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References

Aktuell

Beauchamp 2016

Jonathan P. Beauchamp, *Genetic evidence for natural selection in humans in the contemporary United States.* PNAS **113** (2016), 7774–7779.

Recent findings from molecular genetics now make it possible to test directly for natural selection by analyzing whether genetic variants associated with various phenotypes have been under selection. I leverage these findings to construct polygenic scores that use individuals' genotypes to predict their body mass index, educational attainment (EA), glucose concentration, height, schizophrenia, total cholesterol, and (in females) age at menarche. I then examine associations between these scores and fitness to test whether natural selection has been occurring. My study sample includes individuals of European ancestry born between 1931 and 1953 who participated in the Health and Retirement Study, a representative study of the US population. My results imply that natural selection has been slowly favoring lower EA in both females and males, and are suggestive that natural selection may have favored a higher age at menarche in females. For EA, my estimates imply a rate of selection of about -1.5 mo of education per generation (which pales in comparisonwith the increases in EA observed in contemporary times). Although they cannot be projected over more than one generation, my results provide additional evidence that humans are still evolving—albeit slowly, especially compared with the rapid changes that have occurred over the past few generations due to cultural and environmental factors.

Keywords: natural selection | human evolution | educational attainment | menarche | polygenic scores

Significance: I leverage recent advances in molecular genetics to test directly whether genetic variants associated with a number of phenotypes have been under natural selection in the contemporary United States. My finding that natural selection has been slowly occurring for genetic variants associated with educational attainment and (suggestively, in females) for variants associated with age at menarche provides additional evidence that humans are still evolving—albeit slowly and at a rate that cannot account for more than a small fraction of the large changes that have occurred over the past few generations.

Courtiol 2016

Alexandre Courtiol, Felix C. Tropf & Melinda C. Mills, *When genes and environment disagree, Making sense of trends in recent human evolution.* PNAS **113** (2016), 7693–7695.

The studies by Beauchamp (1) and Conley et al. (9) mark a milestone in our understanding of human evolution and natural selection in contemporary populations. These authors fill the gap between SNP-based studies reporting natural selection acting in the past and phenotypic studies suggesting it is acting now. Because natural selection occurs on phenotypes that have a genetic basis, phenotypic studies suggest that natural selection should still be acting at the genetic level in contemporary populations (3). Despite limitations, Beauchamp (1) and Conley et al. (9) provide unambiguous evidence in support of this hypothesis.

Eklund 2016

Anders Eklund, Thomas E. Nichols & Hans Knutsson, *Cluster failure, Why fMRI inferences for spatial extent have inflated false-positive rates*. PNAS **113** (2016), 7900–7905.

The most widely used task functional magnetic resonance imaging (fMRI) analyses use parametric statistical methods that depend on a variety of assumptions. In this work, we use real resting-state data and a total of 3 million random task group analyses to compute empirical familywise error rates for the fMRI software packages SPM, FSL, and AFNI, as well as a nonparametric permutation method. For a nominal familywise error rate of 5 %, the parametric statistical methods are shown to be conservative for voxelwise inference and invalid for clusterwise inference. Our results suggest that the principal cause of the invalid cluster inferences is spatial autocorrelation functions that do not follow the assumed Gaussian shape. By comparison, the nonparametric permutation test is found to produce nominal results for voxelwise as well as clusterwise inference. These findings speak to the need of validating the statistical methods being used in the field of neuroimaging.

Keywords: fMRI | statistics | false positives | cluster inference | permutation test

Significance: Functional MRI (fMRI) is 25 years old, yet surprisingly its most common statistical methods have not been validated using real data. Here, we used resting-state fMRI data from 499 healthy controls to conduct 3 million task group analyses. Using this null data with different experimental designs, we estimate the incidence of significant results. In theory, we should find 5 % false positives (for a significance threshold of 5 %), but instead we found that the most common software packages for fMRI analysis (SPM, FSL, AFNI) can result in false-positive rates of up to 70 %. These results question the validity of some 40,000 fMRI studies and may have a large impact on the interpretation of neuroimaging results.

Iyengar 2016

Satish Iyengar, *Case for fMRI data repositories*. PNAS **113** (2016), 7699–7700.

The motivation in the study by Eklund et al. (5) comes from their earlier work (14), in which they used SPM software on 1,484 resting states for task-based, single-subject fMRI analyses, and found that the falsepositive rates were as high as 70 % rather than the expected 5 %. To understand the sources of the higher error rates, they expanded their scope by including the three most common software packages, SPM, FSL, and AFNI, generally using each package's default settings. They used resting state fMRI data from 499 healthy controls from three sites obtained from the 1000 Functional Connectomes Project. They then mimicked several activity paradigms, and used one-sample and two-sample t tests, controlling for the FWE rates for both voxel-wise and cluster-wise inference.

Anthropologie

Qiu 2016

Jane Qiu, *The Forgotten Continent*. nature **535** (2016), 218–220.

Fossil finds in China are challenging ideas about the evolution of modern humans and our closest relatives.

Another possibility is that some of the Chinese fossils, including the Dali skull, represent the mysterious Denisovans, a species identified from Siberian fossils that are more than 40,000 years old. Palaeontologists don't know what the Denisovans looked like, but studies of DNA recovered from their teeth and bones indicate that this ancient population contributed to the genomes of modern humans, especially

Australian Aborigines, Papua New Guineans and Polynesians — suggesting that Denisovans might have roamed Asia.

María Martinón-Torres, a palaeoanthropologist at University College London, is among those who proposed that some of the Chinese making a push in that direction. Qiaomei Fu, a palaeogeneticist who did her PhD with Paabo, returned home last year to establish a lab to extract and sequence ancient DNA at the IVPP. One of her immediate goals is to see whether some of the Chinese fossils belong to the mysterious Denisovan group. The prominent molar teeth from Xujiayao will be an early target. “I think we have a prime suspect here,” she says.

But all agree that Asia — the largest continent on Earth — has a lot more to offer in terms of unravelling the human story. “The centre of gravity,” says Petraglia, “is shifting eastward.

Bibel

Knohl 2009

Israel Knohl, *The Dark Side of Isaiah’s Prophecy.* In: Nili Sacher Fox, David A. Glatt-Gilad & Michael J. Williams (Hrsg.), *Mishneh Todah, Studies in Deuteronomy and Its Cultural Environment in Honor of Jeffrey H. Tigay.* (Winona Lake 2009), 1-26.

We perforce must accept the vision in its simple meaning: Isaiah began his prophesying with a vision in which he is appointed by God to block the path of repentance for the people. He thereby aids God in bringing a holocaust upon the people, a cataclysm that shall annihilate the people almost in their entirety. This vision was not preceded by any chastisement or call for repentance by the prophet. Since this vision was not preceded by reproach and a call for repentance, it cannot be given a rational and moral explanation. Even if the people had sinned, the rules of justice and morality would require God to first admonish the people and allow them to repent before decreeing such a horrendous punishment for them. The vision, in its entirely, is in the sphere of the holy and the numinous, beyond reason and morality.

The burning fire is the outstanding symbol of this sanctity, and as Weiss explains, the seraphim represent the all-consuming divine fire. It is in this fire, that is embodied in the burning alter coal, that the prophet’s lips are refined and cleansed; and it is this terrible blaze that shall burn and consume the major part of the people.

Knohl 2016

Israel Knohl, *The Original Version of the Priestly Creation Account and the Religious Significance of the Number Eight in the Bible.* unknown (2016), preprint, 1–28.

In my view, the original version of the Priestly account of creation (Gen 1:1–2:4a), was based on the number eight. However, later editors from the “Holiness School” changed the text to reflect the more popular sanctity of the number seven, with the Sabbath day as the culmination of the story. However, the esoteric sanctity of eight did not disappear, but continued to be transmitted within some biblical circles.

Thus, the original version of the Priestly account of creation was a very sophisticated example of sacred architecture. The numerical symbolism collapsed in the wake of the redactional process of the H editors, which stands behind the present version. The editors were not interested in the numbers 52, 26, 17 and 8, which are all connected to the Tetragrammaton. They cared only for the number 7 and the numbers derived from it (7 x 7 = 49).

However, we might raise the possibility that the eight-day framework was chosen in order to express gratitude to God, whose most sacred name, YHWH, is represented by the “base number,” eight.

Klima

Gronenborn 2012

Detlef Gronenborn, *Das Ende von IRD 5b, Abrupte Klimafluktuationen um 5100 denBC und der Übergang vom Alt- zum Mittelneolithikum im westlichen Mitteleuropa.* In: Regina Smolnik (Hrsg.), *Ausgrabungen Siedlungsstruktur und Kulturwandel in der Bandkeramik, Beiträge der int. Tagung “Neue Fragen zur Bandkeramik oder alles beim Alten?!” Leipzig 23. bis 24. September 2010.* Arbeits- und Forschungsberichte zur sächsischen Bodendenkmalpflege, Beiheft 25 (Dresden 2012), 241–250.

During the Holocene, climate cycles partly originating from the North Atlantic have an influence on north-western Eurasia: ice rafting detritus events (IRD) and fresh water spells from the shrinking Laurentidian ice shield affect the thermohaline circulation and with it the climatic effects of the North Atlantic on Europe. These cycles are connected to shifting solar activity patterns which can be fixed chronologically through the 14C-production curve. Notably the shifts from an active to a calm sun and vice versa seem to have been dominated by strong climatic anomalies. One such period is the end of IRD 5b around 5100 den BC. This period is contemporaneous with the termination of the LBK. However, a high-resolution comparison between archaeological chronologies and palaeoclimatic age-models shows that simplistic climate determinism is inappropriate. Only with the application of the ecology-based adaptive cycle model does the complex interrelation between climate fluctuations and culture change become comprehensible.

Methoden

Morgan 2013

Johanna Morgan, *The Invisible Hunger, Is Famine Identifiable from the Archaeological Record?* Antrocom **9** (2013), 115–129.

Famine, as defined by an acute (short-term) or chronic (long-term or cyclical) period of starvation, is identifiable in the historical period from written records and potentially with archaeological corroboration, but in prehistory other approaches must be employed. Several of these are discussed including studies of diet and nutrition, paleodemography, environmental catalysts, and funerary ritual. Despite a multifactorial analysis integrating palynology, dendrochronology, stable isotope analyses, osteoarchaeology, and social archaeology, difficulties in contemporizing paleodemographic events them with osteological assemblages are substantial enough that the detection of a famine is not possible solely from the archaeological record. More significant is the conclusion that all apparent indicators for acute or chronic starvation are also representative of epidemic disease. Because of this uncertainty, it is not possible to identify famine in prehistory.

Keywords: palaeodiet | prehistory | bioarchaeology | palaeodemography | palaeopathology