Demographic Techniques: Inverse Projection

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Abstract

Inverse projection, designed in the late 1960s by Ronald Lee, is a method for reconstructing populations where vital registration data are available but age details are scarce and population census is lacking or unreliable, as it is often the case of historical populations. Since its introduction, several modifications have been made to Lee's original procedure in order to address some of its shortcomings and to make the procedure suitable to the existing sources. Inverse projection and its developments have produced important innovations in the field of population reconstruction.

Origins

Inverse projection (IP) is a method for reconstructing populations where vital registration data are available but age details are scarce and population censuses are lacking or unreliable, as it is often the case of historical populations. The technique has been devised by Ronald Lee in the late 1960s as part of his PhD dissertation, which was a study of the broad macro determinants and consequences of aggregate population change in preindustrial England (Lee, 2004). It then appeared in an article published in 'Population Studies' in 1974. IP estimates accurate demographic indicators – life expectancy, gross and net reproduction ratios – and population age structures just using time series of deaths and births and an estimate of the initial population size. The projection is hence logically inverted because instead of using age-specific rates to estimate totals of births and deaths and population age structures, as conventional projection techniques do, it derives age-specific rates and population age structures from counts of births and deaths.

The inverted projection routine offers a solution to the problem of analyzing the demographic characteristics of past populations in the case of lack and incompleteness of sources. As in the case of family reconstitution – the microdemographic technique devised by Louis Henry in the 1960s – IP is suitable to the available documentation for past populations because it uses parish registration data, which for European countries before the nineteenth century are often more available than data on the size of the population and its age and sex structures. However, unlike Henry's nominative technique, IP requires only aggregate data thus overcoming some important limits that result from the family reconstitution and that were at the center of a lively debate among scholars of the time. 'Moving families', which may differ from 'stable families' for social and demographic characteristics, are difficult to detect and thus they can escape the family reconstitution. Hence given the difficulty of extending the reconstruction to all households in the village studied, results from the nominative technique may result unrepresentative. Other obstacles refer to the inability to aggregate results related to single villages and to consider these as representative of wider areas. Furthermore, although researchers today can avail themselves of computer programs for linkage, it must be recognized the enormous amount of energy needed to reconstruct a village made up of only a few families. Instead, with little effort, IP is able to reconstruct the demographic history of entire, even large populations over long periods of time, producing surprisingly accurate demographic indicators, by requiring only aggregate data. As Lee has pointed out (2004) "Some good ideas just don't work out in practice, while other ideas that seem to be based on very questionable assumptions, surprise us by working better than one could reasonably expect. Inverse Projection certainly falls in this second category". However, it must be said that historical demographers today are broadly in agreement in considering the aggregative technique of IP and the nominative reconstitution of families as two different techniques to be used profitably in a quite complementary way.

Method

In the study of past populations, the lack of complete data inevitably leads to the use of techniques that rely on models. This is also the case of IP that, in fact, presupposes the use of age schedules of mortality, fertility, and migration. To initiate the projection, IP requires the total population at the beginning of the period, an initial age structure of the population (obtained from either a census or a model), and counts of births and deaths for each interval. Under the hypothesis of closed population, to project the initial population at the subsequent instant, deaths occurred in the time interval must be subtracted for each age. But, since only the total number of deaths is known, this total is distributed by age through a series of probabilities of death that, applied to a given age structure, gives precisely the number of deaths observed in the considered time interval. This particular series of probabilities is determined by linear interpolation between two adjacent age schedules of mortality chosen from a single-parameter family of life tables. An adjustment factor, k_t, which is proportional to the difference of the two age schedules chosen as standard, locates the current series of probabilities of death. This variable can be viewed as an index of the force of mortality.

By removing the hypothesis of closed population, the procedure requires the knowledge of the total population not only at the beginning, but also at the end of the period considered, or, better, at instants subsequent to the initial. The projected total, derived just adding the counts of births and subtracting the counts of deaths, is subtracted from the observed total population to obtain an estimate of net migration. Net migration is then apportioned equally among the intervening periods. In case of long periods, net migration is apportioned among the intervening periods through a more sophisticated solution based on the amount of the population and the number of intervals included in the period. Once the number of migrants in each interval is determined, they are distributed by age according to a standard pattern of age-specific rates.

Once the age distribution of the population is estimated, it is then possible to estimate the most important measures of mortality and fertility. The gross reproduction ratio is estimated from the number of birth, the age structure of the population, and a normalized age pattern of fertility which changes over time by a proportional factor, f_t, at all ages. This variable can be viewed as an index of the force of fertility. Models of fertility, therefore, affect only the estimates of the relative measures, since they are not used to estimate the number of births that are already known at the beginning of the procedure.

Theoretically, IP can generate estimates of nuptiality measures. Of course, in order to obtain these estimates, it is necessary to consider as inputs an age schedule of marriage, the marital status of the initial population, and the time series of marriages. But apart from the objective (and not negligible) difficulty to find these information for historical populations, IP that, also in this case, as for mortality and fertility, assumes a model of marriage rates with proportional changes over time at all ages, is not suitable to the analysis of a complex phenomenon such as nuptiality (Brunborg, 1976 cited in Lee, 2004; Breschi, 1990).

Over time, some extensions have been added to the original IP formulation. The first enhancement has been the extension of the number of age groups beyond age 55. The final open-ended group was in fact originally fixed at age 55 because computer was slow and expensive but it has been shown that this limit produces bias when life expectancy improves (Brunborg, 1976 cited in McCaa and Barbi, 2004). Another important enhancement was the implementation of annual projections in place of 5- or 10-year periods (Biraben and Bonneuil, 1986; McCaa and Brignoli, 1989). Also, the IP method is not well suitable to capture age patterns of mortality for particular conditions of mortality such as epidemics, famine, civil war etc. Mortality crises were frequent in historical populations and they often affected selectively the population, thus determining substantial changes in the age profile of mortality. These changes, however, are not captured by IP since the underlying hypothesis in the IP algorithm is that mortality varies over time only by an age-independent factor, which is proportional to the difference between two adjacent age schedules of mortality. Thus IP will produce estimates of the probabilities of death disproportionately high at younger and older ages, leading hence to a distorted reconstruction. A solution was to set a mortality ceiling considered normal for the study period. The number of deaths below this threshold is apportioned according to the IP method while the exceeding part is apportioned proportionally to the size of the population of each age group (Biraben and Bonneuil, 1986; McCaa, 1993).

Many applications have highlighted the extreme adaptability of the procedure to the available documentation. Its robustness with respect to the choice of age patterns of vital events and the initial age structure, guarantees a good stability of the estimates and therefore it is a great advantage for those who, due to lack of information, are forced to make arbitrary choices. Many studies have shown that any wrong choice of the age structure and the mortality model have only a negligible impact on the estimates of the various demographic indicators (Lee, 1974, 1985; McCaa, 1989; McCaa and Vaupel, 1992; McCaa, 1993). The differences in the estimates obtained with two different initial age structures are quite strong in the early cycles of the projection, but diminish rapidly as the projection continues. Wachter has shown (1986) that the weak ergodicity theorem is extendible also to IP. In the long run, vital rates determine the population, not its initial state. The population hence quickly forgets its past age distribution. With regard to the mortality model, the effects of different hypotheses are more modest than those caused by different initial age structures, but appear to be more persistent over time. On the other hand, IP requires good vital registration data. As shown by Brunborg (1976), and McCaa and Vaupel (1992), quality of data is the most important factor for successfully applying the method (McCaa and Barbi, 2004).

Thanks to McCaa (1989) and McCaa and Brignoli (1989), who devised the user-friendly program 'populate', the IP could be readily applied by several researchers around the world.

Developments

Back projection was developed by Wrigley and Schofield for their massive reconstruction of the population of England, 1541–1871, as a means of dealing with the closure problem (Wrigley and Schofield, 1981; Oeppen, 1993b). Most populations, over the long run, are not closed, and England is no exception. While forward IP takes into account authentic migration data, Lee's method cannot produce migration flows (Lee, 1993). Back projection seeks to generate migration estimates from a terminal age structure by backcasting the population against the flow of births and deaths. While it might seem commonsensical to begin with the best, i.e., most recent, data and project backwards, Lee argues that this ignores the weak ergodicity theorem. In Lee's words (1993), "the problem originates with the attempt to resurrect people who have died into the oldest age group, an attempt that is, in practice, hypersensitive to error". The Cambridge team used iteration procedures to settle upon a single series of best estimates. However, beyond the Cambridge team, back projection has attracted few proselytes.

Generalized inverse projection (GIP) responds to Lee's criticisms of back projection and broadens the method into an analytical system which exploits whatever data are available as well as a broad range of assumptions or constraints, including components derived from back projection (Oeppen, 1993a,b). Lee's IP and back projection may be seen in fact as members of a same class of constrained projection models. In the worst situation of data scarcity – i.e., in the back projection frame, when only series of births and deaths and the final population age structure are known – generalized inverse projectionists argue that the method can endogenously estimate migration flows as well as population totals and age structures by using a standard nonlinear optimization algorithm which maximizes the consistency between assumptions and data. The starting age structure can be also estimated using a stable population assumption. Since there are more parameters to be estimated (migration and mortality) than empirical observations (death totals and age groups of the final population), additional assumptions and/or data are required. Despite its flexibility, GIP has to solve an 'ill-posed' problem because of the uncertainty of the uniqueness and stability of the final solution. In Oeppen's words (1993b), "The selection of extra targets is somewhat arbitrary, which is in part a virtue since it allows a researcher to use whatever is available, but it also makes the estimates dependent on these extra targets". Lee (1993) remains unpersuaded, arguing that "…one can easily construct an infinity of radically different trajectories of population size, net migration, fertility and mortality which exactly match the given data".

Trend projection (Biraben and Bonneuil, 1986; Bonneuil, 1993) reconstructs past populations using series of births and deaths but in the absence of any census count or age structure. Given a birth and death series, the method finds a single value for which the trend in life expectancy after the initial date of the burial series is equal to the assumed value before. The method works well for closed populations but is ill-suited to open ones.

The flexibility and the potentiality of the IP method could not be ignored by Italian demographers given the rich availability of historical record of parish data of exceedingly high quality. In Italy, the first attempt to reconstruct a past population using the IP method is the work by Marco Breschi (1990) who tried to trace the demographic evolution of Tuscany from 1640 to 1940. The case of Tuscany, where demographic-statistical documentation is particularly detailed, allows Breschi to fully exploit the method and to develop a first and experimental version of two-sex projections. Results from Breschi's reconstruction demonstrated that the growth of the population of Tuscany starting from the middle of the eighteenth century was probably due, as in the case of England, to a rise in fertility rather than to a fall in mortality.

Since Breschi's work, new flavors of the method were developed, on the one hand, to exploit all available information and, on the other, to overcome some limits of Lee's IP.

The *differentiated IP* (Rosina, 1993, 1996; Rosina and Rossi, 1993) arises from the richness of data available in historical-demographic sources of some Italian regions where the age at death is faithfully reported. The procedure is based on the distribution of death by big age classes or, more simply, by only two age classes: infant and adult ages. In this case, the age-differentiated version of IP takes into account two life tables which, following Lee's procedure, have to fulfill two constraints: the first life table has to be such as the probabilities of death, applied to the young population, yield the total number of deaths recorded for infants and children and the second one has to be such as the probabilities of death, applied to the adult population, yield the total of deaths recorded at adult ages.

The aim of the age-differentiated procedure is to overcome possible shortcomings, already mentioned in Section Method, deriving from Lee's original assumption about the estimation of the age structure of the mortality function which, as said, varies over time only by a proportionality factor, the k_t variable, which does not depend on age but refers to the time-independent differences between two life tables from the same family. This assumption can lead, in exceptionally low or high mortality conditions, to probabilities of death greater than one or less than zero! This matter is particularly important in the past when age-selective mortality crises shifted not only the level but also the profile of mortality. It has been shown (Rosina and Rossi, 1994) that the distribution of deaths by as few as three age classes leads to an improvement of the fit to the observed data of about 80%. The differentiated IP has more explanatory power than the original IP as demonstrated by Rossi and Rosina in the study on the transition in the Venetian area (1998). However, since the age structure of the initial population has to be consistent with the information on deaths by age, the differentiated version of IP is, on the one hand, more rigorous, on the other, due to the larger number of constraints, less flexible with respect to Lee's procedure. This feature, especially in single-year projections, with the occurrence of a heavy mortality crisis, may lead to impossible probabilities of death (Barbi, 1997). The features of the method and an overview of various applications are described by Rosina (2004).

To make the profile of the mortality function more sensitive to possible changes over time and to avoid estimates of 'negative' population or 'births' at adult or old ages, Salvatore Bertino (1995) suggested some others modifications to Lee's method. Of particular interest is a model that estimates the mortality function at each time through a recursive procedure. The adjustment factor at each time t, k_t, is still determined through Lee's technique but the mortality function at each time t is estimated through a linear combination of the mortality functions estimated at time $t-1$ and $t-2$ with coefficients respectively equal to $1 + k_t$ and $-k_t$. Furthermore, the procedure imposes some convenient limits to the probabilities of death in the extreme ages (besides the obvious limits of 0 and 1) and then the adjustment factor is determined in an iterative way. Unfortunately, the robustness of Bertino's idea cannot be assessed in practice because, up to now, no software has been devised to implement his formulas.

An innovative more recent algorithm is the *stochastic inverse projection* (SIP) devised by Salvatore Bertino and Eugenio Sonnino in (1995) and appeared in an article published on Mathematical Population Studies in 2003. This procedure reconstructs past populations through a microsimulation approach. First, similar to Lee's procedure, a linear variation of the mortality function between two life tables relative to the beginning and the end of the studied period is hypothesized. Additionally, it is possible to enter two additional models for dealing with years where unusual conditions of mortality prevailed. Then, it is assumed that each individual in the population follows, over the entire life span, a nonhomogeneous Poisson process with intensity equal to the force of mortality obtained by approximation from step 1. Assuming that all individuals behave independently from each others, the

Poisson theory allows one to calculate the probability that a mortality event occurring at time *t* is to be attributed to an individual of age *x*. Generating a realization of the random variable 'age at death', according to the probability distribution just determined, it is possible to assign, by simulation, an age of death to the individual. The procedure is replicated for all recorded deaths so as to obtain the distribution of deaths by age, which is necessary to project the population. Similarly, fertility statistics are also determined by simulation. Although methodologically different, both forward and backward projections are possible with the stochastic method.

Instead of a single deterministic solution as with usual reconstruction methods, the stochastic approach offers a set of different reconstructions for the same time *t*. Then, the average scenario and the variability in a population's evolution are also evaluated. The results of all these alternative simulations differ by chance only and are equally coherent because they are governed by the same data and models. A comparison between the behavior of the IP technique, the differentiated version, and the stochastic method in various simulated scenarios of exceptional mortality (Barbi, 1997) shows that the stochastic approach proceeds in a way, which closely reflects empirically observed patterns. The estimated probabilities of death are based not only on theoretical risks (the intensity of the Poisson process) but also on the proportion of the population at each age. This is a key point, especially in the reconstruction of small populations. The stochastic approach recognizes the eventuality that very few mortality events or even none may be attributed in some old age classes where individuals are few although their theoretical mortality risks are high.

Barbi and Oeppen (2004) compared the results from the GIP and the SIP in the back projection frame (when the terminal age structure of the population is specified) and showed that both the techniques reconstruct demographic scenarios coherently with recorded data. However, Lee (2004), while appreciates the stochastic approach because it provides an estimate of the uncertainty in the IP results, and Oeppen's generalized version because of its flexibility to incorporate demographic information that are available, does not see any advantage to running SIP backward and continues to be critic with respect to GIP when running in the back projection frame in the absence of input data on migration.

IP and its variations have produced important innovations in the field of population projection. Their strategy is to exploit specific existing documentation so as to lead to coherent demographic reconstructions. Desirable developments should look at an even more flexible approach that takes benefit of any bit of demographic information, a general model able "to cover situations in which one did not have full time series of births and deaths, and perhaps had more information of other kinds, such as censuses" (Lee, 2004). Toward this direction is the approach devised recently by Bonneuil and Fursa (2011, 2012). Combining the Lotka–McKendrick population model with stochastic optimization, the authors reconstruct the demographic dynamics, even by civil status, from partially missing or flawed demographic data. (Large part of this Section is reprinted from McCaa and Barbi, 2004, © Springer-Verlag Berlin-Heidelberg 2004, with kind permission of Springer Science + Business Media.)

See also: Demographic Techniques: Family Reconstitution; Population Dynamics: Mathematic Models of Population, Development, and Natural Resources; Population Forecasts.

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