RECENT ADVANCES IN PALAEODEMOGRAPHY

Recent Advances in Palaeodemography

Data, Techniques, Patterns

edited by

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Recent Advances in Palaeodemography: Data, Techniques, Patterns

Written demographic records mainly cover the last few centuries. Since the emergence in Africa of *Homo ergaster*, our direct human ancestor, and its expansion through Eurasia around 1.8 million years ago until few centuries ago, there are no written records to reconstruct human demographic history in a form that can be interpreted using the conventional tools of demography. However, to be tested with any validity, the main demographic theories from Malthus to Boserup (and combinations) require knowledge of long-term or even very long-term trends. Therefore, sources of information other than written records need to be used, as well as techniques other than standard demographic methods. The information provided by archaeological research and archaeological models of interpretation therefore provides essential input. The intention of this book is to cover three broad topics, some of which were discussed during the 2005 international population conference:

- Palaeodemographic data, represented by the space-time distribution of archaeological remains (sites, 14C dates, urban) and of skeletons by age from burial sites;
- Techniques of demographic inference from the distributions and densities of palaeodemographic data, and methods to derive estimates of demographic parameters.
- Detection of demographic signals in archaeological data, such as those indicating the approaching limits of carrying capacity during the Middle Palaeolithic, or a major demographic change, like the Neolithic demographic transition on a worldwide scale.

INTRODUCTION

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The written data used by demographers essentially cover the last five centuries. Since *Homo ergaster* moved out of Africa around 1.8 million years ago and until the sub-contemporary periods, there is no data allowing us to reconstruct a demographic history that can be interpreted with the traditional tools of demography. If we want to be able to tackle demographic issues over a long evolutionary duration, trying to reconstitute our human demographic history and thinking out and testing macro-demographic theories, we need to draw on sources other than written data and on techniques other than those commonly used by demographers. This necessarily means using information of every kind, from archaeology, physical anthropology, paleontology, primatology or genetics, along with relevant models of interpretation.

The volume presented here has been developed from a core of papers selected for the paleodemographic session of the 25th World Population Congress (July 2005, Tours, France), to which further requested contributions have been added. The publication covers recent paleodemographic innovations, in terms of data, techniques and the detection of patterns making it possible to highlight hitherto unknown prehistoric demographic processes. Now that the anxiety over ways of defusing the population "time bomb", which mobilized mainstream demographic thinking as from the 1960s (see, for authority, Bogue and Tsui 1979; Demeny 1979) has largely been dissipated, the focus has shifted to other important issues.

Looking back in time, there is the issue of the long duration of the human metapopulation's demographic past, such as the planetary colonization scenario or the demographic transitions that were experienced over two million years. Looking forward, we have the issue of the future of an age pyramid in which, after the current accelerating decline in fertility and

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possibly even its collapse, we will see hundreds of millions of old people having to provide for themselves without any pension funds and almost without any children, in the former Third World countries which had always been the world's reservoir of young people. Now that the demography of the human metapopulation has become an object of scientific study, shedding its burden of demographic policy contingencies, the place of paleodemography within the IUSSP, which was episodic before its 24th Congress (Salvador, Brazil, 2001; see also the 1969 Congress in London, with JN Biraben, L Henry and J Nemeskeri), is tending to become permanently established. In the interests, perhaps, of seeking a dialogue with demographers, the papers given at the Congress mainly gave demographic narratives on archaeological data, rather than addressing methodological or technical questions, despite the well-known fact that there is no consensus over even basic paleodemographic techniques. The volume's subtitle, "Data, Techniques and Patterns", reflects a necessarily loose subdivision among chapters, since so many of these items are embedded in one another.

In the first part, we look into two radically different categories of data: genetic data, with a critical re-reading of their interpretation models in demographic terms, and space-time distributions of archaeological remains, as reconstituted from systematic field surveys. The first data concern periods of humanity going back several hundreds of thousands of years to the Pleistocene. The second category concerns ancient Greece. The very different nature of these data is almost a caricature of the inevitable eclecticism of paleodemographic information. There is no such thing as a version of human demographic history written for genetic or archaeological semiotics. What does exist is simply the demographic history that we try to reconstruct from the mists of the past, using whatever comes to hand and, whenever possible, comparing the results. Because we are setting end to end the chronological periods with which various categories of data are coupled, we have to get used to the juxtaposition of eclectic data. It is important to remember that one of main goals of demography is simply the enumeration of human beings, otherwise known as the "census population size". The census population size does not mean exactly the same thing to an economist, a historian or an evolutionary biologist. But it is generally agreed that the overall interpretation of the size of a census population is a measurement of success – of an economic system, a society or an adaptation.

For a long time now, the genetic variation of a population has provided us with an estimator of this number, via the so-called "effective population size" (Wright, 1931). For the Pleistocene, the literature on genetic anthropology usually gives a number of 10,000 individuals, while carefully written demographic literature (see Hawks below) usually gives 300,000. Why such a large discrepancy – of 1:30 – between these estimates? In chapter 1, John Hawks questions this discrepancy. Contrary to an insistent suggestion, he reminds us that genetic data are not, in themselves, demography. They need to be interpreted via a model, that of Wright-Fisher. In reality, there are any number of conditions of deviation from the model. Hawks reviews many of them and concludes, pessimistically, that the link between human genetic variation during the past million years and "*the relative importance of demography, selection and changing environments (. . .) remain unclear*".

In chapter 2, Jean-Nicolas Corvisier describes the grid surveys made of archeological sites on the scale of Ancient Greece. The sheer number of surveys makes it possible to estimate the space-time distribution of settlement units, from cities to villages, hamlets and individual farms. But these distributions raise several primarily technical questions as to the influence of the grid size of archeological site surveys on their interpretation, in other words, as to the resolution degree of spatial distributions. Next, on a more strictly theoretical level, as Jean-Nicolas Corvisier writes, "*in a world dominated by the City-state phenomenon, does the civic phenomenon have any influence on the spatial distribution of the population, or is the logic simply that of urbanization, i.e. the creation of urban centres once human settlements have reached a certain level of concentration in the same place?*" (Corvisier, this volume: p. 34).

The techniques described in the next three chapters are designed to deal with two interconnected problems: estimating an age distribution of skeletons and its confidence interval. Two approaches are described to estimate an age distribution. Chapter 3 presents an iterative Bayesian procedure used by Jean-Noël Bacro and myself. This gives an age distribution from the distribution of an age indicator of physical anthropology in a cemetery. This is given in the knowledge, on the one hand, of the information provided by an anthropological reference collection and representing the relationship between biological age indicator and chronological age and, on the other hand, of the mortality law from which the cemetery was inferred. The statistical procedure varies the prior probability of two broad classes of preindustrial mortality: ordinary mortality (also called attritional mortality in the paleontological literature) and catastrophic mortality. These prior probabilities are kept in the procedure, which makes it possible to obtain the best approximation of the observed distribution of the age indicator in a cemetery. But, as always with this kind of approach, there is never any certainty of having the "true" prior probabilities, only the best of the two broad classes of models proposed. A confidence interval for the distribution is then determined by bootstrapping the likelihood matrix of the reference anthropological collection, which represents the main source of error in the estimate (Bocquet-Appel and Masset, 1996).

In chapter 4, in order to estimate an age distribution, Isabelle Séguy, Luc Buchet, Arnaud Bringe, Carole Perraut, Nadège Couvert and Paul Beurnier have built up an array of pre-industrial Model Life-tables, obtained through successive linear regressions, in the manner of Coale, Demeny Vaugham (1983) or Ledermann (1969). The array input is one of the non-conventional demographic indicators observed in cemeteries, such as the various ratios of child and adult age classes (5–14/20+, 5–19/5+), or the average age at 20 years+. The limits indicated for the confidence intervals are those of the computed regressions, which the user will have to add the variation in the non-conventional demographic indicators that were used as input. Under the usual conditions of model life-table use, this new set would then have to replace the arrays built up from industrial populations or, worse, from archaeological populations (see Jackes and Meiklejohn, this volume: p. 179)

Now that we have an age distribution of skeletons, obtained not overall as in the approaches used in the two preceding chapters, but by grouping individual age estimates produced by any anthropological technique, with a confidence interval for each individual age, the question then is how to move from the individual confidence interval to the overall confidence interval of the distribution? In chapter 5, Marc A Luy and Ursula Wittwer-Backofen suggest drawing the individual age estimates in random sequences many times over (say 1000 distributions/cemeteries simulated), within their respective confidence interval limits, and building up the corresponding life table of each simulated distribution. The dispersion limits of the age-specific deaths in the 1000 life-table samples (the dx's of the life-table), at the level $1 - \alpha$, then provide an estimate of the confidence interval for the age distribution.

The final section of this volume covers the archaeological signatures left by identifiable demographic phenomena in (pre-)historical information, i.e. paleodemographic patterns. Here as in other areas, we need a demographic model of interpretation in order to move from an observable pattern in the data to demography. An initial set from the literature contains the simplest patterns, expressed by profiles representing skeleton age distribution, assuming, of course, that such profiles are constructible using current techniques. These age distribution profiles are directly interpretable simply by virtue of their resemblance to historical distributions, such as those produced by attritional mortality, warfare mortality – civilian or military – or plague epidemics (see Chamberlain, 2006; Gowland and Chamberlain, 2005;

Margerison and Knüsel, 2002; Paine, 2000; Keckler 1997). But when we depart from the catalogue of historical resemblances, the identification of a non-referenced signal which is not – or not adequately – measured in aggregate data from government offices, or which is unknown in ethno-historical demography (i.e. caused by a new demographic process), becomes more complex. A second set of paleodemographic patterns brings together signals that express temporal or space-time changes in variables compared to former stable states. This can be the case with an abrupt increase in frequencies, for example of hundreds of radiocarbon dates, interpreted as representing a re-colonization during the Late Glacial in Europe (Gamble et al., 2005), or even in the percentage of immature skeletons in more than 130 cemeteries, interpreted as the effect of a Neolithic demographic transition (Bocquet-Appel and Naji, 2006; Bocquet-Appel, 2002). It can also be the case with the variation in the space-time distribution of archaeological sites across Europe, reflecting an hitherto unknown distribution of populations under severe climatic constraint (Bocquet-Appel et al., 2005). But in these examples, which link up signatures and the demographic processes generating them, the distance is short and the model is simple. As we go further back in time, direct signatures of demographic processes become scarcer or non-existent. To come closer to demography, models for the interpretation of archaeological remains must become complex, with one or more additional layers of interpretation.

In chapter 6, from subtle changes in the archeozoological distributions of Mediterranean sites of the Late Pleistocene through Holocene periods, Mary C Stiner, Joseph E Beaver, Natalie D. Munro and Todd A Surovell detect a process of hunting intensification, where others might only have seen a simple change in fauna distribution due to climatic variations. This intensification is interpreted as indicating an increase in demographic density at the sub-continental scale. This detection of intensified hunting (and perhaps also of the law of diminishing returns) during OIS 2 was made possible thanks to a model where prey animals are classified on the one hand according to their long-term persistence (resilience) and on the other hand according to the expected return for the hunter-gatherer on his investment in time. This model provides an economic reference against which the observed data can be appraised. Stiner, Beaver, Munro and Surovell's approach can be extended to other sites and periods.

In chapter 7, Nathan B Goodale, Ian Kuijt and Anna M. Prentiss attempt a demographic interpretation of the Upper Columbia area of the Canadian Plateau between 4000 and 500 years ago, drawing on data representing variations in the temporal density of pithouses and C14 dates. These data are used as proxy variables of human density. According to the authors, a small-scale society seems to have existed in Upper Columbia prior to the full onset of the Neo-glacial climatic period, at 3800–4200 calBP, and was replaced by a society of "complex" gatherers at 1400–2200 calBP. The detection by Goodale, Kuijt and Prentiss of major regional economic and social changes, under conditions of very low demographic density, has led them to take up a position in the ongoing debate on the validity of the Boserupian paradigm of the creative force of population pressure on cultural change.

The next two chapters focus on the increase in fertility during the transition from a forager to a producer economy, as measured by skeleton distributions in cemeteries. In chapter 8, Mary Jackes and Chris Meiklejohn present the distributions of skeletons dug up from three important Portuguese sites in European prehistory, including two Mesolithic shell midden cemeteries which they personally excavated. The authors' tenacity along the years in gathering information on skeletal data which, in some cases, have been mixed up or dispersed since the first campaigns of the 1880s, must be underlined. Jackes and Meiklejohn then provide an in-depth ecological contextualisation of population data. Finally, tools for fertility estimation are presented. As will be seen, Jackes and Meiklejohn do not subscribe to the idea of a Neolithic demographic transition[1], which I have set out elsewhere. But this is a matter of scientific debate.

In chapter 9, Richard S Meindl, Robert P Mensforth and C Owen Lovejoy update their analysis of Libben, a Late Woodland forager cemetery (Northern Ohio, USA). We know that a skeleton age distribution, assuming of course that it can be obtained, is not in itself demography. To become demography, such a distribution has to be interpreted using a model. The preferred model is a Lotka stable population model, with its single parameter represented by the growth rate. This model is simple in its assumptions (the temporal stability of input/output parameters in a population) and robust in its results, having proven its reliability beyond reasonable doubt in countries where statistics are inadequate (Bourgeois-Pichat, 1994). Meindl, Mensforth and Lovejoy give a bounded continuum of a priori existing solutions, making it possible to provide a demographic interpretation (explanation) of their Libben age distribution, when fertility (and therefore their growth rate) varies, via the age-specific fertility rates of natural fertility populations (summarized by their TFR). The authors then set Libben within the long duration of evolutionary time in order to emphasize the need to take the growth rate into account in the demographic interpretation of skeleton distribution, because, as the authors write: "*it is the evolutionary nature of human populations to grow*".

Finally, in chapter 10, Stephan Naji, Matthew Bandy and myself return to the paradigmatic question initially raised 30 years ago by Mark Cohen (Cohen, 1977): What were the consequences of the Neolithic demographic transition on the population' s health? We know that in the five main centers of invention of plant domestication (the Levant, Meso-America, North America, Peru and Southern China), the transition from a forager to a horticulture-farming economy did not occur at the same time, ranging from 12,000 calBP to 500 calBP in North America alone. One of the main difficulties involved in answering Cohen's question concerns the integration of biodemographic information, taking its space-time dispersion into account. How, for example, can we compare the effects of a transition occurring between 12000–8000 BP in the Levant and 500 AD in Eastern North America? As with the detection of the signal of the Neolithic Demographic Transition, Naji, Bandy and myself provide an integrated representation of the pattern of change in a number of bioarchaeological indicators, positioning them in the reference frame of a relative chronology.

It is to be hoped that following the IUSSP meetings, other volumes will be published on paleodemography, reporting on progress in an active field of research as well as on the emergence of a consensus on methodologies and problematics, because it seems that the time has come to tackle the reconstruction of the demographic history of our global village. Finally, I am glad to acknowledge Lounès Chikhi, Christian Theureau, Monique Tersis and Ilona Bossanyi for their contribution to this volume.

NOTE

[1] I have not found, in Deevey (1960), the reference given by Jackes and Meiklejohn to a "demographic transition", a concept that was developed between 1929 and 1945 by several scientists, including CP Blacker, K Davis, A Landry, F Notestein and W Thompson (see Kirk, 1996); the concept of a Neolithic demographic transition was set out by the demographer Livi-Bacci (1992) and, independently, by myself (Bocquet-Appel, 2002). The reality of the concept is based, now, on more than 130 cemeteries across the entire northern hemisphere (Bocquet-Appel and Bar-Yosef, 2007).

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Chapter 1

FROM GENES TO NUMBERS: EFFECTIVE POPULATION SIZES IN HUMAN EVOLUTION

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Abstract: The effective population size has become a central aspect of our understanding of the ancient structure of human populations. It is through this concept that the genetic variation of present-day humans may inform us about the number and relationships of humans in the past. However, effective population size itself is not a demographic parameter. If the theoretical model does not apply accurately to human evolution, then inferences based on the estimates of effective population size may be in error. Here, I present the theoretical basis of effective population size, including many of the demographic and evolutionary conditions that can confound the relationship of genetic variation and population size.

Demography is the engine of evolution. Changes in allele frequencies require differential births and deaths of the individuals who carry the alleles. Under natural selection, these births and deaths approximate a deterministic process favoring the survival and reproduction of carriers of a particular allele. The histories of alleles themselves are demographic phenomena: the fitness advantage of a selected allele may be expressed as a relative intrinsic growth rate; its frequency over time follows a logistic growth curve.

In the absence of selection, allele frequencies vary as a stochastic process. The parameters influencing this process are themselves demographic: population size and mating pattern. Ultimately, the rate of evolution of a population must be constrained by these parameters. This means that the observable genetic characteristics of populations are to some extent natural estimators of demographic characteristics. The relationship between the demographic parameters of a population and its genetic characteristics may in some cases be approximated by a single parameter: the "effective population size." Effective population size refers the demographic complexity of some real population to the simplicity of some ideal

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