

Dead ends and new paths in historical demography

Daniel Courgeau

Historical demography has recently known two important trends in the realm of methodological approaches: the first is the adoption of behaviour genetics to explain demographic outcomes and the second is the development of fully Bayesian approaches. In this contribution, I argue that the first trend leads us to a dead end, but that further development of fully Bayesian approaches provides an important way forward for historical demographers.

1. Behaviour genetics: a dead end

Until 2005, historical demography sought the determinants of the evolution of a population in society itself. Society was seen as characterized by its social rules, the economy, the political system, and geographic and climatic conditions (Bengtsson *et al.* 2004). At the time, biology and genetics were clearly regarded as secondary. More recently, however, these latter two factors have been assigned an increasingly important role. Should historical demographers strengthen their research efforts further in this direction in future? I argue that they should refrain from doing so, as the path of behaviour genetics leads us to a dead end.

Even if the emergence of behaviour genetics can be dated to around 1960, it developed from the works of Galton in the nineteenth century and Fisher in the early twentieth century. In particular, the subsequent development of behaviour genetics relied heavily on the hypotheses and concepts of Fisher (1918), which were later applied to human populations. Fisher held that a trait is determined by a large number of polygenes, either uniquely or in combination with polygenes associated with another trait – an assumption that came to be known as the polygenic hypothesis. He also assumed that there is an infinite number of polygenes, and that genes and environment act additively and operate independently. Behavioural genetics, as it currently tends to be used with increasing frequency by (historical) demographers, followed in the footsteps of these premises. Hence we find studies

in the field of historical demography arguing that genes have an independent effect on behavioural outcomes in the realm of fertility, mortality, morbidity, etc. (for example, Bengtsson & Mineau 2008).

However, our understanding of the human genome has dramatically advanced since the theory of behaviour genetics was first elaborated. While, at the time, biologists believed that humans might count around 2 million protein-coding genes, we now know that we have only 19,797 of them. The amount of coding DNA that a human body contains is much lower than previously thought, and forms only about 2% of the total of our DNA. As the human characteristics that behavioural genetics study are innumerable – fertility, nuptiality, longevity, intelligence, homosexuality, alcoholism, femininity, autism, maniac depression, aggression, happiness, spatial and verbal reasoning, criminal behaviour, obesity, political participation, and so on – it is implausible to think that they are all linked to so small a number of genes. Similarly, the human organism produces well over a million proteins: the polygene hypothesis cannot explain this with only 19,797 genes at the body's disposal. The advancement of our understanding of genes has settled that human traits are always shaped by an interaction of genes and environment, not by genes alone. As, for example, Gottlieb (2001) clearly states:

“It is now known that both genes and environments are involved in all traits and that it is not possible to specify their weighting or quantitative influence on any trait... This has been a hard-won scientific insight that has not yet percolated to the mass of humanity.”

Genes and environment operate through interaction, not through addition. We can, therefore, conclude that the use of the concept of heritability, as linked to Fisher's assumptions, leads to a dead end. The problem to be studied is the interaction between genes and environment, and behaviour genetics cannot provide the answer. Considerable further research in molecular genetics and epigenetics will be required to unravel the complex ties between nature and culture, and we may even ask if this will ever be possible.

Beyond its scientifically inaccurate results, behaviour genetics hint at a desire for control over human destinies that strangely resembles Galton's eugenics – routinely resurrected since Nazism and, more recently, by governments seeking to improve society by locking up persons regarded as genetic misfits. Rather than to follow the blind alley of heritability, historical demography will do better to consider the social, economic, political, climatic and geographic factors to which they can have access.

What, then, is the way forward for historical demographers in the realm of methodology?

2. A truly Bayesian approach: new paths

Demographers – whether studying the present or the past – have long taken an objectivist view of the probability of events. Under this approach, first presented by

Pascal and Fermat in 1654, probability is seen as a measure assigned to the elements of sets. The population sets observed in the major large-scale surveys, censuses and registers are large enough for us to assume that demographic phenomena can be repeated in identical conditions at a given point in time. Probabilities can therefore be measured by their frequencies. For objectivists, the ‘probability’ of a hypothesis is thus meaningless. All that can be calculated is the probability of obtaining a given sample.

More recently, however, the Bayesian approach has emerged in various branches of historical demography. Under this approach, first given by Bayes in 1763, probability is no longer a measure assigned to sets, but to states of knowledge. The role of experience is now to modify this knowledge in a consistent manner; in other words, by transforming the *prior* probabilities into improved *posterior* probabilities. As a result, the probabilities of different hypotheses become truly meaningful and can be estimated and compared.

I argue that further development of Bayesian approaches provides an important way forward. One possible field of application, which illustrates the potential benefits, is paleodemography.

Paleodemography, a discipline based on archaeological data, seeks to estimate its various demographic parameters with the aid of skeletal remains. From a reference population and under the assumption of biological uniformity, it notably aims to determine the sex and age structure of the population of a given site, for which the only available evidence is the structure by stage of the biological evolution of a set of indicators. Moreover, the number of skeletons observed is very often small – sometimes no more than a few hundred individuals.

Until 2010, the methods prescribed by objectivists were unable to take fully into account the variability of some of the observations. While the methods proposed by Bocquet-Appel, Hoppa, Vaupel and others used Bayes’ theorem, the paradigm on which they were based was actually objectivist and the results obtained were highly unstable; in some cases, the population size of specific age groups was even estimated as zero. In 2010, with Henri Caussinus, I proposed a fully Bayesian method that avoids all these negatives. Our method starts from a prior distribution – chosen to reflect the researcher’s knowledge – to arrive at a posterior distribution obtained with the aid of observations. This approach has proved far more effective than its predecessors when working on populations whose mortality is known from other sources. It avoids the aberrant results obtained with non-Bayesian methods and offers more robust conclusions about the structure of the observed population.

The recent use of Bayesian methods in historical demography across diverse fields and around the world is now growing. For example, under some assumptions, approximate Bayes computation (ABC) permits, by coupling historical data with genetic data, the estimation of models of population expansion and dispersal at the continental scale over long past periods. Similarly, Bayesian population reconstruction also makes it possible to estimate past populations by age, fertility

and mortality rates, and net international migration, with fully probabilistic statements of uncertainty and expert opinions.

I therefore advocate the use of the Bayesian paradigm for a greater number of historical demographic questions. Doing so will permit historical demographers to judge states of knowledge about the studied population.

References

- Bengtsson, T., Campbell, C. & Lee, J. Z. (Eds.) (2004). *Life under pressure*. Cambridge, MA: MIT Press.
- Bengtsson, T. & Mineau, G. (2008). *Kinship and demographic behaviour in the past*. Dordrecht: Springer.
- Caussinus, H. & Courgeau, D. (2010). Estimating age without measuring it: a new method in paleodemography. *Population-E*, 65 (1), 117-144.
- Fisher, R. A. (1918). The correlation between relatives on the supposition of Mendelian inheritance. *Transactions of the Royal Society of Edinburgh*, 52, 399-423.
- Gottlieb, G. (2001). Genetics and development. In: Smelser, N.J. & Baltes, P.B. (Eds.). *International Encyclopedia of the Social and Behavioral Sciences, Genetics, Behavior and Society*. New York: Elsevier.

Biography

Daniel Courgeau is a demographer and Research Director Emeritus of the French National Demographic Institute (INED) in Paris. His main research interests are the theory and practice of demographic approaches from period to multilevel analysis, methodology and epistemology in the social sciences, and the application of Bayesian methods to the study of paleodemographic evidence.