

References

Aktuell

COHEN 2020

Andrew N. Cohen & Bruce Kessel, *False positives in reverse transcription PCR testing for SARS-CoV-2*. [medRxiv 2020, 20080911](https://doi.org/10.1101/2020.04.26.20080911), 1–11. DOI:10.1101/2020.04.26.20080911.

Background: Large-scale testing for SARS-CoV-2 by RT-PCR is a key element of the response to COVID-19, but little attention has been paid to the potential frequency and impacts of false positives.

Methods: From a meta-analysis of external quality assessments of RT-PCR assays of RNA viruses, we derived a conservative estimate of the range of false positive rates that can reasonably be expected in SARS-CoV2 testing, and analyzed the effect of such rates on analyses of regional test data and estimates of population prevalence and asymptomatic ratio.

Findings Review of external quality assessments revealed false positive rates of 0-16.7%, with an interquartile range of 0.8-4.0%. Such rates would have large impacts on test data when prevalence is low. Inclusion of such rates significantly alters four published analyses of population prevalence and asymptomatic ratio.

Interpretation The high false discovery rate that results, when prevalence is low, from false positive rates typical of RTPCR assays of RNA viruses raises questions about the usefulness of mass testing; and indicates that across a broad range of likely prevalences, positive test results are more likely to be wrong than are negative results, contrary to public health advice about SARS-CoV-2 testing. There are myriad clinical and case management implications. Failure to appreciate the potential frequency of false positives and the consequent unreliability of positive test results across a range of scenarios could unnecessarily remove critical workers from service, expose uninfected individuals to greater risk of infection, delay or impede appropriate medical treatment, lead to inappropriate treatment, degrade patient care, waste personal protective equipment, waste human resources in unnecessary contact tracing, hinder the development of clinical improvements, and weaken clinical trials. Measures to raise awareness of false positives, reduce their frequency, and mitigate their effects should be considered.

DEARLOVE 2020

Bethany Dearlove, Eric Lewitus, Kayvon Modjarrad & Morgane Rolland et al., *A SARS-CoV-2 vaccine candidate would likely match all currently circulating variants*. [PNAS 117 \(2020\), 23652–23662](https://doi.org/10.1073/pnas.2008281117). DOI:10.1073/pnas.2008281117.

[pnas117-23652-Supplement.pdf](https://doi.org/10.1073/pnas.2008281117)

The magnitude of the COVID-19 pandemic underscores the urgency for a safe and effective vaccine. Many vaccine candidates focus on the Spike protein, as it is targeted by neutralizing antibodies and plays a key role in viral entry. Here we investigate the diversity seen in severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) sequences and compare it to the sequence on which most vaccine candidates are based. Using 18,514 sequences, we perform phylogenetic, population genetics, and structural bioinformatics analyses. We find limited diversity across SARS-CoV-2 genomes: Only 11 sites show polymorphisms in >5% of sequences;

yet two mutations, including the D614G mutation in Spike, have already become consensus. Because SARS-CoV-2 is being transmitted more rapidly than it evolves, the viral population is becoming more homogeneous, with a median of seven nucleotide substitutions between genomes. There is evidence of purifying selection but little evidence of diversifying selection, with substitution rates comparable across structural versus nonstructural genes. Finally, the Wuhan-Hu-1 reference sequence for the Spike protein, which is the basis for different vaccine candidates, matches optimized vaccine inserts, being identical to an ancestral sequence and one mutation away from the consensus. While the rapid spread of the D614G mutation warrants further study, our results indicate that drift and bottleneck events can explain the minimal diversity found among SARS-CoV-2 sequences. These findings suggest that a single vaccine candidate should be efficacious against currently circulating lineages.

Keywords: SARS-CoV-2 | evolution | vaccine

Bethany Dearlove, Eric Lewitus, Hongjun Bai, Yifan Li, Daniel B. Reeves, M. Gordon Joyce, Paul T. Scott, Mihret F. Amare, Sandhya Vasani, Nelson L. Michael, Kayvon Modjarrad & Morgane Rolland

Significance: The rapid spread of the virus causing COVID-19, SARS-CoV-2, raises questions about the possibility of a universally effective vaccine. The virus can mutate in a given individual, and these variants can be propagated across populations and time. To understand this process, we analyze 18,514 SARS-CoV-2 sequences sampled since December 2019. We find that neutral evolution, rather than adaptive selection, can explain the rare mutations seen across SARS-CoV-2 genomes. In the immunogenic Spike protein, the D614G mutation has become consensus, yet there is no evidence of mutations affecting binding to the ACE2 receptor. Our results suggest that, to date, the limited diversity seen in SARS-CoV-2 should not preclude a single vaccine from providing global protection.

WATSON 2020

Clare Watson, *Stillbirth Rate Rises During Coronavirus Pandemic*. [nature](#) **585** (2020), 490–491. .

Emerging data link disrupted antenatal services to a rise in pregnancy complications in several countries.

Anthropologie

BÖHME 2019

Madelaine Böhme, *Wie wir Menschen wurden, Eine kriminalistische Spurensuche nach den Ursprüngen der Menschheit – Spektakuläre Funde*. (München 2019).

PETR 2020

Martin Petr & Janet Kelso et al., *The evolutionary history of Neanderthal and Denisovan Y chromosomes*. [science](#) **369** (2020), 1653–1656. [s369-1653-Supplement.pdf](#)

Ancient DNA has provided new insights into many aspects of human history. However, we lack comprehensive studies of the Y chromosomes of Denisovans and Neanderthals because the majority of specimens that have been sequenced to sufficient coverage are female. Sequencing Y chromosomes from two Denisovans and three Neanderthals shows that the Y chromosomes of Denisovans split around 700 thousand years ago from a lineage shared by Neanderthals and modern human Y chromosomes, which diverged from each other around 370 thousand years ago.

The phylogenetic relationships of archaic and modern human Y chromosomes differ from the population relationships inferred from the autosomal genomes and mirror mitochondrial DNA phylogenies, indicating replacement of both the mitochondrial and Y chromosomal gene pools in late Neanderthals. This replacement is plausible if the low effective population size of Neanderthals resulted in an increased genetic load in Neanderthals relative to modern humans.

Martin Petr, Mateja Hajdinjak, Qiaomei Fu, Elena Essel, H el ene Rougier, Isabelle Crevecoeur, Patrick Semal, Liubov V. Golovanova, Vladimir B. Doronichev, Carles Lalueza-Fox, Marco de la Rasilla, Antonio Rosas, Michael V. Shunkov, Maxim B. Kozlikin, Anatoli P. Derevianko, Benjamin Vernot, Matthias Meyer & Janet Kelso

RUTHERFORD 2017

Adam Rutherford, *A brief history of everyone who ever lived, The stories in our genes.* (London 2017).

SCHIERUP 2020

Mikkel Heide Schierup, *The last pieces of a puzzling early meeting.* [science](#) **369** (2020), 1565–1566.

Y chromosomes transferred from Homo sapiens to Neanderthals between 350,000 to 150,000 years ago.

A rapid and total replacement of both the Y chromosome and mitochondrion seems too much of a coincidence to be driven by chance alone, especially given the relatively small contribution of H. sapiens to the Neanderthal nuclear genome. Some form of natural selection must have contributed. It is as yet anyone’s guess what the selective agent might have been. Because both the Y chromosome and mitochondrion are inherited as nonrecombining units, it is exceedingly difficult to locate targets of natural selection on them.

WOOD 2020

Bernard A. Wood & David B. Patterson, *Paranthropus through the looking glass.* [PNAS](#) **117** (2020), 23202–23204.

We do not know what the temporal and geographic ranges of an extinct hominin taxon like P. boisei were. Its presence at a fossil site is evidence that it was living at that time and in that place, but we should not assume that existing site samples circumscribe the temporal or geographic range of a taxon. Each site is like a window that gives us access to what is going on in just one room within a large house, but it is likely that important events in the evolutionary history of a taxon took place in presently windowless rooms.

Datierung

CHENG 2020

Hai Cheng et al., *Timing and structure of the Younger Dryas event and its underlying climate dynamics.* [PNAS](#) **117** (2020), 23408–23417.

[pnas117-23408-Supplement0.pdf](#), [pnas117-23408-Supplement1.xlsx](#), [pnas117-23408-Supplement2.xlsx](#)

The Younger Dryas (YD), arguably the most widely studied millennial-scale extreme climate event, was characterized by diverse hydroclimate shifts globally and severe cooling at high northern latitudes that abruptly punctuated the warming trend from the last glacial to the present interglacial. To date, a precise understanding of its trigger, propagation, and termination remains elusive.

Here, we present speleothem oxygen-isotope data that, in concert with other proxy records, allow us to quantify the timing of the YD onset and termination at an unprecedented subcentennial temporal precision across the North Atlantic, Asian Monsoon-Westerlies, and South American Monsoon regions. Our analysis suggests that the onsets of YD in the North Atlantic (12,870 \pm 30 B.P.) and the Asian Monsoon-Westerlies region are essentially synchronous within a few decades and lead the onset in Antarctica, implying a north-to-south climate signal propagation via both atmospheric (decadal-time scale) and oceanic (centennial-time scale) processes, similar to the Dansgaard–Oeschger events during the last glacial period. In contrast, the YD termination may have started first in Antarctica at \approx 11,900 B.P., or perhaps even earlier in the western tropical Pacific, followed by the North Atlantic between \approx 11,700 \pm 40 and 11,610 \pm 40 B.P. These observations suggest that the initial YD termination might have originated in the Southern Hemisphere and/or the tropical Pacific, indicating a Southern Hemisphere/tropics to North Atlantic–Asian Monsoon-Westerlies directionality of climatic recovery.

Keywords: Younger Dryas | timing | structure | event phasing | climate dynamics

Hai Cheng, Haiwei Zhang, Christoph Spötl, Jonathan Baker, Ashish Sinha, Hanying Li, Miguel Bartolome, Ana Moreno, Gayatri Kathayat, Jingyao Zhao, Xiyu Dong, Youwei Li, Youfeng Ning, Xue Jia, Baoyun Zong, Yassine Ait Brahim, Carlos Prez-Mejias, Yanjun Cai, Valdir F. Novello, Francisco W. Cruz, Jeffrey P. Severinghaus, Zhisheng An & R. Lawrence Edwards

Significance: The Younger Dryas (YD) was an \approx 1,300-y period of extreme climate that dramatically reversed the course of global warming that brought the last Ice Age to a close. Understanding what mechanisms triggered and terminated this event remains enigmatic, but it is fundamental for gaining insights into the inner workings of Earth’s climate system. In this study, we used a combination of well-dated speleothem and ice-core records to pinpoint the timing of its onsets and terminations in various climatic regimes around the world. We show that the YD event occurred first at high northern latitudes and then propagated southward into the tropical monsoon belt through both atmospheric and oceanic processes, ultimately reaching Antarctica before reversing the course to its eventual termination.

WENINGER 2020

Bernhard Weninger & Kevan Edinborough, *Bayesian ^{14}C -Rationality, Heisenberg Uncertainty, and Fourier Transform, The Beauty of Radiocarbon Calibration*. *Documenta Praehistorica* (2020), preprint, 1–38.

Following some 30 years of radiocarbon research during which the mathematical principles of ^{14}C -calibration have been on loan to Bayesian statistics, here they are returned to Quantum physics. The return home is based on recognition that ^{14}C -calibration can be described as Fourier Transform. Following its introduction as Fourier Transform, there is need to reconceptualise the probabilistic ^{14}C -analysis. The main change will be to replace the traditional (one dimensional) concept of ^{14}C -dating probability by a two-dimensional probability. This is entirely analogous to the definition of probability in Quantum physics, where the squared amplitude of a wave function defined in Hilbert space provides a measurable probability of finding the corresponding particle at a certain point in time/space, the so-called Born rule. When adapted to the characteristics of ^{14}C -calibration, as it turns out, the Fourier Transform immediately accounts for practically all known so-called quantization properties of archaeological ^{14}C -ages, such as clustering, age-shifting, and amplitude-distortion. This also applies to the frequently observed chronological lock-in properties of larger data sets, when analysed by Gaussian wiggle matching (on the ^{14}C -scale) just as by Bayesian sequencing (on the calendar time-

scale). Such domain-switching effects are typical for a Fourier Transform. They can now be understood, and taken into account, by application of concepts and interpretations that are central to Quantum physics (e.g. Wave diffraction, Wave-Particle Duality, Heisenberg Uncertainty, Correspondence Principle). What may sound complicated, at first glance, simplifies the construction of 14C-based chronologies. The new Fourier-based 14C-analysis supports chronological studies on previously unachievable geographic (continental) and temporal (Glacial-Holocene) scales, for example, by temporal sequencing of hundreds of archaeological sites, simultaneously, with minimal need for development of archaeological prior hypotheses, other than those based on the geo-archaeological Law of Stratigraphic Superposition. As demonstrated in a variety of archaeological case studies, just one number, defined as a gauge-probability on a scale 0–100 %, can be used to replace a stacked set of subjective Bayesian priors.

Keywords: Radiocarbon Calibration | Fourier Transform | Born Probability | Santorini

Klima

GARBE 2020

Julius Garbe, Torsten Albrecht, Anders Levermann, Jonathan F. Donges & Ricarda Winkelmann, *The hysteresis of the Antarctic Ice Sheet*. [nature 585 \(2020\), 538–544](#).

n585-0538-Supplement1.mp4, n585-0538-Supplement2.mp4

More than half of Earth’s freshwater resources are held by the Antarctic Ice Sheet, which thus represents by far the largest potential source for global sea-level rise under future warming conditions¹. Its long-term stability determines the fate of our coastal cities and cultural heritage. Feedbacks between ice, atmosphere, ocean, and the solid Earth give rise to potential nonlinearities in its response to temperature changes. So far, we are lacking a comprehensive stability analysis of the Antarctic Ice Sheet for different amounts of global warming. Here we show that the Antarctic Ice Sheet exhibits a multitude of temperature thresholds beyond which ice loss is irreversible. Consistent with palaeodata² we find, using the Parallel Ice Sheet Model^{3–5}, that at global warming levels around 2 degrees Celsius above pre-industrial levels, West Antarctica is committed to long-term partial collapse owing to the marine ice-sheet instability. Between 6 and 9 degrees of warming above pre-industrial levels, the loss of more than 70 per cent of the present-day ice volume is triggered, mainly caused by the surface elevation feedback. At more than 10 degrees of warming above pre-industrial levels, Antarctica is committed to become virtually ice-free. The ice sheet’s temperature sensitivity is 1.3 metres of sea-level equivalent per degree of warming up to 2 degrees above pre-industrial levels, almost doubling to 2.4 metres per degree of warming between 2 and 6 degrees and increasing to about 10 metres per degree of warming between 6 and 9 degrees. Each of these thresholds gives rise to hysteresis behaviour: that is, the currently observed ice-sheet configuration is not regained even if temperatures are reversed to present-day levels. In particular, the West Antarctic Ice Sheet does not regrow to its modern extent until temperatures are at least one degree Celsius lower than pre-industrial levels. Our results show that if the Paris Agreement is not met, Antarctica’s long-term sea-level contribution will dramatically increase and exceed that of all other sources.

SADAI 2020

Shaina Sadai, Alan Condron, Robert DeConto & David Pollard, *Future climate response to Antarctic Ice Sheet melt caused by*

anthropogenic warming. *Science Advances* **6** (2020), eaaz1169.
[DOI:10.1126/sciadv.aaz1169](https://doi.org/10.1126/sciadv.aaz1169).

[SciAdv06-eaaz1169-Supplement.pdf](#)

Meltwater and ice discharge from a retreating Antarctic Ice Sheet could have important impacts on future global climate. Here, we report on multi-century (present–2250) climate simulations performed using a coupled numerical model integrated under future greenhouse-gas emission scenarios IPCC RCP4.5 and RCP8.5, with meltwater and ice discharge provided by a dynamic-thermodynamic ice sheet model. Accounting for Antarctic discharge raises subsurface ocean temperatures by $>1^{\circ}\text{C}$ at the ice margin relative to simulations ignoring discharge. In contrast, expanded sea ice and 2° to 10°C cooler surface air and surface ocean temperatures in the Southern Ocean delay the increase of projected global mean anthropogenic warming through 2250. In addition, the projected loss of Arctic winter sea ice and weakening of the Atlantic Meridional Overturning Circulation are delayed by several decades. Our results demonstrate a need to accurately account for meltwater input from ice sheets in order to make confident climate predictions.

Religion

RENNIE 2015

Bryan Rennie, *Religion and Art Behavior—A Theory and an Example, The Biblical Prophets as Postcolonial Street Theater*. *Journal for the Study of Religion, Nature and Culture* **9** (2015), 312–334.

Enough has been written on the cognitive and evolutionary bases of both art and religion to permit a theoretical understanding of these closely related behaviors. My argument is that religion and art are descendants of a common ancestral behavior that cannot be identified as either one or the other but has identifying features of both. It is my contention that such an understanding facilitates an improved comprehension of the history of religion as well as a coherent theoretical explanation of religious pluralism. As an example of the application and implication of this theory I will undertake a brief analysis of Biblical Prophecy as a complex of art forms bearing significant similarities to contemporary postcolonial literature and street theater. Both complexes communicate individual emotional responses to the environment that are transmitted and retained in the local culture and contribute to assured and persistent behavior.

Keywords: Cognition | evolution | art | religion | divination | prophecy | street theater.

Story or Book

STAIRS 2020

Allen Stairs, *Understanding quantum cause and effect*. *science* **369** (2020), 1573.

Correlations at a distance needn't necessarily be “spooky”.

Synchronicity. Paul Halpern. Basic Books, 2020. 304 pp.

More generally, instead of looking for an explanation for quantum entanglement, we might consider it part of our basic explanatory machinery. Quantum states fit together in Hilbert space, an elegant abstraction from ordinary physical space that Halpern describes fancifully as akin to “a kind of network of utility corridors behind the scenes of an active office building.” If each of two particles is represented

by a Hilbert space, the only way to build a Hilbert space for the pair guarantees the existence of entangled states, with their attendant unorthodox statistical predictions. So-called spooky correlations could exist in such a scenario without causal mechanisms.