

PUBLIC HEALTH FOUNDATION OF INDIA







Certificate Course in

**Healthcare Technology (CCHT)** 

Module 1 : Introduction to Health care Technology and its practical application



Understanding health care data and digital epidemiology





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### **Understanding health care data and digital epidemiology**

#### **Overview of Session:**

Epidemiology is the study of health and disease in populations. Googles Flu Trends, Flowminder, Healthmap, Biodiaspora are several examples of digital epidemiology already in play. Engineered systems that are built from and depend upon, the seamless integration of computational algorithms and physical components is how National Science Foundation defines the field of cyber physical systems (CPS). Digital Epidemiology can be viewed as a health care application of CPS. The foundations of CPS include a focus on the modelling of dynamic systems with attention to integrating computing, communication and control in uncertain and heterogeneous environments. Modelling paradigms include linear and non-linear, stochastic, discrete-event and hybrid models that are analyzed by methods of optimization, probability theory and dynamic programming.

#### **Detailed Reading Content:**

Digital Epidemiology is a new field that has been growing rapidly in the past few years, fuelled by the increasing availability of data and computing power, as well as by breakthroughs in data analytics methods.

Digital Epidemiology has come a long way in the past 10 years. What started as a small and diverse group of researchers from various fields mining the increasing amount of internet data for epidemiological purposes has now turned into a nascent field of its own. The number of scholarly publications, scientific events, and academic groups dedicated to digital epidemiology has grown steadily over the past few years. In these early years of digital epidemiology, its growth has been fueled by the rapid growth of digital data, the widespread penetration of mobile phones and internet usage, and the increasing power of machine learning that is necessary to make sense











of the available data. As these underlying developments are continuing, the growth of the field of digital epidemiology will continue alongside with it.

The goal of epidemiology, very broadly speaking, is to understand the patterns of disease and health dynamics in populations as well as the causes of these patterns, and to use this understanding to mitigate and prevent disease, and to promote health. The goal of digital epidemiology is exactly the same. So, what differentiates (non-digital) epidemiology from digital epidemiology? Digital epidemiology is epidemiology that uses data that was generated outside the public health system, i.e. *with data that was not generated with the primary purpose of doing epidemiology*.

#### Digital epidemiology - an outlook

The original growth of digital epidemiology was largely fueled by the rapidly increasing amounts of data generated on the internet, particularly also on social media. Google Flu Trends (GFT) was among the earliest well known examples of digital epidemiology, leveraging symptomatic search queries for the purpose of syndromic tracking of influenza-like illnesses (Ginsberg et al., 2009). The specific problems with GFT have been well described and discussed (Cook et al., 2011; Olson et al., 2013; Lazer et al., 2014), but the larger problem with GFT was the private ownership of the underlying data, which meant that the algorithm could not be reproduced and investigated independently. In other words, the public health community had no deep insight into the algorithm and the underlying data, was not able to directly contribute to its improvement, and had no say in the decision to shut down the system. It is understandable that no public health authority would be particularly keen on using such a black box system over which it has absolutely no control. However, the implementation of digital epidemiology into the daily workflow of public health authorities is perhaps the key goal of digital epidemiology in the future. Therefore, the field needs to focus on finding ways to make data openly accessible, at least to health authorities and researchers, and ideally to the community at large. This, however, is at odds with the current trend of major internet services substantially reducing the access to data.

There are multiple responses to this trend, of which two are highlighted The first response, ironically, is to do less digital epidemiology in the strict sense, namely to rely less on third-party data that was not generated for epidemiological purposes, and for the public health system to generate their own digital data streams that do not exclusively depend on corporate actors. Academic labs could play an important role in this development by creating the prototype systems, which, once their usefulness is established, could be supported, extended and maintained by public health authorities. Existing successful case studies of innovative approaches coming out of academic labs include HealthMap (Brownstein et al., <u>2008</u>) and InfluenzaNet (Paolotti et al., <u>2014</u>).











The second response is to build on the increasing legal reality that data generated by individuals, no matter through which corporate service, belongs to the individuals who generated it - or that, at least, the individual has a right to a copy of his or her data. It is conceivable that a representative fraction of the population could be convinced to share health-related data with public health authorities, either directly or through third parties such as health cooperatives.

Beyond the data-related trends, another major trend is concerned with the analytics of the data, rather than the data itself, and can be captured by the term "machine learning". Machine learning, broadly defined as the ability for computers to learn patterns from data without being explicitly programmed, has seen enormous developments in the past decade, particularly also in the subfields of image recognition and natural language comprehension. The breakthroughs in these subfields were themselves mostly realized using a branch of machine learning called deep learning (LeCun et al., 2015), which builds on artificial neural networks that can be constructed in such a way as to learn rapidly from large amounts of data to correctly map an input (such as an image or a sentence) to an output (such as a diagnosis or a sentiment). Recent high-profile examples in the health domain include the demonstration that a deep learning algorithm trained on almost 130,000 clinical images of skin lesions performed on par with 21 board-certified dermatologists when performing skin cancer classification (Esteva et al., 2017). Such demonstrations now appear almost daily in the scientific literature, underlying the rapidly growing interest in this field, and artificial intelligence (AI) in general. The fact that these large neural networks are currently mostly black boxes whose inner workings are poorly understood is often leveled as a major criticism against them. However, this criticism may not be valid for very long, as substantial resources are currently invested towards a better understanding of how exactly they work.

Interestingly, the deep learning approach itself is currently highly dependent on the availability of very large datasets from which neural networks can learn. Thus, in order to reap the benefits from this technology, one needs access to large datasets. The need for large, open datasets for digital epidemiology will therefore only continue to grow. Due to the strong open source software movement particularly also from academia, most of the algorithms underlying deep learning are openly and freely available. The same is not generally true for data, and access to large, high quality datasets is thus becoming the limiting factor in the development of AI.











#### Syndromic Surveillance-Impact of the internet and social networks

#### Syndromic surveillance

Traditional vs syndromic surveillance

- Traditional: laboratory tests of respiratory specimens, mortality reports
- Syndromic: 'clinical features that are discernable before diagnosis is confirmed or activities prompted by the onset of symptoms as an alert of changes in disease activity' <sup>15</sup>

Issues in considering a syndromic surveillance system

- Sampling bias
- Veracity and reliability of syndromic data
- Granularity of space- and time-resolution
- Change point detection versus forecasting

Broad consensus is that syndromic surveillance provides some early detection and forecasting capabilities but nobody advocates them as a replacement for traditional disease surveillance.

<sup>15</sup>K Hope, DN Durrheim, ET d'Espaignet, C Dalton, *Journal of Epidemiology and Community Health*, 2006

Suggested Readings on Syndromic Surveillance

- Simon Hay and colleagues: <u>https://scholar.google.co.in/citations?user=SxiyFuQAAAAJ&hl=en&oi=sra</u>
- There has been work in H1N1
   <u>https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0019467</u>
- Flu tracking <u>http://www.aclweb.org/anthology/N13-1097</u>
- In Global south spaces, there is some work there is work on search behavior and disease tracking: <u>https://journals.plos.org/plosntds/article?id=10.1371/journal.pntd.0005295</u> <u>https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0064323</u>
- Some of Lakshmi Subramanian's students were working on dengue from mainstream media news sources: <u>https://dl.acm.org/citation.cfm?id=2442906</u>











#### Epidemiology: paradigms

- Communicable Epidemics / Pandemics
- Non-Communicable Diseases
  - Somatic (CVDs, Cancer, Respiratory, Neurodegenerative, ...)
  - Genetic / Inherited / Germline
  - Haemetological, Skeletal, Neuromuscular, Dermatological, Immune
  - Deficiency, Lysosomal Storage, Autoimmune, neurodevelopmental,

Environmental Epidemiology (somatic)
 Precursors to Computational Epidemiology



#### Modelling in Epidemiology











- Applications of Models in Epidemiology
- Modelling Paradigms
  - Simulation Models and Studies
  - Compartmental Models in Epidemiology
  - Spatial Models Patch Based, Cellular Automata
  - Network Models for Communicable Diseases
  - Graphical Dynamical Systems Models in Epidemiology

Models are abstractions of Complex Systems that permit us to

- Understand phenomena / Explore Scenarios
- Explore Hypotheses
- Create intervention strategies

Strategic/Tactical/Operational

- Formulate Policy

#### S-I-R Models (Kermack and McKendrick (1927)) Susceptible Infected Recovered

#### Compartmental SIR Model

- Kermack and McKendrick
  - DTDS vs CTCS
  - Critical Parameters
- Population of N individuals. Each individual begins in one of 3 states
  - Susceptible: has never had the disease and is susceptible to being infected
  - Infected: currently has the disease and can infect others
  - Resistant: does not have the disease, cannot infect others and cannot be infected.
- Discrete Evolution. In each time step:
  - Each susceptible individual draws a uniformly random person from the population. If the person drawn is infected, the susceptible











individual changes state to infected with probability  $\boldsymbol{\beta}$  (infectivity parameter)

- Each infected individual change state to resistant with probability γ (infectious period parameter)
- Each resistant individual stays resistant
- Let X(t), Y(t) and Z(t) denote the number of susceptible, infected and resistant individuals in the population at time t. X(t) + Y(t) + Z(t) = N for all t.
- Expected values:

$$\begin{split} \mathsf{E}[\mathsf{X}(t+1)] &= \mathsf{X}(t) \cdot (1 - (\mathsf{Y}(t)/\mathsf{N}) \cdot \beta) \\ \mathsf{E}[\mathsf{Y}(t+1)] &= \mathsf{X}(t) \cdot ((\mathsf{Y}(t)/\mathsf{N}) \cdot \beta) + \mathsf{Y}(t) \cdot (1 - \gamma) \\ \mathsf{E}[\mathsf{Z}(t+1)] &= \mathsf{Y}(t) \cdot \gamma + \mathsf{Z}(t) \end{split}$$

Difference equations to differential dynamics (DTDS to CTCS)

$$\begin{split} \frac{dX(t)}{dt} &= -\beta \cdot X(t) \cdot \frac{Y(t)}{N}, \\ \frac{dY(t)}{dt} &= \beta \cdot X(t) \cdot \frac{Y(t)}{N} - \gamma \cdot Y(t), \\ \frac{dZ(t)}{dt} &= \gamma \cdot Y(t). \end{split}$$

Variable substitutions S(t) = X(t)/N; I(t) = Y(t)/N; R(t)=Z(t)/N

$$\begin{split} \frac{dS(t)}{dt} &= -\beta \cdot S(t) \cdot I(t), \\ \frac{dI(t)}{dt} &= \beta \cdot S(t) \cdot I(t) - \gamma \cdot I(t) \\ \frac{dR(t)}{dt} &= \gamma \cdot I(t). \end{split}$$











**200** runs of the discretetime,discrete-space model with a population size of 100,000 individuals, 100 of whom are initially infected and the rest susceptible.  $\beta$ ,  $\gamma$ = 0.4, 0.2

Mean Field Approximation – justification in compartment model

- Which Diseases Become Epidemics?
  - Basic Reproduction Number  $R_0 = \beta/\gamma$

$$- R_0 > 1$$



- Extension 1 : More complex population structures
  - e.g., a natural birth/death process that removes individuals from all compartments and introduces individuals into the susceptible compartment. In this model, µ is the birth/death rate.





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$$\frac{dS}{dt} = -\beta \cdot S \cdot I + \mu \cdot (I + R),$$

$$\frac{dI}{dt} = \beta \cdot S \cdot I - \gamma \cdot I - \mu \cdot I$$

$$\frac{dS}{dt} = -\beta \cdot S \cdot I,$$

$$\frac{dR}{dt} = \frac{dE}{dt} = \beta \cdot S \cdot I - \sigma \cdot E,$$

$$\frac{dI}{dt} = \sigma \cdot E - \gamma \cdot I,$$

$$\frac{dR}{dt} = \gamma \cdot I.$$

• Extension 2: progression.

More complex disease

 e.g., introduce a latent period of the disease, between the susceptible and infected compartments. In this model, E stands for the exposed compartment of infected individuals in the latent stage of infection, and σ is the rate at which these individuals progress to the active stage of infection.

SEIR Model

#### Limitations of Compartmental SIR Model

 Based on the estimates of R<sub>0</sub> in the range (2.2,3.6),SARS should have caused a great world pandemic with cases numbering easily in the millions. However, for the entire SARS outbreak (from November 1,2002 to July 31,2003),only 8,096 cases were reported with 774 deaths. Why?











- Diseases often spread differently in different age groups, have varying incubation periods in different age groups, spread differently depending on the type of contact; e.g., contacts at home tend to be more intimate than contacts at work. Also, disease spread is affected by geographic location and seasonality.
- Researchers have built very high-fidelity models using agent-based simulations, where each individual is tracked as they move from home to work and back

#### **References:**

- Digital epidemiology: what is it, and where is it going? Marcel <u>https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5754279/#CR6</u>
- <u>https://healthheatmapindia.in/digital-epidemiology</u>

#### Suggested Readings:

- Exponential Technologies and the Perfect Storm for Digital Health <u>https://link.springer.com/article/10.1007/s41745-020-00203-3</u>
- Statistical Models in Epidemiology, The Environment and clinical Trials" Halloran & Berry, IMA Vol 116, Springer 2000. pages 219-236
- <u>http://www.thehindu.com/sci-tech/health/emerging-infectious-diseases-one-health-and-india/article19285575.ece</u>





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## Presentations







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Indian Institute of Space Science and Technology

## Certificate Course in

## **Healthcare Technology (CCHT)**

## **Computational Epidemiology and Covid-19**



## **Prof. Vijay Chandru**



Vijay Chandru is computational mathematician who is an INAE Distinguished Technologist and an Adjunct Professor at the Indian Institute of Science (IISc) in Bangalore. He co-founded Strand Life Sciences, a spinoff of IISc in precision medicine which he led as executive chairman from inception in 2000 till his retirement in 2018. He also co-founded several non-profit organizations - CHET, Metastring and OPFORD Foundations which are dedicated to health policy, the democratization of data and healthcare access for the underserved orphan diseases. A former president of ABLE, the biotechnology industry apex body, Professor Chandru is a technology pioneer of the World Economic Forum where he has served on the industry advisory council on the future of health.

## **Learning Objectives**

## Epidemiology

- Epi (on) + Demos (population)
  - Study of health and disease in populations
- History
  - Hippocrates (disease decriptions), Galileo Galilei (quantitative measurement), John Gaunt (mortality, gender), P-C Alexandre Louis (numerics, statistics), John Snow (cholera, water), Rudolf Virchow (social Sciences), Joseph Goldberger (NCDs)

### Mass action compartmental Models



- Susceptible (S): An individual has never had the disease and is susceptible to being infected;
- Infected (I): An individual who currently has the disease and can infect other individuals, and
- Resistant/Recovered (R): An individual does not have the disease, cannot infect others, and cannot be infected (sometimes called removed)

Where I is referred to as the *transmission rat*e, and is the recovery rate. A key parameter in such a model is the *reproductive number*, denoted by  $R_0 = /$  At the start of an epidemic, much of the public health effort is focused on estimating  $R_0$  from observed infections.

### Dynamics in Compartmental Models

$$\frac{ds}{dt} = -\beta is$$
$$\frac{di}{dt} = \beta is - \gamma i$$
$$\frac{dr}{dt} = \gamma i$$

- $\frac{di}{dt} > 0$  (leads to a large epidemic) if  $\frac{\beta s}{\gamma} > 1$
- $\blacksquare$  At the start of epidemic: spprox 1
- $R_0 = \beta / \gamma$ : reproductive number
- Large epidemic if and only if  $R_0 > 1$
- Modeling epidemic = estimating  $R_0$
- Controlling epidemic: reducing R<sub>0</sub>



Effect of  $R_0$  on the dynamics<sup>3</sup>

<sup>3</sup>Dimitrov and Meyers, *INFORMS*, 2010

## **Limitations of Compartmental SIR Model**

- Based on the estimates of R<sub>0</sub> in the range (2.2,3.6),SARS should have caused a great world pandemic with cases numbering easily in the millions. However,for the entire SARS outbreak (from November 1,2002 to July 31,2003),only 8,096 cases were reported with 774 deaths. Why?
  - Diseases often spread differently in different age groups, have varying incubation periods in different age groups, spread differently depending on the type of contact; e.g., contacts at home tend to be more intimate than contacts at work. Also, disease spread is affected by geographic location and seasonality.
- Researchers have built very high-fidelity models using agent-based simulations, where each individual is tracked as they move from home to work and back



## **Data Science and Epidemiology**

"In more traditional epidemiological studies, data might be gathered or generated by manual means, such as in-person interviews, voluntary surveys or other types of deliberate, purposeful data collection. Nowadays, researchers and computer scientists are turning to novel sources of data, including cell phone records, blog posts, Tweets and flight data, to draw new, highly experimental, though sometimes questionable, inferences about the world at large."

-Mathew Braga "The rise of the digital epidemiologist: Using big data to track outbreaks and disasters,"

Google's Flu Trends, Flowminder, Healthmap, Biodiaspora are several examples of digital epidemiology already in play.

Big Data and Analysis for Infectious Disease research: Operations and Policy Workshop Proceedings, National Academies Press, 2016

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### Big data problem

- Synthesis of realistic networks
  - Data is noisy and time-lagged
  - Need new methods for information fusion and ML: Currently using 34 databases
- Large complex networks
  - > 100GB input data: 300M people , 22B edges, 100M locations, 1.5B daily activities
  - Irregular network: Dimension reduction techniques (e.g. renormalization group techniques) do not apply
  - Coevolving behaviors and networks
- Large experimental design ⇒ multiple configurations





## BIOCOMPLEXITY

#### University of Virginia

- Madhav Marathe
- Anil Vullikanti
- Srini Venkataraman

# The Perfect Storm for Digital health:



C. Viruses, munity S Stork

### **Science City Responds**

Chakraborty, Arup K.

Pandemics, and Immunity

Illustrations Philip JS Stork

Andrey S Shaw

MIT Press 2020

#### **Exponential Laws in Technology**



## **The Beast**





#### Genomic epidemiology reveals multiple introductions and spread of SARS-CoV-2



#### Karnataka

Multiple lineages of SARS-CoV-2 in Karnataka



Contact graphs showing lineages, clinical state and geographical location of clusters



Chitra Pattabhiraman, Neurovirology, NIMHANS

Pattabiraman et al., Preprint on Medrxiv doi: https://doi.org/10.1101/2020.07.10.20150045

### Stephen Massey and Bhubaneswar Mishra BioMimicry and Signalling Games J of Royal Society Interface 2018



Types of Mimicry (molecular, organism, social)

- Batesian (Asymptotic Patients)
- Mullerian (Bees and Wasps)
- Mimicry Rings (tRNA signalling Ribosomes)
- Cue Mimicry (Chameleon, Cancer Cells hiding in tissue by surface antigen masking)
- Complexity & Stability extinction of species
- Costly Signaling teriary structure of proteins, sexual ornamentation in animals, risk taking by health workers.

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#### HOW SIGNALING GAMES EXPLAIN MIMICRY AT MANY LEVELS: FROM VIRAL EPIDEMIOLOGY TO HUMAN SOCIOLOGY WILLIAM CASEY, STEVEN E MASSEY, BUD MISHRA (pre-print)



Invasion of a Mullerian molecular mimicry ring by SARS-CoV-2 spike protein polybasic cleavage site. Polybasic cleavage sites (PCSs) are found in an array of host proteins, and are cleaved by endogenous proteases, including furin. The PCSs act as cooperative Mullerian co-mimics, forming a molecular mimicry ring. SARS-CoV-2 spike protein also contains a PCS, which leads to cleavage of the spike protein by endogenous proteases including furin, increasing the infectivity of the virus, and has directly contributed to the devastating effects of the COVID-19 pandemic

## COVID-19 is a wicked social problem! [Rittel & Webber 1973]

- 1. There is no definitive formulation of a wicked problem
- 2. Wicked problems have no stopping rule
- 3. Solutions to wicked problems are not true or false, but good or bad
- 4. There is no immediate or no ultimate test of a solution to a wicked problem
- 5. Every solution to a wicked problem is a "one shot" operation; because there is no opportunity to learn by trial and error , every attempt counts
- 6. Wicked problems do not have an exhaustive describable set of potential solutions, nor a set of permissible operations that can be used in a plan.
- 7. Every wicked problem is essentially unique
- 8. Every wicked problem can be considered to be a symptom of another problem
- 9. The existence of a discrepancy in representing a wicked problem can be explained in numerous ways
- 10. The planner has no right to be wrong

Approaches: Authoritative, Competitive, Collaborative

## **Decision Support**

Predicting regions of vulnerabilities and showing estimated result of choosing different intervention strategies.





Risk heatmap

Change badging protocol Expected risk decrease : 30%

**Possible Intervention Strategies** 







Quarantining parts of campus Expected risk decrease : 45%



### Game Theoretic Framework – Inavamsi Enaganti, Corollary Health

## **Tapestry Pooling for COVID19 Labs**

IIT-B, NCBS, InStem, TMH, Malabar Hospital, Harvard Wyss Institute Tata Health Tapestry Pooling Inc.

#### **Compressed Sensing**

- As sensitive as individual PCR
- Faster Results with Single Round Test
- Prevalence Rates upto 12%
- Handle each sample only once
- >100% increase in Testing Capacity
- Quantitative Results
- Easy to Use (Web App)
- Clinically Validated on 3000+ samples\*

#### **Save Lives**

kits, reagents, time, effort, PPE, plasticware

\*Manuscript in preparation



### **X Prize Entrant**

#### Identifies each sample +ve or -ve 2% infected → 100 tests in 1 round for 1000 people

### GoCoronaGo

#### Yogesh Simmhan, Tarun Rambha, et al.,

- GCG records the proximate devices and timestamps in a backend cloud server
  - We link all this data to form a global contact network, at Institute Scale
  - Know at what time and duration they were close to each other
- Can be used for primary, secondary and tertiary contact tracing, *rapidly*
- Can identify high-risk individuals, before they get infected – *Proactively*
- Analytics for users: Proximity alerts, contact timelines, social distancing scores, 2-hop contact neighbourhood

Supported by RAKSHAK (DST) Developed at IISc Deployed at IISc, In progress at IIT-Jodhpur, IIIT-H





## **Screening and Testing**

- A test has high accuracy meaning high sensitivity (few false negatives) and high specificity (few false positives). Usually a diagnostic test protocol requires regulatory approval, and the results are reported to the subject (patient).
- A screen can have less sensitivity and less specificity than a test. Typically a screen is used to decide whether or not to test a subject. The results of the screen are sometimes not reported to individual patients.
- For example **antibody screens (sero-surveillance)** for infection or **contact tracing** based on mobile apps - may not be accurate enough to inform individual patients but may be useful for campus health monitoring purposes

## **Screening and Testing**

#### **RNA Testing:**

Open RT-PCR systems (Bio Rad, ABI,...) Reagents/Kits (Atma nirbhar) Closed Systems (Roche, Cepheid, MICO BioMed/ MediSys, TrueNat – BigTecMolBio\*) Mass Array Platforms: Agena, Star Array (NTU) Next generation Genome Sequencing: Illumina, Nanopore, MGI, ... CRISPR POC

### AntiBody (IgM) IgG Testing:

ELISA Tests (ICMR-Zydus Cadilla, Syngene-HiMedia, ...) ABBOTT (chemiluminescent microparticle immunoassay (CMIA)

### Antigen Testing:



COVID-19 Aq

COVID-19

SD BIOSENSOR



**NEXT INS** 

#### FELUDA-CRISPR TEST: COVID-19

Slide 20

Maximum decrease in mortality & morbidity per rupee spent

- **Campus:** "people, buildings, and grounds affiliated to a given institution"
- Site of productive activity
- People in close proximity
   through the working day
   •
- Keep people safe
- Help people feel safe
- Regulatory compliance

### Uncompromisables:

- Reflex to State Health and ICMR guidelines for all clinical actions
- Respect personal liberties
- Maintain highest ethical standards of consent, information, fairness
- Equity in access for all services

#### Agent – based Simulation platform for Decision Support DST Rakshak: Chiru Bhattacharya (PI), Vijay Chandru, Rajesh Sundaresan, Nidhin Koshy



Badging system

Slide 22

## **Dengue in Singapore:** Atlanta Chakraborty, BSc (Research), IISc 2018 **Predictive Non-parametric Model using Gaussian Processes**





#### **Gaussian Processes:**

Mathematical Extension of both Deep Learning Artificial Neural Nets and Support Vector Machines.



### **EECS @ IISc RESPONDS TO COVID-19 - Podcasts by Native Voices**

- **1. Sound Acoustics and Covid 19 infection** [Sriram Ganapathy et al.]
- 2. Privacy Respecting digital contact tracing for Covid 19 :

**Challenges and opportunities** [YS, TR,..]

- **3. Modelling testing strategies for Covid 19: Insights from theory and practice** [A Gopalan, H Tyagi]
- 4. Covid 19 infection rate estimation [Navin Kashyap et al.]
- 5. Unlocking the lockdown: agent based city scale epidemic simulator and workplace readiness tool [Rajesh Sundaresan, Nidhin Koshy, et al.]
- 6. Suppress, not just flatten: Strategies for rapid suppression of Covid 19 transmission in small world communities [Chiru Bhattacharya, V Vinay]
- 7. Spatiotemporal predictive modelling framework for infectious disease spread [SG, DS]
- 8. Project PRAANA: Crisis engineering of an electro-mechanical ventilator [Gaurab Banerjee]

## Take home messages

## **Activity/ assignment**

Activity / assignment for the participant related to the submodule can be a subjective questions which is to be uploaded by participant to move to next submodule



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