Liste erstellt am 2021-01-11

References

Aktuell

BRAUNER 2020

Jan M. Brauner et al., *The effectiveness of eight nonpharmaceutical interventions against COVID-19 in 41 countries.* medRxiv **2020**, 20116129. DOI:10.1101/2020.05.28.20116129.

Governments are attempting to control the COVID-19 pandemic with nonpharmaceutical interventions (NPIs). However, it is still largely unknown how effective different NPIs are at reducing transmission. Data-driven studies can estimate the effectiveness of NPIs while minimising assumptions, but existing analyses lack sufficient data and validation to robustly distinguish the effects of individual NPIs. We gather chronological data on NPIs in 41 countries between January and the end of May 2020, creating the largest public NPI dataset collected with independent double entry. We then estimate the effectiveness of 8 NPIs with a Bayesian hierarchical model by linking NPI implementation dates to national case and death counts. The results are supported by extensive empirical validation, including 11 sensitivity analyses with over 200 experimental conditions. We find that closing schools and universities was highly effective; that banning gatherings and closing high-risk businesses was effective, but closing most other businesses had limited further benefit; and that many countries may have been able to reduce R below 1 without issuing a stay-at-home order.

Keywords: COVID-19 | SARS-CoV-2 | nonpharmaceutical intervention | countermeasure | Bayesian model

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CHANG 2021

Serina Chang, Emma Pierson, Pang Wei Koh, Jaline Gerardin, Beth Redbird, David Grusky & Jure Leskovec, *Mobility network models of COVID-19 explain inequities and inform reopening.* nature **589** (2021), 82–87. DOI:10.1038/s41586-020-2923-3.

n589-0082-Supplement.pdf

The coronavirus disease 2019 (COVID-19) pandemic markedly changed human mobility patterns, necessitating epidemiological models that can capture the effects of these changes in mobility on the spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)1. Here we introduce a metapopulation susceptible–exposed–infectious–removed (SEIR) model that integrates fine-grained, dynamic mobility networks to simulate the spread of SARS-CoV-2 in ten of the largest US metropolitan areas. Our mobility networks are derived from mobile phone data and map the hourly movements of 98 million people from neighbourhoods (or census block groups) to points of interest such as restaurants and religious establishments, connecting 56,945 census block groups to 552,758 points of interest with 5.4 billion hourly edges. We show that by integrating these networks, a relatively simple SEIR model can accurately fit the real case trajectory, despite substantial changes in the behaviour of the population over time. Our model predicts that a small minority of ‘superspreader’ points of interest account for a large majority of the infections, and that restricting the maximum occupancy at each point of interest is more effective than uniformly reducing mobility. Our model also correctly predicts higher infection rates among disadvantaged racial and socioeconomic groups2–8 solely as the result of differences in mobility: we find that disadvantaged groups have not been able to reduce their mobility as sharply, and that the points of interest that they visit are more crowded and are therefore associated with higher risk. By capturing who is infected at which locations, our model supports detailed analyses that can inform more-effective and equitable policy responses to COVID-19.

Chen 2021

M. Keith Chen, Judith A. Chevalier & Elisa F. Long, *Nursing home staff networks and COVID-19.* PNAS **118** (2021), e2015455118. DOI:10.1073/pnas.2015455118.

pnas118-e2015455118-Supplement.pdf

Nursing homes and other long-term care facilities account for a disproportionate share of COVID-19 cases and fatalities worldwide. Outbreaks in US nursing homes have persisted despite nationwide visitor restrictions beginning in mid-March. An early report issued by the Centers for Disease Control and Prevention identified staff members working in multiple nursing homes as a likely source of spread from the Life Care Center in Kirkland, WA, to other skilled nursing facilities. The full extent of staff connections between nursing homes—and the role these connections serve in spreading a highly contagious respiratory infection—is currently unknown given the lack of centralized data on cross-facility employment. We perform a large-scale analysis of nursing home connections via shared staff and contractors using device-level geolocation data from 50 million smartphones, and find that 5.1 % of smartphone users who visited a nursing home for at least 1 h also visited another facility during our 11wk study period—even after visitor restrictions were imposed. We construct network measures of connectedness and estimate that nursing homes, on average, share connections with 7.1 other facilities. Traditional federal regulatory metrics of nursing home quality are unimportant in predicting outbreaks, consistent with recent research. Controlling for demographic and other factors, a home’s staff network connections and its centrality within the greater network strongly predict COVID-19 cases.

Keywords: nursing homes | COVID-19 | complex networks | smartphone data

Significance: Nursing homes account for 40 % of US COVID-related fatalities as of August 31, highlighting the urgent need to reduce SARSCoV2 transmission routes in these facilities. Our large-scale analysis of smartphone location data reports half a million individuals entering a nursing home following the March 13 federal ban on visitors. With 5.1 % of these individuals entering two or more facilities, a nursing home snapshot network emerges. More connections, likely arising from contractors and staff working at multiple facilities, are highly predictive of COVID-19 cases, whereas traditional regulatory quality metrics are unimportant in predicting outbreak size. With an estimated 49 % of nursing home cases attributable to crossfacility staff movement, attention to highly connected nursing facilities is warranted.

Contreras 2020

Sebastian Contreras, Jonas Dehning, Sebastian B. Mohr, F. Paul Spitzner & Viola Priesemann, *Low case numbers enable long-term* *stable pandemic control without lockdowns.* arXiv (2020), 2011.11413. <`http://arxiv.org/pdf/2011.11413`>.

The traditional long-term solutions for epidemic control involve eradication or herd immunity1; 2. Neither of them will be attained within a few months for the COVID-19 pandemic. Here, we analytically derive the existence of a third, viable solution: a stable equilibrium at low case numbers, where test-trace-and-isolate policies partially compensate for local spreading events, and only moderate contact restrictions remain necessary. Across wide parameter ranges of our complementary compartmental model3, the equilibrium is reached at or below 10 daily new cases per million people. Such low levels had been maintained over months in most European countries. However, this equilibrium is endangered (i) if contact restrictions are relaxed, or (ii) if case numbers grow too high. The latter destabilisation marks a novel tipping point beyond which the spread self-accelerates because test-trace-and-isolate capacities are overwhelmed. To reestablish control quickly, a lockdown is required. We show that a lockdown is either effective within a few weeks, or tends to fail its aim. If effective, recurring lockdowns are not necessary — contrary to the oscillating dynamics previously presented in the context of circuit breakers4;5;6, and contrary to a regime with high case numbers — if moderate contact reductions are maintained. Hence, at low case numbers, the control is easier, and more freedom can be granted. We demonstrate that this strategy reduces case numbers and fatalities by a factor of 5 compared to a strategy focused only on avoiding major congestion of hospitals. Furthermore, our solution minimises lockdown duration, and hence economic impact. In the long term, control will successively become easier due to immunity through vaccination or large scale testing programmes. International coordination would facilitate even more the implementation of this solution.

DAVIES 2021

Nicholas G. Davies et al., *Estimated transmissibility and severity of novel SARS-CoV-2 Variant of Concern 202012/01 in England.* unknown (2021), preprint, 1–35.

A novel SARS-CoV-2 variant, VOC 202012/01, emerged in southeast England in November 2020 and appears to be rapidly spreading towards fixation. We fitted a two-strain mathematical model of SARS-CoV-2 transmission to observed COVID-19 hospital admissions, hospital and ICU bed occupancy, and deaths; SARS-CoV-2 PCR prevalence and seroprevalence; and the relative frequency of VOC 202012/01 in the three most heavily affected NHS England regions (South East, East of England, and London). We estimate that VOC 202012/01 is 56 % more transmissible (95 % credible interval across three regions 50-74 %) than preexisting variants of SARS-CoV-2. We were unable to find clear evidence that VOC 202012/01 results in greater or lesser severity of disease than preexisting variants. Nevertheless, the increase in transmissibility is likely to lead to a large increase in incidence, with COVID-19 hospitalisations and deaths projected to reach higher levels in 2021 than were observed in 2020, even if regional tiered restrictions implemented before 19 December are maintained. Our estimates suggest that control measures of a similar stringency to the national lockdown implemented in England in November 2020 are unlikely to reduce the effective reproduction number R t to less than 1, unless primary schools, secondary schools, and universities are also closed. We project that large resurgences of the virus are likely to occur following easing of control measures. It may be necessary to greatly accelerate vaccine roll-out to have an appreciable impact in suppressing the resulting disease burden.

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C. Tully, Sam Abbott, Amy Gimma, William Waites, Kerry LM Wong, Kevin van Zandvoort, CMMID COVID-19 Working Group, Rosalind M. Eggo, Sebastian Funk, Mark Jit, Katherine E. Atkins, W. John Edmunds

MA 2021

Kevin C. Ma & Marc Lipsitch, *Big data and simple models to track COVID-19.* nature **589** (2021), 26–28.

Understanding the dynamics of SARS-CoV-2 infections could help to limit viral spread. Analysing mobile-phone data to track human contacts at different city venues offers a way to model infection risks and explain infection disparities.

Although the goal of this mechanistic modelling was not to provide a forecast8, confirming that the model has reasonable predictive power is often a necessary first step in trying to draw any conclusions about mechanisms that might underlie the observed patterns.

In addition to trying alternative fitting approaches, the authors analysed how sensitive particular outcomes were to the parameters of the model, finding that model outputs are consistent over a range of plausible parameter values. These give confidence that, although simple, the assumptions underlying this model generate predictions that match the data better than do equally plausible alternatives, which increases the persuasiveness of the hypotheses generated about interventions.

SCHMELZ 2021

Katrin Schmelz, *Enforcement may crowd out voluntary support for COVID-19 policies, especially where trust in government is weak and in a liberal society.* PNAS **118** (2021), e2016385118. DOI:10.1073/pnas.2016385118.

pnas118-e2016385118-Supplement.pdf

Effective states govern by some combination of enforcement and voluntary compliance. To contain the COVID-19 pandemic, a critical decision is the extent to which policy makers rely on voluntary as opposed to enforced compliance, and nations vary along this dimension. While enforcement may secure higher compliance, there is experimental and other evidence that it may also crowd out voluntary motivation. How does enforcement affect citizens' support for anti–COVID-19 policies? A survey conducted with 4,799 respondents toward the end of the first lockdown in Germany suggests that a substantial share of the population will support measures more under voluntary than under enforced implementation. Negative responses to enforcement—termed control aversion—vary across the nature of the policy intervention (e.g., they are rare for masks and frequent for vaccination and a cell-phone tracing app). Control aversion is less common among those with greater trust in the government and the information it provides, and among those who were brought up under the coercive regime of East Germany. Taking account of the likely effectiveness of enforcement and the extent to which near-universal compliance is crucial, the differing degrees of opposition to enforcement across policies suggest that for some anti–COVID-19 policies an enforced mandate would be unwise, while for others it would be essential. Similar reasoning may also be relevant for policies to address future pandemics and other societal challenges like climate change.

Keywords: social norms | institutions | state capacities | cooperation | crowding out intrinsic motivation

Significance: This paper makes three contributions. First, it provides insights from Germany on people's agreement with policy choices that all countries face in addressing the COVID-19 pandemic. My findings point to dimensions relevant for policy makers when deciding between voluntary as opposed to enforced measures. These insights include the essential role of trust in government. Second, the paper contributes to the small but important literature on the intersection of policy design, state capacities, and the interplay of obedience and voluntary compliance. Third, my finding that even 30 y after reunification those who have experienced state coercion in East Germany are less control-averse concerning anti–COVID-19 measures than West Germans contributes to the literature on endogenous preferences and comparative cultural studies.

Bibel

Herzer 2014

Jens Herzer, *Was ist falsch an der “fälschlich so genannten Gnosis”? Zur Paulusrezeption des Ersten Timotheusbriefes im Kontext seiner Gegnerpolemik*. Early Christianity **5** (2014), 68–96.

The notion of the “falsely so-called Gnosis” in 1 Tim 6:20 is the only explicit reference to a religious group of a Gnostic type in the New Testament. Within the Pastoral Epistles, however, the religious profile of the “heretics” is highly disputed, because these letters describe different types of opponents with particularly Jewish, Christian, and Gnostic characteristics. The paper argues that in order to understand the problem within the Pastoral Epistles it is inappropriate to suppose a mixed type of “heresy,” i. e. of a Jewish-Christian Gnosis. From the perspective that each of the letters has its specific challenge only 1 Tim pertains to the quarrels of the church with the raising Gnostic movements in the first half of the second century. The main instrument in First Timothy’s struggle against Gnostic opponents and for an internal consolidation of the church is a significant transformation of Pauline Ecclesiology.

Keywords: Pastoralbriefe | 1. Timotheusbrief | Paulustradition | Gnosis | Ekklesiologie | Markion | Valentin | Irenäus

Luther 1912

Die Bibel oder die ganze Heilige Schrift des Alten und Neuen Testaments, nach der deutschen Übersetzung D. Martin Luthers. (München 2020).

Moffatt 1926

A new translation of The Bible, Containing the the Old and the New Testament – James Moffatt. (London 1926).

Datierung

Demján 2020

Peter Demján & Peter Pavúk, *Clustering Of Calibrated Radiocarbon Dates, Site-Specific Chronological Sequences Identified By Dense Radiocarbon Sampling*. Radiocarbon (2020), preprint, 1–10. DOI:10.1017/RDC.2020.129.

Radiocarbon2021.01-Demjan-Supplement.zip

Calibrated radiocarbon (14C) determinations are commonly used in archaeology to assign calendar dates to a site's chronological phases identified based on additional evidence such as stratigraphy. In the absence of such evidence, we can perform dense 14C sampling of the site to attempt to identify periods of heightened activity, separated by periods of inactivity, which correspond to archaeological phases and gaps between them. We propose a method to achieve this by hierarchical cluster analysis of the calibrated 14C dates, followed by testing of the different clustering solutions for consistency based on silhouette coefficient and statistical significance using randomization. Separate events identified in such a way can then be regarded as evidence for distinct phases of activity and used to construct a site-specific sequence. This can be in turn used as a Bayesian prior to further narrow down the distributions of the calibrated 14C dates. We assessed the validity of the method using simulated data as well as real-life archaeological data from the Bronze Age settlement of Troy. A Python implementation of the method is available online at http://github.com/demjanp/clustering_14C.

Keywords: clustering | phasing | radiocarbon | randomization testing.

HUTCHINSON 2020

Ian Hutchinson, *Spatiotemporal Variation in ΔR on the West Coast of North America in the Late Holocene, Implications for Dating the Shells of Marine Mollusks.* American Antiquity **85** (2020), 676–693.

Radiocarbon ages on mollusk shells, which account for about half of the more than 8,000 dates from cultural deposits on the west coast of North America, need to be corrected for the local marine reservoir effect (DR) to yield true ages. Assays on "prebomb" shells show that DR increases poleward, echoing the age gradient in offshore waters. The meridional gradient in DR is not appreciably affected by the transition either from an upwelling regime to a downwelling regime north of 40°N-45°N or from a winter maximum-high alkalinity river discharge pattern to a summer maximum-low alkalinity pattern at the same latitude, probably because these changes are offset by increasing storminess and tidal energy in coastal areas. Mesoscale variations in DR along this gradient are attributable to contrasts in shore morphology and exposure. Data from 123 shell-wood pairs reveal similar patterns of temporal variation in DR in the late Holocene in the coastal ecoregions. The characteristic temporal pattern echoes phases of variable El Nino-Southern Oscillation (ENSO) activity. The high degree of variability in DR argues against the indiscriminate application of regionally uniform or trans-Holocene DR values and demands improvements in spatiotemporal resolution if shell is used to date cultural deposits.

Keywords: radiocarbon | marine reservoir | DR | North America | Pacific coast | spatiotemporal variability | ocean currents | river discharge | El Nino

Islam

LEPPIN 2018

Hartmut Leppin, *Die frühen Christen, Von den Anfängen bis Konstantin.* (München ^{2}2019).

Judentum

ADLER 2018

Yonatan Adler, *The Hellenistic origins of Jewish ritual immersion.* Journal of Jewish Studies **69** (2018), 1–21.

The present study explores the origins of Jewish ritual immersion – inquiring when immersion first appeared as a rite of purification and what the reasons may have been for this development specifically at this time. Textual and archaeological evidence suggest that immersion emerged at some point during – or perhaps slightly prior to – the first half of the first century bce. It is suggested here that the practice grew out of contemporary bathing practices involving the Hellenistic hip bath. Through a process of ritualization, full-body immersion emerged as a method of purificatory washing clearly differentiated from profane bathing. By way of a subsequent process of 'hyper-ritualization', some ventured further to distinguish purificatory ablutions from profane bathing by restricting use of 'drawn water' for purification and by assigning impurity to anyone who bathed in such water. Before us is an enlightening example of one of the many ways wherein Jewish religious practices evolved and adapted in response to Hellenistic cultural innovations.

Klima

Bauch 2020

Martin Bauch, Thomas Labbé, Annabell Engel & Patric Seifert, *A prequel to the Dantean Anomaly, The precipitation seesaw and droughts of 1302 to 1307 in Europe*. Climate of the Past **16** (2020), 2343–2358.

ClimPast16-2343-Supplement.zip

The cold/wet anomaly of the 1310s ("Dantean Anomaly") has attracted a lot of attention from scholars, as it is commonly interpreted as a signal of the transition between the Medieval Climate Anomaly (MCA) and the Little Ice Age (LIA). The huge variability that can be observed during this decade, like the high interannual variability observed in the 1340s, has been highlighted as a side effect of this rapid climatic transition. In this paper, we demonstrate that a multiseasonal drought of almost 2 years occurred in the Mediterranean between 1302 and 1304, followed by a series of hot, dry summers north of the Alps from 1304 to 1306. We suggest that this outstanding dry anomaly, unique in the 13th and 14th centuries, together with cold anomalies of the 1310s and the 1340s, is part of the climatic shift from the MCA to the LIA. Our reconstruction of the predominant weather patterns of the first decade of the 14th century – based on both documentary and proxy data – identifies multiple European precipitation seesaw events between 1302 and 1307, with similarities to the seesaw conditions which prevailed over continental Europe in 2018. It can be debated to what extent the 1302–1307 period can be compared to what is currently discussed regarding the influence of the phenomenon of Arctic amplification on the increasing frequency of persistent stable weather patterns that have occurred since the late 1980s. Additionally, this paper deals with socioeconomic and cultural responses to drought risks in the Middle Ages as outlined in contemporary sources and provides evidence that there is a significant correlation between pronounced dry seasons and fires that devastated cities.

Ozeanien

Pugach 2021

Irina Pugach, Alexander Hübner, Hsiao-chun Hung, Matthias Meyer, Mike T. Carson & Mark Stoneking, *Ancient DNA from Guam and the peopling of the Pacific*. PNAS **118** (2021), e2022112118.

pnas118-e2022112118-Supplement.pdf

Humans reached the Mariana Islands in the western Pacific by ≈3,500 y ago, contemporaneous with or even earlier than the initial peopling of Polynesia. They crossed more than 2,000 km of open ocean to get there, whereas voyages of similar length did not occur anywhere else until more than 2,000 y later. Yet, the settlement of Polynesia has received far more attention than the settlement of the Marianas. There is uncertainty over both the origin of the first colonizers of the Marianas (with different lines of evidence suggesting variously the Philippines, Indonesia, New Guinea, or the Bismarck Archipelago) as well as what, if any, relationship they might have had with the first colonizers of Polynesia. To address these questions, we obtained ancient DNA data from two skeletons from the Ritidian Beach Cave Site in northern Guam, dating to ≈2,200 y ago. Analyses of complete mitochondrial DNA genome sequences and genome-wide SNP data strongly support ancestry from the Philippines, in agreement with some interpretations of the linguistic and archaeological evidence, but in contradiction to results based on computer simulations of sea voyaging. We also find a close link between the ancient Guam skeletons and early Lapita individuals from Vanuatu and Tonga, suggesting that the Marianas and Polynesia were colonized from the same source population, and raising the possibility that the Marianas played a role in the eventual settlement of Polynesia.

Keywords: ancient DNA | Micronesia | Polynesia | human settlement

Significance: We know more about the settlement of Polynesia than we do about the settlement of the Mariana Islands in the western Pacific. There is debate over where people came from to get to the Marianas, with various lines of evidence pointing to the Philippines, Indonesia, New Guinea, or the Bismarck Archipelago, and over how the ancestors of the present Mariana Islanders, the Chamorro, might be related to Polynesians. We analyzed ancient DNA from Guam from two skeletons dating to ≈2,200 y ago and found that their ancestry is linked to the Philippines. Moreover, they are closely related to early Lapita skeletons from Vanuatu and Tonga, suggesting that the early Mariana Islanders may have been involved in the colonization of Polynesia.