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REJOINDER

Andrei Rogers
International Institute for Applied Systems Analysis, Schloss Laxenburg, Austria
Jacques Ledent
Division of Economic and Business Research, University of Arizona, Tucson, Arizona 85721

Schoen states that "Rogers and Ledent claimed (1976, p. 289) that the general increment-decrement life table model set forth in Schoen (1975) was correct only for the special case of a single radix." But a careful examination of our statement will reveal that we never put forward such a claim. We never have disputed that the Schoen (1975) *model* could be used to construct a multiradix life table. What we did claim was that "His formula for life table *rates* in equation (2), however, is correct only for the special case of a single radix" (italics added). For a multiradix situation, Schoen does not provide a computational formula for calculating life table rates that are based on the spatial dynamics of the *life table* population. His equation (2) in the original paper is simply a definitional relationship which defines the unknown quantity d as the product of M and L. It cannot be used in a multiradix case as a computational formula for obtaining d as a function *only* of the life table l's and L's. Although Schoen is quite correct in observing that his flow and orientation equations "can readily be generalized to recognize each person's state at the beginning of the interval" and that this additional recognition (implemented by means of an extra superscript) is what "permits more than one positive radix," the generalization was not part of his original paper. And it is precisely this generalization that is the major point of the life table rate section of our "Comment."

Our "claim," therefore, might be reexpressed as follows: In order to develop a computational formula for determining life table rates m using only the information about the evolution of the life table population, one must keep track of the place of birth (or place of previous residence) of the various cohorts throughout the calculations. This necessitates the use of an additional superscript and leads to the matrix formulation we proposed, i.e., the use of $\mathbf{l}$ and $\mathbf{L}$ *matrices* instead of $\{l\}$ and $\{L\}$ *vectors.*

This is a subtle point and perhaps needs some elaboration. A way of focusing on the crux of the issue is to relax the assumption that the two sets of rates, M and m, respectively, are equal. Keyfitz (1970), for example, does this and develops an iterative algorithm for constructing a single-radix life table that reproduces exactly the age-specific mortality rates that are its basis, subject to allowances made for differences between the distributions of population and deaths within age groups in the observed population and in the stationary population of the life table. One could not carry out such an iterative procedure in the multiradix case without a formula for life table rates such as ours.

Another way of focusing on the basic issue is to assume that $m = M$, but to imagine that we do not know how to connect the transition matrix $\mathbf{P}$ with the matrix $\mathbf{M}$. We could start by selecting an arbitrary initial approximation of $\mathbf{P}$, compute a multiradix life table, and obtain the matrix $\mathbf{m}$ using our formula (8). We then could compare $\mathbf{m}$ with $\mathbf{M}$, observe a discrepancy, and somehow use this discrepancy to obtain an improved approximation of $\mathbf{P}$, repeating the entire procedure until $\mathbf{m} = \mathbf{M}$.

REFERENCES

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