The Faculty of Medicine of Harvard University
Curriculum Vitae

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Place of Birth: Ankoun, Lebanon

Education:

7/2001	BSc high distinction	Chemistry	American University of Beirut
5/2005	MD CM	Medicine	McGill University
5/2015	MSc	Biostatistics	Harvard School of Public Health

Postdoctoral Training:

Internships and Residencies

6/2005 - 6/2006	Intern	Internal Medicine	Massachusetts General Hospital
6/2006 - 6/2008	Resident	Internal Medicine	Massachusetts General Hospital

Clinical and Research Fellowships

7/2008 - 6/2012	Clinical Fellow	Harvard Combined Pulmonary and Critical Care Medicine Fellowship	Beth Israel Deaconess Medical Center, Brigham and Women's Hospital, and Massachusetts General Hospital
3/2010-6/2016	Postdoctoral Research Fellow	Harvard Pulmonary and Critical Care Medicine (mentored by Megan Murray, MD ScD & Pardis Sabeti, MD DPhil)	HMS Department of Global Health and Social Medicine

Faculty Academic Appointment:

7/2012 - 11/2016	Instructor	Medicine	Harvard Medical School
12/2016 -	Assistant Professor	Biomedical Informatics	Harvard Medical School

Appointments at Hospitals/Affiliated Institutions:

9/2011 - 6/2012	Graduate Assistant	Medicine	Massachusetts General Hospital
7/2012 - 4/2014	Assistant	Medicine	Massachusetts General Hospital
5/2014 -	Assistant Physician	Medicine	Massachusetts General Hospital

Committee Service:

Local

2006 - 2010	IRB Committee	Partners Member/Protocol Reviewer
2013 – 2018	Residency Coaching Program	Massachusetts General Hospital Resident Coach
2018 – 2019	Curriculum committee	Harvard Masters of Biomedical Informatics Member
2017 – 2018	Admissions committee	Harvard Masters of Biomedical Informatics Member
2017 –	Admissions Committee	Harvard Bioinformatics and Integrative Biology PhD Member
2018-2019	Junior Faculty Search Committee	Harvard Department of Biomedical Informatics

National

2019 -	International Expert Panel on the use of big data to assess the risk of HIV	Expert Member

International

2019-	American Thoracic Society Planning Committee	Invited Member

2020-	American Thoracic Society Assembly Program Committee	Invited Member
2020-	American Thoracic Society TB Working Group	Invited Member
2020-	International Union Against TB and Lung Disease –TB Science Scientific Review Committee	Invited Member

Professional Societies:

2005 – 2008	American Medical Society	Member
2005 – 2010	Massachusetts Medical Society	Member
2005 – 2008	American College of Physicians	Member
2008 -	American Thoracic Society 2008 – Pulmonary infections and TB assembly –PI-TB	Member
2014-	International Union against Tuberculosis and Lung Disease	Member

Grant Review Activities:

2015- 2017	Grant review committee	Harvard Dubai Center for Global Health Delivery Grant Reviewer
2019 -	Ad hoc study section	NIH/NIAID Grant Reviewer

Editorial Activities:

- **Ad hoc Reviewer**

PLoS Medicine
Nature Communications
Nature Microbiology
Genome Biology
Science Advances
American Journal of Pulmonary and Critical Care
Lancet Respiratory Medicine
Clinical Infectious Disease
Journal of Infectious Disease
Bioinformatics
PLoS Genetics
PLoS One
Antimicrobial Agents and Chemotherapy
Journal of Antimicrobial Chemotherapeutics
International Journal of Tuberculosis and Lung disease
Tuberculosis

Scientific Reports
Clinical Epidemiology
BMJopen
Database

Honors and Prizes:

2000	Said Frieha Award	Lebanese Ministry of Education	Academic excellence
2001	Phillipe Hitti Award,	American University of Beirut	Academic excellence
2002	James Q. Bliss Book Prize	McGill University Faculty of Medicine	Academic excellence
2002	Mary and Louise Streicher Prize	McGill University Faculty of Medicine	Academic excellence
2002	Joseph Hils Prize	McGill University Faculty of Medicine	Academic excellence
2002	Francis McNaughton Prize	McGill University Faculty of Medicine	Academic excellence
2002-4	James McGill Award	McGill University Faculty of Medicine	Academic excellence
2003	Sutherland Prize	McGill University Faculty of Medicine	Academic excellence
2003	Joseph Morley Drake Prize	McGill University Faculty of Medicine	Academic excellence
2004	McConnell scholarship	McGill University Faculty of Medicine	Academic excellence
2005	Award of Quebec Association of Francophone Physicians		Academic excellence
2005	Holms Gold Medal	McGill University Faculty of Medicine	Highest Faculty award for Academic excellence
2006	Abstract competition awardee	ACP Massachusetts	Research and presentation excellence
2008	Humanism Award	MGH Internal Medicine Residency	Humanism
2011	Fellow's Symposium award	American Thoracic Society	Research excellence
2011, 2012, 2015	Excellence in Tutoring Award	Harvard Medical School	Excellence in tutoring

2014	Parker B Francis Fellowship	Parker B Francis Foundation	Research excellence
2015	Abstract Award	American Thoracic Society Assembly on Tuberculosis and Pulmonary Infections.	Research excellence
2016	Finalist Massachusetts General Hospital Innovation Program	MGH Department of Internal Medicine	Research excellence
2018	Burke Global Health Fellowship	Harvard Institute of Global Health	Research excellence
2020	Young Mentor Award	Harvard Medical School	Mentorship excellence

Report of Funded and Unfunded Projects:

Past

9/2012-9/2013	Identification of GyrA/B Mutations that Predict Fluoroquinolone Resistant TB Harvard University Center for Aids Research (CFAR) feasibility grant NIH/NIAID P30 AI060354 PI ($40,000) The study of genetic determinants of fluoroquinolone resistance in tuberculosis using targeted sequencing and minimum inhibitory concentration measurements.
3/2014-9/2015	CETR Integrated Discovery and Development of Innovative TB diagnostics NIH/NIAID U19-AI109755 CoI The overarching goal is to develop and test an array based molecular diagnostic for TB drug resistance, and collect translational data on pediatric samples for drug resistance testing.
7/2013-6/2016	Genetic Determinants of Drug Resistance in Mycobacterium tuberculosis American Lung Association Biomedical Research Grant RG-270912-N PI ($80,000) To develop a predictive model for TB drug resistance from genomic data and a platform to disseminate to research and laboratory end users
7/2014-9/2017	Genetic Determinants of Drug Resistance in Mycobacterium tuberculosis Parker B. Francis Foundation Award PI ($95,250) To make novel associations between the drug resistance phenotype and TB genomic variants using phylogenetic convergence.

9/2016- 8/2018	A toolkit for genome-wide association in bacteria Genome Canada CoI, (PI Jesse Shapiro UdeM, Montreal) A collaborative project that allows the dissemination of current tools for bacterial genome wide association through a web-based platform. Include the development of new tools for the study host-pathogen interactions.
10/2017 - 2/2019	NIH Commons Credit Program NIH BD2K K01 ES026835 PI ($7,750) Cloud compute credits to support
7/2018- 6/2019	Harvard Burke Global Health Fellowship PI ($75,000) A big data approach to tuberculosis and drug resistance epidemiology
1/2018- 8/2019	Statistical methods for challenging problems in public health microbiology Canadian Statistical Science Institute Collaborative Research team award CANSSI Co-I, PI: Leonid Chendelvitch S. Fraser University, Vancouver BC A collaborative project on development of tools for bacterial genome sequence analysis for the study of infectious disease.
9/2017- 11/2019	Building capacity in Pune city, India for rapid diagnosis of tuberculosis (TB) and multidrug-resistance Harvard Dubai Center for Global Health Delivery Cooperative Grant Co-Investigator with Dr. Sachin Atre from Pune, India – $75,000 To conduct a pathways to care study of TB drug resistance in the suburbs of Pune, India
10/2015- 6/2020	New Tools for the interpretation of Pathogen Genomic Data with a focus on Mycobacterium tuberculosis NIH/NIAID/BD2K Initiative K01 ES026835 PI ($815,000) To develop genome wide association methods and tools to identify the genetic determinants of infectious diseases.

Current

9/21/2020 – 8/30/2025	Investigating bacterial contributions to TB treatment response: a focus on in-host pathogen dynamics R01 PI ($1,009,734) – 30% effort Patients with tuberculosis (TB) can benefit greatly if we could identify signs of poor response earlier and adjust therapy intensity accordingly. Innovations in DNA isolation and sequencing technologies now enable the study of TB pathogen populations in an individual patient with very high resolution. Here, we propose to use these technologies and a highly

well-characterized cohort of South African TB patients to investigate how pathogen population genetic changes link to pathogen survival and treatment response, laying the foundation for improvements in clinical treatment monitoring using DNA sequencing.

Pending (Select) :

Pending; Impact factor 20	Are Mycobacterium tuberculosis genetic lineages adapted to specific human sub-populations? A genomic epidemiology study to guide TB control R21
4/2021 - 3/2023	PI ($507,791) - 10% effort It is suspected that *Mycobacterium tuberculosis* is genetically adapted to different human populations and is less infectious between humans of different ancestry. As this has implications for how we investigate tuberculosis outbreaks, here we propose to definitively study genetic adaptation been humans and *Mycobacterium tuberculosis* through an innovative and efficient genetic study repurposing tuberculosis surveillance data across three countries.
Pending; Submitted	Transcriptome plasticity and antibiotic resistance in Mycobacterium tuberculosis
7/2021- 6/2024	Smith Family Foundation ($300,000) Studying the effect of resistance-associated mutations on the pathogen transcriptome can shed light on novel cellular mechanisms involved in antibiotic resistance. The integration of genome and transcriptome data will also generate basic generalizable knowledge on transcriptional regulation in bacteria

<u>Report of Local Teaching and Training:</u>

Teaching of Students in Courses:

2010 -	HMS Cardio-pulmonary pathophysiology course tutor HMS-II students	HMS 3 2-hour sessions per week for 3 weeks
2011, 2012	Tutor on mechanical ventilation and pulmonary physiology HST-III students	Harvard School of Technology 1 2-hour session per week for 3 weeks
2014 -2016	OSCE examiner HMS-IV students	HMS 1-2 4-hour sessions annually

2017-	DBMI 722 Topics in Biomedical Informatics Masters of Biomedical Informatics 1st year graduate students	HMS 3 hours per week for 14 weeks
2017-	Summer Institute in Biomedical Informatics (SIBMI) Summer interns in biomedical informatics	HMS 1-hour annually
2018-	AISC 610 Computationally Enabled Medicine HMS-III students	HMS 3-hour visiting lecture every spring semester
2019-	Bioinformatics and Integrative Genomics Seminar PhD candidates	HMS 30-minutes annually

Formal Teaching of Residents, Clinical Fellows, and Research Fellows (post-docs):

2013 – 2016	RACU core curriculum: Gas exchange 1st and 2nd Year Pulmonary Fellows	MGH 1-hour session every 6 months
2014 – 2016	Pulm Crit Care Fellows Research Retreat: sessions on choosing the right mentor, and Epi/translational research 1st year pulmonary fellows	MGH 2-hour session per year
2018-	Pulmonary function test interpretation 1st and 2nd year internal medicine residences on ambulatory rotation	1 hour per year

Clinical Supervisory and Training Responsibilities

2012-	Teaching Service inpatient Medical Students, Internal Medicine Residents and Pulmonary and Critical Care fellows	MGH 6-weeks per year

Formally Mentored Harvard Medical, Dental and Graduate Students:

6-9/14	Chidi Akusobi, MSc MD/PhD candidate on summer research experience
9-12/15	Kevin Ma, Undergraduate in Molecular and Cellular Biology and Statistics, Harvard College Mentored on genotyping methods for tuberculosis Current Position: PhD Student Harvard School of Public Health
3/17-6/18	Gunjan Thakur, PhD Postdoctoral fellow in machine learning for genotype to phenotype interpretation. Current Position research scientist at Merck Research Labs

5/17-6/18	Braden Tierney, PhD candidate in Harvard BBS program (secondary mentor)
9/17- 6/19	Gabriel Fregoso, HMS Class of 2019 (scholar in medicine) Current Position: Resident in Anesthesia Massachusetts General Hospital
6/18 - 7/19	Jiaqi Xie, Masters' in biomedical informatics Class of 2019 Current Position: PhD student in Genetics at Johns Hopkins
11/18- 5/19	Maria Nakhoul Masters' in biomedical informatics Class of 2020
8/16 -	Avika Dixit, MD MPH MBI Postdoctoral fellow in pediatric infectious diseases. Current position: Instructor Boston Children's Hospital
3/17-	Luca Freschi, PhD Postdoctoral fellow in microbial evolutionary genomics
6/17 – 5/20	Michael Chen, Harvard Undergraduate Class of 2020 Current Position: Medical Student. Stanford
9/17-	Roger Vargas, PhD candidate in Harvard Systems Biology
7/18- 7/20	Jessica El Halabi, MD Masters' Biomedical informatics Class of 2020 Postdoctoral fellow in biomedical informatics Current Position: Resident in Internal Medicine, the Cleveland Clinic
3/19-	Maximilian Marin, PhD candidate in Harvard Systems Biology
6/19 -	Matthias Gröschel, MD PhD Postdoctoral Research Fellow
7/19 -	Anna Green, PhD Postdoctoral Research Fellow
8/19 -	Nicoletta Commins, PhD candidate in Harvard BBS program
9/19 -	Carter Nakamoto, Harvard Undergraduate Class of 2021
10/19-	Chang-Ho Yoon, MD Masters' Biomedical informatics Class of 2020 Capstone Mentor

	Current Position: PhD student at Oxford University
10/19- 5/20	Ruojun Wang, MD Masters' Biomedical informatics Class of 2020 Capstone Mentor
12/19-	Hussain Poonwala, MD Masters' of Public Health Class of 2021 Practicum mentor
11/20-	Aliya Moreira, MD Candidate University of Michigan, MPH Candidate Harvard Chan School of Public health Practicum mentor

Other Mentored Trainees and Faculty

2013 - 2016	Hanna Nebenzahl-Guimaraes MPH, PhD candidate University of Minho, Braga, Portugal and RIVM Netherlands Mentored on the use of phylogenetic convergence for TB genome wide analysis. Current Position: Post-doctoral fellow Instituto De Higiene E Medicina Tropical, University of Lisbon.
3-6/2014	Philipp Heindl Bioinformatics undergraduate student, University of Applied Sciences Upper Austria Campus Hagenberg Bioinformatics Class of 2016. Mentored on the design and development of a genomic database. Current Position: Software Developer, Greiner Bio-One GmbH, Linz
6-8/2015	Lanhao Chen, Undergraduate in Business analytics George Washington University (Joint with IQSS). Mentored on machine learning applications and development level scripting. Current Position: NIH Data Mining Specialist
3-7/2017	Sonny Doddi premedical postbac intern, Started medical school at University of Virginia in 8/17. Mentored on database building, bacterial variant calling from NGS data. Current Position: MD candidate University of Virginia Medical School
6-8/2017	Nicholas King, undergraduate BD2K summer intern, Yale Biology Class of 2018 Current Position: Medical Student at Boston University
6-8/2017	Mary Swadener, undergraduate BD2K summer intern, University of Washington Seattle, Biology Class of 2018 Current Position: Associate Computational Biologist, Adaptive Biotechnologies Corp., Seattle

11/17-3/18	Hongya Zhu, undergraduate in Applied Bioscience Zhejiang University. Currently Position: PhD student at Cornell University in Biology
2/18-7/20	Rakesh Dhiman, MPH candidate Umass Amherst (MPH practicum advisor)
4-6/2018	Stefan Bassler, Masters of Bioinformatics Candidate at the University of Heidelberg, Germany Current Position: PhD student EMBL-EBI
6/18-10/20	Yasha Ektefaie, undergraduate intern Harvard Summer Program in Biomedical Informatics (SBMI), Engineering and computer science Major at UC-Berkley: Now PhD Student in the Harvard BIG PhD program
6-8/18, 6-8/19	Shandukani Mulaudzi, undergraduate intern Harvard Summer Program in Biomedical Informatics (SBMI), computer science Major at Columbia. Now PhD Student in the Harvard BIG PhD program
6-8/19	Jerry Yang, undergraduate intern Harvard Summer Program in Biomedical Informatics (SBMI), computer science Major at UC-Berkley
9/2018-6/2020	Suha Kadura, Pulmonary fellow at St. Elizabeth's Medical Center Mentored in conducting a systematic review and in using electronic health record data to study multidrug resistant organism clearance after ICU admission. Current position: Pulmonary Hypertension Fellow, University of Washington Seattle
6-8/20	Naomi Rankin, undergraduate intern Harvard Summer Program in Biomedical Informatics (SBMI), computer science Major at Howard.
6-8/20	Corinne Bintz, undergraduate intern Harvard Summer Program in Biomedical Informatics (SBMI), computer science and Global Health double major at Middlebury College, VT. Current Position: Data Scientist at the Institute for Health Metrics and Evaluation (IHME), Seattle
6-8/20	Monica Iram, undergraduate intern Harvard Summer Program in Biomedical Informatics (SBMI), applied math major at University of Minnesota.

Formal Teaching of Peers:

No presentations below were sponsored by outside entities

2013	Critical care ultrasound Beth Israel Deaconess Critical Care Course (CME)	Single Presentation followed by hands on instruction using mannequins

		Boston
2015 -	Lecture on TB and antibiotic resistance Harvard Pulmonary and Critical Care Course (CME)	Single presentation annually Boston

Local Invited Presentations:
No presentations below were sponsored by outside entities

2012 Novel genes associated with Mycobacterium tuberculosis drug resistance/Seminar
Broad Institute Infectious Disease Initiative seminar series

2012 Drug Resistant TB diagnostics/ Seminar
Brigham and Women's Pulmonary research seminar

2013 Association testing in a Mycobacterium tuberculosis genome wide study
Channing Laboratory Statistical Genetics research seminar

2013 Genomic analysis can inform accurate and thorough TB diagnostics
Massachusetts General Hospital and Beth Israel Deaconess combined fellowship

2015 A power calculator for matched microbial genome wide association studies
Harvard TB Center for Excellence in Translational Research monthly scientific

2015 Drug Discovery for Tuberculosis: A large-scale study of genetic determinants of drug resistance/Seminar
Harvard School of Public Health

2016 Research in Progress
Massachusetts General Hospital Pulmonary Research Series

2017 B3D Series/Seminar
HMS Department of Biomedical Informatics and Harvard Chan School of Public Health

2017 Speaker at "Resistance movement: Drugs, bugs and the fight against über-germs,"
Longwood seminar, HMS

2018 Antibiotic Resistance and Novel Diagnostic Approaches
Massachusetts General Hospital – Surgical Intensive Care Unit Symposium

2018 Tuberculosis in 2018/Grand Rounds
St. Elizabeth Medical Center Medical

2019 Can Mycobacterium tuberculosis population genetics inform TB patient care?
Broad Institute Infectious Disease and Microbiome Program Seminar

2019 Speaker at Diagnostic technologies and host-pathogen interactions in TB
Broad Institute 3rd annual Tuberculosis Research Program Retreat

2020	Novel approaches in the era of MDR/XDR-TB Tufts University Northeast World TB Day Symposium 2020

<u>Report of Regional, National and International Invited Presentations:</u>

No presentations below were sponsored by outside entities.

Regional:

2006	Who develops active TB? A multifactorial risk assessment tool for determining risk of active TB/ (Selected oral presentation) American College of Physicians Massachusetts annual meeting Waltham, MA
2012	Whole genome tests for positive selection in drug resistant TB/ (Selected oral abstract) New England Tuberculosis Meeting Boston, MA
2015	Innovations for mycobacterial disease and emerging drug resistance/Invited Speaker American Society for Microbiology New England Chapter Meeting. Randolf, MA
2018	Heterogeneous populations/Invited Speaker Boston Bacterial Meeting Cambridge, MA
2018	Resistance and Transmissibility of Mycobacterium tuberculosis: what has pathogen whole genome sequencing taught us/ Invited Speaker Rutgers/NJMS Newark, NJ
2019	Tuberculosis Resistance and Transmissibility through a genomic and evolutionary lens/ Invited Speaker Boston University/Brown Tuberculosis Interest Group Boston, MA
2020	New England Tuberculosis Day Symposium. Organized by Tufts University/Invited Speaker (Event canceled due to COVID19) Boston, MA
2020	Antibiotic Resistance Panel/Invited Discussant Boston Bacterial Meeting Cambridge, MA (Virtual)
2021	Mtb WGS to leverage rare variants in predicting treatment response and bacterial contribution to transmission, Invited Speaker, North America Region, Union of TB, Virtual due to COVID

National:

2011	Molecular determinants of isoniazid resistance/ (selected oral presentation) Respiratory Disease Young Investigator's Forum. Atlanta, GA.
2015	Large Scale Sequencing of Genetic Determinants of Drug Resistance in Mycobacterium tuberculosis: Implications for Diagnostic Design/ (selected oral presentation) ATS international meeting. Denver, CO
2017	Machine Learning for Predicting the TB drug resistance phenotype Critical Path to Tuberculosis Drugs Annual Workshop/ Invited Speaker Washington, DC
2017	Implications of Whole Genome Sequencing in TB/Invited Speaker 11th Annual TB Medical Consultant's Meeting West Orange, NJ
2018	Heterogeneity and other considerations for the use of Microbial whole genome sequencing for the diagnosis of antibiotic resistance/ Invited Speaker Pharmaceutical Sciences and Pharmacogenomics Seminar Series, UCSF San Francisco, CA
2018	Women who code (WECODE) conference on Global Health Informatics/ Invited speaker Boston, MA
2018	Clinical implications of pathogen sequencing for TB care/ Invited Speaker Continuing Education session for TB clinicians Hartford, CT
2020	UCSD Biomedical Informatics PhD Seminar/Invited Speaker. Mycobacterium tuberculosis resistance evolution in space and time San Diego, CA
2021	North America Regional Tuberculosis Meeting. Virtual due to COVID Invited Speaker
2021	Microbial Genomics: From Public Health to Personalized Care/ Invited Speaker Baylor College of Medicine, Pulmonary, Critical Care and Sleep Grand Rounds Virtual due to COVID

International:

2014	TB data sharing and database development/ Invited speaker New Diagnostics Working Group for Tuberculosis symposium London, UK

2014	Development needs for TB database development/Invited speaker New Diagnostics Working Group for Tuberculosis 2nd meeting Barcelona, Spain
2015	Genome wide association studies in bacteria/ Invited speaker University of Helsinki, School of Veterinary Medicine. Helsinki, Finland
2015	GenTB: A Web-based Interface to Explore and Analyze Mycobacterium tuberculosis Whole Genome Sequence & Phenotype Data/ --(selected oral presentation) International Union of Tuberculosis and Lung Disease Meeting. Cape Town, South Africa.
2016	Tuberculosis Big Data for drug resistance/ Invited Speaker Critical Path to TB Drug Regimens (CPTR) forum. London, UK
2017	The use of whole genome sequencing technology in TB clinical care/ Invited Speaker Tuberculosis Union North America Annual Meeting Vancouver, Canada
2017	A Web-Based Interface to Explore and Analyze Mycobacterium Tuberculosis Whole Genome Sequence Data / Invited talk American Thoracic Society 2017 International Conference Washington D.C.
2017	Can whole genome sequencing replace traditional cultures and drug susceptibility testing / Invited Spearker McGill 30th Annual Doctor Dorothy Wiselberg Seminar Montreal, Canada
2017	Microbial evolution and implications for molecular epidemiology and medicine/ Invited Speaker Microbial Darwinian Medicine: A Workshop at the Interface of Medicine and Microbial Ecology and Evolutionary Biology The Lorentz Center, Netherlands
2017	Microbial Genome-Wide Association Studies/Invited speaker Microbial GWAS Genome Quebec, Consortium Meeting, University of Montreal Montreal, Canada
2017	Whole Genome Sequencing to Diagnose Drug Resistant TB/ Invited Speaker Dr. D.Y. Patil Medical College, Hospital & Research Center Pune, India
2017	Genomic Applications in Healthcare and Translational Research/ Invited speaker Institute of Bioinformatics and Applied Biotechnology (IBAB) Bangalore, India

2018	Machine Learning for resistance prediction in the session on Data Science to advance TB research/Invited lecture International Union against TB and Lung Disease The Hague, Netherlands
2019	Biological and Clinical Consideration to guide statistical prediction of antibiotic resistance/ Invited Speaker Simon Fraser University, Burnaby, Canada
2019	TB Union Meeting Data Science Symposium/ Organizer, invited speaker and moderator Hyderabad India
2019	In-host population dynamics of *Mycobacterium tuberculosis* during treatment failure/ (accepted oral presentation) TB Union Meeting Data Science Symposium Hyderabad India
2020-21	American University of Beirut WiDS: Women in Data Science International Conference Invited Speaker (Rescheduled till 2021 due to COVID19)
2020	TB Science at the International Union for Tuberculosis and Lung Disease meeting, Valencia Spain (conducted virtually due to COVID19). Invited speaker on "Antibiotic resistance heterogeneity and relevance to clinical care" & Invited panelist on the Antibiotic resistance panel
2021	Machine learning to predict antibiotic resistance in Mycobacterium tuberculosis. UCL Artificial Intelligence Society, Women in Health Series. Guest Speaker, Virtual due to COVID (United Kingdom)

Report of Clinical Activities and Innovations

Current Licensure and Board Certification:

2003	USMLE Step 1
2005	USMLE Step 2
2005	Canadian Licensing Exam
2007	USMLE Step 3
2008	Massachusetts Medical License
2009, 2019	Certification, American Board of Internal Medicine
2010	Certification, American Board of Medical Specialties – Pulmonary Medicine
2011	Certification, American Board of Medical Specialties – Critical Care Medicine

Practice Activities:

7/2012-	Pulmonary and critical care medicine	Inpatient, MGH	Attending 6-weeks per year

2014-2016	House-staff (Bigelow) general medicine teaching service	Inpatient, MGH	Attending 2-weeks every other year

Clinical Innovations:

Web based open access tool (2006)	Development of a risk prediction calculator to aid clinicians in interpreting the tuberculin skin test. Available at: http://www.tstin3d.com/
Web based open access tool (2015)	Development of a web interface for prediction of drug resistance. Available at: http://gentb.hms.harvard.edu/

Report of Education of Patients and Service to the Community

2013-2016	Participant in the Global Health Delivery Online Community. Contribute to discussions around tuberculosis, drug resistance, and diagnostics.

Report of Scholarship

Peer reviewed scholarship in print or other media: Also available at http://www.ncbi.nlm.nih.gov/sites/myncbi/1f5e_XTK7evQc/bibliography/45264981/public/?sort=date&direction=ascending (except for preprints)

Research Investigations (published and preprints under peer review):

1. **Farhat M**, Greenaway C, Pai M, Menzies D. False-positive tuberculin reactions due to non-tuberculous mycobacterial infections. Int J Tuberc Lung Dis 2006 10(11): 1192
2. Menzies D, Gardiner G, **Farhat M**, Greenway C, Pai M. Thinking in three dimensions: a web-based algorithm to aid the interpretation of tuberculin skin test results. Int J Tuberc Lung Dis 2008 12(5): 498
3. Colijn C, Brandes A, Zucker A, Zucker J, Lun DS, Weiner B, **Farhat MR**, Cheng TY, Moody DB, Murray M, Galagan JE. Interpreting expression data with metabolic flux models: predicting Mycobacterium tuberculosis mycolic acid production. PLoS Comput Biol. 2009 5(8):e1000489
4. Karvellas CJ, **Farhat MR**, Sajjad I, Mogensen SS, Leung AA, Wald R, Bagshaw SM. Meta-analysis of early vs late RRT in the critically ill. Crit Care. 2011;15(1):R72. doi: 10.1186/cc10061. Epub 2011 Feb 25. PubMed PMID: 21352532.
5. **Farhat MR***, Shapiro BJ*, Kieser KJ, Sultana R, Jacobson KR, Victor TC, Warren RW, Streicher EM, Calver A, Sloutsky A, Kau D, Posey JE, Plikaytis B, Oggioni MR, Gardy JL, Johnston JC, Rodrigues M, Tang PK, Kato-Maeda M, Borowski ML, Muddukrishan B, Kreiswirth BN, Kurepina N, Galagan J, Gagneux S, Birren B, Rubin EJ, Lander ES, Sabeti P, Murray M. Genomic analysis identifies targets of convergent positive selection in drug-resistant Mycobacterium tuberculosis. Nat Genet. 2013 Oct;45(10):1183-9. doi: 10.1038/ng.2747. Epub 2013 Sep 1. PubMed PMID: 23995135.

- Editorial Coverage: News & Views. Warner, D and Mizrahi V. Complex genetics of drug resistance in Mycobacterium tuberculosis Nat Genet. 2013. 45(10): 1107-8.
- Covered in Nature News, The Scientist, The Independent, El Mundo Salud, SciDev.net, and HMS news.

6. Nebenzahl-Guimaraes H, Jacobson KR, **Farhat MR**, Murray M. A systematic review of mutations that confer drug resistance in Mycobacterium tuberculosis. J Antimicrob Chemother. 2014 Feb;69(2):331-42. doi: 10.1093/jac/dkt358. Epub 2013 Sep 20. Review. PubMed PMID: 24055765.

7. **Farhat MR**, Shapiro BJ, Sheppard SK, Colijn C, Megan M. A phylogeny-based sampling strategy and power calculator informs genome-wide associations study design for microbial pathogens. Genome Med. 2014 Nov 15;6(11):101. doi: 10.1186/s13073-014-0101-7. eCollection 2014. PubMed PMID: 25484920.

8. **Farhat MR**, Mitnick C, Franke M, Devinder K, Sloutsky A, Murray M, Jacobson KR. Concordance of *Mycobacterium tuberculosis* Fluoroquinolone Resistance testing: implications for treatment. Int J Tuberc Lung Dis. 2015 Mar;19(3):339-41. doi: 10.5588/ijtld.14.0814. PubMed PMID: 25686144.

9. Ramly EP, Bohnen JD, **Farhat MR**, Razmdjou S, Mavros MN, Yeh Dante, Lee J, Butler K, De Moya M, Velmahos G, Kaafarani MA. The epidemiology, clinical outcomes, and financial impact of intraoperative adverse events in emergency surgery. Am J Surg. 2015 Oct 23. PubMed PMID: 26601649

10. **Farhat MR**, Jacobson KR, Franke MF, Kaur D, Sloutsky A, Mitnick C, Murray M. Gyrase mutations are associated with variable levels of fluoroquinolone resistance in Mycobacterium tuberculosis. J Clin Microbiol. 2016 Jan 13. pii: JCM.02775-15. PMID:26763957

11. **Farhat MR**, Razvan S, Bozeman S, Iartchouk O, Galagan J, Sisk P, Nebenzahl-Guimaraes H, Jacobson K, Sloutsky A, Kaur D, Posey J, Kreiswirth BN, Kurepina N, Rigouts L, Streicher EM, Victor TC, Warren RM, Van Soolingen D, Murray M. Genetic Determinants of Drug Resistance in Mycobacterium Tuberculosis and their diagnostic value. Am J Respir Crit Care Med. 2016 Feb 24 [Epub ahead of print] PMID: 26910495

    - Editorial coverage: Small PM. Making Tuberculosis Care and Control Easy Again. AJRCCM 2016; 194(5)::537-8. PMID: 27585381

12. Andre E, Isaacs C, Affolabi D, Alagna R, Brokmann D, Cambau E, Churchyard G, Cohen T, De Jong BC, Delmee M, Delvenne JC, Denkinger C, Digovich K, **Farhat MR**, Habib A, Holme P, Kashongwe Z, Keshavjee S, Khan A, Moore D, Moreno Y, Mundade Y, Pai M, Nyaruhirira A, Rocha LEC, Takle J, Trebucq A, Van Soolingen D, Creswell J, Boehme C. Connectivity of diagnostic technologies: combining data sources to improve surveillance and accelerate TB elimination in the post-2015 era. International Journal of Tuberculosis and Lung Disease 2016 Aug;20(8):999-1003. PMID: 27393530

13. Nebenzahl-Guimaraes H*, van Laarhoven A*, **Farhat MR***, Koeken V, Mandemakers J, Netea M, Murray M, van Crevel R, van Soolingen D. Convergent evolutionary analysis identified genetic markers of Mycobacterium tuberculosis transmissibility that are associated with altered cytokine and neutrophil response. American Journal of Respiratory and Critical Care Medicine. (*Co-first authors)

15. **Farhat MR**, Jacobson KR, Franke MR, Kaur D, Murray M, Mitnick C. Fluoroquinolone resistance mutation detection is non-inferior to culture based drug sensitivity testing for predicting MDR TB treatment outcome: A retrospective cohort study. Clin Infect Dis. 2017 Oct 15;65(8):1364-1370. doi: 10.1093/cid/cix556.

16. Dixit A and **Farhat MR**. Cautious interpretation of antibiotic course recommendations. Letter to the Editor. The BMJ. 2017 July. Available at: http://www.bmj.com/content/358/bmj.j3418/rr-16

17. Pollack N, Dhiman R, Daifalla N, **Farhat MR**, Compos-Neto A. Unique *Mtb* protein found in urine of TB patients Discovery of a unique Mycobacterium tuberculosis protein through proteomic analysis of urine from patients with active tuberculosis. Microbes and Infection. 2018 Jan 3. doi: 10.1016/j.micinf.2017.12.011

18. **CRyPTIC Consortium**. Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. N Engl J Med 2018; 379:1403-1415 DOI: 10.1056/NEJMoa1800474

19. Schubert B, Maddamsetti R, Nyman J, **Farhat MR**, Marks DS. Genome-wide discovery of epistatic loci affecting antibiotic resistance using evolutionary couplings. Nat Microbiol. 2019 Feb;4(2):328-338. doi: 10.1038/s41564-018-0309-1

20. **Farhat MR**, Sixsmith J, Calderon R, Hicks N, Fortune S, Murray M. Rifampicin and rifabutin resistance in 1003 MTB clinical isolates. J Antimicrob Chemother. 2019 Feb 21. pii: dkz048. doi: 10.1093/jac/dkz048.

21. Michael L. Chen, Akshith Doddi, Jimmy Royer, Luca Freschi, Marco Schito, Matthew Ezewudo, Isaac S. Kohane, Andrew Beam, **Maha Farhat**. Deep Learning Predicts Tuberculosis Drug Resistance Status from Whole-Genome Sequencing Data. EBioMedicine. 2019. https://www.biorxiv.org/content/early/2018/03/03/275628

22. Yang Yang, Timothy M Walker, A Sarah Walker, Daniel J Wilson, Timothy E A Peto, Derrick W Crook, Farah Shamout, **CRyPTIC Consortium**, Tingting Zhu, David A Clifton, DeepAMR for predicting co-occurrent resistance of *Mycobacterium tuberculosis*, *Bioinformatics*, Volume 35, Issue 18, 15 September 2019, Pages 3240–3249, https://doi.org/10.1093/bioinformatics/btz067

23. Dixit A, Freschi L, Vargas R, Calderon R, Sacchettini J, Drobniewski F, Galea JT, Contreras C, Yataco R, Zhang Z, Lecca L, Kolokotronis SO, Mathema B, **Farhat MR.** Whole genome sequencing identifies bacterial factors affecting transmission of multidrug-resistant tuberculosis in a high-prevalence setting. Sci Rep. 2019 Apr 3;9(1):5602. doi: 10.1038/s41598-019-41967-8. PubMed PMID: 30944370.

24. **Farhat MR**, Freschi L, Calderon R, Ioerger T, Snyder M, Meehan CJ, de Jong B, Rigouts L, Sloutsky A, Kaur D, Sunyaev S, van Soolingen D, Shendure J, Sacchettini J, Murray M. Genome wide association with quantitative resistance phenotypes in Mycobacterium tuberculosis reveals novel resistance genes and regulatory regions. Nature Communications 2019. bioRxiv 429159; doi: https://doi.org/10.1101/429159

    - Featured on the home page of Nature Communication

25. Vargas R[#], Freschi L, Marin M, Epperson LE, Smith M, Oussenko I, Durbin D, Strong M, Salfinger M, and **Farhat MR**. In-Host Population Dynamics of *M. Tuberculosis* during Treatment Failure. BioRxiv Preprint. *Genomics*, 2019 Aug 6. https://doi.org/10.1101/726430. (#mentee)

26. Hunt M, Bradley P, Grandjean Lapierre S, Heys S, THomsit M, Hall M, Malone K, Wintringer P, Walker T, Cirillo D, Comas I, **Farhat M**, Fowler P, Gardy J, Ismail N, Kohl T, Mathys V, Merker M, Niemann S, Vally Omar S, Sintchenko V, Smith G, van Soolingen D, Supply P, Tahseen S, Wilcox M, Arandjelovic I, Peto T, Crook D, Iqbal Z. Antibiotic resistance prediction for Mtb from genome sequence data with Mykrobe. Wellcome Open Research 2019.

27. Vargas R[#], **Farhat MR**. Antibiotic treatment and selection for glpK mutations in patients with active TB disease. Proc Natl Acad Sci U S A. 2020 Feb 25;117(8):3910-3912. doi: 10.1073/pnas.1920788117. Epub 2020 Feb 19. PubMed PMID: 32075922.

28. Ektefaie Y[#], Dixit A, Freschi L, **Farhat MR.** Tuberculosis resistance acquisition in space and time: an analysis of globally diverse M. tuberculosis whole genome sequences BioRxiv 837096; November 2019 doi: https://doi.org/10.1101/837096 (#mentee) *In Press* Lancet Microbe.

29. Gaitanidis A[#], Bonde A[#], Mendosa A, Sillesen MH, El Hechi M, Velmahos G, Kaafarani H*, **Farhat MR***. Identification of a new genetic variant associated with cholecystitis: a multicenter genome-wide association study. Feb 2020 Journal of Trauma and Acute Care Surgery *co-senior (#mentee)

30. Wilson, Daniel J., The CRyPTIC Conssortium. GenomegaMap within-species genome-wide dN/dS estimation from over 10,000 genomes. *Molecular Biology and Evolution*. 2020 March 13. doi: https://doi.org/10.1093/molbev/msaa069.

31. Gröschel MI[#], Meehan CJ, Barilar I, Diricks M, Gonzaga A, Steglich M, Conchillo-Solé O, Scherer IC, Mamat U, Luz CF, Bruyne KD, Utpatel C, Yero D, Gibert I, Daura X, Kampmeier S, Rahman NA, Kresken M, Werf TS, Alio I, Streit WR, Zhou K, Schwartz T, Rossen JWA, **Farhat MR**, Schaible UE, Nübel U, Rupp J, Steinmann J, Niemann S, Kohl TA. The Global Phylogenetic Landscape and Nosocomial Spread of the Multidrug-Resistant Opportunist Stenotrophomonas Maltophilia. 2020 April 27. Nature Communications. https://doi.org/10.1101/748954. (#mentee)

32. Kadura Suha[#], King Nicholas[#], Nakhoul Maria[#], Zhu Hongya[#], Theron Grant, Koser Claudio U, **Farhat MR**. Systematic review of mutations associated with resistance to the

new and repurposed Mycobacterium tuberculosis drugs bedaquiline, clofazimine, linezolid, delamanid and pretomanid. *Journal of Antimicrobial Chemotherapy.* 2020 May. (#mentee)

33. El Halabi J#, Palmer NP, Fox K, Golub JE, Kohane I, **Farhat MR**. Measuring healthcare delays among privately insured tuberculosis patients in the United States: an observational cohort study. *The Lancet Infectious Diseases.* In Press. (#mentee)

34. Lemieux J, Siddle KJ, Shaw BM, Loreth C, Schaffner S, Gladden-Young A, Adams G, Fink T, Tomkins-Tinch CH, Krasilnikova LA, Deruff KC, Rudy M, Bauer MR, Lagerborg KA, Normandin E, Chapman SB, Reilly SK, Anahtar MN, Lin AE, Carter A, Myhrvold C, Kemball M, Chaluvadi S, Cusik C, Flowers K, Neumann A, Cerrato F, **Farhat MR,** Slater D, Harris JB, Branda J, Hooper D, Gaeta JM, Baggett TP, O'Connell J, Gnirke A, Lieberman TD, Philippakis A, Burns M, Brown C, Luban J, Ryan ET, Turbett SE, LaRocque RC, Hanage WP, Gallagher G, Madoff LC, Smole S, Pierce VM, Rosenberg ES, Sabeti P, Park DJ, MacInnis BL. Phylogenetic analysis of SARS-CoV-2 in the Boston highlights the impact of superspreading events. Science Dec 10th 2020 DOI: 10.1126/science.abe3261

35. El Moheb M, Naar L, Christensen MA, Kapoen C, Maurer LR, **Farhat MR**, Kaafarani. Gastrointestinal Complications in Critically Ill Patients With and Without COVID-19. *JAMA.* Published online 2020 September 24. doi:10.1001/jama.2020.19400

36. Freschi L#, Vargas Jr R, Hussain A, Kamal SMM, Skrahina A, Tahseen S, Ismail N, Barbova A, Niemann S, Cirillo DM, Dean AS, Zignol M, **Farhat MR.** Population structure, biogeography and transmissibility of Mycobacterium tuberculosis. BioRxiv 2020 September 29. https://doi.org/10.1101/2020.09.29.293274. (#mentee)

37. Atre S, Jagtab J, Faqih M, Dumbare Y, Sawant T, Ambike S, Bhawalkar J, Bharaswadka S, Jogewar P, Hodgar B, Jadhav V, Mokashi N, Golub J, Dixit A, **Farhat MR.** Measuring and Understanding Delays in Multidrug-Resistant Tuberculosis Care in India. Lancet Preprints. https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3717571

38. Fregoso, G, Dhiman, R, Lanuti, M, Wain, J, Hurtado, R, Richards, C, O'Donnell, W, **Farhat, MR.** Surgical Resection Compared to Medical Management in localized Mycobacteria Avium Complex Pulmonary Infections-A Case Control Study. Preprint 2020 Dec 10. https://www.researchsquare.com/article/rs-122939/v1

39. Alser O, Mokhtari A, Naar L, Breen K, El Moheb M, Kapoen C, Gaitanidis A, Christensen M, Maurer L, Mashbari H, Bankhead-Kendall B, Parks J, Fawley J, Saillant N, Mendoza A, Paranjape C, Fagenholz P, King D, Lee J, **Farhat MR**, Velmahos G, Kaafarani H. Multi-Organ System Outcomes and Predictors of Mortality in Critically Ill Patients with COVID-19. Preprint on SSN (the Lancet preprint server). link

Other peer-reviewed scholarship:

40. **Farhat MR**, Loring S, Riskind P, Weinhouse G. Disturbance of Respiratory Muscle Control in a Patient with Early Stage Multiple Sclerosis. Eur Respir J. 2013 Jun;41(6):1454-6.

41. Invited expert, Lorentz Center Workshop consortium on Darwinian Microbial Medicine. Anderson SB, Shapiro, BJ, Vandenbroucke-Grauls C, and de Vos MGJ. *Microbial Evolutionary Medicine: from theory to clinical practice*. Lancet Infectious Diseases. 2019 Aug 1. 19(8):PE273-E283 https://peerj.com/preprints/26969/

42. Meehan CJ, Serrano GAG, Kohl T, Verboven L, Dippenaar A, Ezewudo M, **Farhat MR**, Guthrie J, Laukens K, Miotto P, Ofori-Anyinam B, Dreyer V, Supply P, Suresh A, Utpatel C, van Soolingen D, Zhou Y, Ashton P, Brites D, Cabibbe A, de Jong B, De Vos M, Fabrizio M, Gagneux S, Gao Q, Heupink T, Liu Q, Loiseau CM, Rigouts L, Rodwell T, Tagliani E, Walker T, Warren R, Zhao Y, Zignol M, Schito M, Gardy J, Cirillo D, Niemann S, Comas I, Van Rie A. Whole genome sequencing of Mycobacterium tuberculosis: current standards and open issues. *Nature Reviews Microbiology*. 2019. 17:533-545.

Non-peer reviewed scholarship in print or other media:

41. A 59-year-old woman with diabetic renal disease and non-healing skin ulcers. (Case presenter: Case records of the Massachusetts General Hospital) N Engl J Med 2007; 356: 1049-1057.
42. Cobelens FG, Menzies D, **Farhat M**. False-positive tuberculin reactions due to non-tuberculous mycobacterial infections-author's reply. Int J Tuberc Lung Dis. 2007 11(8); 934
43. **Farhat M** Chapter 47: Lung Cancer. In: Hess DR, MacIntyre NR, Mishoe SC, Galvin WF, and Adams AB. Respiratory care: Principles and Practice. 2rd ed. Jones & Bartlett Learning: Burlington, MA. 2011: 971.
44. **Farhat M** and Brenner L. Chapter 45: Lung Cancer. In: Hess DR, MacIntyre NR, Mishoe SC, and Galvin WF. Respiratory care: Principles and Practice. 3rd ed. Jones & Bartlett Learning: Burlington, MA. 2015: 1053
45. Major Data Contributor: Technical report on critical concentrations for drug susceptibility testing of medicines used in the treatment of drug-resistant tuberculosis: World Health Organization – 2018 Available at: https://www.who.int/tb/publications/2018/WHO_technical_report_concentrations_TB_drug_susceptibility/en/
46. Rankin N#, Groschel M#, **Farhat MR**. When our internship went virtual we needed a new approach. Science Magazine 2020. (#mentee)

Professional educational materials or reports, in print or other media:

1. Chronic Pain. MGH Primer of Outpatient Medicine. 2006
2. Tuberculosis. MGH Handbook of Global Medicine. 2007
3. Mechanical Ventilation. MGH House staff manual. 2007

Abstracts, Poster Presentations at Professional Meetings (Select):

1. **Farhat MR**, Sultana R, Murray M. High Synonymous Mutation Rate In Ribosomal Protein Encoding Genes Of M. Tuberculosis. American Thoracic Society. 2011 May; pp. A3339-A3339. doi.org/10.1164/ajrccm-conference.2011.183.1_MeetingAbstracts.A3339
2. **Farhat, MR**, Murray M. Molecular determinants of isoniazid resistance. New England Tuberculosis Meeting. Boston, MA June. 2011 Poster presentation.
3. **Farhat MR**, Shapiro J, Sultana R, Murray M. Understanding The Evolution Of Drug Resistant Tuberculosis Through Whole Genomes Tests For Natural Selection. American Thoracic Society. 2012 May; pp. A3262-A3262. doi.org/10.1164/ajrccm-conference.2012.185.1_MeetingAbstracts.A3262
4. **Farhat MR**, Murray M. Several genes show evidence for positive selection in drug resistant TB. Keystone Symposium on TB resistance and Persistence, 2012, Uganda. Poster presentation
5. **Farhat MR**, Murray M, Franke M, Mitnick C, Jacobson K. Quantitative vs Qualitative Fluoroquinolone drug resistance testing. 2014 Harvard Center for AIDS research (CFAR) meeting Boston. Poster presentation
6. **Farhat MR**, Choirat C, Prasad R, Crosas M, Murray M. A Web-Based Interface To Explore And Analyze Mycobacterium Tuberculosis Whole Genome Sequence Data. American Thoracic Society. 2017 May; pp. A7324-A7324. doi/abs/10.1164/ajrccm-conference.2017.195.1_MeetingAbstracts.A7324
7. **Farhat MR**, Calderon R, Ioerger T, Snyder M, Meehan C, de Jong B, Rigouts L, Sloutsky A, Kaur D, van Soolingen D, Shendure J. Genome Wide Association Study of Mycobacterium Tuberculosis Reveals Multiple Novel Genes Associated with Large Increase in Drug Minimum Inhibitory Concentrations. American Thoracic Society. 2018 May; pp. A1153-A1153. doi/abs/10.1164/ajrccm-conference.2018.197.1_MeetingAbstracts.A1153
8. Dixit A, Freschi L, Calderon R, Ioerger T, Kolokotronis S, Methema B, Galea JT, Contreras C, Yataco R, Zhang Z, Lecca L, **Farhat MR**. Genomic Epidemiology of Tuberculosis in Lima, Peru. Abstract accepted at the ASM Microbe 2018 conference
9. Freschi L, Vargas R, **Farhat MR**. Redefining the Population Structure of Mycobacterium tuberculosis Using WGS Data. American Society for Microbiology Microbe 2019 conference
10. Ektefaie Y, Dixit A, Freschi L, **Farhat MR**. TB Resistance Acquisition in Space and Time: An Analysis of Globally Diverse M. tuberculosis Whole Genome Sequence. The TB Union international meeting. Hyderabad, India 2019

Narrative Report:

I am a practicing pulmonary and critical care physician and an early stage investigator. My work is interdisciplinary spanning epidemiology, bioinformatics, computational and evolutionary biology. I dedicate 75% of my time to research activities, 15% of my time to clinical work, 7% of my time to education and 3% of my time to administrative duties.

My area of excellence is investigation and there specifically, I am interested in how pathogens evolve and adapt to environmental, antibiotic and immune pressures, and how this can inform control of infectious disease. I have dedicated most of my career thus far to investigating the single pathogen responsible for the most deaths, *Mycobacterium tuberculosis*, and this grew out of early clinical experiences in South Africa as an Internal Medicine Resident. I am passionate about exploring and repurposing a wide variety of data to answer meaningful and impactful questions related to pathogen evolution and infectious disease surveillance and care. To date among my most prominent achievements is pioneering work in combining epidemiological studies and field data with microbial molecular signatures to understand transmission and drug resistance of *Mycobacterium tuberculosis*. For example, using patient *Mycobacterium tuberculosis* isolates from several drug resistant outbreaks in South Africa, the US, Peru, and Russia, we performed whole genome sequencing and developed a method for the detection of novel genes under positive selection in the drug resistant group while correcting for population structure. Our study was among the first of its kind performing a “Genome wide association study” for bacteria. I have followed this up with methodological work suggesting sampling and analysis strategies for microbial whole genome sequence data. In addition, I have been conducting work of a more translational nature, building prediction algorithms for drug resistance diagnostics using machine learning, integrating these into a public web-based analysis tool: gentb.hms.harvard.edu, and conducing case control studies associating genetic mutations with response to antibiotic therapy and treatment outcome. I have also developed an increasing interest in using clinical informatics data to understand diagnostic delays and pathways to care for TB, and in integrating environmental data such as pollution to understand disease trends over time. I have also been leading and contributing to field work for clinical, epidemiological and molecular data collection nationally and internationally. I am current actively competing for peer reviewed grants, and since becoming faculty member I have been awarded the Harvard Dubai Grant in Global Health Delivery, the Burke Global Health Fellowship, an NIH Cloud computing pilot grant an NIH NIAID R01, and a have a highly scored R21 with NIAID pending. My trainees have successfully competed for travel scholarships (Dr. Dixit and Yasha Ektefaie), and career development awards (Boston Children’s career development award, Charles King Fellowship both to Dr. Dixit, and German Research Foundation to Dr. Matthias Groeshel).

I believe strongly in the academic mission for education and diversity and see my primary role as a faculty member is to support the growth and career development of young physicians and scientists. I co-teach a Master’s level class BMI 722 every fall to the first year MBI students, my co-instructor and I developed the curriculum for this class from scratch and continue to improve upon it annually. We have received very positive feedback about the class and it’s unique format that includes student led seminars moderated by us and close engaged participation of other students. I have also mentored and continue to mentor undergraduates, masters students, PhD students, postdoctoral research scientists and hospital clinical fellows in conducting research. I believe strongly that any passionate dedicated mentee can be very successful if encouraged and given close mentorship and support. I hence don’t only take on trainees that have demonstrated extreme success but judge their passion and willingness to learn our field of study. My lab group has grown very rapidly and I continue to receive regular requests for rotations in our group and have been nominated twice for the HMS mentorship award since starting as faculty in Nov 2016 and won this award in 2020. I also sit on multiple DAC and PQE committees across HMS. I also provide clinical training to medical students, residents and fellows in my capacity as pulmonary critical care attending physician at MGH.

At the same time as I pursue my primary focus area of investigation, and education activities, I continue to dedicate time to clinical patient care at MGH and to pursue the highest standards of clinical excellence. I will be applying for funding from the Cystic fibrosis foundation to begin a non-tuberculous mycobacterial research program at MGH and I believe this will help me contribute further to the hospital and medical schools mission to serve our local community and the integration of clinical care and research. I plan to continue to find opportunities integrate my research and clinical practice over time. I am also committed to my department of biomedical informatics and its research and academic mission. I have volunteered to be a member of both the Masters and the PhD admissions committees at DBMI and also volunteered on faculty search committees and I am a strong advocate for diversity in recruitment. I have also volunteered to support departmental activities towards a new clinical informatics PhD program.

In summary, my primary area is investigation and I am passionate about continuing to grow my research program. I believe strongly that my track record in impactful publications, peer-reviewed grant support and the national and international recognition that I have gained as a pioneer in my field set me up well for continued success. It is a critical time period for me as I compete for larger scale grant support and projects and I am grateful to the Medical School for their continued investment and support of our work.