INTERNATIONAL SYMPOSIUM ON HEALTH ANALYTICS AND DISEASE MODELING (HADM 2018)
MARCH 8-9, 2018
NATIONAL ACADEMY OF MEDICAL SCIENCES AUDITORIUM, NEW DELHI, INDIA

Organized by
Indian Council of Medical Research
National Institute of Medical Statistics, New Delhi, India

and
University of Pittsburgh
Public Health Dynamics Laboratory,
Graduate School of Public Health, Pittsburgh, PA, USA
International Symposium on Health Analytics and Disease Modeling (HADM 2018)
Questions can be emailed to hadm@pitt.edu.

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INTRODUCTION

The text starts with an introduction to the symposium, mentioning its title, date, and location. It also highlights the key aspects of the agenda, including registration, welcome remarks, keynote talks, and invited talks.

AGENDA

The agenda for Thursday, March 8, 2018, is detailed as follows:

8:00 a.m. Registration
9:00 a.m. Welcome: Dr. M. Vishnu Rao, Director, ICMR-NIMS
          Opening Remarks: Secretary, Department of Health Research & Director General, ICMR
          Inauguration: Additional Director General, ICMR
9:30 a.m. Keynote Talk
          Mathematical Modeling as a Tool for Improving Population Health
          Dr. Mark Roberts, University of Pittsburgh, USA
10:30 a.m. Tea Break
10:45 a.m. Plenary Talk
          Modeling of High-dimensional Human Immuno-phenotypic Diversity
          Dr. Saumyadipta Pyne, University of Pittsburgh, USA
11:30 a.m. Invited Talk
          Modeling Epidemiological and Economic Impact of Vaccines
          Dr. Kaja Abbas, London School of Hygiene & Tropical Medicine, UK
12:00 p.m. Invited Talk
          DHR/ICMR Virus Research and Diagnostic Laboratory Network:
          Analysis of Dengue Surveillance Data
          Dr. Manoj Murhekar, ICMR-National Institute of Epidemiology (NIE), Chennai, India
12:30 p.m. Lunch
1:30 p.m. Plenary Talk
          Improving Data Access and Standardization for Epidemic Modeling in Global Health
          Dr. Wilbert Van Panhuis, University of Pittsburgh, USA
2:15 p.m. Invited Talk
          Turning Traditional Surveillance Systems into Big Data: Vietnam as a Case Study
          Dr. Marc Choisy, University of Montpellier, France
2:45 p.m. Invited Talk
          Climate and Dengue Modeling: A Big Data Analytics Perspective
          Dr. Daphne Lopez, Vellore Institute of Technology, Vellore, India
3:15 p.m. Invited Talk
          Climatic and Socio-economic Factors of Dengue Transmission in a City like Delhi
          Dr. Olivier Telle, Centre for Policy Research, New Delhi, India
3:45 p.m.  
**Tea Break**

4:00 p.m.  
**Special Talk**

*Penetrating Modeling at Administrative Units for Enhanced Decision Making*

Professor Nirmal Kumar Ganguly, Translational Health Science and Technology Institute (THSTI), Faridabad, India

4:30 p.m.  
**Panel Discussion**

*Communicable Disease Modeling*

Chair: Professor Nirmal Kumar Ganguly, THSTI, Faridabad, India
Discussant: Professor Arvind Pandey, ICMR-NIMS, India

5:00 p.m.  
**Conclusion of Day 1**

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**Friday, March 9, 2018**

9:30 a.m.  
**Keynote Talk**

*Forecasting Epidemics*

Dr. Roni Rosenfeld, Carnegie Mellon University, USA

10:30 a.m.  
**Tea Break**

10:45 a.m.  
**Plenary Talk**

*A Mathematical Model of CD8 T Cell Responses Calibrated with Human Yellow Fever Vaccine Data*

Professor Carmen Molina-París, University of Leeds, UK

11:30 a.m.  
**Invited Talk**

*A Stochastic Multi-scale Model for Mechanisms of Infection*

Dr. Martín López-García, University of Leeds, UK

12:00 p.m.  
**Invited Talk**

*Complexity of Infectious Disease Modeling for Malaria Prediction*

Dr. Himanshu Chaturvedi, ICMR-NIMS, New Delhi, India

12:30 p.m.  
**Lunch**

1:30 p.m.  
**Invited Talk**

*Application of Big Data Analytics in NCD Surveillance*

Professor R.M. Pandey, All India Institute of Medical Sciences (AIIMS), New Delhi, India

2:00 p.m.  
**Invited Talk**

*TBA*

Dr. Prashant Mathur, Scientist-G and Director, ICMR-NCDIR Bangaluru, India
2:30 p.m.  **Invited Talk**  
*Big Data Analytics in Nutrition and Health*  
Dr. M. Vishnu Vardhana Rao, ICMR-NIMS, New Delhi, India

3:00 p.m.  **Invited Talk**  
*Small Area Estimation in Health Sector by Combining Demographic Health Survey and Census Data*  
Dr. Hukum Chandra, Indian Agricultural Statistics Research Institute, Indian Council of Agricultural Research, New Delhi, India

3:30 p.m.  **Tea Break and Certificate Distribution**

3:45 p.m.  **Special Talk**  
*Healthcare Delivery During the Information Age*  
Dr. P.S. Reddy, SHARE INDIA, India

4:15 p.m.  **Panel Discussion**  
*Health Informatics for Non-communicable Diseases*  
Chair: Dr. D.K. Shukla, ICMR-NIMS, New Delhi, India  
Discussants: Dr. Prashant Mathur, National Centre for Disease Informatics and Research, Indian Council of Medical Research, Bengaluru, India  
and Dr. P.S. Reddy, SHARE INDIA, India

4:45 p.m.  **Closing Remarks**  
Dr. Clareann Bunker, University of Pittsburgh, USA  
**Vote of Thanks**  
Dr. Ajit Mukherjee, ICMR-NIMS, New Delhi, India

5:00 p.m.  **Conclusion of Symposium**
SPEAKER AFFILIATIONS

Dr. Kaja Abbas
Assistant Professor, Department of Infectious Disease Epidemiology
Affiliated Faculty, Center for Mathematical Modeling of Infectious Diseases
London School of Hygiene and Tropical Medicine (LSHTM), London, UK

Dr. Clareann Bunker
Associate Professor Emerita, Department of Epidemiology
Graduate School of Public Health, University of Pittsburgh, PA, USA

Dr. Hukum Chandra
National Fellow and Principal Scientist,
Indian Agricultural Statistics Research Institute
Indian Council of Agricultural Research, New Delhi, India

Dr. Himanshu K. Chaturvedi
Scientist F, Indian Council of Medical Research (ICMR)
National Institute of Medical Statistics (NIMS), New Delhi, India

Dr. Marc Choisy
Scientist, University of Montpelier, France
National Institute of Hygiene and Epidemiology (NIHE), Hanoi, Vietnam

Professor Nirmal Kumar Ganguly
Visiting Professor of Eminence
Translational Health Science and Technology Institute (THSTI), Faridabad, India
Former Director General, Indian Council of Medical Research (ICMR), New Delhi, India

Dr. Daphne Lopez
Professor and Assistant Dean
Vellore Institute of Technology (VIT), Vellore, Tamil Nadu, India

Dr. Martin Lopez-Garcia
Lecturer, School of Mathematics
University of Leeds, Leeds, UK

Dr. Prashant Mathur
Scientist-G and Director, National Centre for Disease Informatics and Research
Indian Council of Medical Research, Bengaluru, India

Professor Carmen Molina-Paris
Professor, School of Mathematics
University of Leeds, Leeds, UK
Dr. Ajit Mukherjee  
Scientist F, Indian Council of Medical Research (ICMR)  
National Institute of Medical Statistics (NIMS), New Delhi, India

Dr. Manoj Murhekar  
Scientist G and Director, Indian Council of Medical Research (ICMR)  
National Institute of Epidemiology (NIE), Chennai, India

Dr. Arvind Pandey  
Advisor, Indian Council of Medical Research (ICMR)  
National Institute of Medical Statistics (NIMS), New Delhi, India

Dr. R.M. Pandey  
Professor and Head, Department of Biostatistics  
All India Institute of Medical Sciences (AIIMS), New Delhi, India

Dr. Saumyadipta Pyne  
Scientific Director, Public Health Dynamics Laboratory  
Graduate School of Public Health, University of Pittsburgh, Pittsburgh, PA, USA  
Adjunct Professor, ICMR-NIMS

Dr. M. Vishnu Vardhana Rao  
Scientist G and Director, Indian Council of Medical Research (ICMR)  
National Institute of Medical Statistics (NIMS), New Delhi, India

Dr. P.S. Reddy  
Founder and Chairperson of SHARE India  
Professor of Medicine  
Department of Medicine, Division of Cardiology  
University of Pittsburgh

Dr. Mark Roberts  
Director, Public Health Dynamics Laboratory (PHDL)  
Professor and Chair, Department of Health Policy and Management  
Graduate School of Public Health, University of Pittsburgh, PA, USA  
Professor of Medicine, Industrial Engineering and Clinical and Translational Science

Dr. Roni Rosenfeld  
Professor, Machine Learning, Language Technologies, Computer Science and Computational Biology  
Carnegie Mellon University (CMU), Pittsburgh, PA, USA

Dr. D.K. Shukla  
Scientist G and Director-In-Charge, Indian Council of Medical Research (ICMR)  
National Institute of Medical Statistics (NIMS), New Delhi, India
Dr. Olivier Telle  
Senior Visiting Fellow, Centre for Policy Research, New Delhi, India  
Centre National de la Recherche Française (CNRS)  
UMR Géographie-cité (Paris-Sorbonne), France

Dr. Wilbert Van Panhuis  
Assistant Professor, Department of Epidemiology  
Affiliated Faculty, Public Health Dynamics Laboratory (PHDL)  
Graduate School of Public Health, University of Pittsburgh, Pittsburgh, PA, USA

KEYNOTE SPEAKERS

Mark Roberts is Professor and Chair, Health Policy and Management, and Director, Public Health Dynamics Laboratory (PHDL) at the Graduate School of Public Health, University of Pittsburgh, PA, USA. He is a practicing general internist and has conducted research in decision analysis and the mathematical modeling of disease for over 25 years. Dr. Roberts has expertise in cost effectiveness analysis, mathematical optimization and simulation, and the measurement and inclusion of patient preferences into decision problems. He has used decision analysis to examine clinical, cost, policy and allocation questions in liver transplantation, vaccination strategies, operative interventions, and the use of many medications. His recent research has concentrated in the use of mathematical methods from operations research and management science, including Markov Decision Processes, Discrete Even Simulation and integer programming to problems in health care.

Roni Rosenfeld received his PhD in Computer Science from Carnegie Mellon University in the previous century, and his undergraduate degree in Math and Physics from Tel-Aviv University even earlier, in the previous millennium. He is Professor of Machine Learning, Language Technologies, Computer Science and Computational Biology at Carnegie Mellon. His current research interests are in epidemic forecasting, and the use of speech and language technologies to aid international development. In past decades he has worked on statistical language modeling, machine learning, speech recognition, and viral evolution. He has published over 100 scientific articles in academic journals and conferences and is the recipient of the Allen Newell Medal for Research Excellence.
PLENARY SPEAKERS

**Saumyadipta Pyne** is the Scientific Director in the Public Health Dynamics Laboratory (PHDL) at the University of Pittsburgh, Graduate School of Public Health. His research interests include Big Data in Life Sciences and Health Informatics, Computational Statistics and High-dimensional Data Modeling. Dr. Pyne received his PhD in computer science from the State University of New York at Stony Brook and was a senior research fellow at the Indian Statistical Institute and a postdoctoral associate at Broad Institute of MIT and Harvard University. He is a remote research associate of the Broad Institute and adjunct professor of the Indian Council of Medical Research. Formerly, Dr. Pyne held the prestigious P.C. Mahalanobis Chair while professor and head of bioinformatics in the C.R. Rao Advanced Institute of Mathematics, Statistics and Computer Science. He worked for years with Harvard Medical School and the Indian Institute of Public Health and was awarded the DBT Ramalingaswami Fellowship. Dr. Pyne is the founder Chairman of Computer Society of India’s Special Interest Group on Big Data Analytics, and leads the Health Analytics Network. He edited the Springer title ‘Big Data Analytics’ in 2016, and the 2-volume ‘Handbook of Statistics: Disease Modelling and Public Health’ published by Elsevier in 2017.

**Wilbert Van Panhuis** is Assistant Professor of Epidemiology, and a Faculty member, Public Health Dynamics Laboratory (PHDL) at the Graduate School of Public Health, University of Pittsburgh. Dr. Van Panhuis is an infectious disease epidemiologist specializing in (inter)national disease surveillance systems, vector-borne and vaccine preventable diseases and global cooperation for disease data sharing and disease control. He is the lead scientist of Project Tycho that aims to provide open access to newly digitized, standardized US weekly disease surveillance data in a dynamic online user environment. He works with colleagues, students and partner organizations in the United States, Southeast Asia and Latin America to assess disease surveillance systems to use high resolution surveillance data for studies on the spatiotemporal spread of infectious diseases. He is developing technology and policy solutions to advance the use of high resolution disease data for dynamic computational modeling in support of decision making, bridging the gap between data, analytics, and policy making. His aim is to establish a central online access point to integrated, standardized country disease surveillance data in the public domain as a core resource for technological innovation, scientific advancement, and more effective investments in global health. His research is focused on data systems and epidemiological analysis of infectious diseases, in particular dengue and vaccine preventable childhood diseases such as measles or pertussis. He is a co-investigator of the Vaccine Modeling Initiative (VMI) funded by the Bill & Melinda Gates Foundation and a co-PI of the Modeling of Infectious Diseases Agent Study (MIDAS) funded by NIH.
Carmen Molina-París is Professor of Applied Mathematics in the School of Mathematics at the University of Leeds, UK. She leads the Mathematical Immunology team, which is part of the Mathematical Biology and Medicine Group in the School of Mathematics. She was appointed a Lecturer in Applied Mathematics at the University of Leeds in September 2002. At that time, her research effort was devoted to the successful unravelling of fundamental problems in the broad area of semiclassical gravity, which deals with the complicated interactions between quantum matter and the gravitational field, as for example in the Early Universe. Since then, she has transitioned from Theoretical Physics to Theoretical Immunology, to Experimental Immunology and to Clinical Immunology, and in doing so, she has established and developed a new research group in the School of Mathematics that has successfully led and coordinated three large international FP7 networks, as well as collaborations with some of the best T cell immunologists in the world. Her team is currently supported by the Smith Institute, EPSRC, H2020, Unilever, Dstl, AstraZeneca and the University of Leeds. She is interested in developing mathematical models, in close collaboration with immunologists, that help us understand the molecular mechanisms behind immune responses. Stochastic Markov process are extremely useful to describe the time evolution of different immune cell populations.

**INVITED SPEAKERS**

Kaja Abbas is an Assistant Professor in Disease Modeling in the Department of Infectious Disease Epidemiology at the London School of Hygiene and Tropical Medicine. His research focus is epidemiological and economic modeling of infectious diseases at the interface of infectious disease system dynamics and public health systems research. He received his BTech from the Indian Institute of Technology Kharagpur, MS and PhD from the University of North Texas, and MPH from the University of Rochester.

Manoj Murhekar is currently working as a Scientist G and Director, National Institute of Epidemiology (NIE), Indian Council of Medical Research (ICMR), Chennai. He received his medical degree from the Government Medical College, Nagpur, and completed his post-graduate work in Preventive & Social Medicine from the same college. He has 25 years of research experience and his areas of interest include infectious disease epidemiology, vaccine preventable diseases, disease surveillance and outbreak investigations. He is a recipient of ICMR’s Major General Saheb Singh Sokhey award for outstanding contribution in the field of viral hepatitis among the tribal population of Andaman and Nicobar. He has more than 125 publications to his credit.
Marc Choisy holds a MSc degree in Ecology and Evolutionary Biology (1999), a MSc degree in Mathematical Statistics (2000) and a PhD in Integrative Biology (2004), all from the university of Montpellier, France. His research interests focus on the transmission of infectious diseases in host populations and his approach combines mathematical and computational modeling together with data analysis borrowing more and more from machine learning techniques. He is particularly interested in understanding the seasonality of epidemics, how diseases spread in space and in developing optimal disease control strategies. After a post-doctoral position at the university of Georgia, Athens (USA) he joined the French Institute of Research for Sustainable Development (IRD, www.ird.fr) in 2007 and moved to Vietnam in 2012 where he became jointly affiliated to the Oxford University Clinical Research Unit (OUCRU, www.oucru.org) in Hanoi. There, he’s based at the National Institute of Hygiene and Epidemiology (NIHE, aka Pasteur Institute of Hanoi) and works on measles, influenza and dengue. Since his relocation to Vietnam, he’s been collaborating closely with PHDL (www.phdl.pitt.edu) of the university of Pittsburgh on data projects, including Tycho Project (www.tycho.pitt.edu) and others. He started organizing the Computational Biology for Infectious Diseases (CBID, www.cbid.asia) summer school in 2016.

Daphne Lopez is Professor of the School of Information Technology and Engineering, VIT, where she has been since 1994. She worked for Wipro Technologies, India and Farmers Insurance, USA for a brief period. She received a BSc from Madurai Kamaraj University and a MCA from St. Joseph’s College in 1990. During the early stages of her professional career, she worked in Software Consultancy Services and eventually joined as a Lecturer. She received a PhD in Computer Science from Mother Teresa University.

Her research interests span data mining, analytics and distributed computing. Much of her work has been on improving the understanding and application of analytics in various domains. In the health arena, she has worked on characterizing the transmission of H1N1 based on spatio temporal factors. She has explored the hot spots and identified the mobility of patients and applied spatial graph clustering to predict the patterns. She has received funds from ICMR for analyzing the H1N1 transmission. Currently her focus is on the analysis of changing climate big data and its impact on public health. She has worked on change detection algorithms and has explored the implications of the climate changes on dengue incidences. In addition she has made contributions to the modeling of diseases and analysis on social media data. Professor Daphne is editor of HCI Challenges and Privacy Preservation in Big Data Security (IGI Global Publishers, 2016) and has authored a number of papers on Data Mining, Big Data Analytics and Cloud Computing.
M. Vishnu Vardhana Rao is the director of the National Institute of Medical Statistics (NIMS), Indian Council of Medical Research, New Delhi. He is a trained mathematical statistician and data scientist. He has a Masters and a PhD in Statistics from Osmania University, Hyderabad, India, and M.Tech (IT) from Punjabi University. He has over three decades of experience in planning, executing and analyzing data for several large-scale community and clinical based research studies in the domain of nutrition and health. His research focuses on the development and application of innovative and appropriate statistical methods for analysis of large and complex data. He led several interdisciplinary groups in designing, data collection and interpretation of large data with the ultimate goal of addressing important Nutrition and Health related issues faced by the communities, in particular, and the country at large. His work also encompasses several evidence based and policy relevant research studies. He is passionate about teaching and training and is a resource person and guest faculty with many universities and institutes of higher education across the country. In 2006, he served as an international consultant for UNICEF at Maldives, Ministry of Health, to help and train officials on surveys and data analysis. Earlier, he was Scientist F – Sr. Deputy Director with ICMR-National Institute of Nutrition, Hyderabad.

Dr. Rao played a pivotal role in establishing the Bioinformatics Centre at NIN, where he collected and computerized large volumes of data pertaining to health and nutrition. Under his leadership, the Bioinformatics team brought out the Nutrition Atlas (http://218.248.6.39/nutritionatlas/home.php) and Count What You Eat (http://218.248.6.43:8080/CountWhatYouEat/Home.do) which are online, virtual, interactive tools that draw from various datasets to provide an overview of nutrition and health scenarios from macro to micro levels in India. He guided several post graduates toward obtaining a PhD degree in the areas of multivariate data analysis, meta-analysis and statistical methods in big data analytics.

Olivier Telle is a researcher at the National Center for Scientific Research (CNRS) currently affiliated with CPR and leading the territorial axe of Centre de Sciences Humaines. The general aim of his research is to better understand how socio-spatial dynamics of cities are connected to epidemic diffusion, in India (Delhi) as well as Asia, integrating human mobility, socio-economic, infra-structural and governance disparities. He is particularly interested in reconnecting sanitation – in the broad meaning - with urban health. Before being recruited by CNRS, Dr. Telle conducted a three-year postdoc at Institut Pasteur Paris (Functional Genetic of Infectious Diseases). He has coordinated projects in India for the past eight years.

Martín López-García is a Lecturer and a Medical Research Council (MRC) Fellow at the Department of Applied Mathematics at the University of Leeds, United Kingdom. He carried out his PhD studies at the Complutense University of Madrid, Spain. In 2016, Dr. López-García was awarded the Vicent Caselles award by the Spanish Mathematical Royal Society for his PhD research work on the mathematical modelling of population dynamics and epidemic processes.
During 2013-2016, he was a Research Fellow at the Mathematical Biology and Medicine Group at the University of Leeds, UK, and his research focused on the stochastic modelling of receptor-ligand molecular dynamics. His current research interests are mathematical modelling of infectious diseases at different scales: from within-host infection dynamics to epidemic processes occurring at the population level. He was recently awarded a Skills Development Fellowship by the MRC, with the project entitled “Mathematical modelling of the emergence and spread of antibiotic resistant bacteria in healthcare settings: a stochastic approach”. In this project, the main aim is to develop new stochastic models for the spread of bacteria in hospital settings, which could lead to identifying effective infection control strategies that can be put in place during bacterial outbreaks.

During the last few years, Dr. López-García has participated in a number of outreach activities to move his research closer to the general public, including participation in the Be Curious 2016 festival in Leeds, the Leeds Science Festival 2018, or the MRC Festival 2018. In 2015, he participated in SET for BRITAIN, where he had the opportunity to present his research to the Members of Parliament in the House of Commons. He has also participated in a number of development assistance projects, teaching stochastic processes and their applications in Mozambique and El Salvador, and his research has been recently featured in the Spanish media.

Himanshu K. Chaturvedi completed his MSc and PhD in Statistics from TM Bhagalpur University, Bhagalpur, a small town of Bihar, INDIA. Dr. Chaturvedi has received many honour and awards. He is a distinguished senior level Scientist at National Institute of Medical Statistics of ICMR, New Delhi, and Ph.D. Supervisor in Medical Statistics of GGSIP University, New Delhi, India. He served as a PI/Co-PI of many National Level projects and also as a member of many scientific committees in India and abroad. The area of his research work is epidemiological studies of harmful substance usage, risk factors of non-communicable disease, estimation of disease burden of malaria and health seeking behaviour of people. Besides that many training workshops on statistical methods, clinical and epidemiological research has been organized by him. He has published more than 50 papers in peer reviewed national and international journals.

Hukum Chandra is ICAR-National Fellow & Principal Scientist at ICAR-Indian Agricultural Statistics Research Institute, New Delhi. He did his PhD from the University of Southampton, United Kingdom and Post Doctorate Research from University of Wollongong, Australia. His main research areas include Sample Survey Design and Analysis, Small Area Estimation, Bootstrap Methods, Statistical Modelling and Data Analysis, Statistical Methodology for Improvement of Agricultural Statistics. He has received number of awards and appreciations for his research contribution such as National Award in Statistics by the Ministry of Statistics and Programme Implementation, Govt of India, ICAR-National Fellow award, Cochran-Hansen Award by the International Association of Survey Statisticians, Lal Bahadur Shastri Outstanding Young Scientist Award of ICAR, P.V. Sukhatme Gold Medal Award and Dr. D.N. Lal Memorial Award of Indian Society of Agricultural Statistics, Young Researcher/Student award of the
American Statistical Association. He is recipient of Commonwealth Scholarship by the Commonwealth Scholarship Commission, United Kingdom. He is Fellow of National Academy of Agricultural Science, India. He has published 90 research papers in number of reputed national and international journals of high impact factor. He has also published three books, several technical bulletins, book chapter etc. He also has delivered number invited talks in many national and international platforms of repute. He is council member of International Association of Survey Statisticians, elected member of International Statistical Institute and International Consultant Sampling for the Food and Agricultural Organization of the United Nations.

**SPECIAL TALK SPEAKERS**

**P.S. Reddy** is Professor of Medicine, University of Pittsburgh, Pennsylvania, USA, and Chairman, SHARE Foundations, USA and India. He graduated from Gandhi Medical College, Hyderabad; qualified MRCP, Edinburgh, UK; completed medical residency and fellowship in cardiology from Montefiore Hospital and Presbyterian University Hospital, Pittsburgh. He joined the faculty of medicine at the University of Pittsburgh in 1971 and served as director of Cardiac Catheterization laboratories. He was promoted to Professor of Medicine in 1987 and became a tenured professor.

Professor Reddy founded SHARE (Science Health Allied Research & Education) in USA (1981); SHARE INDIA (1986), a research foundation to promote research in Medical Colleges of India; and SHARE MEDICAL CARE (1987) to promote service and medical education which established MediCiti Hospital (1993) and MediCiti Institute of Medical Sciences (MIMS, 2001).

Professor Reddy has been an interventional cardiologist and his research was focused on intracardiac phonocardiography to elucidate mechanisms of heart sounds and murmurs and hemodynamics, particularly related to pericardial diseases. He introduced mitral valvuloplasty to cardiologists in Cairo, Egypt.

He has authored more than 100 articles in refereed journals as well as a book, Pericardial Disease. He has received innumerable awards including Peter Safar Pulse of Pittsburgh Award of the American Heart Association (2010); University of Pittsburgh Chancellor’s Distinguished Public Service Award (2000); American College of Chest Physicians outstanding Community Service Award (2001); University of Pittsburgh School of Medicine Excellence in Education Award (2008); Tamil Nadu Dr. M.G.R. Medical University Madras Doctor of Science degree (1996); and American Association of Cardiologists of Indian Origin- Outstanding Physician Scientist award.

For the last 30 years he has spent 50% of his time in India imparting training in research in rural health care delivery to medical faculty. Projects REACH, CATCH, LIFE, MILES, TETRA and HELP are major studies (see SHARE Foundations for details) mentored by him and being implemented by the medical faculty of MIMS.
Nirmal Kumar Ganguly was formerly a Distinguished Biotechnology Research Professor, Department of Biotechnology, Government of India. He was formerly President of the Jawaharlal Institute of Postgraduate Medical Education and Research (JIPMER), as well as that of the Asian Institute of Public Health, Bhubaneswar, Odisha. He is the former Director General, Indian Council of Medical Research (ICMR), New Delhi; former Director, PGIMER (Chandigarh); and former Director, National Institute of Biologicals (Noida).

Professor Ganguly has published more than 778 research papers. His major areas of research have been Tropical Diseases, Cardiovascular Diseases and Diarrhoeal Diseases. His interest encompasses the disciplines of Immunology, Biotechnology and Public Health. Professor. Ganguly is a Fellow, Imperial College Faculty of Medicine, London; Royal College of Pathologists, London; International Academy of Cardiovascular Sciences, Canada; Third World Academy of Sciences, Italy; International Medical Sciences Academy, New Delhi; National Academy of Medical Sciences, New Delhi; Indian National Science Academy, New Delhi; National Academy of Sciences, Allahabad; and the Indian Academy of Sciences, Bangalore. He sits on many advisory boards and is a member of numerous scientific groups.

In 2015 he was selected for the award of Helmholtz International Fellow by Helmholtz Center for Infection Research, Germany for significant contribution to the field of infectious diseases. He has received 118 Awards, including 7 International and 113 National Awards. He has been honoured with the prestigious Padma Bhushan Award by Her Excellency, the President of India on 26th January, 2008 in the field of “Medicine”.

DISCUSSANTS

Arvind Pandey is an Advisor at ICMR-NIMS. He received his PhD in statistics from Banaras Hindu University in India and did his postdoctoral work in biostatistics at the University of North Carolina at Chapel Hill. He was Assistant Professor at the International Institute for Population Sciences (IIPS) for seven years, became Associate Professor at IIPS in 1989, Professor at IIPS in 1998, then served as director of NIMS for 16 years. His areas of research include modelling, estimation and projections of HIV/AIDS epidemic in India, population health statistics, sample surveys, evaluation research and clinical biostatistics. He has more than 222 publications and 12 books. He established the national data repository for the Clinical Trials Registry in India and a robust system for the HIV estimation as nodal person under the aegis of NACO, MOHFW. He has received numerous honors and awards and has held many positions with national and international professional bodies.
D.K. Shukla, Scientist-G, ICMR-NIMS, started his career in 1980, completing almost 38 years of service working in different agencies (NIC, AIIMS & ICMR) and going to be superannuated on June, 2018.

He completed his PhD from the Department of Biostatistics at AIIMS, New Delhi, in 1996. His doctoral work was in the area of applied biostatistics (Prediction model in Coronary Heart Disease(CHD) and Hypertension). Prior to this, he completed his Masters in Statistics (MStat) from the Institute of Social Sciences, Agra University, followed by two years of professional training under PSCC Course and a Diploma in Agricultural Statistics from the Indian Agricultural Statistics Research Institute(ICAR), New Delhi.

He started his career with the National Informatics Centre (NIC) and worked on an ICMR project at the Department of Biostatistics, AIIMS, New Delhi, working at ICMR in various capacities (RO/SRO/AD/DD/DDG(DG)/Scientist-G) for the last 34 years in the Division of NCD/ICMR-NIMS. During this time, he had additional responsibilities as Head (NCD) during 2013-2016 and Director In-Charge during February 2017-December 2017, ICMR-NIMS. His specialties are in the area of NCD Surveillance, Burden of Diseases, NCD Risk factors. He has contributed to completion of most of the ICMR Task Force Projects in the Division of NCD during 1983-2016.

Prashant Mathur is a Pediatrician who completed his post-graduate and PhD in Pediatric Gastroenterology & Hepatology from the All India Institutes of Medical Sciences (AIIMS), New Delhi. He has more than 40 peer-reviewed publications in national and international journals and chapters in 18 books and is a reviewer of 21 national and international journals. He joined NCDIR as the Director, National Center for Disease Informatics - National Cancer Registry Program, Bengaluru, in May 2016. Previously, at the ICMR Headquarters, New Delhi, he was Program Officer for extramural research in the areas of Non-communicable Disease Surveillance, Obesity & Metabolic Syndrome, Chronic Disease Epidemiology, Tobacco and Gastroenterology. He initiated several multi-centric task force programs in these areas of public health relevance. He is the Member Secretary of the National Technical Working Group on NCD Surveillance, representing ICMR. He coordinated the implementation of the national NCD risk factor surveys in 2007-2008 under the Integrated Disease Surveillance Program of the Ministry of Health in seven states of the country. He steered the ICMR’s collaboration with the Medical Research Council, UK, Canadian Institutes of Health Research and Global Alliance for Chronic Disease. He has worked closely with the WHO Offices of the South East Region and India Office, including serving as Temporary International Professional on Capacity Assessment for NCD Prevention, Control and Analysis of NCD related Policies in SEAR Countries. He has been actively involved as a member of the Core Group of the ICMR Strategic Plan, MoHFW Standing Committee on Tertiary Cancer Care Centers/State Cancer Institutes, Sub group for Health Effects on Electronic Nicotine Delivery System (ENDS), Karnataka State Cancer Control Committee, Karnataka Think Tank on Health, and other various committees at different institutions across the country.
CLOSING REMARKS

**Clareann Bunker** earned an MPH in Epidemiology at Johns Hopkins University, and a PhD in Epidemiology at the University of Pittsburgh (USA). She underwent postdoctoral training in cardiovascular disease epidemiology at the University of Pittsburgh. Currently, she is an Associate Professor (Emerita) in the Department of Epidemiology, Graduate School of Public Health, University of Pittsburgh. She has been a teacher and mentor for more than 30 years. Her research has focused on large, international cohort studies of non-communicable diseases. She was the Co-PI of the recently completed five year U.S. NIH Fogarty training program, D43 TW009078, SHARE INDIA University of Pittsburgh Population and Intervention Research Training. She is currently the Co-PI of the Fogarty eCapacity education grant, R25TW009717, Empowering Indian Health Researchers with Computational Modeling Tools. The goal of this education grant is to build capacity among Indian researchers to use cutting-edge technology to address health policy-relevant questions. This education program will result in increased knowledge among researchers of the kinds of data needed to inform models and basic methods in modeling, particularly agent-based modeling.

**Ajit Mukherjee** was born in a remote village of District Burdwan, West Bengal. His school, college and university education was from Delhi. He obtained his degree of Doctorate in Statistics from the Institute of Social Sciences, Agra. He is a Fellow of Society of Medical Statistics (FSMS) and is the recipient of the prestigious Dr. B.G. Prasad award of Indian Society of Medical Statistics (ISMS) for the best published work in the area of Epidemiology in the year 2003. He is currently working with the National Institute of Medical Statistics (NIMS), Indian Council of Medical Research (ICMR), New Delhi, in the capacity of Deputy Director (Sr. Grade)/ Scientist F. He has authored over 40 national and international research publications and books in the area of biostatistics, epidemiology and medical research. He has also delivered several professional talks and has made over 60 research presentations in different parts of the country and abroad. He has been a member of various committees and expert groups set up by GOI on health issues of national importance. He has been a reviewer for many important and prestigious national and international research journals, such as IJMR, Statistics in Medicine, Bulletin WHO, JHPN, IJPVM and Demography India. He has been on the editorial board of Indian Journal of Research in Homeopathy and ISMS Bulletin.
**SYMPOSIUM TALK ABSTRACTS**

**Keynote Talk:** *Mathematical Modeling as a Tool for Improving Population Health, Mark Roberts*
Historically, medicine and healthcare have relied on the randomized controlled trial to understand the most effective treatments for a disease. However, many questions in medicine, and many questions in public health, cannot be answered by randomized trials, for both pragmatic and ethical reasons. This talk will explore the use of mathematical models to inform decisions made in support of public health goals. Although complex mathematical models are currently routinely used in some fields such as weather prediction, their use in public health has been more limited. The goal of a model in the context of public health decision making is to be able to predict the likely consequences of decisions prior to having to implement those decisions. Using examples from infectious disease, disaster preparedness, and cardiovascular health, illustrations of how models can inform public policy are presented. Techniques used to verify and validate models and to provide confidence in their use will be presented.

**Plenary Talk:** *Modeling of High-dimensional Human Immuno-phenotypic Diversity, Saumyadipta Pyne*
Platforms to model and predict vulnerabilities and challenges to population health and bio-security with algorithmic efficiency and robustness play an important role towards our strategic preparedness for public health epidemiology, including disease diagnostics and surveillance. Immuno-phenotypes may provide critical insights into possible disease dynamics and clinical classification of the studied populations, but a major obstacle in the efforts of precise characterization of the human immuno-phenome is the immense diversity therein. While new platforms such as mass cytometry can capture rich multi-parametric data on diverse immuno-phenotypes of infectious and non-communicable diseases, such data also present great challenges for current analytical methods due to their high dimensionality, large number of observations, as well as complex distributional features such as multimodality, asymmetry, and other non-normal characteristics. Our statistical models address these key issues in a systematic and rigorous manner.

**Invited Talk:** *DHR/ICMR Virus Research and Diagnostic Laboratory Network: Analysis of Dengue Surveillance Data, Manoj Murhekar*
The Department of Health Research (DHR) and Indian Council of Medical Research (ICMR) are establishing a network of virology laboratories to strengthen the laboratory capacity in the country for providing timely diagnosis of disease outbreaks. The fully functional network would consist of 120 laboratories at the medical college level, 30 state level and 10 regional level laboratories. VRDLs receive samples from the district public health authorities for laboratory confirmation of disease clusters/suspected outbreaks and also provide virological diagnosis to patients seeking healthcare at the medical colleges where the laboratories are located. VRDLs follow a uniform protocol for laboratory testing and have facilities to test up to 27 viral etiologies. The ICMR-National Institute of Virology, Pune, serves as a resource centre for laboratory testing and the ICMR-National Institute of Epidemiology (NIE), Chennai, serves as a data-management centre.

During January 2014 to December 2017, the 52 functional VRDLs investigated nearly 180,768 patients with acute febrile illness, of whom, 27% were sero-positive for dengue. During the same period, these
laboratories provided diagnosis to 811 suspected outbreaks, 196 of which were due to dengue. The number of dengue fever cases increased from the month of June and peaked in the month of October and decreased thereafter. About two-thirds of these cases were in the age group of 15-45 yr, and 71% were from urban areas. The DHR’s initiative to establish the VRDLs is an important step toward establishing a public health laboratory network system for surveillance of infectious diseases in India. This network, besides providing early diagnosis to disease outbreaks, is also generating case-based data on important viral diseases in India.

Plenary Talk: Improving Data Access and Standardization for Epidemic Modeling in Global Health, Wilbert Van Panhuis
In 2013, we released the first version of Project Tycho, an open access resource for infectious disease data containing weekly disease case counts for 50 notifiable conditions reported by health agencies in the United States between 1888 and 2014. Over the past 3.5 years, more than 3500 users have registered to use Project Tycho and over 40 creative works, including peer-reviewed papers, have been published that use Project Tycho data. This year, we released Project Tycho 2.0, a new iteration of Project Tycho that has a global scope, includes more data, and is more extensively standardized. Project Tycho 2.0 includes case counts for 28 additional notifiable conditions for the US and dengue case count data for 100 countries between 1955 and 2010, obtained from the World Health Organization and national health agencies. Project Tycho 2.0 data conform to a standard data format that improves interoperability between Project Tycho data and other datasets. In the near future, we aim to make disease surveillance, and related data, more compliant with FAIR (Findable, Accessible, Interoperable, and Reusable) guiding principles for data management, towards a network of standardized data for epidemiology and global health.

Invited Talk: Turning Traditional Surveillance Systems into Big Data: Vietnam as a Case Study, Marc Choisy
Disease notification data collected by national surveillance systems are a primary source of information for public health policies. Notification data are useful to characterize disease dynamics including patterns of seasonality and spatial spread. When analyzed with mathematical models, we can also use notification data to better understand the mechanism of transmission, which is particularly relevant for estimating the impact of public health interventions. The epidemiological dynamics of infectious diseases are influenced by multiple drivers related to the host population (e.g. size, density, immunity, age and spatial structures, and socio-economic factors, such as income or education). Other drivers of disease dynamics are the environment (e.g. elevation, land use, distance to the coast line) and local weather and climatic conditions (e.g. temperatures, absolute humidity, rainfall). Integrating population, environmental, and climate variables in epidemiological models can improve model forecasting accuracy. In the big data era, there are more and more opportunities to conduct such so-called ecological studies using data from various sources, collected for various purposes. However, combining co-variables of multiple types in epidemiological studies remains technically challenging, computationally intensive, and time consuming. These challenges limit the utility of available data for public health researchers and practitioners. To overcome these challenges of data integration, we introduce the multepiX project that provides: (1) a method for integration of
public health data and co-variables; (2) a set of tools for data integration in R; and (3) a set of open-access, country-specific, databases (in the form of R data packages).

**Invited Talk: Climate and Dengue Modeling: A Big Data Analytics Perspective, Daphne Lopez**

Climate change rapidly accelerates the need for data revolution around the world. It is a pressing need of society to catalyze climate innovation and influence decision-making on a global level by providing data to vetted public health researchers who can analyze it for the public good. While traditional sources of climate data help describe how and to what extent the climate is changing, they do not always illustrate the solutions that are likely to be most effective in helping to build community resilience. New sources of big data from geographies can be applied to construct a more complete picture, thereby significantly enhancing the understanding of the deeply interrelated relationships between human health and climate change.

This study attributes to the spread of infectious diseases including vector-borne, water-borne, air-borne, and food-borne. The research focus is to identify the factors that influence the dengue incidence in Vellore. Meteorological data collected from various weather stations and centres provide valuable insights for the forecast of short-term weather. However, the traditional data mining algorithms and statistical methods are not adequate to store and process the big climate data. There is a need for a scalable distributed framework to process the big climate data to provide more meaningful change information in the seasonal climate. A big data processing framework is designed to integrate climate and health data, and the next stage change detection method is applied to determine the changes in the climate. Spatial cumulative sum algorithm with a Local Indicator Spatial Association is used to enhance the algorithm. Prediction of dengue incidence is determined using Gaussian Process Regression and my research findings indicate that temperature directly impacts the transmission. New, adaptive machine learning techniques have the potential to exploit data and will help the beginning of a new and enabling ecosystem.

**Invited Talk: Climatic and Socio-economic Factors of Dengue Transmission in a City like Delhi, Olivier Telle**

Mosquito-borne diseases rising in Asia is a true critical issue: severe dengue is, for example, a leading cause of serious illness and death among children in some Asian and Latin American countries. In India, CNRS and CPR collaborate with National Institute of Malaria Research (ICMR), South Municipal Corporation of Delhi and Institut Pasteur on a public health project which aims to understand the structural factors involved in VB diseases emergence, such as urbanisation, increased international/regional/urban mobility and unequal governance of diseases. We recently explored dengue geography in the Delhi trough surveillance system and fieldworks realized in several parts of the city. This presentation aims to sum up the finding of this study.

**Special Talk: Penetrating Modeling at Administrative Units for Enhanced Decision Making, Nirmal Kumar Ganguly**

India is home to more than one-tenth of the global populations and bears a disproportionate burden of diseases. There is a major push in India toward policy changes that is evidence supported using
modelling for policy prioritization and resource allocations. However, there is a low uptake of proven strategies which needs to be provided to the policy makers and health leadership through the use of modelling-associated scenario building (e.g. for cholera, leprosy and others). Modelling can be a valuable tool to aid healthcare policy development and management. A key role of a model is to steer decision-makers in the right direction. In many cases, a model cannot give the “right” answer to a question, but it can be a useful tool in characterizing the problem and finding ways to resolve it. The bottoms-up approach holds a key role in the current scenario of public health in India. In this, it is important to empower and strengthen the decision-making capacity at the district level or even the lower administrative levels. Estimations and projections, through the modelling exercises, at the administrative units would be a powerful tool for the programme implementers to make in-time, independent and evidence-based decisions.

Penetrating modelling at administrative units for enhanced decision making would require a strong capacity building campaign. In India, modelling is still evolving and there is a lack of capacity and training to develop models. But it is important that we need not wait for the best model before the penetration starts, rather a parallel and balanced approach should be adopted to make use of available models at administrative units. Otherwise, there would be a high risk of lagging behind. There already exist a few examples of subnational estimations and projections, a good example being HIV. There is a need to learn from available structures and thereafter institutionalizing modelling to administrative units.

Keynote Talk: Forecasting Epidemics, Roni Rosenfeld

Epidemics can and should be forecast, to improve decision making by governments, institutions and individuals. The goal of the Delphi group at Carnegie Mellon University is to make epidemiological forecasting as universally accepted and useful as weather forecasting is today. I will describe the statistical forecasting system we developed, which won several forecasting competitions including the most recent flu prediction competition run by CDC. It includes both Bayesian and frequentist components, and careful attention to the details of the surveillance signal.

A critical open problem in epi-forecasting is nowcasting – real-time estimation of epidemic intensity. Google search query fraction and other real-time sources have been used to try to nowcast epidemic intensity, with mixed results. Better results might be achievable by combining many such proxies: electronic health records, internet search queries, social media, relevant retail purchases, and online information-seeking behavior. However, these sources are correlated, dynamically changing, sporadic, of variable geographic and temporal resolution, of variable reporting delays, and have variable historical training data. Conventional statistical estimation techniques are inadequate for dealing with these challenges, resulting in a variety of ad-hoc approaches. I will describe a novel method for nowcasting that is derived from sensor fusion theory. It combines an arbitrary number of heterogeneous and sporadic sources to produce real-time estimates. Unlike regression-based methods, it is robust to missing data and follows a disciplined approach to combining sources of variable geographic resolution. I will demonstrate our method on a large set of both traditional and novel digital flu surveillance sources, and provide a retrospective analysis of its performance, including ablation experiments showing its robustness.
Plenary Talk: A Mathematical Model of CD8 T Cell Responses Calibrated with Human Yellow Fever Vaccine Data, Carmen Molina-París

Once activated by antigen presenting cells (APCs), naive (N) CD8+ T cells proliferate and differentiate to functionally diverse central (C) and effector memory (M), and effector cells (E). Novel experimental techniques allow us to track antigen-specific cellular responses, yet we still lack a complete understanding of the temporal dynamics of T cell responses: how and when lineage differentiation takes place. We have made use of mathematical and statistical modelling to describe CD8+ T cell dynamics during an immune response. The model includes N, C, M and E T cells and three spatial compartments, draining lymph nodes, blood and resting lymph nodes, and tissues. We hypothesise that (1) CD8+ T cell differentiation follows the decreasing potential model and (2) a single T cell-APC interaction drives a programme of division-linked differentiation events (see Figure 1). We have made use of: 1) yellow fever vaccination data; and 2) Approximate Bayesian Computation (ABC) to estimate some of the parameters of the model. The rest of the parameters have been obtained from previously published studies. The number of CD8+ T cell clonotypes that are driven into the immune response has been estimated with ABC methods. We find that increasing the number of clonotypes reduces the number of divisions required for naive cells to differentiate into central memory cells and for central memory cells to differentiate into effector memory cells, but it does not affect the number of divisions required for effector memory cells to differentiate into effector cells. Thus, our model provides a mathematical framework to quantify human immune responses.

Invited Talk: A Stochastic Multi-scale Model for Mechanisms of Infection, Martín López-García

We present a multi-scale stochastic model of the within-phagocyte, within-host and population level infection dynamics of Francisella tularensis. Our within-host model is based on the mechanistic one proposed by Wood et al. 2014 [1], which incorporates key aspects of the interaction between host phagocytes and extracellular bacteria. The main aim of the within-host model is to obtain the probability of response, and mean time until response, of an infected individual as a function of the initial infection dose. In ref. Wood et al. 2014 [1], it is assumed that when each infected phagocyte ruptures, a fixed number of bacteria are released. Here, a multi-scale extension to this model is proposed that links the within-host infection dynamics with stochastic within-phagocyte dynamics. A Bayesian approach is applied to parametrise both the within-phagocyte and within-host models using infection data. We then compute the probability mass function of the number of bacteria released by a rupturing phagocyte. Our results suggest that the number of bacteria released upon rupture in ref. Wood et al. 2014 [1] was slightly overestimated. This rupture size distribution is the main link between the within-phagocyte and the within-host scales. Finally, we show how dose response probabilities at the individual level can be used to estimate the airborne propagation of Francisella tularensis in indoor settings (such as a microbiology laboratory) at the population level, by means of a deterministic zonal ventilation model.

Invited Talk: *Complexity of Infectious Disease Modeling for Malaria Prediction, Himanshu K. Chaturvedi*

Infectious disease modelling is mainly focused for early prediction of disease occurrence that can help in planning and policy decision to control the disease outbreak. Malaria is an infectious disease causing severe morbidity which may result in fatality if the diagnosis is delayed. Despite scientific knowledge and community level programs to control malaria, its eradication is yet a challenging problem for many countries in the world. Infectious disease modelling is an important research area to understand the transmission dynamics of various pathogens related to disease outcome among human population. Classical modelling approach in malaria is a theoretical framework mainly based on division of human host parasite population into categories such as susceptible (S), exposed (E), infectious (I), and recovered (R), e.g. named as SEIR model. These models are described as a mathematical expression in the form of differential equation of infection rates. Besides that there were several statistical methods used for infectious disease of modelling, such as Markova Chain Monte Karlo, Simulation approach, Baysian models and time series models for prediction of malaria. These models were based on stochastic process of disease occurrence related to the chance of spreading disease in a given population with time.

The complexity of models increases when the role of climate fluctuation, such as inter-annual changes in rainfall patterns in determining the inter-annual variability of disease occurrence, and small increase in temperature leads to large increases in the vectorial capacity of mosquitoes, are also included for more reliable prediction of malaria. The variability in disease occurrence may be explained by change of location (one place to other in larger area) and time (seasonal/periodical change). The modelling becomes more complicated if we incorporate directional variability with time using geospatial analysis, but it may not be possible to incorporate many more parameters related to localized transmission related to occurrence of malaria.

The validity and sustainability of these prediction models are also important issues for building confidence and future research interest in modelling.

Invited Talk: *Small Area Estimation in Health Sector by Combining Demographic Health Survey and Census Data, Hukum Chandra*

The demand for small (local-level) area statistics has increased tremendously, particularly in countries where a decentralised approach to governance and service provision has been adopted. Most of these countries lack local-level statistics to aid policy decisions and planning. Sample surveys such as the Demographic and Health Survey provide a wide range of invaluable data at the national and regional level but cannot be used directly to produce reliable district-level estimates due to small sample sizes. The small area estimation technique overcomes the sample size challenges and can generate representative and reliable estimates at the local (or small area) level by linking outcome of interests that are recorded in survey with auxiliary data from census or administrative datasets. This paper illustrates the application of small area estimation techniques to generate model-based district-level estimates of health related indicators by combining Demographic and Health Survey and Population Census data. The diagnostics measures show that the model-based estimates are precise and robust when compared to the direct survey estimates. In countries where small area statistics are non-existent, small area estimation techniques could be crucial for designing effective policies and strengthening local-level governance.
ABOUT THE ORGANIZERS

**National Institute of Medical Statistics, Indian Council of Medical Research**
Situated at New Delhi, the National Institute of Medical Statistics (NIMS) aims to promote and undertake research in statistical techniques and methodology in the field of health research, exercise surveillance to ensure the statistical adequacy and validity in various programmes of the Council and Government of India.

Learn more at [http://nims.icmr.nic.in](http://nims.icmr.nic.in).

**Public Health Dynamics Laboratory, Graduate School of Public Health**
Since 1948, as Pennsylvania’s first fully accredited graduate school of public health and the 13th in the nation, the University of Pittsburgh Graduate School of Public Health has been educating leaders, engaging in service and research, and translating research into public health practices and policies to improve the health of people regionally, nationally, and globally.

The Public Health Dynamics Laboratory (PHDL) at the University of Pittsburgh Graduate School of Public Health was established in 2009 as a catalyst for development of interdisciplinary computational approaches to understand and solve the world’s most challenging public health issues. The PHDL brings together epidemiologists, biostatisticians, behavioral scientists, public health policy experts, and computational scientists to produce the next generation of tools for public health analysis.

Learn more at [www.phdl.pitt.edu](http://www.phdl.pitt.edu).

**SHARE India**
In 1981 a seed of a noble thought was planted that would later on become a flourishing tree of health and happiness for a huge segment of people. That life transforming seed was SHARE.

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Choosing picturesque and peaceful environs, at Medchal Mandal (County) about 35 kms Hyderabad, the Capital City of the state of Telangana, they went about their mission. Thus was born a world-class medical centre which today, is a proud institution of health and happiness covering 80 villages in the two nearby mandals (Medchal and Shameerpet) and providing world-class care to the needy.


**Health Analytics Network**
Health Analytics Network is a research consortium that brings together data analysts, statisticians, biomedical scientists, public health researchers and policy experts around the globe to address public health challenges and develop inter-disciplinary solutions for translation of health data to effective policy.

Learn more at [http://www.healthanalytics.net/HADM2018/](http://www.healthanalytics.net/HADM2018/).
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