Comparing the Results from Generalised Inverse Projection and Stochastic Inverse Projection

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1 The Issues and Challenges of Generalised Inverse Projection and Stochastic Inverse Projection

Since the introduction of Lee's Inverse Projection (IP - [7]), several modifications have been made to overcome some of its methodological limitations and make the procedure suitable for the existing sources, which may be very different from country to country. In this field, two procedures in particular instigated a lively discussion among demographers in the 1990s, due to their completely different approaches: Generalised Inverse Projection (GIP - [11, 12]) and Stochastic Inverse Projection (SIP - [2, 3]).

GIP offers the opportunity for simultaneously estimating the migration and population totals, as well as the age structures and derived demographic parameters. In Lee's original formulation, migration and population totals were determined exogenously. GIP also abandons the requirement to specify a starting age structure. If one is available it can be used, but the program can also estimate the starting age structure using a stable population assumption. The price paid for this flexibility is that there are more parameters to be estimated than there are constraints, whereas in IP there are equal numbers. Additional constraints, or targets, must be specified and these may be assumptions or data. The program then finds a solution to the reconstruction problem that maximises the consistency between the estimated population surface and the data and assumptions. Some of the differences between IP and GIP have been discussed by Lee and Oeppen in Reher and Schofield [9, 12].

Later, Bertino and Sonnino devised a stochastic approach to inverse projection. The usual inverse projection methods - Lee's Inverse Projection [7, 8],

¹ An example of using a combination of these can be found in van Leeuwen and Oeppen's [10] reconstruction of the population history of Amsterdam.

Back Projection [16], Trend Projection [4, 5], Differentiated Inverse Projection (IPD - [13, 14]) as well as GIP - reconstruct past populations using a deterministic method. They provide the only reconstruction that is compatible with the data and the assumptions. SIP, by contrast, is a micro-simulation method based on a non-homogeneous Poisson process. SIP is thus able to produce multiple simulations from the same data and assumptions and, hence, to determine the average scenarios and the standard deviations. The results of these simulations differ by chance only and are equally coherent because they are governed by the same rules and input data. As the past is unknown and, hence, it is difficult to check the validity of population reconstruction, it may be more informative and, at the same time, more prudent to handle several possible scenarios that offer a coherent idea of what might have happened in the past. SIP is able to carry out both forward and backward projections. Barbi [1] has discussed some of the differences between IP, IPD and SIP.

This chapter shows the results from a study aimed at stressing the differences between these two methods in the back projection frame (when the terminal population age structure is specified) and their performance when data are scarce, as it is often the case in historical populations. The two models are applied to the same data set, for which population totals and age structures are known, and the reconstructed population surfaces and the estimates of the demographic parameters are compared with these known values.

2 Data

The Nordic countries offer perhaps the best opportunity for testing inverse projection models. In Sweden, which we have chosen to use here as a case study, the collection of data on both the stocks and flows of demography was made compulsory in 1749. Thus, we have two and a half centuries of births, deaths by age, and population age structures: all differentiated by sex. While there are some questions about under-registration in the early period, Nordic data probably form the best and longest series we can find. Demographers are fortunate that John Wilmoth has made the data from 1751, and the matching life-table estimates, available in the Berkeley Mortality Database.²

The Swedish data offer a stern test for any population reconstruction technique. The demographic transition has seen mortality fall from relatively high

² The site also gives a description of the construction of the data and its sources. The web address is http://demog.berkeley.edu/wilmoth/mortality. The Berkeley Mortality Database (BMD) has been recently replaced by the Human Mortality Database (HMD; http://www.mortality.org), a project co-sponsored by the University of California, Berkeley, USA and the Max Planck Institute for Demographic Research, Rostock, Germany. However, mostly for comparison purposes, the BMD is still accessible.

levels, with severe epidemics, to a position today where the Swedish are one of the longest-lived populations. Swedish fertility has also followed a remarkable decline, but with a recent swing from being one of the lowest to one of the highest in Western Europe. Even more critical for these methods is the fact that the nineteenth century saw massive emigration from Sweden to North America. Today, Sweden has net in-migration, but for male cohorts born between 1861 and 1875, net emigration levels reached twenty percent, and about fifteen percent of the females left. If our methods work for national populations with these levels of migration, we can have some confidence that they will work for sub-national units.

In this study, we reconstruct the Swedish population for the period 1790-1860, using both GIP and SIP with, as far as it is possible, the same input data. The choice of time-period involved two factors. Firstly, micro-simulation is time-consuming which, at the initial stage of the research, makes selecting a very long time-period inadvisable. Secondly, the current version of SIP is better suited to conditions where mortality dominates migration. While the period chosen satisfies these criteria, the disadvantage is that any inaccuracy in the data is more likely in the early years of the data. Calculating annual totals of net-migration using the residual method shows that the female data has been manipulated - a tiny but constant number of women appeared to emigrate annually over the period 1750 to 1815. This seems to derive from Sundbärg's 1907 publication [15], rather than from the Berkeley Mortality Database compilation, but similar estimates for men do not show this feature.

3 Results and Discussion

The projections presented here were performed using time series of births and deaths and the terminal age structure reported for 1861. The 1790 and 1861 life tables were assumed for SIP and the 1858-62 life table for GIP. As said before, these data were extracted from the Berkeley Mortality Database. The same standard age-schedules for fertility (corresponding to a mean age at maternity equal to 31 years) and migration were assumed for both GIP and SIP. With these data and assumptions, we have performed two different tests: one accounting for only the terminal census as population target, the other considering all the population totals as input. Regarding time series of events and population totals, SIP, conversely to GIP, does not require input data distinct by sex.³ When necessary, age data were converted to single years of age

³ SIP performs projections distinct by sex using sex-specific age structures and mortality functions but without requiring deaths and population totals by sex. A new version of the program for the stochastic backward inverse projection gives the option to specify population by sex, if available.

by standard procedures. The stochastic backward projections were performed with 50 simulations and a data reduction coefficient equal to 100.⁴

Whether the terminal census forms the only population target (Table 1), or all the population totals are given exogenously (Table 2), the maximum discrepancy between the GIP estimates of life expectancy at birth and the recorded values is 8-9 %. However, these values are found just in correspondence of a period including a mortality crisis. With the exception of the period 1805-10, where total deaths surged by more than 30 percent over the previous quinquennium, the discrepancy between recorded values and GIP estimates through the study period is set at much lower values. The algorithm finds that the data and assumptions in the model are highly consistent with the targets, although there is some variation between the reconstructions. The most consistent reconstruction is for the total population in both cases, with the male ones being the worst, although this is not directly reflected in the comparisons between the observed life expectancy values.

Table 1. Life expectancy at birth (recorded and estimated by GIP and SIP with only the terminal census as target. 5-year mean evaluations)

	1790-95			1805-10				
	Males	Females	M+F	Males	Females	M+F		
rec. (31 Dec.)	37.23	40.05	38.64	30.67	34.08	32.35		
GIP (31 Dec.)	37.45	42.21	40.58	28.13	32.94	31.31		
SIP (31 Dec.)	33.44	37.56	35.43	30.39	34.52	32.39		
GIP dev.%	0.6	5.1	4.8	-9.0	-3.5	-3.3		
SIP dev.%	-11.3	-6.6	-9.1	-0.9	1.3	0.1		

	1830-35			1850-55			
	Males	Females	M+F	Males	Females	M+F	
rec. (31 Dec.)	39.21	43.56	41.37	40.30	44.57	42.41	
GIP (31 Dec.)	37.56	42.69	40.72	39.41	43.67	41.80	
SIP (31 Dec.)	39.18	43.55	41.31	41.67	44.15	42.86	
GIP dev.%	-4.4	-2.0	-1.6	-2.3	-2.1	-1.5	
SIP dev.%	-0.1	0.0	-0.2	3.3	-0.9	1.0	

The life expectancy at birth estimated by SIP when only the terminal total population is assumed as target (Table 1) is very close to the recorded value for each sex and total population with the exception of the first period. Note

⁴ In SIP it is possible to apply a coefficient in order to reduce data and, hence, the time of simulation. However, results are given for the whole population.

	1790-95			1805-10			
	Males	Females	M+F	Males	Females	M+F	
rec. (31 Dec.)	37.23	40.05	38.64	30.67	34.08	32.35	
GIP (31 Dec.)	36.99	40.08	38.40	28.36	31.42	29.95	
SIP (31 Dec.)	35.00	38.70	36.78	30.98	35.00	32.92	
GIP dev.%	-0.7	0.1	-0.6	-8.1	-8.5	-8.0	
SIP dev.%	-6.4	-3.5	-5.0	1.0	2.6	1.7	

Table 2. Life expectancy at birth (recorded and estimated by GIP and SIP with the complete population series as target. 5-year mean evaluations)

	1830-35			1850-55			
	Males	Females	M+F	Males	Females	M+F	
rec. (31 Dec.)	39.21	43.56	41.37	40.30	44.57	42.41	
GIP (31 Dec.)	38.97	42.77	40.92	40.24	44.46	42.42	
SIP (31 Dec.)	40.31	44.43	42.32	42.65	44.79	43.70	
GIP dev.%	-0.6	-1.9	-1.1	-0.2	-0.2	0.0	
SIP dev.%	2.7	2.0	2.2	5.5	0.5	3.0	

that, in this case, SIP reconstructs the population in the absence of migration. When the a priori information about migration or, in other words, the complete series of population totals is given as input, one can see an improvement of the estimates in the first period (Table 2). Strangely, a similar improvement is not evident for the later years. The lower values of life expectancy estimated by SIP at the beginning of the period under study in both the simulations may in part be due to the population age structures reconstructed by the procedure. In fact, the probabilities of dying given as inputs have to be considered just as theoretical risks that do not occur necessarily. The age at death determined by SIP depends on those risks but also on the size of the population at each age. The pyramid projected by SIP for 1790 shows greater distortions in certain age groups with respect to that estimated by GIP (Tables 3 and 4). In 1790, SIP over-estimates the population of each sex at young and adult ages but under-estimates populations at young-old ages and, exceedingly, at old ages. The discrepancy between recorded and estimated pyramids is just a bit lower when the complete population totals are considered as targets (Table 4). Thus, in SIP, the observed deaths could largely come from the population at young and adult ages, leading to underestimated values of life expectancy. The better fit found by SIP with respect to that performed by GIP during the crisis period (1805-10) may have a similar explanation (Tables 1 and 2). The stochastic procedure accounts for the fall in births during the mortality crisis and, hence, estimated values of infant mortality are not exceedingly shifted 100

upward as normally occurs in deterministic inverse projections that relies on a generic mortality structure. Consequently, observed and estimated life expectancies are in almost complete agreement even in this period.

Table 3. 1790 age structure (recorded and estimated by GIP and SIP with only the terminal census as target)

_	0-4			5-14			15-24		
	M	F	M+F	M	F	M+F	M	F	M+F
rec. (1 Jan.)	12.41	11.32	11.84	20.99	19.26	20.09	16.95	16.25	16.58
GIP (31 Dec.)	12.36	11.12	11.74	22.41	20.44	21.44	18.44	16.92	17.61
SIP (31 Dec.)	12.41	11.72	12.05	21.66	19.95	20.77	19.38	17.92	18.62
GIP dev. %	-0.4	-1.8	-0.8	6.4	5.8	6.3	8.1	4.0	5.8
SIP dev. %	0.0	3.4	1.7	3.1	3.5	3.3	12.5	9.3	10.9

_	25-49				50-64			65+		
_	M	F	M+F	M	F	M+F	M	F	M+F	
rec. (1 Jan.)	33.51	34.18	33.86	11.27	12.73	12.03	4.88	6.24	5.59	
GIP (31 Dec.)	32.65	33.06	32.99	12.28	14.09	13.26	5.60	7.24	6.37	
SIP (31 Dec.)	34.10	34.67	34.40	9.96	12.07	11.07	2.49	3.67	3.10	
GIP dev. %	-2.6	-3.4	-2.6	8.2	9.6	9.2	12.8	13.8	12.2	
SIP dev. %	1.7	1.4	1.6	-13.1	-5.5	-8.8	-96.2	-70.3	-80.2	

Figures 1 and 2 show that the Gross Reproduction Rate (GRR) estimates from GIP and SIP are generally within about 0.15 of a daughter from Keyfitz and Flieger's figures [6]. Not surprisingly, because of the momentum of population systems, the errors are autocorrelated rather than random. Obviously, since the number of births are given and the fertility schedule used as the basis for estimating age-specific rates is the same in GIP and in SIP, the two methods produce similar trends of GRRs. Estimates performed by GIP run generally above those obtained by SIP, depending on the number of women at fertile age estimated by the two procedures. SIP was particularly able to produce fertility estimates without any information about the size of the female population in both the projections with and without the complete series of total population. Detailed data are often not available for historical periods but SIP is able, however, to capture good estimates of GRR, as well as of male and female life expectancy, even if events and population by sex are not required as inputs. The events and population by sex are determined endogenously with only the support of life tables and population age structures by sex.

Table 4. 1790 age structure (reco	rded and estimated by	GIP and SIF	with complete
population series as target)			

				5-14			15-24		
M	F	M+F	M	F	M+F	M	F	M+F	
12.41	11.32	11.84	20.99	19.26	20.09	16.95	16.25	16.58	
12.15	11.59	12.29	21.75	20.70	21.76	19.38	17.98	18.76	
12.11	11.49	11.78	21.22	19.61	20.38	19.24	17.81	18.49	
-2.1	2.3	3.6	3.5	6.9	7.7	12.5	9.6	11.6	
-2.5	1.4	-0.5	1.1	1.8	1.5	11.9	8.8	10.3	
						<u> </u>			
	12.41 12.15 12.11 -2.1	12.41 11.32 12.15 11.59 12.11 11.49 -2.1 2.3 -2.5 1.4	12.41 11.32 11.84 12.15 11.59 12.29 12.11 11.49 11.78 -2.1 2.3 3.6	12.41 11.32 11.84 20.99 12.15 11.59 12.29 21.75 12.11 11.49 11.78 21.22 -2.1 2.3 3.6 3.5 -2.5 1.4 -0.5 1.1	12.41 11.32 11.84 20.99 19.26 12.15 11.59 12.29 21.75 20.70 12.11 11.49 11.78 21.22 19.61 -2.1 2.3 3.6 3.5 6.9 -2.5 1.4 -0.5 1.1 1.8	12.41 11.32 11.84 20.99 19.26 20.09 12.15 11.59 12.29 21.75 20.70 21.76 12.11 11.49 11.78 21.22 19.61 20.38 -2.1 2.3 3.6 3.5 6.9 7.7 -2.5 1.4 -0.5 1.1 1.8 1.5	12.41 11.32 11.84 20.99 19.26 20.09 16.95 12.15 11.59 12.29 21.75 20.70 21.76 19.38 12.11 11.49 11.78 21.22 19.61 20.38 19.24 -2.1 2.3 3.6 3.5 6.9 7.7 12.5 -2.5 1.4 -0.5 1.1 1.8 1.5 11.9	12.41 11.32 11.84 20.99 19.26 20.09 16.95 16.25 12.15 11.59 12.29 21.75 20.70 21.76 19.38 17.98 12.11 11.49 11.78 21.22 19.61 20.38 19.24 17.81 -2.1 2.3 3.6 3.5 6.9 7.7 12.5 9.6 -2.5 1.4 -0.5 1.1 1.8 1.5 11.9 8.8	

	25-49				50-64			65+		
_	M	F	M+F	M	F	M+F	M	F	M+F	
rec. (1 Jan.)	33.51	34.18	33.86	11.27	12.73	12.03	4.88	6.24	5.59	
GIP (31 Dec.)	32.77	32.81	32.56	11.10	12.74	11.86	5.08	6.46	5.62	
SIP (31 Dec.)	34.21	34.57	34.40	10.40	12.42	11.45	2.83	4.10	3.50	
GIP dev. %	-2.2	-4.2	-4.0	-1.5	0.0	-1.5	3.9	3.3	0.5	
SIP dev. %	2.1	1.1	1.6	-8.4	-2.6	-5.1	-72.4	-52.1	-60.0	

Finally, Figure 3 shows the estimated populations with only the terminal population constraint. Both procedures appear to be more accurate for the total and female populations. This may reflect the rise in migration towards the end of our period, which affects males more than females. It should be noted that the migration schedule used as the basis for estimating age-specific rates in GIP, as well as in SIP, was the same for both sexes and that in GIP, conversely to SIP, population constraints are given distinct by sex.

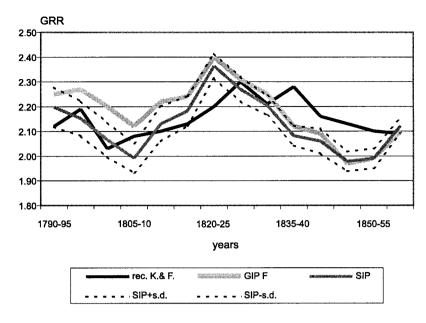


Figure 1. Gross reproduction rate (recorded and estimated by GIP and SIP with only the terminal census as target)

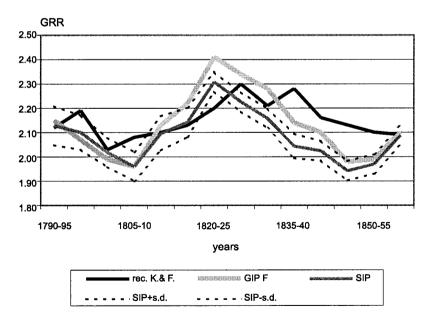


Figure 2. Gross reproduction rate (recorded and estimated by GIP and SIP with complete population series as target)

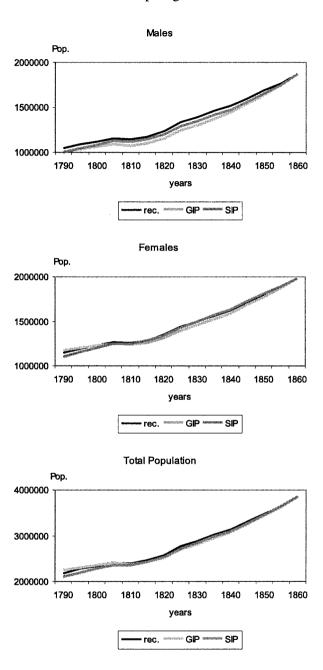


Figure 3. Population series (recorded and estimated by GIP and SIP with only the terminal census as target)

4 Conclusions

Are the two investigated techniques able to reconstruct the unknown past without falling into the field of arbitrary speculations? We have attempted to demonstrate here that they are. Clearly, the two procedures show various weaknesses and potentialities that make one method more suitable than the other depending on the situation under study. GIP may be at an advantage with respect to SIP when the period to be reconstructed is long and no exogenous information on migration is available. On the other hand, SIP showed its ability to estimate highly consistent values of demographic measures when no information is provided about the sex of events and population. This feature is particularly appreciated in measuring fertility rates.

Some of the remaining differences in our results could be attributed to differences in the mortality models. Although the representation is deterministic in GIP and stochastic in SIP, it is possible that their basic character could be brought closer together for comparative purposes. One of the research questions for all inverse projection models is to find the most accurate and simplest representation of changing mortality. This is particularly important when the population is subject to epidemics and wars, and it is here that the stochastic approach of SIP might be most revealing.

One can choose this or that method depending on data, length of period and general knowledge of the population under study. In this paper, we have shown that both GIP and SIP reconstruct demographic scenarios coherently with recorded data. Although this is an encouraging start, the choice of a short time-period, when net international migration was modest, means that the reconstructions are highly constrained by the terminal census, giving little scope for the problems associated with ergodicity.

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