland
Activities: Mentoring PhD student thesis research.

2002 - 2006 Investigator, The Institute for Genomic Research
Research Activities: Development and implementation of technology

and strategies, including computational methods and software tools, necessary for functional analysis of the human and other genomes. Analysis of human gene expression in colon tumors using microarrays, rodent models of heart, lung, blood and sleep disorders and gene expression in Arabidopsis. Director of the TIGR Gene Index Project, providing freely available databases and software to estimate gene content in more than 100 organisms.

2000- 2005 Professor, Department of Biochemistry,
The George Washington University
Activities: Instructor in various courses, curriculum committee for Genomics.

1998 – 2005 Lecturer, The Department of Biostatistics,
The Johns Hopkins University
Activities: Instructor in the Masters In Biotechnology Program

1997 - 2001 Associate Investigator, The Institute for Genomic Research
Research Activities: Development and implementation of technology and strategies, including computational methods and software tools, necessary for functional analysis of the human and other genomes. Analysis of human gene expression in colon tumors using microarrays, rodent models of heart, lung, blood and sleep disorders and gene expression in Arabidopsis. Director of the TIGR Gene Index Project, providing freely available databases and software to estimate gene content in more than 50 organisms.

1997 Assistant Investigator, The Institute for Genomic Research
Research Activities: Development and implementation of technology and strategies, including analytical methods and software tools, necessary for functional analysis of the human and other genomes.

1994 - 1997 Research Associate, Stanford Human Genome Center
Stanford University
Research Activities: Project leader for development and implementation of a transposon-mediated strategy for large-scale genomic DNA sequencing including development and implementation of laboratory protocols, analytical methods, computer software, and instrumentation. Mapping, sequencing, and annotating regions of human chromosomes 4 and 21.

1992 - 1994 Staff Scientist, The Salk Institute for Biological Studies
Research Activities: Development of improved methods for DNA sequencing, combinatoric strategies and devices for screening large libraries, simulation and optimization of single pass sequencing strategies including genome sequence sampling. Project director for the STS content mapping of chromosome 11. Development of methods and software tools to support genome mapping.

1990 - 1992 Postdoctoral Fellow, Department of Physics
University of California, Los Angeles
Research Activities: Research in particle physics, field theory and phenomenology. Founding member of the Antiproton Experiment (APEX) collaboration that set the world's best experimental limit on the lifetime of the antiproton.

1987 - 1992 Visiting Lecturer, Department of Physics
University of California, Los Angeles

1984 - 1996 Physics Instructor, Southern California Science Institute
New College of California

1983 – 1990 Teaching Fellow, Department of Physics
University of California, Los Angeles

1983 - 1990 Research Fellow, Department of Physics
University of California, Los Angeles
Thesis Supervisor: E.T. Tomboulis
Research Activities: Research in elementary particle physics, mathematical physics, field theory focusing on the development of two-dimensional gauge field theory models and the construction of associated string theory models.

Nonacademic Employment

2011-2014 Co-Founder, CEO and Board Chairman, Genospace LLC
Activities: Genospace provides software solutions to operationalize precision medicine through the integration of clinical and genomic data and its presentation to clinical and research users in an intuitive format.

2014-2017 Co-Founder and Board Chairman, Genospace LLC
Activities: Genospace provides software solutions to operationalize precision medicine through the integration of clinical and genomic data and its presentation to clinical and research users in an intuitive format. In January 2017, Genospace was sold to the Hospital Corporation of America to support research and to acquire our world-leading solution for clinical trials matching.

Hospital or Affiliated Institution Appointments:

2003 – 2005 Adjunct Professor, Department of Biostatistics
Bloomberg School of Public Health, The Johns Hopkins University

2005- present Professor, Department of Biostatistics and Computational Biology
Dana-Farber Cancer Institute

2014- present Professor, Channing Division of Network Medicine, Brigham and Women's Hospital

Hospital and Health Care Organization Service Responsibilities:

2005- present Primary research areas are computational and system biology focused on the integration of diverse data types to provide insight into biological processes that drive human disease phenotypes.
Department of Data Science, Division of Computational Biology, Dana-Farber Cancer Institute

2014- present Research at the interface of systems biology and pulmonary disease, exploration of how sex and gender affect disease risk, development of methods to better handle sex differences in systems approaches, and advising faculty in their research and the Director in setting directions for future work.
Channing Division of Network Medicine, Brigham and Women's Hospital

Major Committee Assignments:

1994	National Laboratory Genome Project Visit Review Panel, DOE
1995	Caltech/BAC Library Construction Site Visit Review Panel, DOE
1996-1998	Bioinformatics Grant Review Panel, DOE
1997-2001	Grant Review Panel, DOE
1997	Hollander Fellowship Review Panel, DOE
1997	Five-Year Program Advisory Committee, NCRR
1997	Cancer Chromosome Anatomy Project program Steering Committee, NCI
1998	National Laboratory Functional Genomic Review Panel, DOE
1998	Full-Length cDNA Library Construction and Sequencing Advisory, Committee, NCI
1998	Functional Genomics Panel, Welcome Trust
1998	Genomics Grant Review Panel, NSF SBIR
1998	Special Program in Tropical Disease Research Review, UNDP/World Bank/WHO
1999-2000	Low-Dosage radiation Grant Review Panel, DOE
1999	Bioinformatics Review Panel, NSF
1999	Special Emphasis Review Panel, NHLBI
1999	Microarray Working Group Advisory Panel, NIDCR
1999	Special Emphasis Review Panel, NIMH
1999	Plant Biology Review Panel, NSF
1999-2007	Board of Directors, MGED
2000	Grant Review Panel, NIDA SBIR
2000	Plant Biology Review Panel, USDA
2000	Plant Biology Review Panel, NSF
2000	Exceptional Chromosome Regions Working Group, DOE
2000	Working Group on US Scientific Interactions, NSF
2000-2006	Genome/GCAT study section, NIH
2000-2003	PGA Coordinating Committee, HHLBI
2000-2003	PGA Bioinformatics Committee, NHLBI

2000-2003	PGA Microarray Committee, NHLBI
2000	Working Group on Australia Scientific Interactions, NSF
2001	Review Meeting RFP ES-01-01 National Center for Toxicogenomics (NCT) Microarray Resource, HIEHS
2001-2003	Plant Genome Scientific Advisory Board, University of Georgia
2001-2003	Innovative Technology Review Panel, NCI
2001-2002	Genome Study Section, NIH
2002-2006	GCAT Study Section, NIH
2001	Bioinformatics in Neuroscience and Sleep Research Workshop, NIDDK
2001	Plant Genome Site Visit Panel, NSF
2001-2003	BISTI Review Panel, NIH
2001-2005	Grant Review Panel, NCI
2002	Microarray Supplement Review Panel, NHLBI
2002-2006	Panel on Emerging Issues in Toxicogenomics, NRC
2004-2006	Panel on Applications of Toxicogenomics, NRC
2003-2010	Genome British Columbia Scientific Advisory Board
2005-2014	EPA Board of Scientific Counselors
2005-2011	St. Jude's Children's Research Hospital Scientific Advisory Board
2006-2007	Harvard School of Public Health, Lefkopoulou Award Committee Member
2006	Dana Farber Cancer Institute, Computational Biology Search Chair
2005	EU FP6 Grant Review Panel
2006-2007	Harvard School of Public Health, Seminar Committee Member
2006-2019	Harvard School of Public Health, Curriculum Committee Member
2006-2009	Harvard School of Public Health, Computational Biology Search Chair
2007-present	EU FP7 Genomics Grant Review Panel
2008-present	Lovelace Respiratory Research Institute, Scientific Advisory Board
2008-2010	NAS Panel on Collecting, Storing, and Distributing Biodata linked to Social Science Surveys
2009	RC1 Grant Review "Editorial Review" Panel
2009	RC2 Genomic Science Grant Review
2009	Epigenomics Roadmap Grant Review Panel
2009-2014	Epigenomics Roadmap Advisory Board
2010	NCI EUREKA Grant Review Panel
2010	Chair, NCRR S10 Grant Review Panel
2016	NASA ISS Genomic Applications Study Section
2019	NASA Human Research Program Long-Duration Flight Advisory Panel
2016	21st Century Cures Act Biomarker Advisory Group
2012-2019	Research Oversight Committed, Genome British Columbia
2014-present	Shriner's Hospital standing review panel
2005-present	Various NIH grant review panels, either as an ad hoc member or as an ad hoc reviewer. I typically serve on at least six per year and can provide a more detailed list on request.
2005-present	Various EU and Canadian grant review panels, either as an ad hoc member or as an ad hoc reviewer. I can assemble a detailed list on request.
2017-present	Research Foundation Flanders (FWO) standing review panel.
2018-present	Chair, Department of Biostatistics, Harvard T.H. Chan School of Public Health

Nonacademic Board and Advisory Board Positions (active or past five years):

2012-2017	Genospace LLC, Founder, CEO, Board of Directors; Chairman of the Board
2015-present	Haymakers for Hope, Board of Directors
2013-present	Caris Life Sciences, Scientific Advisory Board
2020-present	Caris Life Sciences, Data Science Advisory Board
2014-present	Shriner's Hospitals, Scientific Advisory Board
2014-present	Olema Pharmaceuticals, Scientific Advisory Board
2019-present	StitchBio, Scientific Advisory Board
2015-present	Lacriscience, Scientific Advisory Board
2017-present	Merck KGaA, Precision Medicine Advisory Board
2018-present	Renalytix AI, Advisory Board
2020-present	Charles River School Health and Safety Committee (COVID Advisory Board)
2020-present	Boston University Academy Health and Safety Committee (COVID Advisory Board)
2021-present	Dover, MA, Board of Health Special Advisor
2021-present	Congreso Futuro International Advisory Board, Chile
2012-2020	Blueprint Genomics, Scientific Advisory Board
2010-2017	Lovelace Respiratory Research Institute, Scientific Advisory Board
2012-2016	SynapDx, Scientific Advisory Board
2005-2016	Nabsys Inc., Scientific Advisory Board
2013-2017	Thomson-Reuters, Genomics Advisory Board

Professional Societies:

1988	American Physical Society	Member
1988	APS Biophysics Division	Member
1988	APS International Physics Group	Member
1988	APS Division of Particles and Fields	Member
1988	World Federation of Scientists	Member
1990	Microarray Gene Expression Data Society (MGED)/ Functional Genomics Data Society (FGED)	Member Board Member President
	(2011-2014)	
1995	The Human Genome Organization (HUGO)	Member
1996	Association of Science Professionals (ASP)	Member
1998	American Association for the Advancement of Science (AAAS)	Member
1999	Center for the Study of the Evolution of Life (CSEOL)	Member
2005	American Association for Cancer Research	Member

Community Service Related to Professional Work:

I have presented more than 350 talks, courses, and workshops since joining Dana-Farber and the Harvard T.H. Chan School of Public Health in 2005; detailed lists will be provided upon request. I have also taught numerous courses and workshops on the

analysis of genomic data and have served as an organizer of the EMBO course on DNA microarray analysis for more than five years.

In addition, I have served on the Scientific Advisory Board of the St. Jude's Children's Research Hospital, the Scientific Advisory Board for the Lovelace Respiratory Research Institute, Research Oversight Committees for various Genome Canada programs, and the Board of Scientific Counselors of the Environmental Protection Agency. I have also been a member of advisory boards for a number of NIH initiatives, including the Roadmap Epigenome Project, the Extracellular RNA Communication Consortium, the Atopic Dermatitis Research Network (ADRN), and the Trans-Omics for Precision Medicine (TOPMed) program.

Since the onset of the COVID19 pandemic, I have served numerous local school and community groups by advising these on policy and practice. I am particularly proud that the two schools I advised instituted a series of policies addressing air quality, masking, distancing, hygiene, and vaccination that allowed them to remain open without any documented cases of in-school transmission during the 2020-2021 and 2021-2022 academic years. I have also become a special advisor to the Dover, MA Board of Health and provide advice to the Dover-Sherborn Regional School District on COVID and other heath-related matters.

(Peer Review for Scientific Journals)

1994-2016	*Genomics*
1994-2009	*BioTechniques*
1996-2010	*Genome Research*
2000-2010	*Genome Biology*
1997-1998	*Analytical Biochemistry*
1997-present	*Nature*
1997-2010	*Nucleic Acids Research*
1999-2010	*Nature Genetics*
1999-2009	*EMBO Reports*
1999-2017	*Nature Biotechnology*
1999-present	*Science*
2000-2016	*Bioinformatics*
2000-2009	*Journal of Theoretical Biology*
2000-2009	*Mammalian Genomics*
2000-2006	*Gene*
2000-2016	*BMC Genomics, BMC Bioinformatics*
2001-2009	*Structural and Functional Genomics*
2001-2010	*Nature Reviews Genetics*
2001-2006	*American Journal of Applied Statistics*
2009-present	*PLoS Computational Biology*
2015-present	*Proceedings of the National Academy of Sciences*
2017-present	Molecular Systems Biology

Editorial Boards:

2000-2009	Editorial Board	*BioTechniques*
2000-2012	Associate Editor	*Bioinformatics*
2000-present	Editorial Board	*BMC Genomics*
2000-2006	Editorial Board	*Genomics*
2006-2017	Editor-in-Chief	*Genomics*
2015-present	Editorial Board	*Cancer Research*

Awards and Honors:

1985 - 1991	**Outstanding Teaching Award (7)**, UCLA Physics Department
1986	**Jun John Sakurai Scholarship**, 24th International School of Subnuclear Physics, Ettore Majorana Centre for Scientific Culture, Erice, Italy
1987	**UCLA Distinguished Teaching Assistant Award**, UCLA Academic Senate
1987	**Prize for Best Student** and **Prize for Best Scientific Secretary**, 25th International School of Subnuclear Physics, Ettore Majorana Centre for Scientific Culture, Erice, Italy
1988	**Graduate Distinguished Scholar Award**, UCLA Alumni Association
1992 - 1997	**SERCA Fellow**, National Human Genome Research Institute
2006	**George D. Wilbanks Lectureship in Gynecological Oncology**, University of South Florida College of Medicine
2007	**President's Distinguished Lectureship**, American Society of Reproductive Medicine
2007	**Leopold G. Koss Lectureship**, Universität Bern, Switzerland
2007	**Distinguished International Advisors** at IEE BIBE, the original and the oldest IEEE flagship international conference in Bioinformatics and Bioengineering.
2008	**Distinguished Lecture in Computer Science**, Wayne State University
2010	**IPM Distinguished Lecture**, Mt. Sinai Medical School, New York
2010	**The Ian Lawson Van Toch Memorial Seminar Series in Computational Biology**, Ontario Cancer Institute
2010	**Harvard-Australia Foundation Fellowship**
2010	**Bancroft Fellow-in-Residence**, Queensland Institute for Medical Research, Queensland, Australia
2010	**Jackson Memorial Fellowship**, Griffith University, Queensland, Australia
2011	**Australia Fellow**, National Health and Medical Research Council, Australia
2013	**White House Open Science Champion of Change**, Office of the President of the United States of America
2016	**Mentor of the Year Award**, Postdoc and Graduate Student Organization, Dana-Farber Cancer Institute
2018	**National Cancer Institute Outstanding Investigator Award** (R35)

Part II: Research, Teaching, and Clinical Contributions

A. Narrative report (*700 words or less*) of Research, Teaching, and Clinical Contributions. Please focus primarily on the areas in which most of your time and effort is spent.

My current research involves development of new analytical methods for the integrated analysis of large-scale biomedical data, including genomic data, to better understand the nature of human diseases, including cancer and pulmonary diseases, with the goal of developing better methods for diagnosis and treatment. Two defining characteristics of my work are a commitment to reproducible research through development of open-source software implementations of analytical methods, and an emphasis on studying sexual dimorphism in health and disease.

A longstanding component of my work is methods development for robust biomarkers. We have applied this to identifying reproducible predictive biomarkers in cancer and have explored reproducibility in large, published data sets, demonstrating that many are inconsistent. In collaboration with Hugo Aerts, I have been working to extend our methods to the analysis of quantitative feature data extracted from radiographic images (an emerging field called "radiomics"), to use these to identify predictive biomarkers, and to link these features to genetic mutations in cancer. I have also come to recognize that while individual "features" such as the expression of genes or specific mutations may not be sufficient on their own to identify drivers of biological states or to predict outcome or response to therapy in disease.

I have also been developing methods for inferring gene regulatory network models using gene expression and other sources of data. We published a method, PANDA, that builds on "message passing" (an idea developed communications theory) to optimize information flow through a gene regulatory network model, allowing us to infer condition-specific networks and to compare these between phenotypes. We have developed many extensions of PANDA that incorporate other data types and have applied these to the study of diseases, including ovarian cancer, colorectal cancer, chronic obstructive pulmonary disease, asthma, and Alzheimer's disease, as well as to the investigation of sexual dimorphism. Consistent with our commitment to open and reproducible science, we have collected these methods (all named for animals) with standardized source code in R, C, Matlab, and Python, into the "Network Zoo" (https://netzoo.github.io/). To support the widespread use of these methods, we developed "netBooks" (http://netbooks.networkmedicine.org/), a collection of online tutorials that use Jupyter notebooks to introduce the use of our methods and, increasingly, to allow all of our published analyses to be rerun by those interested in the analyses.

We have also been exploring the connection between genotype and phenotype, using gene expression as a surrogate for phenotype. We have developed a new approach, CONDOR, to the analysis of expression quantitative trait loci that uses a bi-partite graph to represent associations between gene expression levels and both local (*cis-acting*) and distant (*trans-acting*) significant genetic variants. We find that the overall structure of the graph provides insight not only into how genetic variants work together to influence phenotype, but also into evolutionary constraints on the genetic variants themselves. This

has given us new insight into how many genetic variants of small effect-size can collectively exert strong influence on phenotype.

More recently, we have been asking whether how one can model regulatory networks in the context of genetic background, recognizing that an individual's genotype will manifest its effects through alterations of patterns of gene expression that ultimately will influence the functional processes active in individuals. That method, EGRET, represents an important step forward in the analysis of the link between genotype and phenotype and is the first method for linking genetic cause and phenotypic effect through the action of individual regulatory processes.

Our group also builds and maintains a variety of software tools to support genomic analysis. the TM4 suite of open-source software tools for the analysis of DNA microarray data. The most widely used of these, MeV, is a powerful data mining software tool, that places sophisticated analytical tools behind an intuitive graphical user interface. Developed to be accessible to laboratory biologists, MeV has more than 260,000 users worldwide. We recently transitioned MeV to a cloud-based platform, WebMeV (http://mev.tm4.org) to take advantage of cloud scalability to better handle large sequence-based data. WebMeV now has 3000 registered users and provides more than 100 analysis sessions per day.

I am also very involved in teaching and mentoring. I developed, launched, and direct the Computational Biology and Quantitative Genetics (CBQG) master's degree program, I was co-PI and co-director of the first joint Biostatistics and Bioinformatics training grant in the US and recently stepped down to develop and direct a training grant program as part of the NIH's Big Data to Knowledge (BD2K) program. I also developed and teach an introductory genomics tools and methods course and have co-taught an online course on reproducible research through HarvardX (https://www.edx.org/course/principles-statistical-computational-harvardx-ph527x).

I have trained more than 80 postdoctoral fellows and graduate students (including MS and PhD students whom I have mentored for their thesis projects) and have mentored a number of junior faculty members since joining the Harvard TH Chan School of Public Health and Dana-Farber Cancer Institute in 2005. I have emphasized diversity in hiring postdocs; more than half of my trainees have been female and four of the five postdocs from my group who have moved onto faculty positions in the past year have been female. I also maintains an extensive network of former trainees (and their current trainees) which meets weekly as we continue to work collaboratively in the development and application of network methods.

B. Funding Information

I have had more than twenty-five years of continuous grant support from the NIH and other organizations. My current support includes:

Active Research Support

5R01CA205406-03 (Ng, K.) 3/1/2017 – 2/28/2022

NIH/NCI
Novel Randomized Controlled Trials of Vitamin D Supplementation in Patients with Colorectal Cancer: Impact on Survival and Biology
This project is exploring the biology underlying the effects of vitamin D on survival of colorectal patients.
Role: Co-Investigator

1R35CA220523 (Quackenbush, J.) 9/1/2018 – 8/31/2025

NIH/NCI
Unraveling the Complexities of Risk and Mechanism in Cancer
This NCI Career Award supports Dr. Quackenbush's ongoing work to model genetic processes in cancer and to elucidate the link between genotype and phenotype so as to better understand the drivers of cancer and to identify potential targets for therapeutic intervention, with a particular emphasis on understanding differences between men and women. Role: Principal Investigator

1R01HG011393 (DeMeo, D / Quackenbush, J.) 9/1/2018 – 06/30/2025

NIH/NCI
Network Tools to Understand Sex- and Gender-Specific Drivers of Disease
This project will develop robust methods for handling male and female multi-omic data, with an emphasis on applying these to the inference of gene regulatory network models and the use of such models for gaining insight into the regulatory processes that drive clinical differences in human health and disease. Role: co-Principal Investigator

1U24CA231846-01A1 (Quackenbush, J.) 9/1/2019 – 8/31/2024

NIH/NCI
MeV: A Robust Platform for Intuitive Genomic Data Analysis
As part of the Informatics Technology for Cancer Research (ITCR) program, we will develop and support WebMeV, a robust, scalable data analysis software tool that uses intuitive visual interfaces to provide users with access to advanced data analysis methods for large-scale genomic data in a system that helps ensure their research is reproducible.
Role: Principal Investigator

2P50CA127003-11A1 (Bass, A.) 9/1/2019 – 5/31/2024

NIH (Subcontract: Dana Farber Cancer Institute
Dana Farber/ Harvard Cancer Center SPORE in Gastrointestinal Cancer
The GI SPORE supports state-of-the-art investigator-initiated translational research that will contribute to improved prevention, early detection, diagnosis, and treatment of gastrointestinal cancers. Dr. Quackenbush will serve as Co-Director of the Biostatistics and Bioinformatics Core, which will support the quantitative needs of the investigators in the design of experiments and the analysis of the resulting data.
Role: Co-Investigator/Core Co-Director

C. Report of Current Research Activities other than those mentioned above (bench research, clinical trials, outcome studies, efficacy studies as applicable)

None to report.

D. Report of Teaching (use only those categories that are applicable)

1983 - 1990	Teaching Fellow, Department of Physics, University of California, Los Angeles
1984 - 1996	Physics Instructor, Southern California Science Institute, New College of California
1987 - 1992	Visiting Lecturer, Department of Physics, University of California, Los Angeles
1998 - 2005	Lecturer, The Johns Hopkins University Instructor in the Masters in Biotechnology Program
2000 - 2005	Professor, Department of Biochemistry, The George Washington University
2003 - 2005	Adjunct Professor, Department of Biostatistics, Bloomberg School of Public Health, The Johns Hopkins University Developed program in genomics and bioinformatics; instructor in various courses.
2005-present	Professor, Department of Biostatistics, Harvard TH Chan School of Public Health
2013-present	Director, MS in Computational Biology and Quantitative Genetics

E. Report of Clinical Activities

1. Description of clinical practice (field, areas of major focus, site(s) of practice [private office, HMO, teaching hospital etc.])

None

2. Patient load (indicate complexity of cases, as appropriate)

None

3. Clinical contributions (e.g., introduction of new methods of clinical diagnosis, prevention, treatment, care delivery)

None

4. Other relevant information about clinical role (receipt of clinical awards, locally or nationally, invitation to participate in clinical activities at other sites, special recognition by peers or professional organizations as a leader in a clinical field)

None

Part III: Bibliography (as of January 18, 2022)

Total citations: 84,174

h-index: 102

i10-index: 300

Original Articles (320)

Complete List of Published Works in MyBibliography:
https://www.ncbi.nlm.nih.gov/myncbi/john.quackenbush.1/bibliography/public/

1. **Quackenbush J**. Chiral anomalies in two-dimensional quantum field theory. Physical review D: Particles and fields. 1989;40(10):3408-14. Epub 1989/11/15. PubMed PMID: 10011709.
2. **Quackenbush J**. Twisted world-sheet gauge fields and string models Phys Lett B. 1990;234(3):285-91.
3. Buchanan CD, Cousins R, Dib C, Peccei RD, **Quackenbush J**. Testing CP and CPT violation in the neutral kaon system at a phi factory. Physical review D: Particles and fields. 1992;45(11):4088-107. Epub 1992/06/01. PubMed PMID: 10014315.
4. Geer S, Marriner J, Ray R, Streets J, Lindgren M, Muller T, **Quackenbush J**, Armstrong T. Search for antiproton decay at the Fermilab antiproton accumulator. Physical review letters. 1994;72(11):1596-9. Epub 1994/03/14. PubMed PMID: 10055652.
5. Khristich JV, Bailis J, Diggle K, Rodkins A, Romo A, **Quackenbush J**, Evans GA. Large-scale screening of yeast artificial chromosome libraries using PCR. BioTechniques. 1994;17(3):498-501. Epub 1994/09/01. PubMed PMID: 7818903.
6. **Quackenbush J**. Career issues. Science. 1994;266(5189):1306. Epub 1994/11/25. doi: 10.1126/science.266.5189.1306. PubMed PMID: 17772824.
7. Selleri L, Giovannini M, Hermanson GG, Romo A, **Quackenbush J**, Penny L, Khristich JV, Evans GA. Yeast artificial chromosome cloning of 3.2 megabases within chromosomal band 11q24 closely linking c-ets 1 and Fli-1 and encompassing the Ewing sarcoma breakpoint. Genomics. 1994;22(1):137-47. Epub 1994/07/01. doi: 10.1006/geno.1994.1354. PubMed PMID: 7959760.
8. Kupfer K, Smith MW, **Quackenbush J**, Evans GA. Physical mapping of complex genomes by sampled sequencing: a theoretical analysis. Genomics. 1995;27(1):90-100. Epub 1995/05/01. doi: 10.1006/geno.1995.1010. PubMed PMID: 7665188.
9. **Quackenbush J**, Davies C, Bailis JM, Khristich JV, Diggle K, Marchuck Y, Tobin J, Clark SP, Rodkins A, Marcano S, et al. An STS content map of human chromosome 11: localization of 910 YAC clones and 109 islands. Genomics. 1995;29(2):512-25. Epub 1995/09/20. PubMed PMID: 8666402.
10. Schuler GD, Boguski MS, Stewart EA, Stein LD, Gyapay G, Rice K, White RE, Rodriguez-Tome P, Aggarwal A, Bajorek E, Bentolila S, Birren BB, Butler A, Castle AB, Chiannilkulchai N, Chu A, Clee C, Cowles S, Day PJ, Dibling T, Drouot N, Dunham I, Duprat S, East C, Edwards C, Fan JB, Fang N, Fizames C, Garrett C, Green L, Hadley D, Harris M, Harrison P, Brady S, Hicks A, Holloway E, Hui L, Hussain S, Louis-Dit-Sully C, Ma J, MacGilvery A, Mader C,

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Educational Material: I have taught numerous courses and workshops and make the materials freely available. I developed and co-taught a HarvardX course on reproducible

research (https://www.edx.org/course/principles-statistical-computational-harvardx-ph527x).

Thesis: Gauge Field Theory in Two Space-Time Dimensions: Anomalies and Applications to String Models.

Nonprint Materials, i.e., film strips, films, videotapes and computer-based materials relevant to appointee's academic field. *Include description of item, who commissioned, purpose, users, penetration in field.*

None

Patents

None

Abstracts (*only those containing data not yet published in complete form.)*

None