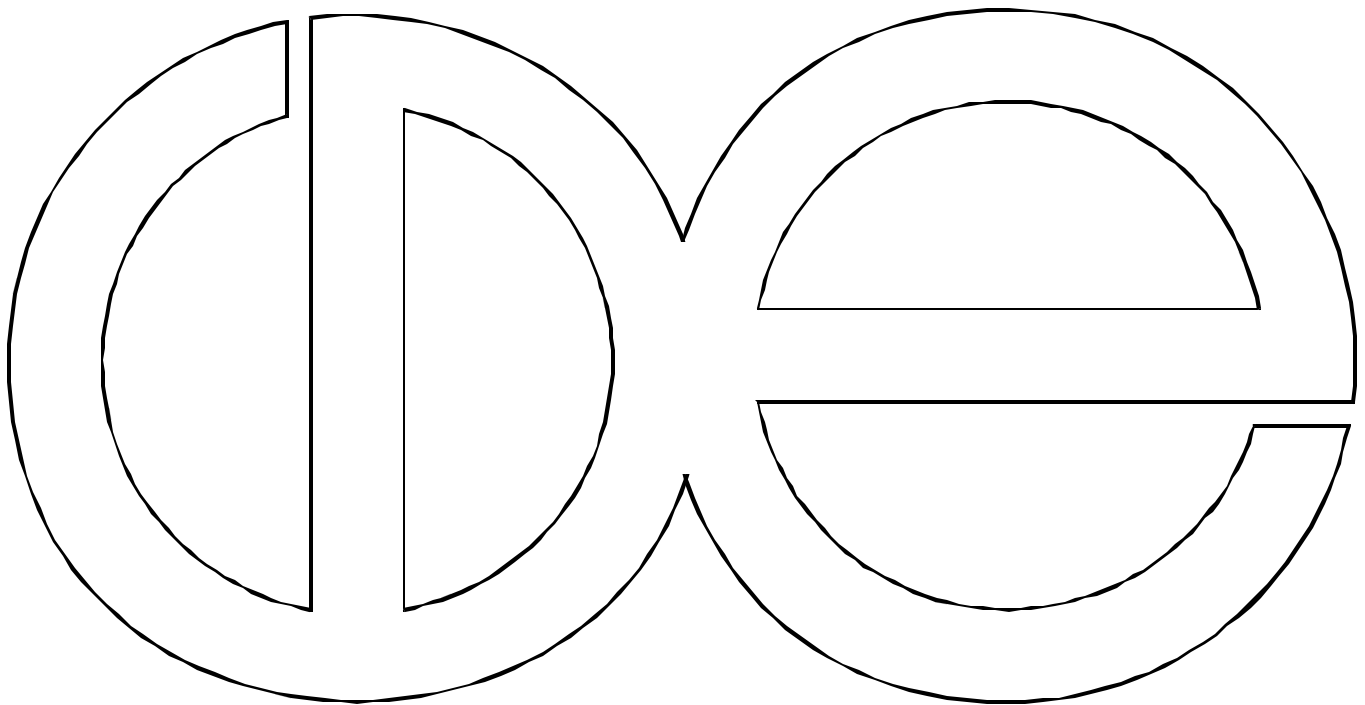# Center for Demography and Ecology

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Demographic Analysis: New Theories, New Models and New Data

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CDE Working Paper No. 2000-01

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1. A brief review of new theoretical developments

Over the last ten years or so demography has made considerable progress on the theoretical front. Old theories have been modified or discarded and new theories have emerged to explain either phenomena not observed before or those that stubbornly resist reduction to conventionally accepted theories. A few examples will suffice to illustrate the point. First, explanations of fertility changes were traditionally fairly loose and imprecise. A case in point is the set of rather disconnected propositions that drawn from the so-called demographic transition framework (Notestein, 1945). More tightness was introduced through contributions by sociologists as Caldwell (1982), Coale and Watkins (1986), Mason(1997), and Retherford (1985), as well as economists as Becker (1960) and Easterlin and Crimmins (1985) who, armed with utility maximization frameworks, lent more rigor though not necessarily more truth, to theories of fertility change. The price paid for this extra amount of rigor was high: for the last twenty years a rigid dichotomy prevailed in the field whereby a paradigm rooted in economic calculus competes with a paradigm where individuals accomodate to social and cultural constraints. However, as illustrated by a recent volume of the US National Academy of Science (1998) such dichotomy is desintegrating as economic theories and corresponding models increasingly incorporate social and cultural factors into the more conventional cost-benefit analysis with rational actors. The new models attempt to explain behavior persistence and change as a function of both individual economic calculations and accommodation to a social and cultural milieu. The models involve complicated feedback mechanisms, and enable us to understand better the exogenous (and sometime endogenous) impact of changes in policies (coordinating agents). Without exception, these models are very demanding of computing technology and empirical information.

Second, although the epidemiological literature on the spread of illnesses benefited very early on from the insights of various deterministic and stochastic models, it remained somewhat stunted and failed to yield the returns expected at the outset. Plagued with mathematical intractability and informational demands that defied even the most ambitious data collection enterprise, the sophisticated machinery developed by Bailey (1975) or Bartholomew (1973), for example, was utilized only

minimally, if at all by demographers. It is only recently and mainly through the influential work by Anderson and May (1991) that such models were revived, fine-tuned, and implemented to answer empirical questions. An example of this are applications to understand the spread of HIV/AIDS. Although these models are still on the shelves of practitioners of demography, there is growing pressure to use them on issues ranging from health and mortality to those regarding relations between events in the life cycle of young adults (Billari, et al., 1999). A very promising avenue of investigation has been pursued by Phillipson and colleagues who embark in an attempt to marry epidemiological models that operate in a social and political vacuum with a utility maximization framework that enables them to introduce rational actors, define mechanism through which their actions can have an impact on aggregate dynamics and those through which aggregate properties of the system influences individual decision making. These, as the aforementioned models involving social interactions, allow feedback to exist between individual decision-making and aggregate properties of the system and, therefore, must face and solve issues related to possibly multiple equilibria.

Third, demographers and sociologists alike have been aware for a long time that some outcomes in the life of individuals--age at marriage, pregnancy, divorce, health status, retirement--are closely connected not just to isolated events or with fixed characteristics acquired in the past, but with entire strings of events and with rapidly changing characteristics. We have even developed a term to refer to this type of strings, namely, ' life cycle stages'. For example, we are now coming to the realization that propensity to divorce may be linked to the kind of family environment and peer groups experienced during early adolescence, and even the propensity to divorce of parents themselves. In social stratification there is a fair amount of research that shows that occupational status at one point in time is a function of the entire past occupational career (as well as marital careers and educational careers), namely, the sequence of status the individual occupied in the past. Similarly, the literature on health status and mortality has produced convincing evidence showing that events in adult life may be traced to events that occurred earlier in life, even in utero (Barker, 1998). Finally, in criminology, a field where demographers and economists have contributed a great deal, we have developed the notion of 'criminal careers' to understand persistent criminal behavior. This conceptualization enables us to

understand how a particular sequence of events in the past locks individuals into a future path where the likelihood of engaging in additional criminal behavior increases.

In all these examples, the key issue seems to be that it is the precise sequence of states that an individual occupies in the past that is relevant for the occurrence (non-occurrence) of events in the future. The study of such phenomena has proven to be quite hard in part because it requires richer data than are commonly unavailable to us. But the difficulties also stem from the fact that this type of approach demands well developed technical tools that most demographers do not know or do not care to learn. An additional obstacle is that feasible and promising procedures are insufficiently developed and have not yet diffused broadly enough in the research community nor have they been tested extensively. Multistate hazard models and sequence analyses are good examples. I will review both below.

Fourth, there are a number of demographic phenomena that require an understanding of how individuals eventually match with each other in terms of some *a priori* defined resources. Marriage is a prototypical example of a matching problem but so are the processes whereby individuals get jobs, or when entire households are involved in decision making about migration of some of their members, or when siblings and parents agree on particular forms of social, material and emotional support, the so-called intra-family intergenerational transfers. Characteristic of all these examples is the existence of some type of dynamic process which requires search and agreement by several actors, all of whom are trying to maximize some sort of benefit in cooperation (competition) with others. Thus, it is not surprising that game theoretical approaches and bargaining models have been brought to bear to elucidate some of them. But the models are difficult, the literature is opaque to most demographers, and the estimation procedures are involved and computer intensive.

Fifth, and lastly, we have known for sometime that exogenous economic, social and cultural changes lead to the transformation of families and households. However, inferences about the occurrence of such transformations from observable family or household configurations--and about the relation between these changes and exogenous factors--are hampered by the simple fact that the same exogenous factors that lead to changes in individual propensities to group under the umbrella of various

family or household forms affect demographic conditions as well. These, in turn, influence the availability of kin thereby constraining the actual frequency of certain family and household configurations (Wachter, Hammel and Laslett,1978; Wachter et al., 1999). The problem is unsolvable except via micro simulation models which enable us to estimate and factor out the magnitude of the impact of changes in demographic conditions, thus leaving a 'uncontaminated' observed change to be explained by the operation of exogenous factors. The first such model was proposed by Wachter and colleagues although a new version by Wachter (Wachter et al., 1999) has been also used. There are a number of alternative models and alternative uses proposed by Ruggles (1987) and Wolf (Wolf et al., 1995) which have not yet found their way into mainstream demography. We will review some of these later in the paper.

Micro simulation models such as these are potentially useful in a number of other context, not just for the study of families and households. And some of our increasingly complex theories will necessitate that we test them using a blend of observed data and micro simulation.

This paper is a brief review of the models and associated estimation procedures being applied in each of the aforementioned. In each case I will present the main features of the models, identify how they enable us to improve over previous models by examining the range of their testable theoretical implications and, finally, review the estimation procedures and associated computational technology needed to make some headway. I hope that my main point is rendered clearly: a substantial amount of improvement is possible but whether we succeed in realizing it or not will depend on our ability to increase the complexity of our explanatory frameworks, formulate novel study designs for the collection of new data and, last but not least, take advantage of new computer technology. The domination of standard statistics is rapidly giving way to alternative approaches that free the analyst from the need to invoke restrictive and sometimes unrealistic assumptions. These approaches, however, are viable only through intensive computing applications. Simultaneously, we should be able to formulate theories incorporating complexities that heretofore could not be reflected in the models designed to test them. Since I am not the first to make this point (see Burch, 1999; Hanemman, 1988; Wachter, 1987), I am not solely responsible for issuing an assessment that could turn out to be wrong.

2. Economic versus ideational theories of fertility

Although the final conclusion of the Princeton fertility study has been recently challenged in at least one country and attributed to incomplete data and faulty modeling (Galloway et al., 1994), it still stands out in the form of a negative sweeping generalization: a significant fraction of the total decline of fertility in Northern and Western Europe during the period 1870-1930 was **not** due to measurable social and economic transformations, as the conventional demographic transition theory would have it. The observation that fertility levels as well as the pace of decline tend to cluster along regional, ethnic and language boundaries prompted the inference that changes were driven by a diffusion mechanism whereby regional, cultural and language barriers could sometimes offer resistance to a wave of change or, vice versa, precipitate further changes.

Whilst the idea that diffusion may drive the process of fertility decline is quite reasonable and attractive, it was never well formulated, that is, the mechanisms through which diffusion was supposed to operate were never spelled out with precision. Further, testing of this weakened version of the hypothesis was rarely done directly and instead proceeded via a residual test, e.g., what could not be explained by measurable ("structural") factors must be attributable to diffusion.

In the aftermath of the Princeton fertility study the field experienced the fierce and rigid opposition between two explanatory frameworks. One reduced fertility behavior to the outcome of rational decision making by individuals seeking to maximize some type of utility. Although in its most rigorous form, this framework was introduced in demography as a direct import from economics, a much looser form had already been applied by demographers (the demographic transition theory is a good example), and was also present in formulations apparently very distanced from the utility maximization framework (Caldwell's intergenerational flows is an illustration of this). The other framework , a much more loosely formulated one, was erected on the idea that fertility decision making was respondent to influences from cultural factors and adherence to practices and beliefs characteristic of ethnic, language or other groups to which actors belong. Waves of ideational change originating in a particular social context could sometimes (and under conditions that usually remain opaque) invade

other social contexts and, if adopted, could go a long way toward explaining the demise of a high fertility regime. An example of this is the idea that 'westernization' is at the root of fertility changes in some developing areas.

Nowhere is the contrast between these two frameworks more starkly formulated than in Cleland and Wilson's rendition (Cleland and Wilson, 1987). In this review the authors describe the differences between the frameworks and mount an attack on the economic explanation showing that all the available evidence regarding fertility decline in developing areas point to the existence of influences associated with ideational factors that far outweigh those associated with individual socioeconomic positions. Whether this is the case or not is not as fundamental as the resolution of two key theoretical issues. First, is it reasonable to reify these two frameworks as if they were truly competing entities in a zero-sum game ? Second, can we conceive of diffusion or ideational processes where a new behavior is adopted **without** incorporating constraints imposed by individual's socioeconomic positions? In my view the answer to both is negative. I will deal with each of them in reverse order.

a. Diffusion processes do not occur in a socio-economic vacuum.

Elsewhere (Palloni, 1998), I offer a definition of diffusion processes that captures the complexities involved in representing the mechanisms through which diffusion occurs: 'A diffusion process is one where selection or adoption (rejection) of a behavior or practice depends on an individual decision-making process that assigns significant influence to the adoption(rejection) behavior of other individuals within the social system" (see also Montgomery and Chung, 1994; Montgomery and Casterline, 1996; Montgomery and Casterline, 1998). The definition implies the adoption of two important premises. First, diffusion results from individual decision making processes and are not, as conventionally thought, the outcome of a somewhat mindless, a-rational choice of behavior. From this point of view the contrast between, on the one hand, a rational actor whose decision depends on prices and individual budgets and, on the other, an impulsive individual whose actions depend on the operation of obscure inclinations toward or against adopting some behavior, is a false one. Second, the distinction between a situation involving diffusion and another that does not is the existence (non

existence) of social influences, that is, effects of other's behavior on ego's behaviors. A key element is thus the identification of the set of 'significant others' for a given individual and for a given behavior.

b. Integrating models I: sociological models

Armed with this definition we can translate theoretical propositions invoking diffusion process into more or less refined models to be tested directly so that the diffusion explanation ceases to be validated by default. There a number of ways of doing this and all involve integration into a single model incorporating factors associated with both individual maximization calculus and social influences. For the sake of brevity of exposition I choose to describe two models, one of sociological and the other of economic inspiration. Unfortunately this does not do justice to the richness of this models (see also Montgomery and Casterline, 1998; Strang and Tuma, 1993; Durlauf, 1999; Brock and Durlauf, 1995; 1999; Durlauf and Walker, 1998; Kohler, 1997)

The first model is one of sociological inspiration. Here we represent individuals choosing among a set of alternative behaviors under a set of individual and social constraints. This can be accomplished most efficiently positing the existence of a system with two states, one representing adoption of the target behavior and the other representing adoption of a different behavior. Subjects are allowed to move between these two states as a function of individuals characteristics associated with social and economic conditions (costs and utilities), external characteristics acting as constraints (or facilitators), influence of external sources of ideas and effects of individual's social networks. To capture the dynamic of this two-state system we can formulate a pair of equations for the risk or hazard of transitions between the two states:

$$\mu_{12i}(t) = \mu_{o12}(t) \exp(\boldsymbol{\$X_i}(t) + \boldsymbol{(Z_i}(t) + \boldsymbol{"W_i(t)G(Y(t))} + g_{i12})$$

$$(1)$$

$$\mu_{21i}(t) = \mu_{o21}(t) \exp(\boldsymbol{\$*X*_i}(t) + \boldsymbol{(Z*_i}(t) + \boldsymbol{"W*_i(t)G*(Y*(t))} + g*_{i21})$$

where $\mu_{12i}(t)$ is the risk of moving from state 1 (non adopter) to state 2 (adopter) for

individual i at time t, $\lambda_{o12}(t)$ is a baseline hazard, $\mathbf{X_i}$ is a vector of 'structural characteristics'
of individual i, $\mathbf{Z_i}$ is a vector valued function containing information on external sources of
information that may influence i's choice, $\mathbf{W_i}$ is a contiguity vector for individual i
containing the weight assigned to the influence of contacts with individuals j=1,...i-1,
i+1,...N, where is N is the total number of members in the system, $\mathbf{G}$ is a functional
transform and $\mathbf{Y}$ is a vector of responses for members j=1,...i-1,i+1,...N. Finally, ε_{12i} is an
error term. The second equation defines the risk of moving from state 2 to state 1
(abandoning the new behavior). It is analogous to the first but with the possibility of
different baselines, different effects, and different matrices of covariates. The contiguity
vector is time dependent to allow for changing influences derived from social networks
during the process. Similarly, the vectors of responses $\mathbf{Y}$ and $\mathbf{Y^*}$ allow for updating of
information about members of the system.

This model confronts a number of problems. The most important one is that its nature is t *ad
hoc* since there is no theoretical formulation from which one can infer or translate specific mechanisms
through which social influences and individual characteristics affect decision making. This problem
disappears if one chooses an economic framework.

b. Integrating models II: economic models

Although there are other formulations involving social learning (Kohler, 1997; Montgomery and
Casterline, 1998) I summarize here an attractive model of effects of social interactions developed by
Brock and Durlauf (1995), Durlauf (1999) and Durlauf and Walker (1998). The appeal of this
formulation is that it effectively marries an individual utility maximization model incorporating social
interactions with discrete choice models that are familiar and estimable from empirical data, at least
when the system is in equilibrium. One starts with a set of actors, i=1,...,I, in some social context; each
actor desires to maximize utility at time t from adoption (non adoption) of a behavior w_{it} that can attain
values 1(adoption) or -1 (non adoption). Their decision depends on maximization of a function V of
individual characteristics X_{it}, perceived (average) response from other actors, w_t^*, and unobserved
external shock, ε_{it}. The fundamental steps in the formulation of the models are to posit the nature of V

and that of g_{it}. First, V is assumed to have a linear structure so that:

$$V(w_{it}, X_{it}, g_{it}(w_{it})) = u(w_{it}, X_{it}) - J/2(w_{it} - w_t^*)^2 + g_{it}(w_{it}) \qquad (2)$$

The model is composed of two types of utility: one is the individual utility embodied in the first component u(.); the other is the social utility represented by the second component. This depends on a parameter J and a measure of social conformity $(w_{it} - w_t^*)$. When J is 0 the model collapses to a classical individual utility maximization problem. Second, the random utility terms are assumed to be extreme value distributed so that their difference is distributed as a logistic function. It is this assumption that renders the model tractable via conventional discrete choice approaches. The next step in the formulation is to solve for the equilibrium mean choice. This solution is sought by investigating the nature of the individual probability of adopting the behavior at each point in time, given the desire of extracting maximum utility. Asymptotically (when the number of individuals grows to be very large) it is verified that the system may have one or three equilibria with distinct mean behaviors. Which equilibria takes place depends on the strength of social utility and the magnitude of the bias toward one choice induced by private utility. In environments where social utility overwhelms individual utility one is more likely to observe multiple equilibria. The model also implies that in the presence of large social effects, small amounts of initial changes motivated, for example, by adoption among a few forerunners, may lead to a cascade of individual changes precipitating a rapid fertility decline.

Either model (1) or (2) implies that (a) individual decision making is not independent from social effects and (b) that adoption behavior takes place in a setting where individual make rational decisions. Applications of either of these models encounter similar difficulties. The first is the need for information about decision-making on the part of other actors, and on who among these may be significant actors for any ego. Admittedly, choosing a matrix of weights for others' choices (required in model (1) but not in the current form of model (2)) is not a trivial matter and must be resolved theoretically. Even if resolved though, one needs to assess such weights empirically and this inevitably entails challenging problems for data collection. None of these models can be estimated with a minimal degree of

robustness without access to longitudinal information.

The second difficulty is that empirical estimation of the models is not simple and usually special techniques and procedures are needed. Model (1) requires to posit the existence of individual heterogeneity which normally leads to serious identification problems and is only solvable at the expense of carrying out complicated integration and, at least in some cases, application of Markov Chain Monte Carlo (MCMC). Estimation of the models derived from the more economic framework above are usually problematic since they involve the assumption that the system has reached a steady state. Finally, confirmatory analysis may require us to perform micro simulations as an aid to decide between alternative feasible formulations.

3. Individual behaviors and systemic properties

Modern demographic applications frequently focus on the following type of problem: individuals occupy a limited number of states, i=1,...k, and transit between them according to an intensity or hazard rate, $:_{ij}(t)$. For example, in the analysis of adult health we postulate the existence of a multistate system with four states, healthy, with chronic illness, with disability and dead. A family demographer may desire to focus on stages in the family life cycle in which case we are interested in states such as marriage and cohabitation, divorce and separation, childbearing. Or, finally, we may wish to test theories regarding fertility in which case one could use the equivalence between states and birth orders. In sum, an impressive array of demographically interesting problems can be so conceptualized. Multistate hazard models have been designed to enable us to estimate basic parameters or functions, namely, the baseline hazard rates (the $:$'s) and the effects of covariates (some fixed and some time dependent) on the baseline hazard rates. Estimation of these models requires fairly detailed information on the timing and order of the events, on the characteristics of individuals, and on the nature of unmeasured characteristics. It must be said that precious little empirical research has made use of these models even though they could yield high returns. Since the data requirements are fairly stiff, formulating the problem at the outset as one involving multistate hazards could enable us to suggest new data collection designs that meet the desiderata for estimation and identification of these models.

But the plain application of these procedures is not the only activity that will enrich demographic

analysis. There are two additional promising lines of work that analysts are beginning to study in some detail. The **first** has to do with the macro implications of micro processes. Estimation of a multistate hazard models on observed sequences of individual processes does not in itself provide information about aggregate properties, e.g . about the net effects of the micro processes (those taking place among individuals) on a macro level (the implied aggregate characteristics). For example, given estimates of the hazard rates and effects of covariates from a multistate model describing health and morbidity, we may want to know what is the implied distribution of the population by health status, by duration in each state and by age. Anderson and May (1991) provide a complete machinery linking individual transition rates and aggregate distributional characteristics. Billari and colleagues (1999) applied some of Anderson and May tools in order to study the steady state characteristics of young adults that corresponds to a particular set of rates at the individual level. These inferences, however, require the assumption of a steady state, the existence of which is by no means assured and should be explored *ex ante* Alternatively, one must focus on the dynamic of the system, that is, on the trajectory of the aggregate system over time, as a function of evolving individual processes. This is not a trivial task because it is frequently plagued by analytic difficulties and requires substantial computing power

The study of the relation between macro and micro processes can also provide tools for **discriminating between different micro models**. Most of these models are non nested and their relative performance cannot be assessed with conventional log likelihood ratio tests but require Bayesian assessments (such as the use Akaike criterion or the BIC measure) . However, it is clear that using the macro implications of an estimable micro-model one could assess the degree to which observed aggregate distributional properties more or less approximate the ones directly implied by the micro models. I have yet to see analyses where this strategy is fully deployed. Take, for example, the estimation of a multistate model for the analysis of fertility. The models can get as complicated as we may wish to make them but, for the sake of simplicity, let us a assume that one has a series of states representing n birth orders and n-1 transition rates to estimate. Estimates of the rates and of the effects of covariates on the rates directly implies a measure of aggregate fertility, such as TFR. If the implied value for TFR does not approximate observed TFR values, then the model is probably incorrect,

regardless of what the likelihood ratio or t-tests may suggest to the analyst.

There are other applications and implications as well. Consider again a multistate model for health, morbidity, disability and mortality. This model is or ought to be the foundation for calculating measures such as Active Life Expectancy (ALE). Yet we know that in most cases ALE estimates are derived from cross-sectional information and one never tests for distortions induced by the fact that what we observe currently is one of many possible stages in a dynamic process. It may be possible, however, to adjust conventional ALE measures using micro simulation in conjunction with estimated multistate models.

The **second** line of research alluded to above regards the formulation, implications and estimation of the influence of characteristics of the aggregate system on individual decision making. This theme is the same as the one just reviewed in the case of diffusion models for fertility but in a context with multiple states. I will provide two examples which should shed light on the problem

a. Occupational choices and aggregate saturation

Suppose we are interested in the occupational behavioral choices of women who face labor markets where there are two types of occupations: female dominated and male dominated. For the sake of illustration let us define a male (female) dominated occupation as one where more than fifty percent of the incumbents are males (females). The theory tells us that female's transition rates into and out of the labor force is a positive function of the density of female dominated occupations, so that the rates are higher as the availability of female dominated occupations exceed some threshold value. This is an example of a phenomenon where individual behavior has an impact on the average characteristics of the system and this, in turn, affects the structure of incentives for individual behavior. Our intuition tells us that the system may either collapse to a unisex occupational structure or that there could be some (one, two, multiple) equilibrium points. The type of asymptotic behavior will most likely depend on the relative magnitude of the baseline rates and the relative magnitude of the effects of relevant covariates on the male (female) transition rates. In some cases an analytic solution to the problem may be available, but in most cases one will need to resort to simulation models in order to investigate the implied dynamics of the system.

b. The spread of disease in social contexts with choice of preventable behaviors

Classical epidemiology tells us that as the prevalence of an infectious disease grows, the prevalence of the disease also increases. In the absence of retreats to immunity or of subgroups with very low infectivity and unconnected with groups of high infectivity, the infection will overwhelm the population. Suppose, however, that individuals are allowed to choose a preventable behavior, such as protected sex or vaccinations, and that the adoption of this behavior depends on prices of adoption and on the perceived (expected) levels of prevalence of the disease. A modified Anderson-May system of differential equations can describe this situation (see also Phillipson, 1998):

$$\frac{\partial S(t)}{\partial t} = b(1 - P(I(t), p(t))) - \boldsymbol{b}\, S(t)\, I(t) - m\, S(t)$$

$$\frac{\partial I(t)}{\partial t} = \boldsymbol{b}\, S(t) I(t) - (\boldsymbol{w} + m)\, I(t) \qquad\qquad (3)$$

$$\frac{\partial R(t)}{\partial t} = b(P(I(t), p(t)) + \boldsymbol{w}\, I(t) - m\, R(t)$$

where S(t), I(t), R(t) are the proportions susceptible, infected and recovered (and then immune) at time t, P(.) is the fraction demanding immunity (say vaccines), and p(t) are prices at time t. The parameters are rates: b for births into the population, $ for infectivity of a contact between an infected and a susceptible individual at time t, T for recovery into immunity, and m for mortality rate. There are all sorts of simplifications in this system, not the least of which is that it completely overlooks the role of age. But for the purpose of illustration, it will suffice.

From this system, it is clear that the rate of change of I(t) is positive provide that $S(t)/(T +m) >1. Suppose that we let actors make decisions about whether to use the preventative behavior. The choice can depend on a decision-making rule involving discounted streams of expected values associated with the susceptible and infectious states, current utility in the two states, as well as the

levels of prevalence and $ (Phillipson, 1998). The outcome of such a formulation is that individuals will adopt the behavior only if prevalence of the disease exceeds a threshold value which is unobserved for all individuals. Under an assumed (any continuous) distribution for individual thresholds, it is possible to show that as long as the individual response to levels of prevalence is sufficiently pronounced, the hazard of becoming infected **decreases** with prevalence. This is contrary to the classic epidemiological scenario. Similarly, to the extent that prevalence decreases to very low values, the attractiveness of adopting the preventative behavior decreases for all individuals who are still susceptible, and this will trigger the emergence of a new stream of infections and new increases in prevalence. This too is contrary to conventional wisdom in classical epidemiological models.

This scheme can certainly be enriched with a number of modifications. For example, individuals may not respond to average levels of prevalence but to average levels observed or expected in selected groups of membership. This will necessitate to define the nature of those groups for each individual in the system. In so doing we approximate the situation faced in the study of diffusion of fertility behavior. More complexity may be needed to apply the model to other areas of behaviors such as residential mobility, deviant behavior, and the like.

Issues revolving around the relation between individual behavior and systemic properties are inherent in the work of sociologists, demographers, and economists. Sociologists and demographers have traditionally avoided explicit formulations to solve the problem whereas economists have resorted to formulations of market mediated actions. Surely neither of these two research practices is sufficient to deal with the complexity of social interactions.

4. Transitions and sequences in life cycle analyses

Suppose we wish to study the following type of situation: we suspect that a particular outcome or behavior, say health status during late adulthood, H(t), depends on behaviors practiced and positions occupied during the past. Among these positions we include types of jobs, type of family environments, and residential choices. The theory may suggest that H(t) is not simply a function of independent effects of all these behaviors and positions but a result of the particular sequence of positions and behaviors followed by the individual. Another example where sequences of events acquire importance is in the

study of onset of family planning programs, F(t). One could argue that in order for the institutionalization of such programs to occur, societies must undergo a series of transitions involving, for example, the formation of a strong central state, the resolution of the conflict of interest between state and Church, the emergence of organized labor, the birth of neighborhood organizations, and the formulation of economic plans involving massive foreign credit programs. Here too, a theory may posit that early adoption of family planning requires the passage through a particular set of stages, and that in its absence early adoption is more difficult or impossible. Other examples can be drawn from the literature on occupations and status attainment, retirement, and from the literature on criminal careers.

All these examples could conceivably be studied using multistate hazard models. However, it is not difficult to show that deploying multistate hazard models could lead to intractability and/to excessive data demands. This is because to test the theory it will not be enough to estimate effects of covariates on the various transitions. What one needs is to estimate the effects of particular configurations of past trajectories on a particular outcome. This can be done using time dependent covariates reflecting states visited in the past, duration of sojourn, frequency of visits and the order of a subset of transitions. As practitioners know well, this can get out of hand quickly if the positions or states are more than a handful, and if trajectories are long.

More recently a number of social scientists have begun to work on sequence analysis (Abbott and Tsay, 1999; Abbott and Barman, 1997). The inspiration for this approach is drawn from tools designed in molecular biology and genetics for the analysis of resemblance/diversity of protein and DNA sequences. In particular, the applications involve the study or ordered arrays using Optimal Matching (OM) algorithms, one of a number of alternative computing algorithms developed to study ordered arrays in a number of different fields.

OM algorithms rest on three key stages: coding, assessing distances, and clustering. **Coding** is a theoretically driven activity to define the various states on which the analyst will focus. This will involve decisions about lumping or splitting events and will, therefore, shape the nature of the sequences that one will use in the remainder of the analysis. For example, one could study careers using officially defined occupations or, alternatively, a theoretically inspired occupational classification that partially

lumps together some of the official categories. In the study of life cycle stages one may want to partition the category ' two parent family of origin' into two subcategories, one with and the other without resident grandparents. Note that it is possible to define a state so that it captures multiple states **and** the order of transitions between them. For example, if one is interested in studying labor force participation, it would be feasible to define as a state the **transition** from unemployed to employed, and as a different state the **transition** from employed to unemployed. Timing is taken into account in simpler ways as well, such as designing arrays where the loci are states or positions occupied on, say a particular year (if year is the appropriate time unit).

The next step is **assessing distances**. This is done by generating matrix of distances between pairs of individual arrays. The dimension of the matrix depends, of course, on the number of cases in the sample. In order to assess distances between arrays or sequences it is first necessary to use three operations that can translate one array into another. These operations are replacements, insertions and deletions. Since the arrays are strings of characters--drawn from the alphabet of states defined in the coding stage--the distance between any two arrays can be measured by counting the minimum number of replacements, insertions or deletions of characters necessary to transform one array into the other. For example, the strings LAZIO and MILAN require a minimum of two replacements to be identical (a maximum of five is ordering of the sequence is relevant), whereas the strings LAZIO and FIORENTINA requires 5 insertions (or deletions) and two replacements (five if order is relevant). But not all replacements and insertions or deletions may be equally important from a theoretical point of view. In order to let these operations have theoretical meaning it is necessary to define a matrix of weights or costs so that certain operations are more heavily taxed (and mean more in terms of distance) than others. This weights must be chosen by the investigator and should be derived from theory rather than being arbitrary. At this stage computing intensive technology comes in: the assessment of distances depends on the application of computer algorithms involving a very large number of operations and, in some cases, one needs to resort to approximation techniques, such as Gibbs sampling, in order to get solutions.

The final stage of OM algorithms is the analysis and utilization of the distance matrix, **D**.

If this is a N x N matrix, it will define N (N/2-1) observed non-redundant distances between the sample arrays. At this point one attempts to reduce the dimensions of the observed distances into a smaller number of **typical** distances. This can be done displaying a number of classification algorithms, such as cluster analysis. In the end, we will be able to map an N(N/2-1) dimensional space into, say, a K dimensional space where, hopefully, K<N/(N/2-1). These K distinct distances (or, more precisely, clusters of distances) are produced by a reduced subset of the N possible sequences. Sequence membership in clusters of sequences is a discrete variable that can be used to explain outcomes or as an outcome to be explained by other factors.

OM algorithms and the entire skeleton of sequence analysis is the object of intense scrutiny and much skepticism (Wu, 1999). The required intensive computation at the second stage of the OM algorithm is an obvious problem. But the Achilles-hill of OL is the definition of the cost matrix: how can one define a non-arbitrary cost matrix? And how sensitive are final analyses to changes in this matrix? An important issue here is that apparently identical replacements may mean different things and different weights ought to be assigned to preserve such differences. Thus, from a theoretical point of view it is not the same to move from unemployed to employed than to move from employed to unemployed (Wu, 1999). Yet, if these are treated as sequences the assessment of distances involves symmetry and the two will be treated alike. Finally, the reduction of the distance matrix using clustering algorithms is another step where arbitrary decisions may influence the analysis and cause lack of robustness. Clustering algorithms are notorious for their sensitivity to a priori specified rules of clustering. Although it is too early to say what the pay off of this methodological approach will be, it is worth exploring and developing further since, in theory at least, offers solutions for testing theoretical complex formulations that are intractable with extant models and procedures.

5. Matching problems

The marriage problem is well known to demographers. It involves understanding the rules that regulate the matching of males and females in a marriage market. What we normally observe are frequencies of matches already made and frequencies of unmatched individuals. Each member of the pair in a match and each unmatched individual possess relevant characteristics such as age, education,

race, etc...More rarely we may observe the dynamic of match making over time, with individuals entering a union, remaining without partners or dissolving the union. In either case the problem is to identify how individual's preferences for partners, for remaining unmatched, or for disrupting a union operate to render the set of observed matches or couples at any point in time.

Job searching and employment are also match-making phenomena. In this case employers seek and attempt to hire workers and workers seek and attempt to get offers from employers. And, here again, what we frequently observe is a cross sectional set of matches (and non-matches) and, more rarely, the evolution of the job-searching and job offering process.

Finally, intra-family transfers from, say, children to parents (and vice versa) is another example of a process whereby individuals attempt to establish a contract so that each member of a partnership makes a commitment to the other to supply services, emotional support, income or to secure access to assets. This particular example, however, introduces a new complication since, by and large, parents confront not one child but several children who may cooperate (or compete) among themselves. Thus, one of the partners in this exchange is a collectivity wherein second order processes may be occurring, namely, siblings may bargain amongst themselves to coordinate the supply of transfers to their parents.

Up until recently the marriage problem as well as the problem of intra family transfers have been approached in rather ad hoc ways, using conventional multi variate techniques that identify the strength of selected individual characteristics on the probabilities that such an individual enters a match. Typically one does not know the context in which choices were made since we have no information on the pool of potential 'partners' available at the time. Therefore, it is difficult to infer individual preferences for one cannot distinguish them from the degree of availability of desirable matches. These approaches are usually atheoretical or based on very loosely formulated theories, and overlook the fact that in all cases the formation (non-formation or dissolution) of a match involves confrontation of two, not one, individuals who make decisions about the gains (losses) associated with each potential match.

In contrast, job search theory in economics uses a rigorous theoretical framework, with explicit formulation of individual preferences and explicit decision-making rules according to which individuals

may decide to form a match or continue searching among a set of potential preferred partners. However, except for rare situations where one normally knows the availability of desirable matches, application of these frameworks is also limited by the same difficulty mentioned above, namely that of discriminating preferences from availability.

In a recent paper devoted to the study of matching between employers and workers, Logan(1996) proposed a Two Sided Logit (TSL) model to estimate the effects that individual preferences have on the observable worker-employer matches. The key element of the procedure is to replace the unobserved choices available to one side in the match by estimates of the preferences of individuals on the other side. These estimates are retrieved from a cross section of matches where there is limited information on employers and/or employee characteristics. In a recent extension of the procedure Logan and colleagues (Logan et al., 1999) tackle the marriage problem when one has full information on individual characteristics that enter in their decision making process. In what follows I will illustrate the main features of the approach for the case of marriage.

One starts from the proposition that a male i has a preference for women j that depends on a limited set of her characteristics, say X_j. Analogously, man j has preferences for remaining single (choosing partner j=0) that depend on his characteristics, X_{io}. The same applies for a woman j. The second proposition is that these preferences can be expressed as utility functions that translate a preference into a (not discounted) utility for each actor. This imply the existence of four equations representing the ith man's utility derived from a woman j and from staying single, and the utility of woman j derived from man's i and from staying single:

$$U_{ij} = ''X_j + g_{ij}$$
$$U_{io} = ''X_{io} + g_{io}$$

(4)

$$V_{ji} = \$Y_i + g_{ji}$$
$$V_{j0} = \$Y_{jo}$$

where U_{ij} is the utility derived by man i from woman j who possesses characteristic X_j, U_{io} is the utility derived from man i from remaining unmatched, " measures the strength of preference and g_{ij} and g_{io} are continuous independent and identically distributed errors. The symbols in the last two equations have analogous interpretations for woman j. The main idea is that men and women proceed to rank potential partners (including staying single) while attempting to maximize their utility. Given a single draw of error terms, each man can order his preferences regarding all women available. The same applies to women. The X's and Y's (as well as the " and $) may be scalars or vectors. Under these conditions the problem is equivalent to a two-sided matching model, well known in economics, and which can be shown to have a fundamental property: there is always a stable state of matches in which no man could find a partner whom he would prefer and who would also prefer him over any other man, with the same holding for women. This property is fundamental for estimation is possible only if one assumes that the observed set of matches is a stable set. This is not as strong assumption as it may sound since it only requires that the stability be transitory, subject to variation as new people enter into the market and when characteristics change. All is needed is that matches be the result of voluntary decisions, not that they be unchanging as individual preferences or characteristics change. However, the uniqueness of this stable set of matched requires the assumption of complete utility transfers and may not hold when there are constraints on both side of the match on the transferability of utility (Buder and Wright, 1994).

The advantage of this formulation over the more simplistic ones available in the standard literature on the subject is that the match making process takes into account the preferences of individuals on one side of the match, and the constraints on availability imposed by the preferences of individuals on the other side of the match.

The objective of an empirical analysis is to retrieve estimates of " and $ from an observed set of matches. This is done utilizing the TSL model which can be reasonably implemented through application of MCMC methods, a technique through which one can approximate the 'true' value of parameters governing complex probability distributions.

Can this procedure be applied to other areas in demography? With some simplifications, one could certainly study intergenerational transfers between parents and children. These have been the

object of study by economists with utility maximization frameworks (see for example Lillard and Willis, 1995; 1997) but neglecting the issue of availability noted above, except in an *ad hoc* manner. The first step to apply the model is to redefine who the actors are: parents can be treated as a one side of the exchange and each child in turn (or all children or a combination of them) as the other side of the exchange. The second step is to define what the matching involves. It could be living arrangements, or monetary support or the supply of services or a combination of all of these. The third step is to formulate an explicit model for preferences that takes into account characteristics of the parents and children and the hypothetical weights (preferences) assigned to these characteristics by each side of the exchange. The final stage is to start from the assumption that the observed configuration of transfers is indeed a stable set and then proceed with the MCMC estimation algorithm.

This set up is not devoid of difficulties. Thus, the fact that transfers are two-sided, in the sense that children provide for parents after parents have invested in children, poses the problem that the latter type of transfers, if they occurred at all, took place in the past and are, for all purposes, unobserved. That is, the observed flow of transfers from children to parents may be a function of past (unobserved) transfers from parents to children. The second problem is that the true nature of the process surely involves bargaining among children themselves and these are thoroughly masked by a reduction of one side of the match to a single actor.

These difficulties that may plague applications of TSL to the study of intergenerational transfers and, no doubt, to other areas where its use could be advantageous, do not detract from the fact that TSL is a reasonable approach for the study of phenomena that have been heretofore intractable.

6. Micro simulation models

Micro simulation models have been around demographers for a long time but their uses have been limited to the study of fertility (Ridley and Sheps, 1966; Wood and Weinstein, 19xx; Larson, 19xx; Barrett, 1971), evaluation of family planning programs (Inoue, 1977), and specially to evaluation of kin availability (Wachter et al., 1999a; 1999b; Ruggles, 1987; Wolf et al., 1995). These micro-simulation models have also been proposed as refined tools for performing more accurate population projection (Land, 1986; Wolf, 1999; Nakamura and Nakamura, 1978). More recently Wachter,

Knodel and Van Landingham (1999b) suggest ways in which micro simulation models can be used to assess the impact on kin availability for the elderly in countries such as Thailand that have been affected by HIV/AIDS. Wolf and Laditka (1996) propose their applicability to studying issues related to active life expectancy.

In order to understand the main properties of these simulation models, it is convenient to introduce a simple example. Suppose one desires to study the process whereby individuals are subject to transitions to and from a limited number of states, say health, chronic illness, disability and death. One starts with an initial or jump-off population distribution by state, usually obtained from secondary data sources or as a result of applications of the micro simulation model itself to data describing transitions in the past. After deciding on an appropriate time scale, the initial population is subjected to the hazard or risk of transitions characterizing the states initially occupied by individuals in the population. These hazard rates are estimated from empirical data or, if projecting into the future, they must reflect the investigator's belief in their future values. Once the hazard rates are identified, transition probabilities are calculated and a waiting time is imputed to each individual by selecting a random number, R, from the unit closed interval. The hazard rates and the probabilities are sequentially applied from the first until the final interval of time, say the Kth interval. In the nth interval of time (n<K) there are two decisions to be made for each individual:

a. Does the individual experience the transition from state i to state j (j=1,2,...i-1, i+1,...S)?

If the transition rate from state i to state j...i in the nth interval is constant and equal to $\vdots_{ij}(n)$, the probability of experiencing the event is given by $h_{ij}(n)=1-\exp(\vdots_{ij}(n) *(n))$, where $*(n)$ is the width of the interval. A random number R_1 is drawn from an unit interval and one decides that the individual will move from i to j if $R_1 <= h_{ij}(n)$.

b. If the event occurs, what is the waiting time?

If the individual moves from state i to state j one must decide the associated waiting time. A second random number is drawn, R_2, and the waiting time in the nth time interval, $) <^*$, is calculated as

$$） = \ln (1-R_2 \, h_{ij}(n))(:_{ij}(n))^{-1}$$

Since individuals will normally be exposed to a number of competing risks--corresponding to each of the feasible transitions out of the state currently occupied--these two decisions ought to be made for all competing transitions. If, as a result of the calculations, an individual is scheduled to experience several events, one choose the one with the smallest associated waiting time. It immediately follows that the frequency of an event, say moving from state 1 to state 2, is calculated aggregating the individual events instead of being, as it happens in macro simulations, the expected number of events in the time interval.

These calculations are applied to each and everyone of the K intervals over which the investigator decides to follow the process. In the end, it will be possible to calculate indicators characterizing the multistate process such as, for example, the mean number of times that an individual visits state j, the distribution of individuals by state at the end of the process etc...

If a Monte Carlo simulation is performed, the calculations are repeated a large number of times, large enough to be able to calculate approximate distributions for the indicators of interest. This is important for it allows the investigator to assess measures of central tendency as well as of dispersion of the distribution, thus enabling one to associate a measure of uncertainty to the calculations.

Unlike micro simulations, macro simulations are designed to calculate expected number of events within each interval thus neglecting the inherent randomness at every time step and rendering impossible the calculation of variances or of other measures of dispersion that reflect randomness. This is a key property distinguishing micro from macro simulations.

A second important feature of micro simulation models is that one can make the state space as complicated as one needs to without running into constraints associated with number of observed frequencies. This is because, as long as one is able to estimate the rates for each pair of transitions, it will be always possible to estimate the frequency of associated events in an arbitrary initial population. In contrast, in macro simulations this is frequently not possible since the estimation of probabilities for a given path of events is made difficult or impossible when the number of cases to which such path is

applicable is too small. Said otherwise, in a micro simulation model the probability measure associated with a given path of events is a result obtained at the end of the simulation, whereas in a macro simulation such probability must be known in advance before obtaining results.

A third property of micro simulation models is that one can introduce individual heterogeneity, measured and unmeasured. Measured heterogeneity is taken into account by defining different rates for individuals with different characteristics such as age, social class, cohort etc...Unmeasured heterogeneity is taken into account choosing for each individual an adjusting factor for each transition rate. Typically one defines a probability distribution to characterize such unmeasured adjusting factors and, in each time step and for each transition rate to which each individual is exposed, we randomly draw adjusting factors and then inflate (deflate) correspondingly the rate before calculating waiting times.

Macro simulations cannot take into account individual heterogeneity (except only as averages) and the scope for measured heterogeneity is limited since, once again, the number of cases in each *a priori* defined category (age, cohort, social class) may be very small thus compromising the stability of the rates.

This machinery is, in principle at least, not overly complicated. It allows representation of processes with many individuals, complex state spaces, measured and unmeasured heterogeneity, and even with stochastic versions of parameters. In addition, micro simulations of kin can also establish and retrieve kin and cognate relations between individuals in the simulated population thus permitting us to examine the effects of variability in demographic rates on the distribution of the population by kin types. These properties make simulation suitable for population projections, for projection of kin frequencies, for the study of kin frequencies in hypothetical demographic regimes, for the study of long term properties of complicated multi state models, for the study of emergence of behaviors that depend on individual membership in social networks, etc... The range of applications is truly formidable.

But there is no free-lunch. Indeed, micro simulations do have limitations. The first and perhaps most important shortcoming is that one must rely on a typically large set of parameters, some of which may not be known or estimated at all and must be guessed. The advantage

of micro simulation in this case is that one can assess--although this is rarely done--the degree of sensitivity of the simulation results to different specification of the unknown parameters.

In addition to a large set of parameters, micro simulations necessitate a jump-off population which is usually estimated from sample data. These data may be subject to sampling errors and may contain missing information that one must impute before proceeding.

Finally, the implementation of micro simulation rests on computer programs that are long and complicated, and where the opportunities for hidden errors ('bugs') abounds. I am not referring here to code errors that result in glaring inconsistencies. I am speaking of code errors that are subtle because they distort calculations only if a set of conditions occur but not at all when those conditions do not apply. The only way in which such errors can be detected is performing costly and time consuming validation tests that investigators are rarely willing to undertake (for an exception to this rule see Wachter et al., 1999b)

A final shortcoming that plagued micro simulations models in the past twenty years was associated with the storage capacity and computer speed limitations inherent in the available computer technology of the time. This is, I think, no longer a relevant obstacle.

7. Summary and conclusions

I have reviewed the development of approaches suitable to test new and more complex demographic theories. The review illustrates the point that demographers have made substantial progress in the sense that simplistic theories have been abandoned and replaced with more precise, albeit more complex, theoretical formulations.

Models translating these new theories and procedures to estimate these models have also evolved in the direction of increasing complexity but their implementation are demanding new and more data--particularly longitudinal observations--and, not trivially, vast amounts of computer power, in terms of both speed and storage capacity. Indeed, rapid changes in computer technology may, for a while at least, drive progress in the modeling and testing front of research and these, in turn, will facilitate the formulation of newer and bolder theories.

I doubt that the progress experienced in the past ten years is a blip in an otherwise irregular

landscape of very slow and gradual improvements. I venture to say that in the near future the unusually rapid developments that I reviewed here will be multiplied several times, completely transforming the way we do demography and social sciences in general.

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