Sahil Loomba

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RESEARCH INTERESTS Network science, Bayesian inference, statistical machine learning, computational social science, computational & systems biology, public health statistics

EXPERIENCE

Wyss Institute for Biologically Inspired Engineering at Harvard University

Post-baccalaureate Fellow in Computational Biology

August 2016 – July 2018

Advisor: Prof. James J. Collins, MIT

Xerox Research Center India

Research Intern in Multimedia Analytics

May - July 2015

EDUCATION

Imperial College London, United Kingdom

PhD in Applied Mathematics

2018 – August 2022 (expected)

Advisor: Prof. Nick S. Jones

Indian Institute of Technology Delhi, India

BTech in Computer Science and Engineering

2012 - 2016

Advisor: Dr. Sumeet Agarwal

Thesis: Causal Computational Models for Gene Regulatory Networks

ACADEMIC AND COMPETITIVE HONORS

Imperial-TUM Global Fellows Programme	2019
Summer Undergraduate Research Award, IIT Delhi	2014
Cargill Global Scholar Award for academic excellence & leadership	2014
IIT Delhi Institute Medal for obtaining highest overall GPA	2013
IIT Delhi Merit Semester Scholarship	2012, 2013

Publications

• Loomba, S., & Jones, N. S. (2021). Geodesic statistics for random network families. arXiv preprint, arxiv:2111.02330. (74 pages)

We derive an analytic distribution of shortest path lengths in sparse conditionally independent edge models, yielding new results on percolation and path-based centralities.

- Loomba, S.¹, de Figueiredo, A.¹, Piatek, S. J., de Graaf, K., & Larson, H. J. (2021). Measuring the impact of COVID-19 vaccine misinformation on vaccination intent in the UK and USA. *Nature Human Behaviour*, 5(3), 337-348, doi:10.1038/s41562-021-01056-1. Through a randomized study, we show that even brief exposure to COVID-19 vaccine misinformation can reduce the intention to definitely vaccinate by as much as 6.2%.
- Gandhi, A., Biswas, A., Shrivastava, K., Kumar, R., Loomba, S., & Deshmukh, O. (2016, March). Easy Navigation through Instructional Videos using Automatically Generated Table of Content. In Companion Publication of the 21st International Conference on Intelligent User Interfaces (pp. 92-96). ACM, doi:10.1145/2876456.2879472.

We demonstrate a pipeline to automatically generate a table of content for video lectures, using saliency scores of visual and spoken words for topic-based segmentation.

Forthcoming

• Götz, F., Maertens, R., **Loomba, S.**, & van der Linden, S. (*Revise & resubmit at Psychological Methods*). Development and Validation of an Algorithmically-Derived Personality Scale.

¹Co-first authors: SL contributed to survey design, did RCT experiment design, designed all statistical models and performed all inference, generated publication figures, co-drafted the paper and responded to referees

We leverage recent advances in transformer-based neural language models that generate human-like text, like GPT-2, for automatic item generation for psychometric scales.

• Duffy, S., Loomba, S., Cartwright, M., Dimitrakakis, N., Scott, J., McCarty, A., Shapiro, N. I., Super, M., & Ingber, D. (*In prep*). Application of MALDI-TOF mass spectrometry for the rapid identification of PAMPs in blood culture negative septic patients using FcMBL-coated magnetic beads.

We develop a rapid diagnostic test from the mass spectra of patient blood/urine samples, using a probabilistic model that leverages the mass spectra of a microbial library.

• Novak, R., Lin, T., Kaushal, S., Sperry, M., Vigneault, F., Gardner, E., **Loomba, S.**, Shcherbina, K., Keshari, V., Vasan, A., Chandrasekhar, V., Takeda, T., Turner, J., Levin, M., & Ingber, D. (*In prep*). Target-agnostic discovery of Rett Syndrome therapeutics by coupling computation and a CRISPR-enabled *in vivo* disease model.

We combine computational modeling with *in vivo* screening in a CRISPR-edited *Xeno*pus laevis tadpole model of Rett syndrome to carry out target-agnostic drug discovery.

Patents

Cartwright, M. J., Duffy, S. C., Grant, J., Ingber, D. E., Loomba, S., Scott, J., & Super, M. (2021). Methods for detection of microbes and microbe components. U.S. Patent Application No. PCT/US21/12717.

Technology has been licensed to BOA Biomedical, with the aim of rapid detection of active infection from a blood sample within 1 hour, which is crucial for treating sepsis.

- Barhate, S. S., **Loomba, S.**, Gandhi, A., Biswas, A., Negi, S., & Deshmukh, O. D. (2018). Method and system for generation of a table of content by processing multimedia content. *U.S. Patent Application No.* 15/203,868.
- Gandhi, A., Biswas, A., Deshmukh, O. D., & Loomba, S. (2018). Method and system for content processing to determine pre-requisite subject matters in multimedia content. U.S. Patent Application No. 15/250,958.

Grants

Synergistic Discovery and Design (SD2)

DARPA/I20, HR001117S0003, \$2M

PI: Prof. James J. Collins

Co-authored research proposal for data-driven discovery and design of biological circuits. Contributed about half of each of the writing, conceptual and methodological content.

Designed core algorithmic pipeline to generate testable circuit designs: going from high-throughput omics data to inferred network structures, to functional network motifs, down to operable biological circuits in traditional and novel host organisms.

Developed sequence and circuit embedding models of E. coli and yeast for motif discovery.

Conference Presentations

Invited talks

• Loomba, S. (2021, November). Misinformation and the pandemic: a tale of two contagions. Invited talk at *Students for Global Health Conference 2021*.

Accepted oral presentations

- Loomba, S., & Jones, N. S. (2021, July). Geodesic statistics for random network families. Oral presentation at *Networks 2021 (Joint Sunbelt and NetSci Conference)*.
- Loomba, S., & Jones, N. S. (2020, July). Scalable statistics for social networks of entire societies. Oral presentation at *Sunbelt XL Conference*.

Accepted poster presentations

- Loomba, S., Hoffmann, T., & Jones, N. S. (2019, July). Social Access Statistic: Linking Social Connectivity to Health Outcomes. Poster presentation at 5th International Conference on Computational Social Science.
- Loomba, S., & Garrod, M. (2019, July). How Far Would You Go? Comparing Urban Access in 10 Global Cities. Poster presentation at *NetMob 2019*.

September 2017

IMPACT

Generated viable drug candidate(s) for treatment of a monogenic disease

Created NeMoCAD, a Network Model for Causally Aware Discovery, that learns from generegulation and perturbative drug-gene interaction data to query for desirable therapeutic states; discovered a new therapeutic for Rett Syndrome which was validated in mouse models. Software licensed to Unravel Biosciences

Impacted public health policy on health misinformation

Research on the impact of COVID-19 vaccine misinformation on vaccine uptake has seen considerable impact on pandemic research (400+ citations in less than a year), and on policymaking (the U.S. Surgeon General's health misinformation advisory cites our work).

Popular Press

UN Verified Is online misinformation threatening our ability to end the pandemic?

Reuters Misinformation could prompt people to turn against COVID-19 vaccines: study

BBC Covid vaccine: Rumours thrive amid trickle of pandemic facts

The Times Herd immunity put at risk by a few lies about Covid vaccine

The Quint Exposure to Misinformation Reduces COVID Vaccine Acceptance: Study

Hindustan Times Misinformation may hit vaccination drive: Study

Ongoing Research

Online informational interventions for improved offline vaccine uptake

Collaborators: Amit Bahl (Facebook CDS), Heidi Larson & Alexandre de Figueiredo (LSHTM) As part of an internship with Facebook CDS (2022), we will design online interventions likely to improve COVID-19 vaccine uptake, run a large-scale randomized trial on Facebook to gauge their causal impact, and study "spillover" effects on peer outcomes. This precedes the goal of closing the loop on monitor-design-intervene for building vaccine confidence online.

Regional relationship of misinformation susceptibility and vaccine uptake

Collaborators: Friedrich Götz (UBC), Rakoen Maertens, Jon Roozenbeek & Sander van der Linden (Cambridge), Alexandre de Figueiredo (LSHTM)

Building on the misinformation susceptibility test (MIST), we collected data on 16k survey respondents across the UK, and learnt a Bayesian spatial model of MIST scores that accounts for spillover between "well-connected" regions. Post-stratification identified regional "hotspots" of susceptibility that are predictive of regional COVID-19 vaccine uptake.

Mapping inequality in access to social connections via a "social Gini" index

 $\label{lem:collaborators: Nick S. Jones, Johannes Happenhofer \& Till Hoffmann (Imperial), Sumeet Agarwal (IIT Delhi)$

We have developed a rational theory for a "social Gini" index which quantifies the distance between people based on how surprising it is to see a social connection between them. Our aim is to map this index sub-nationally for the UK, US, and India. For that, we are building a Bayesian statistical model that learns from data on spatially aggregated friendship counts.

Graduate
Teaching
(Tutorials)

Methods for Data Science (Years 3 & 4, MSc)	October – December 2019
Mathematical Computation in Python (Year 1)	January – March 2019
Probability and Statistics II (Year 2)	October – December 2018

Services Reviewing

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Physical Review E	2019 - present
Nature Scientific Reports	2019 - present
New Journal of Physics	2021 - present
Proceedings of the National Academy of Sciences	$2021-\mathrm{present}$
Vaccine	2021 - present
Social Network Analysis and Mining	$2021-\mathrm{present}$
Healthcare in Low-resource Settings	2022 - present
PC Member	

MENTORING	Amelia French	Year 4, MSci in Mathematics, Imperial College London	2021
	Kushal Kejriwal	Year 2, Dual degree in Electrical Engineering, IIT Bombay	2021
	Siddharth Chandak	Year 2, BTech in Electrical Engineering, IIT Bombay	2019
	Katie Collins	Year 1, Bachelors in Brain and Cognitive Sciences, MIT	2017
Programming Strengths	0 0	on, R, MATLAB, C, C++ l statistical tools: Stan, TensorFlow, PyTorch, scikit-learn	