Journal of Archaeological Science 52 (2014) 549–557

Contents lists available at ScienceDirect

Journal of Archaeological Science

journal homepage: http://www.elsevier.com/locate/jas

Reconstructing regional population fluctuations in the European Neolithic using radiocarbon dates: a new case-study using an improved method

Adrian Timpson [a, b, *], Sue Colledge [a], Enrico Crema [a], Kevan Edinborough [a], Tim Kerig [c], Katie Manning [a], Mark G. Thomas [b], Stephen Shennan [a]

[a] *Institute of Archaeology, University College London, 31-34 Gordon Square, London WC1H 0PY, UK*
[b] *Research Department of Genetics, Evolution and Environment, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK*
[c] *Archäologisches Institut, Albertus-Magnus-Platz, University of Cologne, D-50923 Köln, Germany*

ARTICLE INFO

Article history:
Available online 2 September 2014

Keywords:
Neolithic
Radiocarbon
Demography
Simulation
Europe
Monte Carlo
SPD
Summed probability distribution

ABSTRACT

In a previous study we presented a new method that used summed probability distributions (SPD) of radiocarbon dates as a proxy for population levels, and Monte-Carlo simulation to test the significance of the observed fluctuations in the context of uncertainty in the calibration curve and archaeological sampling. The method allowed us to identify periods of significant short-term population change, caveated with the fact that around 5% of these periods were false positives. In this study we present an improvement to the method by applying a criterion to remove these false positives from both the simulated and observed distributions, resulting in a substantial improvement to both its sensitivity and specificity. We also demonstrate that the method is extremely robust in the face of small sample sizes. Finally we apply this improved method to radiocarbon datasets from 12 European regions, covering the period 8000–4000 BP. As in our previous study, the results reveal a boom-bust pattern for most regions, with population levels rising rapidly after the local arrival of farming, followed by a crash to levels much lower than the peak. The prevalence of this phenomenon, combined with the dissimilarity and lack of synchronicity in the general shapes of the regional SPDs, supports the hypothesis of endogenous causes.

© 2014 The Authors. Published by Elsevier Ltd. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/3.0/).

1. Introduction

Population size and density are key variables in human evolution. They represent important outcomes of evolutionary adaptation, and have strong feedback relationships with key processes such as: the transmission, selection and drift of both genetic and cultural information; infectious disease dynamics; land and resource use; niche construction; economic cycles and sustainability. To understand human evolution it is therefore necessary to estimate regional population fluctuations, and to identify their causes and consequences. Major advances are now being made in this field due to the growing availability of modern and ancient genetic data and associated modelling approaches (e.g. Li and Durbin, 2011). However, estimates of population size from these data generally lack adequate chronological and/or spatial resolution, or the data are too few in number, to draw meaningful inferences about their relationship with these key processes.

Directly dated archaeological site information does not suffer from these problems but, with some recent exceptions (e.g. Bocquet-Appel (2002) using cemetery age distributions, Zimmermann et al. (2004) using site spatial distributions, and Hinz et al. (2012) using summed radiocarbon probabilities), archaeologists, in Europe at least, have been strikingly reluctant to make demographic inferences from such data, and are generally keener to emphasise the pitfalls than the possibilities. When Rick (1987) proposed using summed date distributions as data for the purpose of reconstructing spatial-temporal variation in coastal-highland settlement practices during the Peruvian preceramic period, an important new weapon was added to the archaeologist's armoury. In his inferential chain, Rick laid out three main assumptions that underpin this approach; firstly that more dateable objects will be deposited during periods when the population was

---

* Corresponding author. Research Department of Genetics, Evolution and Environment, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel.: +44 2076794397.

E-mail address: a.timpson@ucl.ac.uk (A. Timpson).

http://dx.doi.org/10.1016/j.jas.2014.08.011

0305-4403/© 2014 The Authors. Published by Elsevier Ltd. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/3.0/).

larger, secondly that more deposits will lead to more objects preserved in the archaeological record, and thirdly that more preserved objects will lead to more dateable material eventually recovered by archaeologists. Joining these together gives us the assumption of a monotonic relationship between the population size and the amount of radiocarbon dates recovered (Collard et al. 2010). Therefore a suitable radiocarbon database can be used to construct a time-series by summing each date's probability distribution, and the fluctuations in this time-series can then be used as a proxy for changing population size.

Of course the extent to which these assumptions are satisfied can be difficult to determine. The law of large numbers predicts that larger sample sizes should more fairly represent the archaeological record, but this may already be a taphonomically biased representation of the original deposits. Some control can be achieved by using radiocarbon dates from a confined spatial region, small enough for taphonomic losses to be considered spatially homogenous. However, this necessarily reduces sample sizes, and so a balance must be found. Even in this simple case, where the analysis deals only with a local pattern, we can expect constant homogenous taphonomic losses to manifest as a gradual loss over time in the archaeological record, and therefore a long-term exponential increase in the summed distribution.

Whilst the utility of this approach is reflected in its increasing application, the biases and assumptions noted in Rick's chain of inference have also been subject to increasing critical scrutiny (Rick, 1987 Fig. 1; Surovell et al. 2009; Williams, 2012; Bamforth and Grund, 2012). Three major issues that persist are; the impact of sample size, fluctuations in the radiocarbon calibration curve – which have the effect of concentrating dates in some time periods and spreading them out across others – and the effect of differential taphonomic and archaeological recovery processes on what is available for dating.

In our previous study (Shennan et al. 2013) we have shown that many of the problems and biases raised by the standard approach of summing radiocarbon dates can be resolved. Despite this, criticisms persist; most recently for example, Contreras and Meadows (2014) again raise these concerns. The authors simulate a radiocarbon dataset by sampling from a prior 'assumed true' population curve (using Bennett's population reconstruction of the European Black Death AD 1000–1700, and McCaa's population reconstruction of Central Mexico AD 1000–1800), and then comment on the dissimilarity between the sampled summed probability distribution and the 'true' population curve from which it was sampled. In principle this is a sensible approach, which should be expected to demonstrate good congruence as the sample size increases; however the authors argue the contrary, that there is poor congruence, and conclude the method is unreliable.

There is a simple explanation for this. Because of the interference effect of wiggles in the calibration curve, spurious fluctuations exist on a scale below c.200 years, rendering this method quite useless for any time-series shorter than a few thousand years. This is simply a matter of analysing at the appropriate scale – the effect of these wiggles is invisible and irrelevant at the scale of tens of thousand years. As with our previous study, we apply this method to dates spanning several thousand years, before trimming the summed distribution down to a 4000 year period of interest, to avoid edge effects. Furthermore we plot a 200 year rolling mean, to discourage the reader from over-interpreting smaller scale features. In contrast, Contreras and Meadows invoke a straw man by simulating dates over the inappropriately short time ranges of 700 years and 800 years, so that the shape of their distribution is dominated by these spurious short-term wiggles. They obfuscate matters further by plotting the simulated distribution over a wider 1200 year range, so as to include yet more spurious edge effects outside the range covered by the sampled data.

Shennan et al. (2013) also showed that a more comprehensive Monte-Carlo simulation-based method, which generates simulated date distributions under a fitted null model, can be used to test features in the observed dataset for statistically significant patterns. The results of this Monte-Carlo Summed Probability Distribution method (MCSPD-method) can be supplemented by comparing the radiocarbon population proxy with other proxies, based on independent evidence and different assumptions. Thus, Woodbridge et al. (in press) compared this population proxy for Britain with independent evidence for forest clearance, based on pollen analysis, which serves as an indicator of human environmental impact and hence population size, and found a strong correlation: peaks in the summed date distribution correspond to more open environments and troughs to more extensive forest cover. Other studies of the European Neolithic have produced the same result (see Hinz et al. 2012; Whitehouse et al. in press; Lechterbeck et al. in press).

Shennan et al. (2013) addressed the question of whether the arrival of farming in the different regions of Europe was associated with a significant departure from a fitted null-model of long-term exponential growth that characterises both global population history (e.g. McEvedy and Jones, 1978) and the increased survival of the archaeological record towards the present. Results for the majority of the European regions showed significant departures from this null model, and indicate that boom and bust fluctuations followed the arrival of farming. The occurrence of population booms – periods of rapid population growth – associated with the local arrival of farming was unsurprising, on the basis of both theory (Ammerman and Cavalli-Sforza, 1971) and inferences of increased growth rates derived from cemetery age-at-death distributions (Bocquet-Appel, 2002). However, the consistent evidence for population 'busts' contradicts standard views about the long-term impact of agriculture on population levels. Furthermore, cross-correlation of the population fluctuations with climate data did not support the hypothesis that the fluctuations were climate-driven.

This paper pursues a similar agenda by examining dates from another twelve European regions (see map Fig. 1, and Appendix 2 for date sources) to see if they continue to support the boom-bust pattern, but does so by means of an improvement to the existing MCSPD-method that was presented in Shennan et al. (2013). We provide a detailed description of the improved method, and demonstrate its power using one of the twelve regions as a test set, by progressively sampling smaller and smaller training datasets and comparing the results. Finally, we examine the population reconstructions for the twelve regions and discuss their implications.

2. Data

As with our previous study, radiocarbon dates for each study area were selected from the EUROEVOL project database. Once again we used a fully inclusive approach on the basis that inaccurate dates would obscure any genuine underlying patterns, thus having a conservative effect, and that the larger the sample, the closer it will approximate the true distribution (see Shennan et al. 2013 for details).

3. Improvement to computational method

By definition, approximately 5% of any SPD (constructed from observed data or simulated data) will be falsely considered unusually high/low density by the existing method, and reported as locally significant (highlighted in red/blue respectively in the figures below). This is because 5% of any random data falls outside its 95% confidence interval, and can be loosely considered as 'false positive'

Download English Version:

https://daneshyari.com/en/article/7442819

Download Persian Version:

https://daneshyari.com/article/7442819

Daneshyari.com