

**Confessions of a Microsimulator:
Problems in Modeling the Demography of Kinship**

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I could not, without effort, constrain myself to the task of either recalling, or constructing into a regular narrative, the whole burthen of horrors which lies upon my brain.

—Thomas De Quincey,
Confessions of an Opium Eater

When I began microsimulating about a decade ago, I had no conception of the dangers involved. It seemed so easy at first. I started with a few basic probability distributions, a random number generator, and lots of simplifying assumptions. But then, slowly at first, my model began to grow. One by one, I began to address those issues that I had once been content to ignore. No more did real data provide me with the thrill it once had; I was in the grip of microsimulation, lost in an unreal world populated by hypothetical individuals.

I have now broken the hold that microsimulation once had over me. I still suffer occasional relapses; I suppose that no one ever fully recovers from microsimulation. But I have gained enough distance from the vice to speak freely of it. This paper will focus on a problem that is almost universally acknowledged by microsimulators, but whose implications are rarely discussed. I call this problem the Whopper Assumption.

Demographers have been constructing models of kinship since the early 1930s. All such models incorporate simplifying assumptions, and most investigators are well aware of the resulting potential for error.¹ This paper argues that the errors in demographic models of kinship are not just miscellaneous misspecifications that will tend to cancel one another out; instead, the assumptions common to all models will lead to errors of consistent direction that will tend to cumulate.

In real populations, members of the same kin group tend to share many of the same characteristics -- what one might term a demographic family resemblance. Family members typically belong to the same ethnic group, class, and religion, and they usually reside in the same region. For these reasons, members of the same kin group usually resemble one another in demographic behavior more than they resemble persons randomly selected from the population as a whole. For example, a kin group in which the members are poor will usually experience systematically higher mortality than a kin group with wealthy members.

By contrast, models of kinship assume that most demographic events occurring within a kin group are independent of one another. That is, the characteristics of one member of group of kin are assumed to be entirely uncorrelated with the characteristics of other members of the kin group. This is the Whopper Assumption.

Because of the Whopper Assumption, models of kinship will produce less variation in the frequency of kin of any particular type than would occur in a real population. Our models will generally underestimate both the proportion of people with many kin and the proportion of

people with few kin. As I will show, the magnitude of error is potentially large. In addition, the Whopper Assumption can affect the expected number of kin in a population.

What follows is presented in the terms of demographic microsimulation models -- currently the technique of choice for analyzing the demography of the family and kinship -- but many of my comments would apply equally to other kinds of kinship models. Very briefly, microsimulation involves creating a hypothetical population by randomly assigning demographic events -- births, deaths, and marriages -- to individuals on the basis of predetermined probabilities. One can keep track of the family relationships within the simulated population, and thus derive estimates of the frequencies of living kin.²

The great advantage of the microsimulation approach, as opposed to macrosimulations or analytic methods, is that they make it easy to estimate the frequency distribution of kin instead of just mean numbers of kin (Ruggles, 1990). The difficulty is that the estimates of distributions are systematically biased.

I will begin with a discussion of the Whopper Assumption as it relates to fertility. Second, I estimate the magnitude of error resulting from the Whopper Assumption of mortality. The third and fourth sections deal with the potential effects of the Whopper Assumption on expected numbers of kin and on the frequency of three-generation families. I conclude with a brief set of suggestions for improving our models.

The Fertility Problem

The correlation between the fertility of mothers and that of their daughters is well known (e.g. Pearson and Lee, 1899; Huestis and Maxwell, 1932; Berent, 1953; Kantner and Potter, 1954; Duncan et. al., 1965; Hendershot, 1969; Johnson and Stokes, 1976), and it seems likely that the fertility of other kin is also correlated. Much of this correlation results from differentials in fertility between population subgroups. For example, in the United States in 1900, fertility behavior varied dramatically according to family background: blacks, farmers, Southerners, Eastern and Southern European immigrants, and much of the working class was characterized by high fertility, whereas low fertility was the norm for the bourgeoisie, families with high education, and residents of the Urban Northeast (King and Ruggles, 1989; Guest, 1982).

Beyond the fertility correlations within population subgroups, there are also fertility correlations introduced at the level of the family. For example, both traditional and modern contraceptive knowledge was probably often transmitted by the family. And to the extent that fecundity is genetic, that would also contribute to fertility correlations within kin groups.

For all these reasons, in real populations some kin groups have systematically high fertility and others have systematically low fertility. In microsimulation models, however, births are assigned to women without reference to the fertility experience of other members of the kin group. Simulations will therefore show less variation between kin groups in total fertility than would be found in real populations. Thus, one would expect that in a real population a woman with high fertility would be likely to come from a family with many children, and her children would be likely to have high fertility. Such a woman would typically end up with large numbers of grandchildren. Conversely, a woman with low fertility in a real population would be likely to

have few grandchildren. Since no such fertility correlations exist in simulated populations, we would expect that such models would yield unrealistically homogeneous overall distributions and grandchildren.

As simulation studies have shown, the frequency of kin such as aunts, uncles, nephews, nieces, and grandchildren in a population is quite sensitive to the level of fertility (e.g. Ruggles, 1987, Appendix D). The more distant the relationship, the greater the potential impact of fertility. For example, the number of great-grandchildren an individual has is influenced not only by the fertility of grandchildren, but also by the fertility of children, since the latter determines the number of grandchildren.³

Table 1 represents an attempt to assess the impact of correlated fertility on the frequency distribution of grandchildren. The figures shown were generated by the MOMSIM kinship microsimulation model (described in Ruggles, 1987). All three runs shown employ demographic parameters designed to mimic the behavior of the United States population around 1900.⁴ The analysis was restricted to very old women (aged 80-84) with at least one ever-married child, in order to maximize the potential for grandchildren.

The left column shows the standard output of the model: like all other models of kinship, it assumes that the fertility of the younger generation is entirely uncorrelated with that of their mothers. In the middle column, I have introduced a small correlation in completed fertility between generations ($r^2=.0132$), and in the right column a larger correlation ($r^2=.0565$).⁵ The magnitude of intergenerational fertility correlation observed in real populations typically falls within this range.⁶

The average number of grandchildren per woman, shown at the top of Table 1, is unaffected by the introduction of fertility correlations; the small differences shown between the three runs are the product of the random element of microsimulation. But the standard deviations -- shown in the second row -- are different, especially for women nearing the end of their childbearing years: the population with no correlations is significantly more homogeneous than the other populations. Even introducing a small correlation leads to an increase in the standard deviation of grandchildren of about 12 percent; the high correlation raises the standard deviation by 26 percent. The last two rows show the percentage of women with no grandchildren and with twenty or more grandchildren in each of the simulated populations. Analysts of kinship are often most interested in estimating the percentage of persons without any living kin of a given type. From this point of view, the most relevant statistic is the percentage of women without any grandchildren. Among the women aged 80-84, assuming a high correlation in completed fertility more than doubles the percentage of women without grandchildren. If even very small correlations in fertility across generations exist in real populations, then our models will systematically overestimate the proportion of women with grandchildren.

This example illustrates the potential impact of only one facet of the Whopper Assumption. Completed fertility is not the only demographic factor that can influence the distribution of surviving grandchildren in a population. Child mortality, age at marriage, proportion marrying, widowhood, remarriage, child spacing and age at cessation of childbearing are all potential influences. All three runs shown in Table 1 assume that these factors are entirely uncorrelated across generations. A truly realistic model that incorporated correlations for all sorts of

demographic behavior would doubtless reveal considerably more dramatic effects on the distribution of grandchildren.

The Mortality Problem

The effect of correlated mortality probabilities between members of the same kin group is similar to the effect of correlated fertility.⁷ Kin groups with consistently high death rates will tend to have few living kin of any particular type, and kin groups with low mortality will tend to have high kin counts. In populations whose mortality is largely a result of contagious diseases, one would expect the correlations of mortality within kin groups to be particularly high. Because simulation models do not take such correlations into account, they will yield a more homogeneous overall distribution of kin than would be found in a real population.

We can observe the effects of the Whopper Assumption of mortality through use of the children surviving variable in the 1900 U.S. census. This variable can be used to calculate the distribution of number of children dying. The same distribution can be estimated by simulation. Once again, I used the MOMSIM model of kinship to simulate the distribution of surviving children in 1900. As in other simulation models, the death of each child was assigned without reference to the mortality experience of the rest of the family.

Table 2 compares the mortality experience of children in the simulated population with that of the observed population. For this example, I restricted the analysis to families in which the mother was 55 to 84 years old; younger women were excluded so that a substantial proportion of the children would be dead, and older women were excluded because internal evidence suggests a high degree of misreporting of children ever born and children surviving among women of advanced years. In addition, I limited the population to women with five children-ever-born, to avoid problems associated with correlation between parity and child mortality.⁸ The age distribution of the simulated mothers was constrained to be identical to that in the observed population. As shown in the first two rows of Table 2, the model performs well on expected number of children dying. The distribution of surviving children is given in the lower part of the table. The expected finding -- that the Whopper Assumption would lead to greater homogeneity of mortality experience in the simulated families than in the census families -- is borne out by these figures. The percentage of women with all their children surviving is almost twice as great in the census population as in the simulated population, while the percentage with all their children dead is about thirty times greater in the census population than the simulation.

The implication is clear: a simulation model which is based on the assumption that everyone in the population has equal chances of dying at a given age will allocate mortality much too evenly across kin groups. As a consequence, the distribution of living kin will be more homogeneous in a demographic model than it would be in a real population. A simulation will underestimate the percentage of people without any living kin of a given type, and will also underestimate the percentage with many living kin of a given type.

The Whopper Assumption and Expected Numbers of Kin

In the preceding examples, the Whopper Assumption resulted in a reduction on the variance of kin frequencies but had no effect on the mean number of kin. In fact, as Thomas Pullum (1987)

has pointed out, errors in the distribution of kin also have the potential to distort the expected numbers of kin, depending on our point of reference for assessing kin frequencies. Specifically, failure to account for correlations in the demographic behavior of different members of the same kin group can bias the mean number of kin downwards.

Consider the case of cousins. To estimate the number of cousins in a simulated population, one must generate at least three generations. The average number of cousins is then determined by counting non-siblings who share the same grandparent. In effect, we estimate the distribution of grandchildren and then assess the number of cousins from the perspective of each grandchild. Thus, kin groups with many grandchildren count proportionately more heavily than kin groups with few grandchildren. Kin groups with many grandchildren will tend to have more cousins than kin groups with few grandchildren. If we increase the number of kin groups with many grandchildren and the number of kin groups with few grandchildren, we will increase the number of cousins because the kin groups with many cousins will be weighted more heavily. In other words, variance in the number of grandchildren in a population is positively associated with the expected number of cousins, even when the mean number of grandchildren is constant. Since the Whopper Assumption biases the variance in grandchildren downwards, simulations of kinship will tend to understate the expected number of cousins.

This pattern is illustrated in Table 3, which shows measures of cousins calculated from the perspective of the same population of grandchildren simulated in Table 1. Even though the mean number of grandchildren in Table 1 was virtually the same across the three simulation runs, the mean number of cousins is highly sensitive to fertility correlations across generations. With increasing correlations the expected number of cousins goes up.⁹

Table 4 illustrates the point that the expected number of siblings can also be biased by the Whopper Assumption. These figures are simply a rearrangement of the data in Table 2; by measuring from the perspective of the surviving children themselves, we are able to estimate the distribution of surviving siblings. Once again, the Whopper Assumption leads to an underestimate of the mean number of kin. The same kinds of errors could be expected to occur in the estimation of kin types such as aunts, uncles, nephews, nieces, and siblings-in-law.

The Whopper Assumption and Three-Generation Families

Historical research on the family has prompted the development of several demographic models of kinship.¹⁰ For the most part, these models are designed to estimate the maximum frequency of three-generation families or stem families under preindustrial demographic conditions. The stem family, as I am using the term, denotes a family in which one child remains in the parental household after marriage, and any other children leave home and establish independent households when they get married. In cross-sectional data on household structure, stem families are usually identified by the presence of a child-in-law or grandchild of the eldest generation.

Despite the theoretical importance of the stem family, our evidence on family structure in preindustrial Western Europe indicates that such families were rare (Wachter et. al., 1978; Ruggles, 1987; see also Berkner, 1972). The historical models of kinship have attempted to assess whether or not the low observed frequency of stem families can be ascribed to the preindustrial Western European pattern of late marriage and early death. For several reasons that

I have elaborated elsewhere, different models have reached different and sometimes contradictory conclusions (Ruggles, 1987, chapter 4). But all these models -- including my own -- substantially underestimate the impact of demographic constraints on the maximum frequency of multi-generational families.

The maximum frequency of three generation families in a population is affected by several demographic factors. The most important of these is probably mother's age at the birth of her children, or generation length. In natural fertility populations generation length is largely a function of marriage age. The limited evidence available suggests that age at marriage can be significantly correlated across generations.¹¹ Generation length is critical because it counts twice; the length of time all three generations are alive simultaneously depends on generation length of both the eldest generation and that of their children.

Because two generation lengths are necessarily involved, this is a prime situation for violations of the Whopper Assumption to occur. Suppose we are looking at a population in which the members of some of the kin groups have systematically long generations and others have systematically short generations. The frequency of grandchildren would be minimized when both parents and children have long generations. Therefore, we would expect that members of the kin groups with long generations would tend to have exceptionally few grandchildren, and many of them would have no grandchildren at all. Among the kin groups with short generations, on the other hand, there would be unusually large numbers of grandchildren.

Models of kinship assume, in accordance with the Whopper Assumption, that all individuals in the population have an equal probability of long generations, regardless of the behavior of the other members of their kin group. The odds of long generations occurring in both the parents' generation and the childrens' generation would be lower in a simulated population than in a real population. Thus, one would expect that the simulated population would contain a smaller proportion of people with exceptionally few grandchildren than would be found in the real population. Most important, the simulated population would contain fewer people at any moment who lacked grandchildren altogether. Since only one grandchild is needed to form a three-generation family, demographic models tend to overstate the overall potential for three-generation families.

In the case of preindustrial stem families, the problem of correlated generation lengths is compounded by the relationship between age at marriage and age at parental death. Since the preindustrial pattern of late marriage was at least partly a consequence of people waiting to receive their inheritance before they married, there was apparently a strong correlation between marriage age and parental longevity.¹² Strictly speaking, this is not an example of the Whopper Assumption as I have defined the term, since it is a correlation between two different demographic variables. Nevertheless, the consequences would be similar. An association between marriage and parental death would minimize the average interval between marriage and parental deaths. It would reduce the amount of time spent after parental deaths and before marriage, and it would also reduce the amount of time spent after marriage and before parental deaths. Therefore, if those who married early tended to have parents who died young and those who married late tended to have long-surviving parents, the overall overlap between the marriage of children and the death of their parents would be minimized.

The effects of this problem could be dramatic. In the most extreme case -- if everyone in the population waited for their parents to die before they married -- there could be no co-residence of parents with married children at all. Obviously, some people in pre-industrial Europe did marry before their parents died. But the demographic models all assume that there is no correlation whatsoever between age at marriage and parental longevity, and they therefore almost inevitably overestimate the potential for formation of stem families.¹³

Correlations of mortality within kin groups would increase the error further. Part of the mortality effect would be to overestimate the frequency of persons with surviving grandchildren, in accordance with the mechanism described earlier in this paper. In addition, the maximum frequency of stem families would be influenced by a correlation between the mortality of husbands and wives. The Whopper Assumption postulates that the death of one partner in a marriage is entirely unrelated to the death of the other. While I know of no data on this for the preindustrial period, there is ample evidence for a correlation of spouses' longevity in the twentieth century, and there is no reason to believe that this is a new phenomenon. A correlation between the life expectancy of husbands and wives is important because it only takes one living member of the elder generation to form a three generation family. If the men and women who survived long enough to form stem families tended to be married to one another -- and therefore concentrated in a minimal number of families instead of randomly dispersed through the population -- the maximum frequency of stem families would be reduced. To the extent that they occurred in combination, the long-surviving members of the eldest generation would be wasted.

This does not exhaust the potential list of effects of the Whopper Assumption on the expected frequency of stem families or three-generation families. Correlations between kin in fertility, proportions never marrying, migration, childlessness, birth spacing, widowhood, remarriage, and age intervals between spouses could all potentially contribute to heterogeneity in the distributions of surviving parents, children-in-law, or grandchildren in real populations. Such heterogeneity would limit the opportunities to form multi-generational families.

We cannot tell how badly these violations of the Whopper Assumption distort the estimates of demographic models of stem and three-generation families. But these examples serve to underscore my comments about the Whopper Assumption in general. To the extent that exaggerated homogeneity of demographic behavior yields exaggerated homogeneity of kin frequencies, demographic models will tend to underestimate the proportion of individuals without any kin of a given type. Since all techniques devised to date incorporate the Whopper Assumption, all of them tend to overestimate the proportion of the population who have one or more available kin of a given type.

Conclusion

The basic principle holds for all demographic characteristics: one would expect greater demographic homogeneity within a kin group than within a group of similar size comprised of individuals selected randomly from the population. Since microsimulations of kinship ignore the correlations in demographic behavior within kin groups, they ordinarily understate the variance of kinship distributions and for many kin types they also underestimate the expected number of kin.

It may not be too difficult to redesign our models to avoid at least the most obvious examples of the Whopper Assumption. What we need to do is incorporate procedures for introducing correlations between demographic events occurring in the same kin group. The hardest part will be figuring out the appropriate patterns of demographic correlations.

Data on demographic correlations between kin are scarce. We will need data on the demographic experience of kin groups as a whole, and such data are intrinsically difficult to gather. In the short run, historians may actually have access to better sources than demographers do. Existing family reconstitution data from seventeenth and eighteenth century France, England and elsewhere can be pressed into service. In addition, two large ongoing genealogical projects on nineteenth century France and the United States should provide a rich body of information on the demography of kin groups (Dupaquier, 1986; Fogel, 1986). While the reliability of these sources is questionable, it is probably no worse than our basic data on demography and family structure in the period.

Both the family reconstitution and the genealogical studies could also be used to tabulate simple distributions of living kin, and such tabulations can be used as a direct test of the reliability of kinship models. It might be argued that any data sufficient to take care of the Whopper Assumption would also be sufficient to obviate the need for demographic models of the family; if we could directly measure frequencies of living kin, there would be little point to constructing a model whose sole purpose was to estimate the same thing. In fact, the historical data may prove adequate for assessing the basic patterns of demographic correlation between near kin, but they probably have too much missing information to construct reliable tabulations of kin frequencies. In addition, models of kinship are good for more than just estimation of kin frequencies. For example, models allow us to explore the sensitivity of kinship to demographic change, and to project our estimates backwards or forwards in time. Moreover, models of kinship can provide the basis for broader models of social structure that incorporate behaviors that are not strictly demographic, such as residential preferences or transfers of wealth. Perhaps most important, if we want to move beyond models of kinship to construct models of family and household structure, it is imperative that we build on the framework of reliable kinship models.

It is possible that we will find that the general pattern of correlations in demographic behavior within kin groups is reasonably consistent across populations. The extent of the problem caused by the Whopper Assumption depends both on the overall heterogeneity of demographic behavior in the population and on the homogeneity within kin groups; both of these factors could vary substantially from population to population. It may turn out, however, that the degree of homogeneity within kin groups can be efficiently predicted by widely available measures of social stratification. If so, we will be able to construct reasonably realistic models of kinship for a broad range of historical and contemporary populations for which we lack direct information on correlations within kin groups.

Microsimulators tend to be a highly cautious breed; we are all aware of the potential for error in our models, and we are masters of the art of qualification (see, for example Wachter, 1987: 215, 218). Despite repeated calls for improved testing of our models against empirical data, such comparisons are still extremely rare. Perhaps this is because microsimulators get caught up in the hypothetical worlds of our own creation, and grow impatient with the imperfect world of real

numbers. But if models of kinship are to have any credibility, we must demonstrate that they can produce moderately realistic distributions of kin in a variety of demographic contexts.

In the meantime, we should regard the results of existing kinship models strictly as lower-bound estimates of the variance of kin frequencies and recognize that in many cases the expected number of kin may also be biased downwards. Until we know more about the effects of the Whopper Assumption, we cannot be confident that our models even tell us much about the sensitivity of kinship to variation in demographic parameters.¹⁴

NOTES

1. The earliest formal model of kinship is probably Lotka (1931). Although several recent writers on the simulation of kinship -- such as Wachter (1987) and Wolf (1986) -- implicitly acknowledge the Whopper Assumption, none of them, to my knowledge, have pointed out the effects of that assumption.
2. For general descriptions of simulation approaches, see Olinick (1978), Dyke and Macluer (1973), Sheps (1969), Menken (1981), Santow (1978), and Hammersley and Handscomb (1964); also see Jaquard and Leridon (1974). Microsimulations of kinship include Howell (1979), Bartlema and Winkelbauer (1986), Wolf (1986), Rossi (1975), Gilbert and Hammel (1966) and the historical models cited below in note 10. Other relevant applications of microsimulation are Orcutt (1961) and Horvitz (1969). The most important analytic and macrosimulation models of kinship are Goodman, Keyfitz, and Pullum (1974), their "addendum" (1975), Pullum (1982) and Bongaarts (1981). On the limitations of analytic techniques, see Sheps (1969), Barrett (1977), and De Vos and Palloni (1984). Also see Pullum's comments (1982: 564).
3. In the case of fertility, the correlation of demographic events can occur not only at the level of kin groups, but also at the level of individuals. Just as some kin groups may be characterized by consistently high fertility or consistently low fertility, so can individual women experience high or low fertility over the course of their childbearing years. Much of this consistency stems from factors that also operate at the level of kin groups, such as race, class, and ethnicity. There may be additional consistency of fertility behavior as a consequence of the individual circumstances of each woman, whether these circumstances are economic, biological, or cultural. The result is that real populations are quite heterogeneous with respect to fertility. Demographic models of fertility behavior have been reasonably successful in capturing this heterogeneity, but the models oriented to kinship analysis tend to be less sophisticated in this respect. If a model understates fertility heterogeneity at the individual level, the biases in kin variance can be even greater than result from understatement of fertility heterogeneity at the level of kin groups. Theoretically, the Whopper Assumption can exist at the individual level for any demographic event that can occur multiple times to the same person, including widowhood, divorce, and remarriage as well as fertility. In populations where most people only marry once during their childbearing period, however, the effects of heterogeneity in marital behavior are probably small. I have chosen to focus on the effects of the Whopper Assumption at the level of kin groups rather than at the level of individuals because the problem of fertility heterogeneity is already recognized by most of the analysts doing kinship microsimulation. A good general discussion of the concentration of parity distributions is King and Lutz (1988); a variety of approaches have been used by microsimulations to introduce heterogeneity; see Crafts and Ireland (1975), Barrett (1971), Ruggles (1987), Venkatacharya (1971). The approaches of Smith (1987), Wachter, Hammel and Laslett (1978) and Bartlema and Winkelbauer (1986) are also of interest, although they probably produce somewhat less realistic parity distributions.
4. The demographic parameters include a median female age at marriage of 22.2, female life expectancy at birth of 48.3, and a total fertility rate of 3.79. For additional details, see Ruggles (1987: 111).

5. The method employed for introducing correlations is described in the Appendix.

6. In the 1910 public use sample of the U.S. federal census (Strong, et. al., 1989) the correlation between the fertility of mothers aged 80-84 and that of their coresident daughters was .221, which is roughly the same as my "High" correlation. For all daughters married 15 years or longer, the correlation with mother's fertility was .171, and for all coresident mothers and ever-married daughters (including a high percentage of daughters married for only 1 or 2 years) the figure was .084. Of course, mothers residing with married daughters may not have been typical of the population as a whole. Although the association of fertility between successive generations has been studied extensively, comparison is problematic because the procedures used by different investigators vary widely. In a study of the British baronetage and peerage, for example, Pearson and Lee (1899) found correlations ranging from .042 to .223, depending on whether more than one daughter from each family was included and whether the mothers with brief marriages were included. My figures represent the correlation between the number of siblings and children born to women whose mothers were aged 80-84; given the advanced ages of the mothers, virtually all the daughters had completed their childbearing. A roughly comparable measure, albeit for a small homogeneous population, is Huestis and Maxwell (1932), who found a correlation of .124 among 638 families sending children to the University of Oregon. In general, the correlations tend to be lower in studies where the daughters were still bearing children. An exception is Berent (1953), who found a correlation of .187 between children and siblings among 1,482 patients of British gynecologists in 1946. By contrast, Kantner and Potter (1954) found a correlation of .09 among women in the Indianapolis Fertility Study; and Duncan et. al. (1965) got virtually the same results from the 1962 Current Population Survey.

7. On family correlations in mortality see Collver (1963); Jaquard (1982); on class differences in mortality as a source of mortality correlations within kin groups, see Pamuk (1985).

8. In the United States in 1900, child mortality was strongly associated with parity (Smith, 1983). In the developed world high fertility has been associated with low economic status since the late nineteenth century; in natural fertility populations, however, the relationship is often the opposite, since the wealthy have the resources needed for early marriage. Thus, assuming that high mortality is associated with low economic status, we might expect an inverse correlation between fertility and mortality in many populations. Microsimulations generally ignore the relationship between fertility and mortality. In general, a positive correlation between these two variables would tend to counteract the Whopper Assumption, whereas a negative correlation would aggravate it.

9. As in Table 1, the standard deviation of kin is lowest when no fertility correlation is assumed. Unlike Table 1, however, the percentage without any cousins is highest when there is no correlation, simply because the low mean number of cousins cancels out the distribution effect. Thus, depending on the perspective of measurement, the general rule that simulations overestimate the proportion of people without kin can be reversed; in this example, at least, the Whopper Assumption actually leads to an underestimate of the proportion without cousins.

10. The analytic models of this sort are Coale (1965), Burch (1970), Glass (1966), Wrigley (1969); also see Wrigley (1978), Brian Bradley and Franklin Mendels (1978), Mendels (1978). The principle historical microsimulation models of family and kin include SOCSIM, described in Wachter, Hammel, and Laslett (1978), Hammel and Wachter (1977), Hammel and Deuer (1977), and Hammel, et. al. (1976); CAMSIM, described in Laslett (1984) and J. Smith (1987); and my own model MOMSIM described in Ruggles (1987), Ruggles (1986) and De Vos and Ruggles (1988); also see LeBras (1973).

11. In the 1910 public use sample (Strong et. al. 1989), the correlation in age at marriage among mothers residing with married daughters was .1672, significant at the .01 level.

12. That a positive correlation existed between marriage age and parental longevity in the preindustrial West is now a commonplace; see for example Ohlin (1961), Wrigley (1978), Hajnal (1982), Berkner (1972), Goody, Thirsk, and Thompson (1976). Recently, Levine (1982) has proposed the revisionist argument that there was an inverse relationship between marriage age and parental longevity in preindustrial England, but his analysis is badly flawed; see Ruggles (1987: 91).

13. One would expect that if parental longevity was the determining factor in age at marriage, exceptionally long generations would tend to be followed by short ones, since the parents would be older at the birth of their children. Although this could reduce the correlation of generation lengths, it would not enhance the possibilities for three generation families as long as the inheritance rule was maintained.

14. The adverse effects of the Whopper Assumption are least serious when analyzing those kin types that are unlikely to occur in combination. For example, the error should not affect the proportion of the population with a living mother, since it is only possible to have one mother and her chance of being alive depends entirely on her own characteristics. Problems can still arise, however, if we are interested in the characteristics of the reference person; for example, the proportion of the married population with a living mother could be biased by a correlation between marriage and parental longevity. But the main problems will occur when we are analyzing combinations of kin. Analyses of orphanhood -- such as Lotka (1931) or LeBras (1973), for example, involve calculating the simultaneous survival of mothers and fathers, and will be distorted by any demographic correlations between the two parents. The larger the group of kin we are analyzing, the greater is the potential for error. It is possible, for example, to have many grandchildren. If grandchildren in a given kin group behave homogeneously with respect to mortality, then the odds are greater that all will have died or that all will survive.

The greater the detail with which we measure kin types, the fewer the problems which will crop up as a result of assuming no systematic relationships between the characteristics of different members of the same kin group. This is because the probability that a category of kin will occur in combination is reduced if categories of kin are defined narrowly. For example, the odds are generally high that an individual will have multiple living siblings, but the odds of having multiple widowed sisters between forty-five and forty-nine years of age are always low. If there is never or almost never more than one individual within a given category of kin, the Whopper

Assumption is largely circumvented. But this strategy creates a new problem: if we divide kin types into narrow categories, the results of a simulation become too unwieldy to interpret.

I have devised a strategy for analyzing the impact of demography on family structure that minimizes the impact of the Whopper Assumption by assuming that it results in constant proportional errors across different populations. This technique, which I call "Standard Propensities," is the subject of Ruggles (1986) and is further described in Ruggles (1987).

APPENDIX: Method of Introducing Fertility Correlations

In the MOMSIM microsimulation model the number of children born to each woman is allocated by generating a single random number between 0 and 1 and then consulting a cumulative probability distribution of fertility. There are separate probability distributions for each of 8 current ages and 38 durations of marriage (for further details, see Ruggles 1987: 163-169, 174-177). Since a single random number is used to assign the number of children born, introducing intergenerational correlations was fairly straightforward. A random number was generated for each woman to represent her independent contribution to fertility. Then a second random number was generated to represent the degree of influence from the previous generation. For the "High" correlation run, the degree of influence was allowed to vary from 0 (no influence of previous generation) to 1 (fertility number determined entirely by previous generation). For the "Low" correlation run, the degree of influence varied from 0 to 0.5. The random number used to allocate fertility for each woman was then calculated as the average of her own random number and the random number used for the previous generation, weighted according to the degree of influence.

An additional step was needed, because this procedure does not yield a flat distribution of random numbers between 0 and 1. An unadjusted correlation between the fertility of mothers and the fertility of daughters will yield an upward bias in the fertility of the daughters; in real populations, this is compensated for because the average daughter has lower fertility than her mother (for a discussion of this phenomenon, see Preston 1976). In addition to the upward bias, the fertility numbers obtained by this method will have too little variance, since the weighted average produces a concentration of random numbers around the mean.

For both of these reasons, it is necessary to adjust the random numbers to obtain a flat distribution between 0 and 1 for each group of mothers. This was carried out by running each version of the model twice: first, to determine the cumulative probability distribution of fertility random numbers produced by the model, and second, to apply that distribution to rescale the random numbers. The procedure was tested for each generation in each run, and the resulting random number distributions were flat.

The correlation in random numbers between generations was considerably higher than the resulting fertility correlations shown in Table 1. This is because the number of children born depends not only on the random number, but also on current age and duration of marriage. The latter factors are influenced by age at marriage, widowhood, remarriage, mother's age, and age intervals between mothers and daughters, all of which were determined independently for each individual. My procedure can be viewed as a means of introducing correlations in the propensity to have children; the actual number of children born depends also on the individual demographic circumstances of each woman.

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Table 1
 Measures of grandchildren under alternate assumptions of
 intergenerational fertility correlations: Women aged 80-84 with one or
 more ever-married children, U.S. 1900 simulations

Association of fertility with number of siblings	None ($R^2 < .0001$)	Low ($R^2 = .0132$)	High ($R^2 = .0565$)
Mean number of grandchildren	10.78	10.84	10.72
Standard Deviation of grandchildren	8.32	9.32	10.50
Percent without grandchildren	4.37	7.18	10.24
Percent with 20+ grandchildren	12.97	15.03	16.91
N	2105	2089	2099

Table 2

Measures of child survival women aged 55-84 with five children-ever-born, simulated and observed populations, U.S. 1900

	Simulation	Census
Percent of children dead	31.6	31.5
Mean number of children dead	1.58	1.58
Standard deviation	1.02	1.36
Distribution of number of children surviving (percents)		
5	14.4	26.3
4	35.0	27.4
3	32.8	21.8
2	13.9	15.0
1	3.7	6.2
0	0.1	3.4
Number of children	6650	1770

Table 3

Measures of cousins under alternate assumptions of intergenerational fertility correlations: Grandchildren of women aged 80-84, U.S. 1900 simulations

Association of fertility with number of siblings	None ($R^2 < .0001$)	Low ($R^2 = .0132$)	High ($R^2 = .0565$)
Mean number of cousins	12.10	13.80	16.03
Standard Deviation of cousins	8.84	10.02	11.28
Percent without cousins	7.94	6.18	4.92
Percent with 20+ cousins	17.01	23.65	31.90
N	22557	22659	22451

Table 4

Measures of siblings surviving:
 Simulated and observed populations, U.S. 1900

	Simulation	Census
Mean number of siblings	2.73	2.96
Standard deviation	0.92	1.04
Distribution of number of siblings surviving (percents)		
4	21.1	38.4
3	40.9	32.0
2	28.8	19.1
1	8.1	8.8
0	1.1	1.8
N	4549	1212