Reinvigorating Descriptive Epidemiology

Matthew Fox



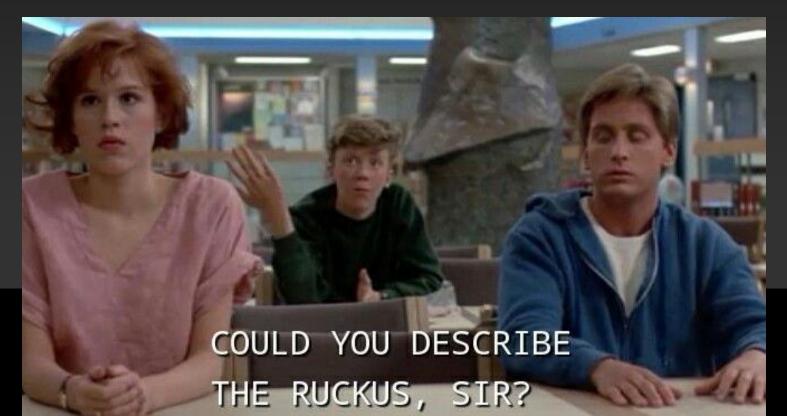




mattpfox.bsky.social



Free Associations, SERious Epi



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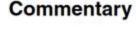












The Epidemiologic Toolbox: Identifying, Honing, and Using the Right Tools for the Job

Catherine R

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Commentary



Matthew

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American Journal of Epidemiology

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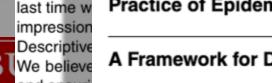
Practice of Epidemiology

A Framework for Descriptive Epidemiology

Catherine R. Lesko*, Matthew P. Fox, and Jessie K. Edwards







epidemiology

epidemiology

what happens when you don't get into med school the first time around.

What is epidemiology?

 Epidemiology is study of the distribution and determinants of disease states in human populations and the application of that knowledge to the control of disease

Catherine R. Lesko*, Alexander P. Keil, and Jessie K. Edwards

public health (12). Loosely speaking, these research goals fall along a spectrum with purely descriptive epidemiology at 1 end; hypothesis generation, prediction, and outbreak investigation somewhere in the middle; and causal effect estimation and program evaluation at the other end. Here, we

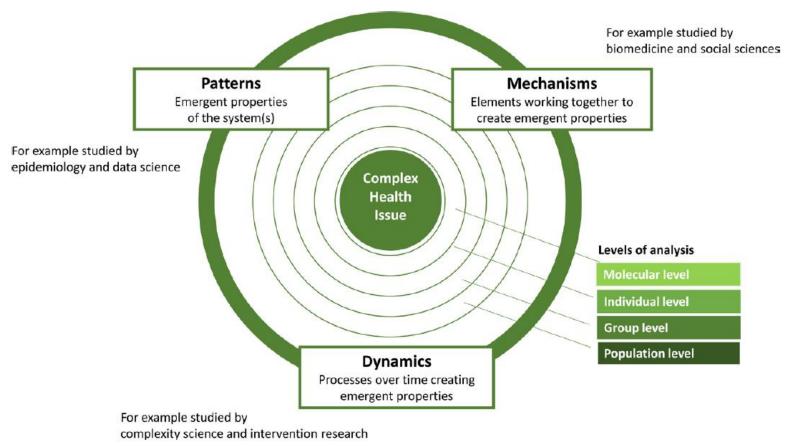
Distribution



Determinants

Complexity in Epidemiology and Public Health. Addressing Complex Health Problems Through a Mix of Epidemiologic Methods and Data

[©]Naja Hulvej Rod,^{a,b} Alex Broadbent,^{c,d} Morten Hulvej Rod,^{b,e,f} Federica Russo,^{b,g,h} Onyebuchi A. Arah^{i,j} and Karien Stronks,^{b,k}





HEALTH COMPLEXITY FRAMEWORK

We suggest that a first, but important, step towards understanding and intervening in complex public health phenomena is to systematically generate and integrate the knowledge of the system(s) that give rise to these phenomena. To operationalize this for public health, we propose an interdisciplinary framework that organizes this knowledge production according to three core dimensions, capturing seven critical features of complex systems (Figure 2). The framework builds upon the idea of methodologic pluralism, ^{18,27,28} and is intended as an overarching framework for interdisciplinary and collaborative research.

The three dimensions involve:

- 1. patterns: describing the health patterns that emerge from complex systems;
- mechanisms: understanding the mechanisms that produce these emergent patterns; and
- 3. dynamics: exploring the dynamics that make mechanisms and patterns change over time.

Each of these dimensions is directly related to key features of complex systems, which are often highlighted in relation to public health.^{21,22} These features include emergence, interactions, nonlinearity, interference, feedback loops, adaptation, and evolution.

FIGURE 2. Overview of the interdisciplinary Health Complexity Framework for producing knowledge on complex health issues.



Search Q

Epidemic Intelligence Service

CDC > EIS > Epidemiology Training & Resources > Chapters



CDC Field Epidemiology Manual

Preface

Chapters

Describing Epidemiologic Data

Acknowledgements





Describing Epidemiologic Data

Print

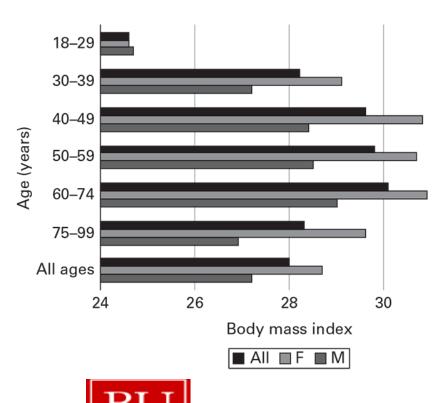
Robert E. Fontaine

"this task, called descriptive epidemiology, answers the following questions about disease, injury, or environmental hazard occurrence: What? How much? When? Where? Among whom?" (4, p. 106).

Person

Place

Mean BMI among adults by Age and Sex in Jordan 2012





Time

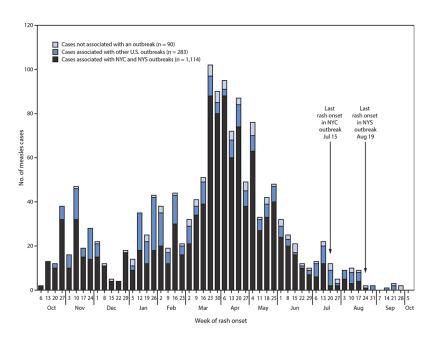
Morbidity and Mortality Weekly Report (MMWR)

National Update on Measles Cases and Outbreaks — United States, January 1–October 1, 2019

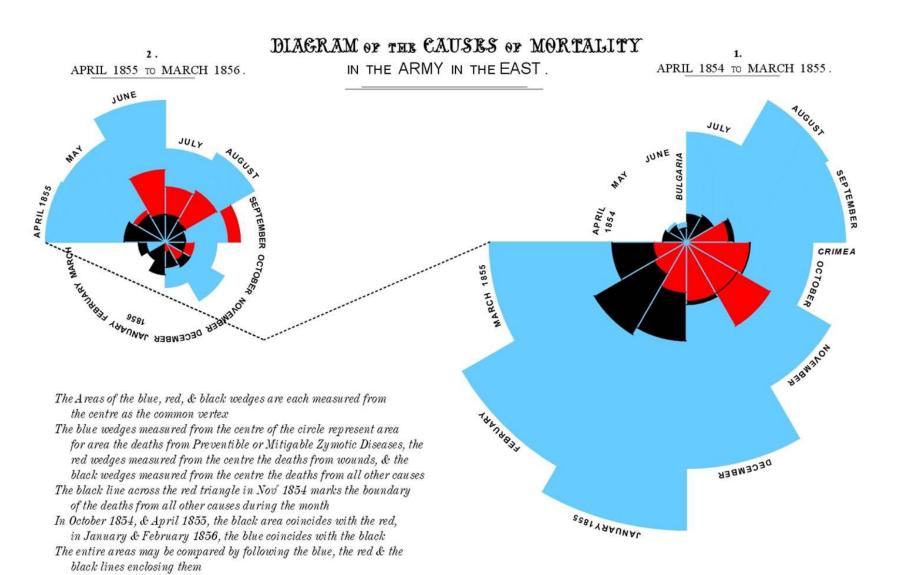
Weekly / October 11, 2019 / 68(40);893-896

On October 4, 2019, this report was posted online as an MMWR Early Release.

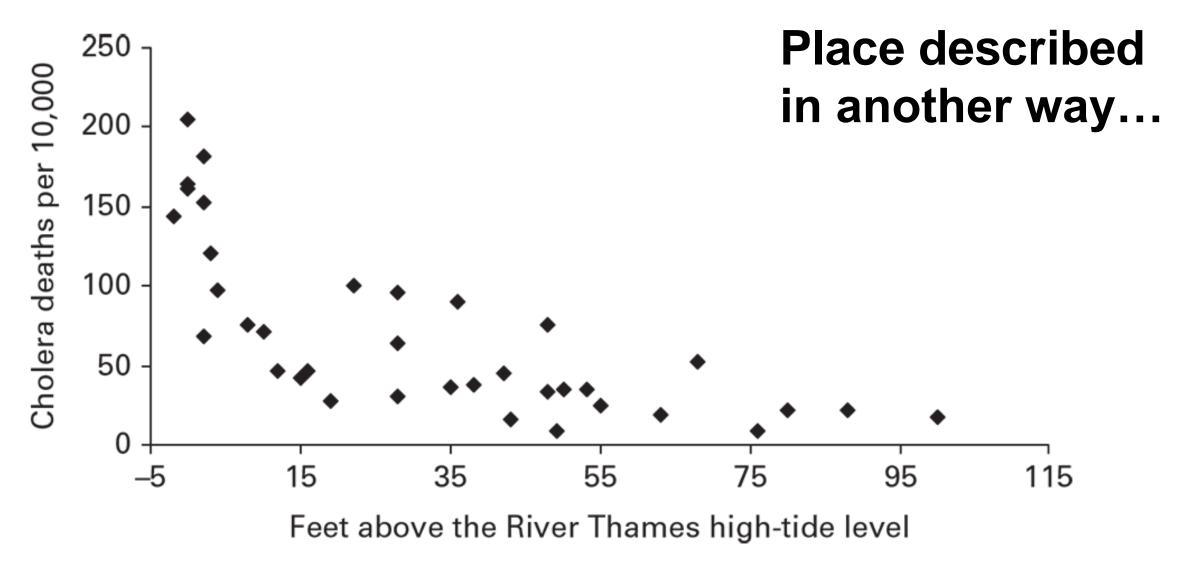
Manisha Patel, MD1; Adria D. Lee, MSPH1; Nakia S. Clemmons, MPH1; Susan B. Redd1; Sarah Poser1; Debra Blog, MD2; Jane R. Zucker, MD34; Jessica Leung, MPH1; Ruth Link-Gelles, PhD1; Huong Pham, MPH1; Robert J. Arciuolo, MPH1; Elizabeth Rausch-Phung, MD2; Bettina Bankamp, PhD1; Paul A. Rota, PhD1; Clindy M. Weinbaum, MD4; Paul A. Gastañaduv, MD1 (VIEW AUTHOR AFFILIATIONS)



Florence Nightingale's Crimean War Rose Diagram





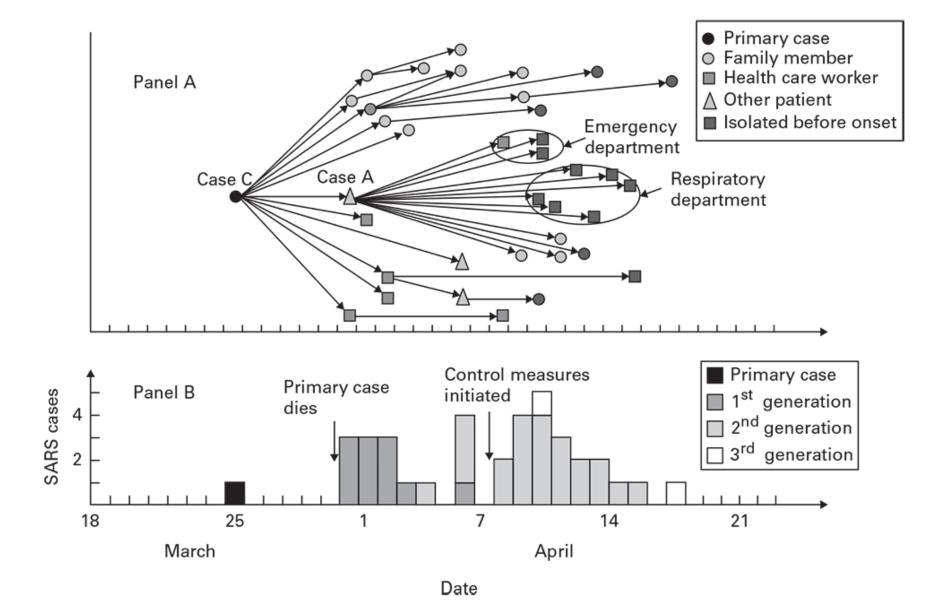




Cholera deaths per 10,000 and altitude above high tide level by district, London, 2849

Time

Contact between severe acute respiratory syndrome (SARS) cases among a group of relatives and health care workers: Beijing, China, 2003.





Characterizing treatment pathways at scale using the OHDSI network

George Hripcsak^{a,b,c,1}, Patrick B. Ryan^{c,d}, Jon D. Duke^{c,e}, Nigam H. Shah^{c,f}, Rae Woong Park^{c,g}, Vojtech Huser^{c,h}, Marc A. Suchard^{c,i,j,k}, Martijn J. Schuemie^{c,d}, Frank J. DeFalco^{c,d}, Adler Perotte^{a,c}, Juan M. Banda^{c,f}, Christian G. Reich^{c,l}, Lisa M. Schilling^{c,m}, Michael E. Matheny^{c,n,o}, Daniella Meeker^{c,p,q}, Nicole Pratt^{c,r}, and David Madigan^{c,s}

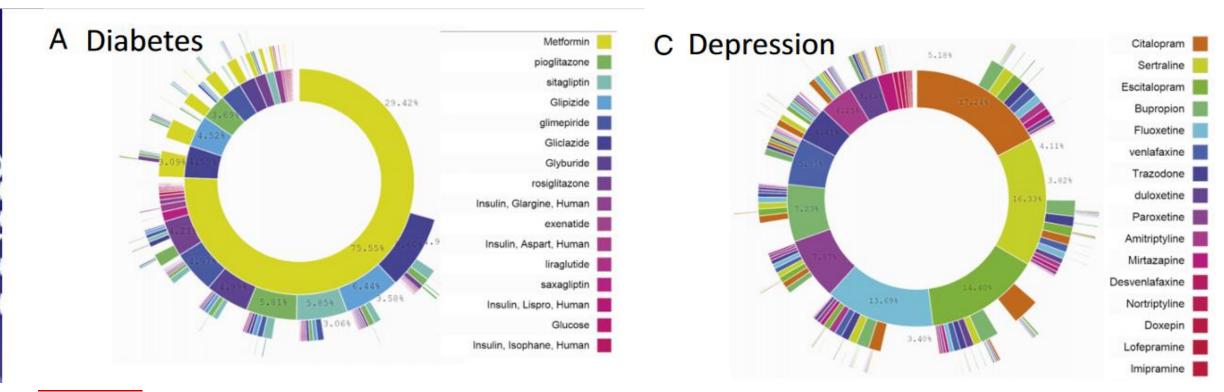
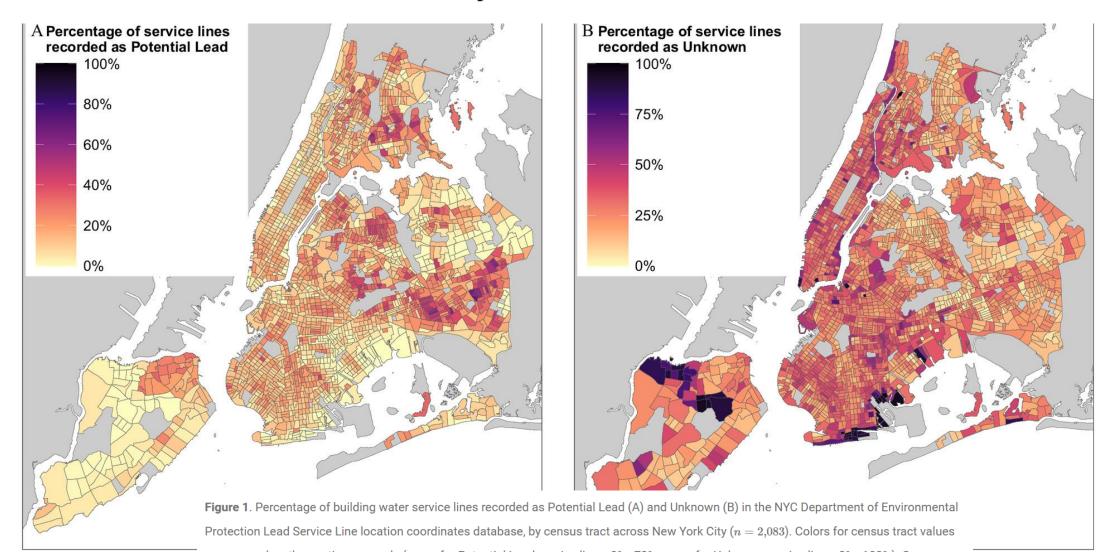


Fig. 2. Treatment pathways for all data sources. For each disease, diabetes (A), hypertension (B), and depression (C), and across all data sources, the inner circle shows the first relevant medication that the patient took, the

second circle shows the second medication, and so forth. Only four levels are shown, but up to 20 medications were recorded. For example, 76% of diabetes patients started with metformin, and 29% took only metformin.

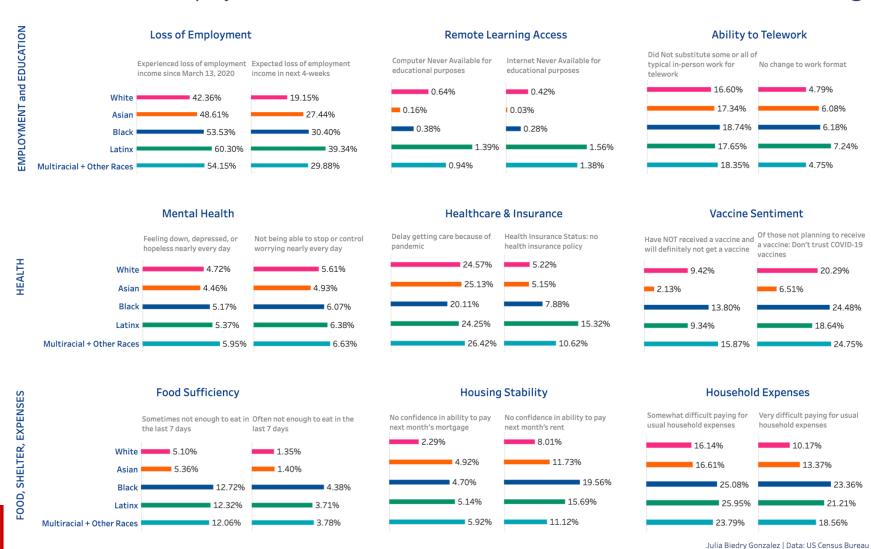
Geospatial Assessment of Racial/Ethnic Composition, Social Vulnerability, and Lead Water Service Lines in New York City



Descriptive Epi for Identifying Disparities

The Inequity Pandemic: 9 Effects of COVID-19 in American Households





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Table 2 Summary of emergency department syndromic surveillance systems (EDSyS) included in the review, by country/territory, with source and format of information used to define syndromic indicators and of areas of public health surveillance supported the EDSyS

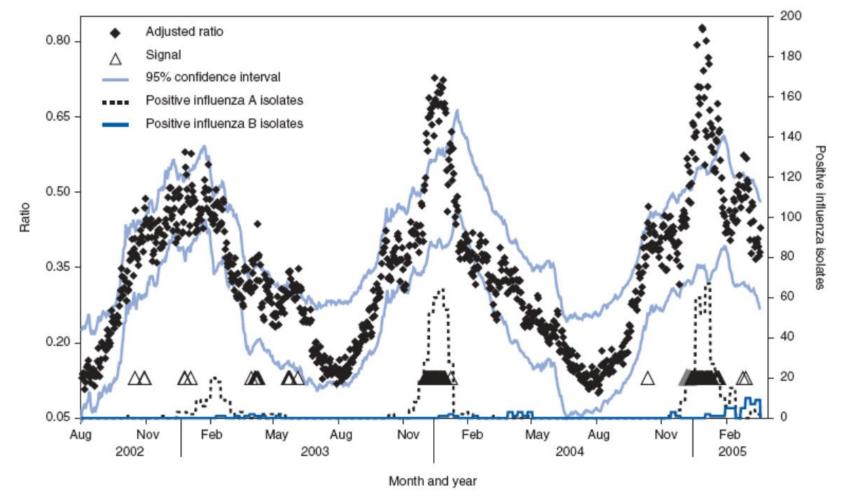
Country/ territory	Syndromic indicator		Infectious diseases			Extreme weather		Other non-infectious		
	Source ^a	Format	Respiratory	Influenza	Gastrointestinal	Heat	Cold	Injury/trauma	alcohol	drug
Albania	diagnosis	coded	✓	✓	✓	_	-	_	_	_
Australia	diagnosis	coded	✓	✓	✓	✓	✓	✓	✓	✓
Canada	chief complaint	text	✓	✓	✓	✓	✓	✓	_	_
China	chief complaint	coded	✓	✓	_	_	_	_	_	_
France	diagnosis	coded	✓	✓	✓	✓	✓	✓	✓	_
Greece	chief complaint	pick list	✓	_	✓	_	_	_	_	_
Italy	chief complaint	text/coded	✓	✓	✓	_	_	_	_	_
Jamaica	"daily analysed data"		✓	_	✓	✓	_	_	_	_
Republic of Korea	diagnosis	coded	✓	✓	✓	_	_	_	_	_
New Zealand	diagnosis	coded	✓	✓	_	_	_	_	_	_
Singapore	unknown	coded	✓	✓	✓	_	_	_	_	_
Spain	chief complaint	coded	✓	✓	✓	_	_	_	_	_
Taiwan	chief complaint	text/ coded	✓	✓	✓	_	_	_	_	_
UK ^b	diagnosis	coded	✓	✓	✓	✓	✓	_	✓	_
USA	chief complaint	text	✓	✓	✓	✓	✓	✓	✓	✓

^a EDSyS may collect more than one data item for syndromic indicators, but each reported a primary field used as standard

^b UK: England & Northern Ireland ✓ relevant EDSyS indicators identified - no relevant EDSyS indicators identified

Descriptive Syndromic Surveillance

FIGURE 1. Citywide trends and signals in the adjusted ratio of influenza-like illness to analgesic over-the-counter (OTC) drug sales and positive isolates of influenza A and B — New York City, August 1, 2001–March 31, 2005*





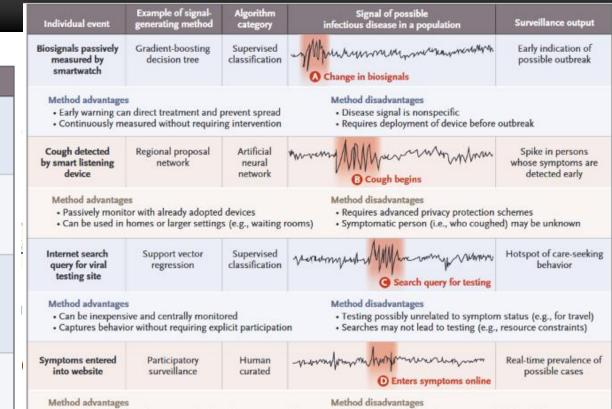
Temporal signals p<0.01 and 95% confidence intervals from daily linear regression. The OTC ratio is adjusted for day of week, major national winter holidays, and the day after these holidays (Thanksgiving, Christmas, New Years, and Martin Luther King observance day).

https://www.nejm.org/doi/full/10.1056/NEJMra2119215

Function	Examples				
Early warning	 Natural-language processing of news sources to identify outbreaks (Freifeld et al., JAMIA 2008) Unsupervised machine learning of social media data to detect unknown infections (Lim, Tucker, and Kumara, J Biomed Inform 2017) 				
Pathogen classification	 Convolutional neural network model for reading antibiograms (Pascucci et al., Nat Commun 2021) Convolutional neural network model to automate malaria microscopy and diagnosis (Liang et al., IEEE 2016) 				
Risk assessment	 Reinforcement learning of Covid-19 positivity rates to target limited testing in Greece (Bastani et al., <i>Nature</i> 2021) Machine-learning models including random forest and extreme gradient boosting to use syndromic surveillance for Covid-19 risk prediction (Dantas, <i>PLoS One</i> 2021) 				
Source identification	 Automated data mining of electronic medical records to uncover hidden routes of infection transmission (Sundermann et al., Clin Infect Dis 2021) Supervised machine learning in combination with digital signal processing for genomic tracing of Covid-19 (Randhawa et al., PLoS One 2020) 				
Hotspot detection	 Neural computing engine to correlate sound from hospital waiting rooms with influenza spikes (Al Hossain et al., <i>Proc ACM Interact Mob Wearable Ubiquitous Technol</i> 2020) Multilayer perceptron artificial neural network model to detect spatial clustering of tuberculosis (Mollalo et al., <i>Int J Environ Res Public Health</i> 2019) 				
Tracking and forecasting	 Real-time stacking of multiple models to improve forecasts of seasonal influenza (Reich et al., <i>PLoS Comput Biol</i> 2019) Machine learning to combine new data sources for monitoring Covid-19 (Liu et al., <i>J Med Internet Res</i> 2020) 				
Figure 1 Various Functions of Artificial Intelligence (Al) for Infectious Disease Surveillance					

Figure 1. Various Functions of Artificial Intelligence (AI) for Infectious-Disease Surveillance.

Shown is a nonexhaustive list of functions of AI-aided infectious-disease surveillance and representative examples from the published literature.²⁻¹³ Each example includes the type of AI algorithm, a brief description of its purpose, and the associated citation. Covid-19 denotes coronavirus disease 2019.



- Information can be disseminated without bureaucratic delay
- Captures mild cases that may not formally test across settings
- · Participants skew toward persons with high health literacy
- · Relies on syndromic definitions that may describe many causes

for virus

Test result positive

Traditional public health surveillance

Human curated Positive test result returned

Official case counts

Method advantages

- Standard diagnostic accuracy
- Mandatory reporting can capture rare and dangerous pathogens

Method disadvantages

- · Verification can be slow and expensive
- Requires resources that may not be available in certain settings

Post on social media about diagnosis Natural-language processing Supervised Vnus

Post diagnosis on social media

Real-time prevalence of confirmed cases

Method advantages

- Rapid collection and dissemination of results
- Wide array of users who may be missed by most other systems

Method disadvantages

- Computationally expensive and difficult to parse signal from noise
- Symptoms nonverified and can be vulnerable to Internet trolls

Mask wearing captured by CCTV Convolutional neural network

Artificial neural network Mask wearing starts

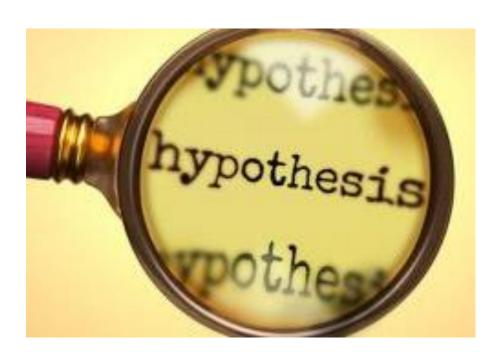
Nonpharmaceutical intervention levels

Done right, descriptive epidemiology saves lives



Descriptive isn't just for hypothesis generation

- We use descriptive epi to determine where disease is occurring, in whom and when
- This allows us to target resources
- During the COVID pandemic, where do we mobilize masks, vaccines, preventive services, implement distancing and lockdowns
- Can do with no assumptions of causation
- It can also be used for hypothesis generation, and this is important, but not necessary





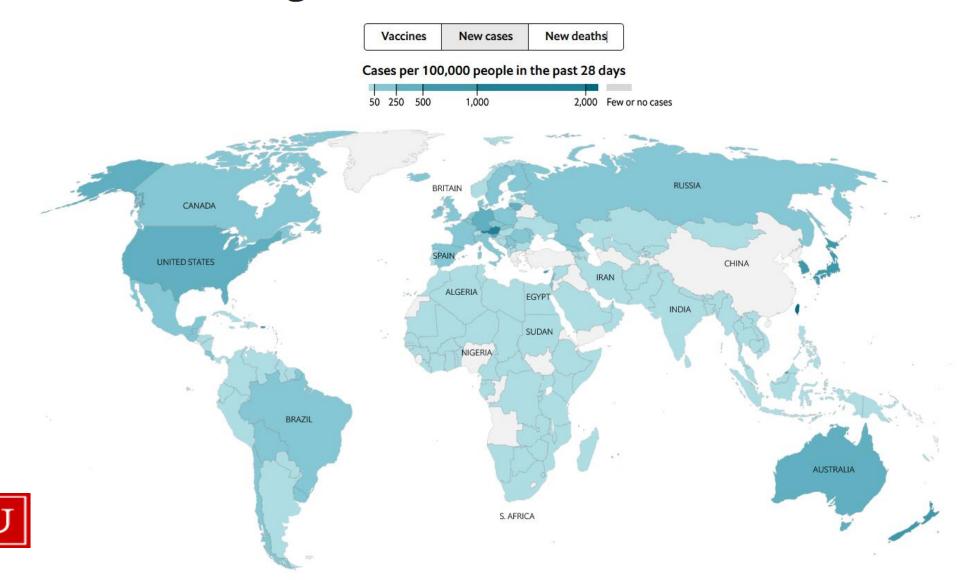
COVID Changed The Way We Look at Descriptive Epidemiology

We went from "so are you a skin doctor" to "when is it going to end"?



Log in

Tracking covid-19 across the world





Coronavirus COVID-19 Global Cases by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins Univ

CANADA

Active Cases

Cumulative Confirmed Cases

167

Total Death

5,476 deaths Italy

3,153 deaths Hubei China

2,206 deaths

1,812 deaths

674 deaths

289 deaths

213 deaths

118 deaths

Netherlands

United Kingdom

Confirmed mage: DAUY

France

Spain

NORWA

adrid

ALGERIA

Accra

NIGE

Total Confirmed 353,692

> Confirmed Cases by Country/Region/Sovereignty

81,496 China

59,138 Italy 35,345 US

33,089 Spain

27,289 Germany

23,049 Iran 16,937 France

8,961 Korea, South

8,547 Switzerland

5,748 United Kingdom

4,763 Netherlands

3,967 Austria

Belgium

2,538 Norway

Admin2 Admin3 Admin1

Last Updated at (M/D/YYYY) 3/23/2020, 10:38:06 AM Vancouver Toronto UNITED STATES n Francisco Los Angeles **REFRESH** M É 💥 C O Mexico City MALI Bogota BRAZIL Esri, FAO, NOAA

health departments, and local media reports. Read more in this blog.

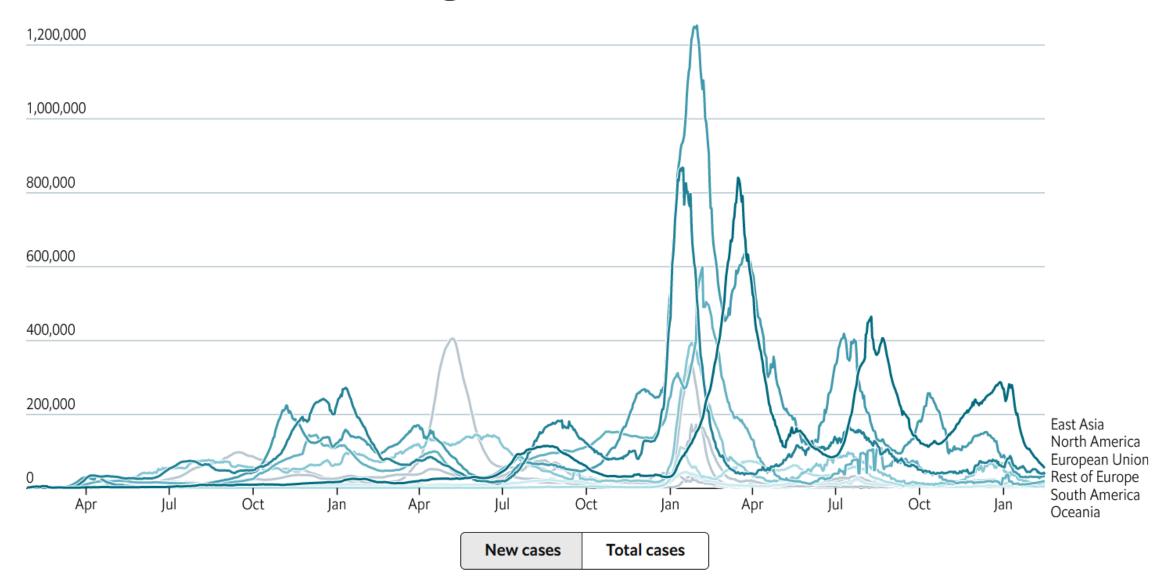
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Log in

Tracking covid-19 across the world



In times of crisis and novelty, descriptive epi is what people crave



COVID-19 in New Zealand and the impact of the national response: a descriptive epidemiological study



Sarah Jefferies, Nigel French, Charlotte Gilkison, Giles Graham, Virginia Hope, Jonathan Marshall, Caroline McElnay, Andrea McNeill, Petra Muellner, Shevaun Paine, Namrata Prasad, Julia Scott, Jillian Sherwood, Liang Yang, Patricia Priest



Summary

Background In early 2020, during the COVID-19 pandemic, New Zealand implemented graduated, risk-informed national COVID-19 suppression measures aimed at disease elimination. We investigated their impacts on the epidemiology of the first wave of COVID-19 in the country and response performance measures.

Methods We did a descriptive epidemiological study of all laboratory-confirmed and probable cases of COVID-19 and all patients tested for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in New Zealand from Feb 2 to May 13, 2020, after which time community transmission ceased. We extracted data from the national notifiable diseases database and the national SARS-CoV-2 test results repository. Demographic features and disease outcomes, transmission patterns (source of infection, outbreaks, household transmission), time-to-event intervals, and testing coverage were described over five phases of the response, capturing different levels of non-pharmaceutical interventions. Risk factors for severe outcomes (hospitalisation or death) were examined with multivariable logistic regression and time-to-event intervals were analysed by fitting parametric distributions using maximum likelihood estimation.

Lancet Public Health 2020; 5: e612-23

Published Online October 13, 2020 https://doi.org/10.1016/ \$2468-2667(20)30225-5

See Comment page e569

Institute of Environmental Science and Research, Porirua, New Zealand (S Jefferies MD, C Gilkison MPH, G Graham BSci, V Hope MPhil, A McNeill PhD, S Paine MAE, N Prasad MPH,

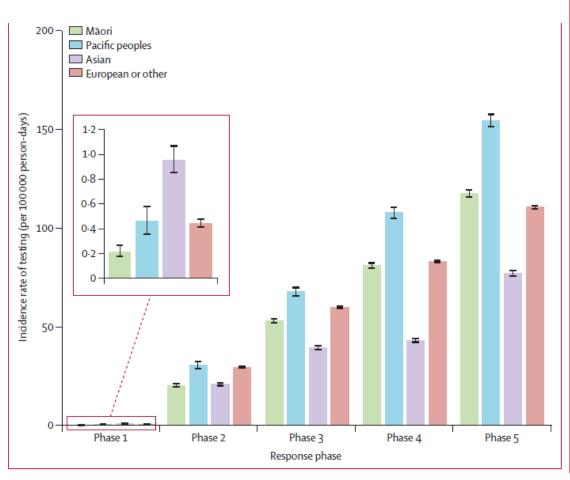
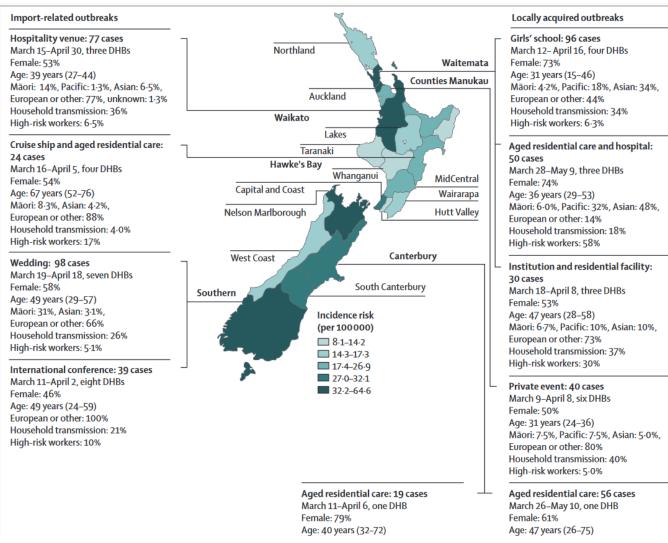
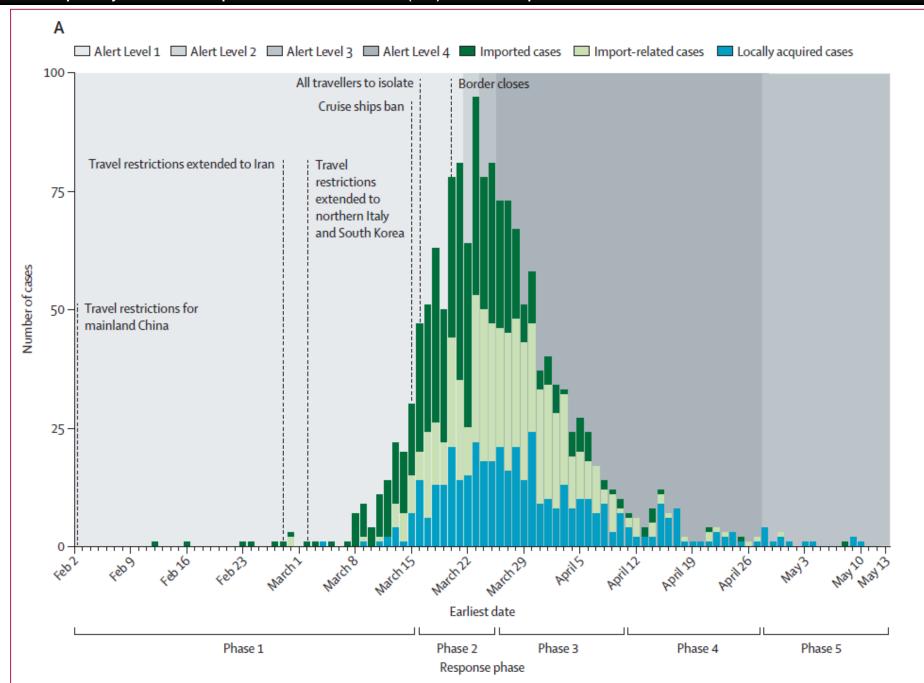
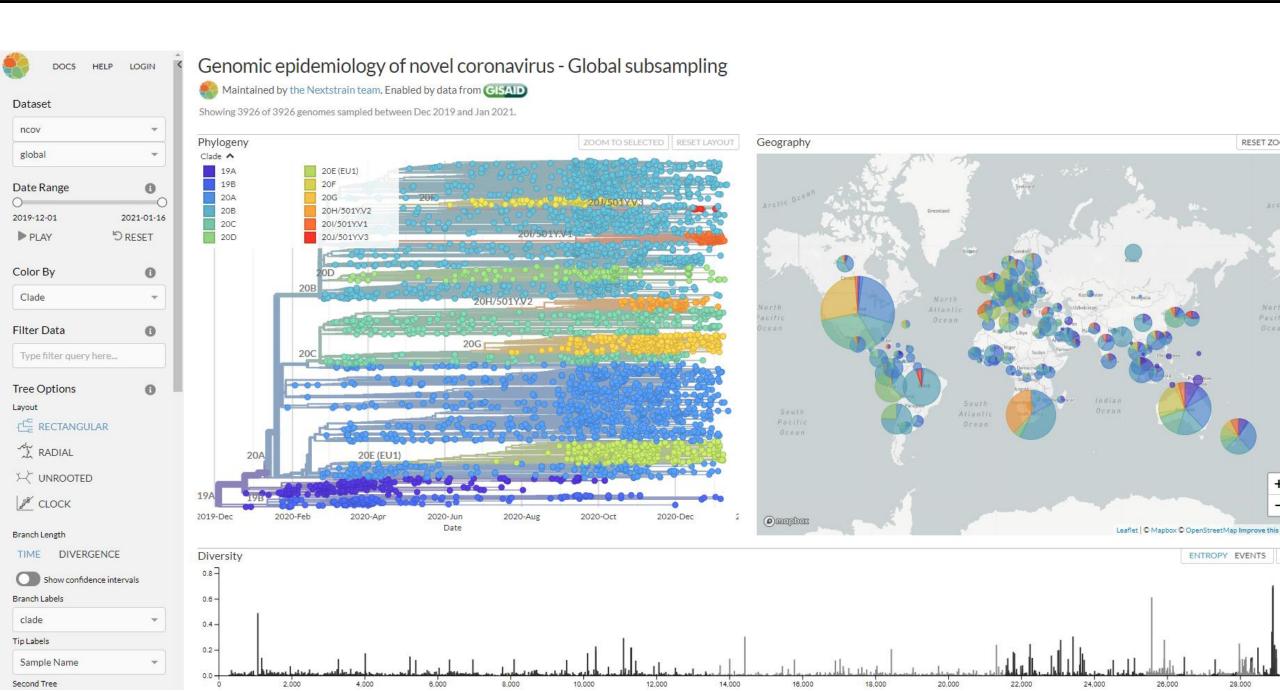


Figure 3: Incidence rates of SARS-CoV-2 testing by sex and response phase (A) and by ethnic group and response phase (B)









Descriptive Epi Has Biases Like All Studies





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Commentary

On the Need to Revitalize Descriptive Epidemiology



Matthew P. Fox*, Eleanor J. Murray, Catherine R. Lesko, and Shawnita Sealy-Jefferson

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Initially submitted March 4, 2021; accepted for publication March 18, 2022.

Nearly every introductory epidemiology course begins with a focus on person, place, and time, the key components of descriptive epidemiology. And yet in our experience, introductory epidemiology courses were the last time we spent any significant amount of training time focused on descriptive epidemiology. This gave us the impression that descriptive epidemiology does not suffer from bias and is less impactful than causal epidemiology.









https://www.the-scientist.com/news-opinion/high-risk-of-bias-in-early-covid-19-studies-meta-analysis-68353



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High Risk of Bias in Early COVID-19 Studies: Meta-**Analysis**

Few peer-reviewed clinical papers on the pandemic contained original data, and many of those that did had poor experimental design.



Max Kozlov Jan 14. 2021 | 5 min read

D PDF VERSION

s scientists led initial investigations into the novel coronavirus last ABOVE: © ISTOCK.COM, winter and spring, journal publishers saw an enormous surge in BRIANAJACKSON COVID-19 publications. A study published January 4 in *BMC Medical* Research Methodology reports that the majority of early clinical studies on the pandemic lacked original data, and those that did were rushed and did not include the appropriate measures to reduce bias.

Raynaud et al. BMC Medical Research Methodology https://doi.org/10.1186/s12874-020-01190-w

BMC Medical Research Methodology

RESEARCH ARTICLE

Open Access

COVID-19-related medical research: a metaresearch and critical appraisal



Marc Raynaud^{1†}, Huanxi Zhang^{2†}, Kevin Louis^{1†}, Valentin Goutaudier^{1,3†}, Jiali Wang², Quentin Dubourg⁴, Yongcheng Wei², Zeynep Demir^{1,5}, Charlotte Debiais¹, Olivier Aubert¹, Yassine Bouatou¹, Carmen Lefaucheur⁶ Patricia Jabre⁷, Longshan Liu², Changxi Wang², Xavier Jouven¹, Peter Reese^{1,8}, Jean-Philippe Empana¹ and Alexandre Loupy¹

Background: Since the start of the COVID-19 outbreak, a large number of COVID-19-related papers have been published. However, concerns about the risk of expedited science have been raised. We aimed at reviewing and categorizing COVID-19-related medical research and to critically appraise peer-reviewed original articles.

Methods: The data sources were Pubmed, Cochrane COVID-19 register study, arXiv, medRxiv and bioRxiv, from 01/ 11/2019 to 01/05/2020. Peer-reviewed and preprints publications related to COVID-19 were included, written in English or Chinese. No limitations were placed on study design. Reviewers screened and categorized studies according to i) publication type, ii) country of publication, and iii) topics covered. Original articles were critically appraised using validated quality assessment tools.

Results: Among the 11,452 publications identified, 10,516 met the inclusion criteria, among which 7468 (71.0%) were peer-reviewed articles. Among these, 4190 publications (56.1%) did not include any data or analytics (comprising expert opinion pieces). Overall, the most represented topics were infectious disease (n = 2326, 22.1%), epidemiology (n = 1802, 17.1%), and global health (n = 1602, 15.2%). The top five publishing countries were China (25.8%), United States (22.3%), United Kingdom (8.8%), Italy (8.1%) and India (3.4%). The dynamic of publication showed that the exponential growth of COVID-19 peer-reviewed articles was mainly driven by publications without original data (mean 261.5 articles ± 51.1 per week) as compared with original articles (mean of 69.3 ± 22.3 articles per week). Original articles including patient data accounted for 713 (9.5%) of peer-reviewed studies. A total of 576 original articles (80.8%) showed intermediate to high risk of bias. Last, except for simulation studies that mainly used large-scale open data, the median number of patients enrolled was of 102 (IQR = 37-337).

Conclusions: Since the beginning of the COVID-19 pandemic, the majority of research is composed by publications without original data. Peer-reviewed original articles with data showed a high risk of bias and included a limited number of patients. Together, these findings underscore the urgent need to strike a balance between the velocity and quality of research, and to cautiously consider medical information and clinical applicability in a pressing, pandemic context.

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Marc Raynaud, Huanxi Zhang, Keyin Louis, and Valentin Goutaudie contributed equally to the article as co-first author. Paris Translational Research Epidemiology and Biostatistics Department Hôpital Necker, 149 rue de Sèvres, 75015 Paris, France Full list of author information is available at the end of the article



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Internal vs external validity in descriptive epi

- Unlike causal epidemiology, descriptive epidemiology does not suffer from confounding, but may still want to stratify, occasionally adjust
- But selection bias, surveillance bias, missing data and measurement error are still issues
- And samples needs to be externally valid
- Early COVID prevalence surveys suffered from selection bias and measurement error
- How well do we teach sampling?



International Journal of Epidemiology, 2021, 410-419 doi: 10.1093/ije/dyab010 Advance Access Publication Date: 22 February 2021 Original article



COVID-19

COVID-19 antibody seroprevalence in Santa Clara County, California

Eran Bendavid , 1* Bianca Mulaney, 2 Neeraj Sood, 3 Soleil Shah, 2 Rebecca Bromley-Dulfano, 2 Cara Lai, 2 Zoe Weissberg, 2 Rodrigo Saavedra-Walker, 4 Jim Tedrow, 5 Andrew Bogan, 6 Thomas Kupiec, 7 Daniel Eichner, 8 Ribhav Gupta, 9 John PA Ioannidis 1 and Jay Bhattacharya 1

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*Corresponding author. Department of Medicine, Stanford University, Stanford, CA 94305, USA. E-mail: ebd@stanford.ed Received 9 September 2000, Editorial decision 18 January 2021; Accepted 21 January 2021

Abstract

Background: Measuring the seroprevalence of antibodies to Severe Acute Respiratory Syndrome Coronavirus 2 (SARS CoV-2) is central to understanding infection risk and fatality rates. We studied Coronavirus Disease 2019 (COVID-19)-antibody seroprevalence in a community sample drawn from Santa Clara County.

Methods: On 3 and 4 April 2020, we tested 3328 county residents for immunoglobulin G (IgG) and immunoglobulin M (IgM) antibodies to SARS-CoV2 using a rapid lateral flow assay (Premier Biotech). Participants were recruited using advertisements that were targeted to reach county residents that matched the county population by gender, racelethnicity and rip code of residence. We estimate weights to match our sample to the county by zip, age, sex and race/ethnicity, We report the weighted and unweighted prevalence of antibodies to SARS-CoV-2. We adjust for test-performance characteristics by combining data from 18 independent test-kit assessments: 14 for specificity and 4 for specificity.

Results: The raw prevalence of antibodies in our sample was 1.5% (exact binomial 95% confidence interval (Cl. 11-2.0%). Test performance specificity in our data was 95.5% (95% Cl 99.2-99.7%) and sensitivity was 82.8% (95% Cl 76.0-88.4%). The unweighted prevalence adjusted for test-performance characteristics was 1.2% (95% Cl 0.7-1.8%). After weighting for population demographics, the prevalence was 2.8% (95% Cl 1.3-4.2%), using bootstrap to estimate confidence bounds. These prevalence point estimates imply that 5300 0195% Cl 26000 to 82000 using weighted prevalence; 23 000

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Commentary

Catherine R. Lesko*, Alexander P. Keil, and Jessie K. Edwards

The Epidemiologic Toolbox: Identifying, Honing, and Using the Right Tools for the Job

A solid understanding of biases that plague single-sample estimation problems is made even more urgent as our modes of communication and transportation and our expectations of privacy evolve. Staple sampling methodologies such as random-digit dialing or using Department of Motor Vehicle registries are becoming less reliable. New sampling methods (e.g., Internet sampling, respondent-driven sampling) can reach hidden populations or return large samples quickly (17–21), but drawing population-level inference may be challenging.



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International Journal of Epidemiology 2013;42:1012-1014 doi:10.1093/ije/dys223

POINT COUNTERPOINT

Why representativeness should be avoided

Kenneth J Rothman, 1,2 John EJ Gallacher and Elizabeth E Hatch 1

¹Department of Epidemiology, Boston University School of Public Health, Boston, MA, USA, ²RTI Health Solutions, RTI International, Research Triangle Park, NC, USA and ³Institute of Primary Care and Public Health, Cardiff University, Cardiff, UK

bers from these other age-groups'. But we in fact acknowledged that there is a role for representativeness is certain circumstances, as when 'public-health wood in a cert professionals may rely on representative samples to cople. derived by gene describe the health status of specific populations'. ocess way

The essence of

always produce fire. The art of discovery is therefore the art of correct generalisation. What is irrelevant, such as the particular shape or size of the piece of wood used, is to be excluded from the generalisation; what is relevant, for example, the dryness of the wood, is to be included in it. The meaning of the term relevant can thus be defined: that is relevant which must be mentioned for the generalisation to be valid. The separation of relevant from irrelevant factors is the heainning of knowledge.

nature works. That process is uncertain, along with everything else in empirical science, but it is not an extrapolation from sample to target population. When Pasteur created the experiment that refuted the theory of spontaneous generation, he used a goose-neck flask to allow air to contact his cooling broth without letting organisms settle into the broth. His concern was to control the conditions in



Measurement Error

- Caused great problems in COVID pandemic
- Surveillance bias/missing data also parts of the measurement conundrum
- Is distinction between nondifferential vs differential and dependent still important?



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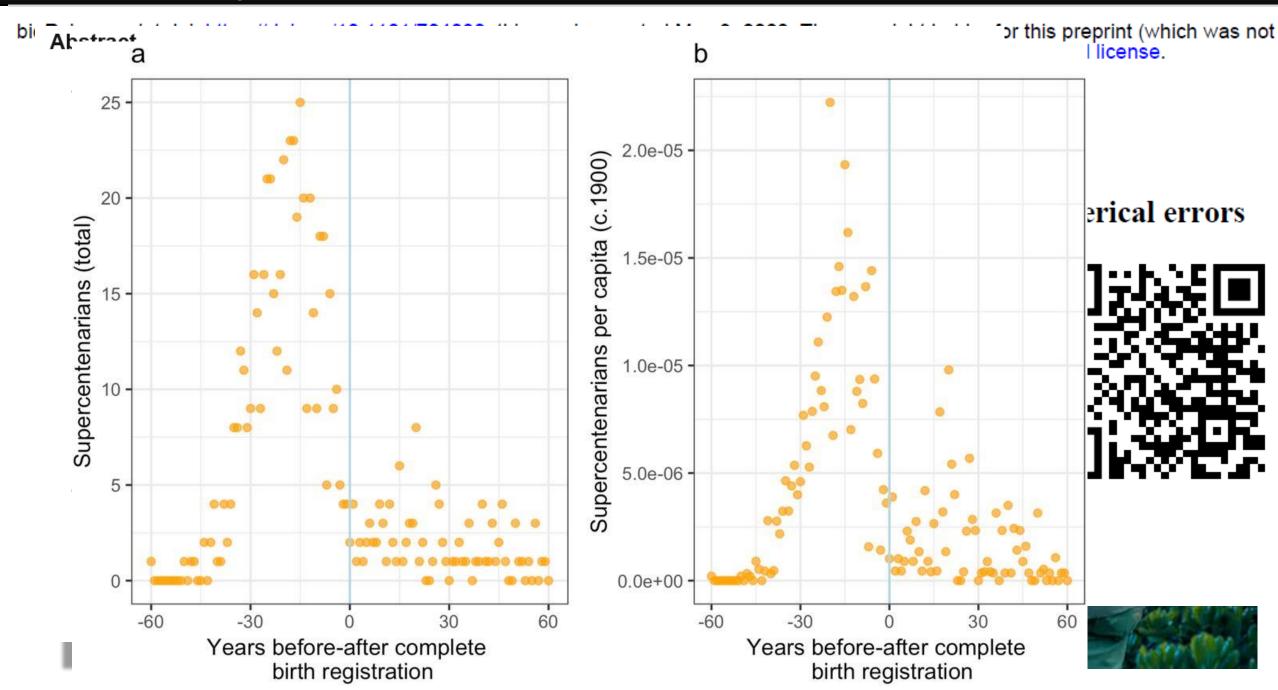
Commentary

On the Need to Revitalize Descriptive Epidemiology

Matthew P. Fox*, Eleanor J. Murray, Catherine R. Lesko, and Shawnita Sealy-Jefferson

Early COVID-19 work provides an example of how a poorly conceived sampling strategy can lead to poor inference in descriptive epidemiology. Early serological surveys enrolled a sample of volunteers interested in knowing their SARS-CoV-2 antibody status (12). These surveys likely oversampled people who had experienced COVID-19-like symptoms during the Spring of 2020, and the resulting prevalence estimates were likely much higher than would have been obtained from a random population sample. Here, measurement error (as the tests used were not perfect at detecting COVID-19 antibodies and, due to low prevalence of COVID-19, false positives probably overwhelmed true positives) also likely biased results. However, in contrast to causal analyses, confounding bias is not an issue (indeed, confounding bias is not defined for this question).







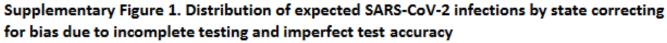
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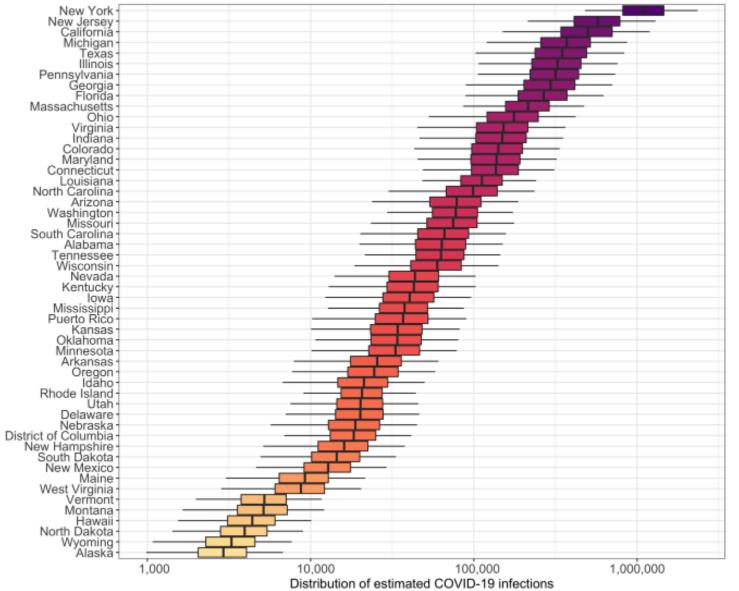
https://doi.org/10.1038/s4

Substantia infection in

Sean L. Wu 1, Andre Stephanie Djajadi 1, Benjamin F. Arnold 6,7,

Accurate estimates of the response. Confirmed COV pandemic because testin severe symptoms due to bias analysis to account estimate 6,454,951 cumu 0.2% of the population) in the number of infections d





nique that attempts to correct for out how the data are biased away bias or misclassification). When are treated as random variables are is known as probabilistic bias an because it defines prior disformal likelihood function to d data²². In cases where a likelimited information to update fully Bayesian approaches lead to certainty in several of the input tment may remain partially g priors. Since our goal was to burden that removed bias due to istics, we decided to use a

mplex mathematical relationship ytic treatment of the induced timates is often intractable, and the nulation. In order to correct bias (preferential testing of accuracy, we developed a simple

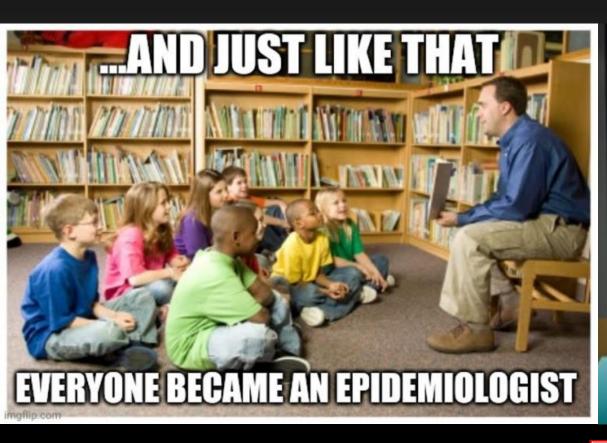
confirmed cases. 86% (simulation interval. 64-99%) of this difference is due to incomplete

model hand on anidomic lowing formula to incompare to this and arms to the

But be careful of our biases...

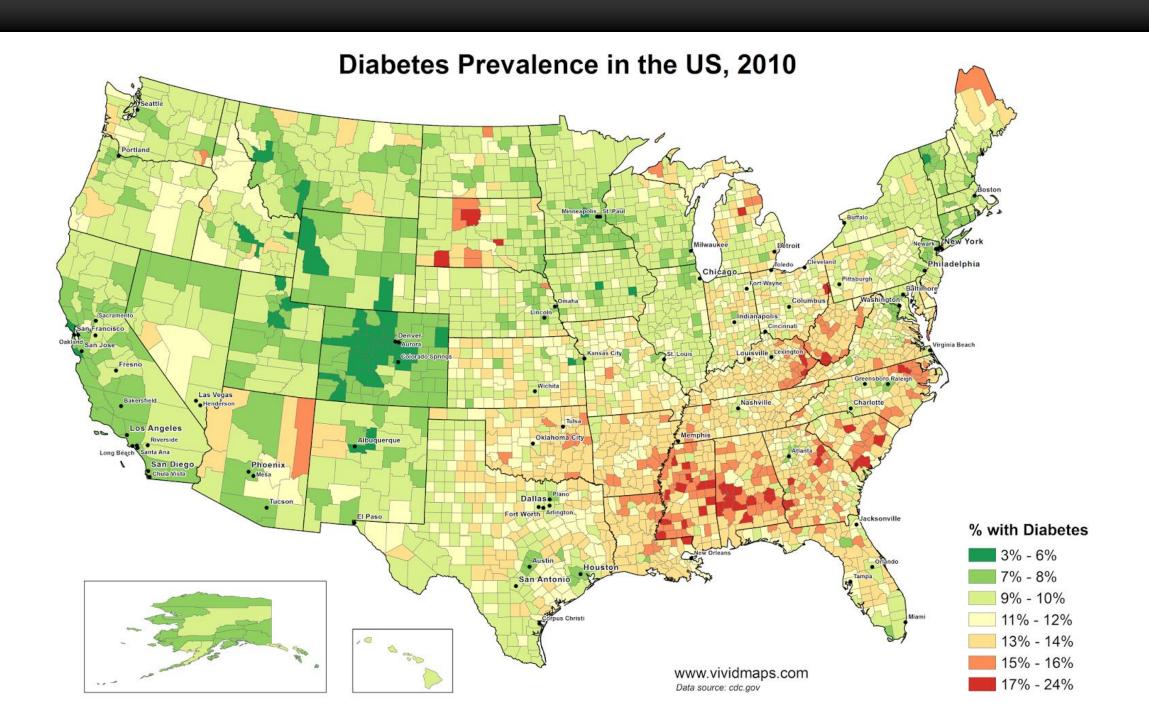


But descriptive is not causal And yet, the world thinks descriptive is easy









Correlation is not causation, but it sure does look like it...



The Washington Post

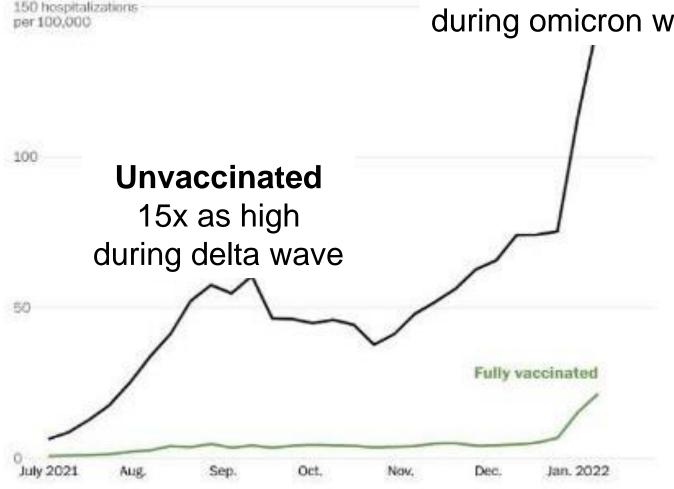
Democracy Dies in Darkness

Coronavirus vaccine protection was much weaker against omicron, data shows

Unvaccinated

7x as high during omicron wave



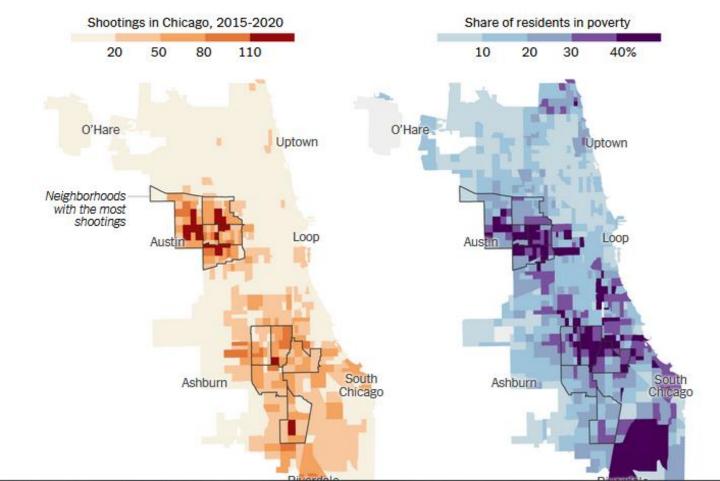




Poverty and violence

There are several factors behind the concentration of violence. A major one is poverty.

In Chicago, violence and poverty closely overlap, as these maps demonstrate:





About

Tools

Developers

Help

Search life-sciences literature (42,047,761 articles, preprints and more)

Advanced search

Visualization aesthetics bias trust in science, news, and social media

Authors: Chujun Lin*, Mark Thornton

Affiliations:

Department of Psychological and Brain Sciences, Dartmouth College; Hanover, NH, USA

* Corresponding author. Email: Chujun.Lin@Dartmouth.edu

Visualization aesthetics bias trust in science, news, and social media

visual appeal, independent of data quality. Here we tested whether the beauty of a graph influences how much people trust it. Across three studies, we sampled graphs from social media, news reports, and scientific publications, and consistently found that graph beauty predicted trust. In a fourth study, we manipulated both the graph beauty and misleadingness. We found that beauty, but not actual misleadingness, causally affected trust. These findings reveal a source of

Conclusions

- Descriptive epidemiology is an essential function of our discipline and yet it doesn't receive the prestige it should
- During the pandemic there was renewed interest in descriptive epi as we recognized its central role in responding to the pandemic
- But to be useful, descriptive epidemiology must be done with care and rigor and with attention to key sources of bias
- Renewed training in descriptive epi could really help improve out outputs



Thank you!



How much time did you spend on descriptive epidemiology in your epi training?







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Commentary

Catherine R. Lesko*, Alexander P. Keil, and Jessie K. Edwards

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it is evident that 1) epidemiologic principles and methods are applicable to many questions beyond causal effect estimation, and 2) epidemiologic curricula and journals have prioritized analytic epidemiology and questions related to identifying (causal) determinants of disease over descriptive epidemiology and questions related to accurately characterizing the health of populations (14, 15). Descriptive epidemiologic studies are frequently excluded from peerreviewed journals for not being generalizable enough. We



Do we value descriptive epidemiology?

- How many of you work primarily on descriptive epidemiologic studies?
- How many of you would feel you had the skills to properly evaluate as a peer reviewer a descriptive study?
- How many of you have more than cursory training in descriptive epidemiology?
- How many of you would be comfortable with your students writing a dissertation that is entirely descriptive epidemiology?





Descriptive Research at NIH



Causal Research at NIH





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Commentary

Catherine R. Lesko*, Alexander P. Keil, and Jessie K. Edwards

The Epidemiologic Toolbox: Identifying, Honing, and Using the Right Tools for the Job

tive courses. An epidemiology curriculum that emphasized descriptive epidemiology might spend the entirety of the first term on single-sample estimation problems and describing the natural course of disease (i.e., the course of disease in the absence of any interventions). This could be framed in terms of designing a target study, or an idealized study that would accurately estimate the descriptive parameter of interest in the absence of real-world constraints like missing data and measurement error (foreshadowing introduction of the target trial as a heuristic for study design for causal effect estimation but encompassing a broader set of questions).



What is the goal of your study?

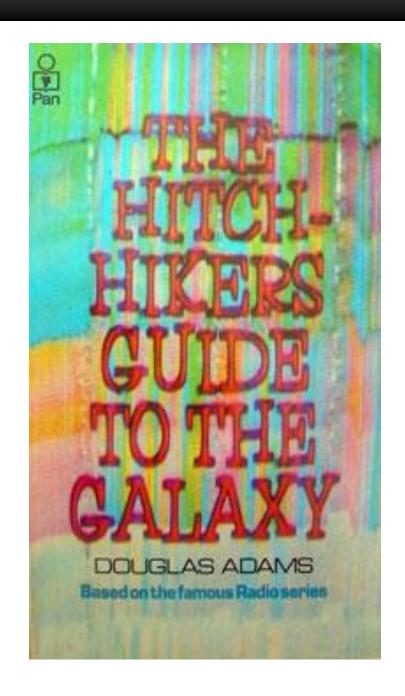


The number 42 is, in *The Hitchhiker's Guide to the Galaxy* by Douglas Adams, the "Answer to the Ultimate Question of Life, the Universe, and Everything", calculated by an enormous supercomputer named Deep Thought over a period of 7.5 million years. Unfortunately, no one knows what the question is. Thus, to calculate the Ultimate



The Answer to the Ultimate Question of Life, The Universe, and Everything





What's the question?

Journal of Orthopaedic & Sports Physical Therapy

Current Issue Just Accepted Archive

A previous Evidence in Practice article explained why a specific and answerable research question is important for clinicians and researchers. Determining whether a study aims to answer a descriptive, predictive, or causal question should be one of the first things a reader does when reading an article. Any type of question can be relevant and useful to support evidence-based practice, but only if the question is well defined, matched to the right study design, and reported correctly. *J Orthop Sports Phys Ther* 2020;50(8):468–469. doi:10.2519/jospt.2020.0703

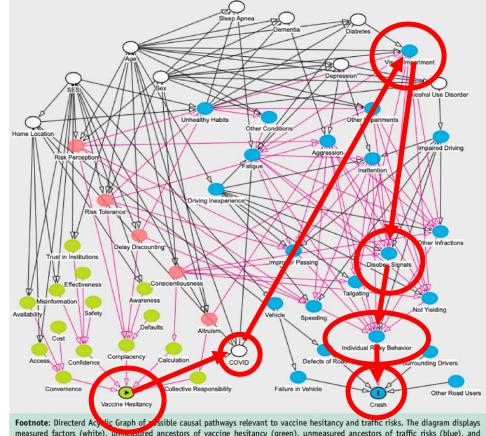
- Likely the biggest problem we have is asking a question that can be translated into statistical notation that can be answered
- Often it isn't clear if interested in description, prediction or causation
- Often simpler with descriptive epi, but the problem doesn't go away

We should know what the question is...



- Causation, description or prediction?
- Seems at first like causation
 - "COVID vaccine hesitancy is a reflection of psychology that might also contribute to traffic safety. We tested whether COVID vaccination was associated with the risks of a traffic crash."
 - Vax wouldn't help here, so not causation.
- Last bullet seems like description
 - Find them so we can give them an intervention for traffic safety, not vax to reduce traffic accident/
 - But then why adjust?
- DAG suggest COVID causes impairments that cause accidents

§2 Directed Acyclic Graph



Footnote: Directerd Acy lic Graph of a sible causal pathways relevant to vaccine hesitancy and traffic risks. The diagram displays measured factors (white), unmeasured ancestors of vaccine hesitancy (green), unmeasured ancestors of traffic risks (blue), and unmeasured ancestors to both vaccine hesitancy and traffic risks (pink). Causal pathways denoted as closed (black lines) or open (magenta lines). Specific causal pathways based on literature review, direct clinical experience (Canada's largest trauma center), and expert consultation (International Traffic Medicine Association).

Description or Association?

- Well, I guess this is just meant to be descriptive as we can't say anything causal for sure, so I just want to see if things are associated...
- So why did you adjust?
- If description is the goal, adjustment is usually not necessary or helpful (there are cases where it is)?
- But the opposite can also be true, it can be so tempting to read causation from description...





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Invited Commentary

Invited Commentary: The Importance of Descriptive Epidemiology



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