## Dynamic Analysis of Spatial Population Systems



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CONCEPTS AND TECHNIQUES IN MODERN GEOGRAPHY

## DYNAMIC ANALYSIS OF SPATIAL

## POPULATION SYSTEMS

by<br>Jianfa Shen<br>( Department of Geography, London School of Economics )

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## DYNAMIC ANALYSIS OF SPATIAL

 POPULATION SYSTEMS
## 1 INTRODUCTION

### 1.1 Purpose and prerequisities

In this monograph we deal with the analysis of spatial population systems. A spatial population system consists of various regional populations. These regional populations are not independent, but are interrelated via population migration. Migration is an important component of population change in a regional population. In the case of the United Kingdom, many places have experienced substantial change in their population size despite the fact of virtually zero growth in the national population for the period 1971-1981. Migration plays an important role in this zero-sum game ( Champion, Green, Owen, Ellin and Coombes, 1987; Champion, 1989). In developing countries such as China and India, there are also substantial migrations between regions of various scale, notably rural to urban migrations (Shen, 1991; Becker et al, 1986 ).

The sizes of regional populations are of much concern to local and central governments as well as various planning and business organizations for the purposes of planning, delivery of services and marketing ( Hobcraft, 1989; Rees, 1991 ). Therefore, population statistics authorities in various countries are charged with the task of making national and sub-national population projections and estimations (Rogers and Woodward, 1991). In the United Kingdom, for example, a series of population estimations are made and updated by the Office of Population Censuses and Surveys (OPCS ) as a population census is only taken once in each decade. A series of subnational population projections are also made and updated by OPCS for purposes of planning. Various procedures are used in making these population estimates and projections ( OPCS, 1981; 1991 ).

Sophisticated spatial population models have been developed by demographers and geographers. The purpose of this monograph is to introduce the principles of spatial population analysis and develop a specific multiregional population model which can be used for dynamic analysis of spatial population systems. There are no complex mathematical principles involved. Thus the only prerequisities for our discussions are a basic knowledge of algebra and mathematics.

There are two major books related to the discussions in this monograph. Mathematical Methods in Human Geography and Planning by Wilson and Bennett ( 1985 ) made a general and concise discussion of spatial population
analysis and models. Spatial Population Analysis by Rees and Wilson ( 1977 ) developed general accounts-based spatial population models in detail and various principles and procedures in the analysis and projection of general spatial population systems. The discussions in this monograph will concentrate on a specific multiregional population model using a forward demographic rates-based approach for the analysis and projection of spatial population systems. It is argued that a forward demographic rates-based approach is a straightforward, easy and simple way for spatial population analysis and projection, and for studying these specialized topics. The level of discussion will be between the classical book Spatial Population Analysis (Rees and Wilson, 1977 ) and the treatment in Mathematical Methods in Human Geography and Planning ( Wilson and Bennett, 1985 ). Undergraduate students should be advised to concentrate on sections 1 and 2, while sections 3, 4 and 5 are probably more suited to staff and graduate students undertaking postgraduate courses or research.

### 1.2 Developments in spatial population analysis

Demographic models have a long history. But they often deal only with single region populations. Since the middle 1960's, multiregional population models have been developed originally by Rogers and his collaborators ( Rogers, 1966; 1973; 1975 ). Parallel to some of these developments, multiregional population accounts and accounts-based multiregional population models have also been developed ( Rees and Wilson, 1975; 1977 ). An important development in spatial population modelling is the introduction of occurrenceexposure demographic rates ( See section 2.3 for a detailed discussion on the definitions of various demographic rates) including mortality, fertility and migration rates (Rees and Wilson, 1977). The three major components of population change are birth, death and migration. Age-specific mortality, fertility and migration rates need to be defined first in any spatial population model. These demographic rates were not clearly defined in previous spatial population models. As pointed out by Rees and Wilson ( 1975 ), most population models have a problem of failing to match exactly the age groups in the numerators and denominators of rate definitions. On the other hand, multiregional population accounts have the basic advantage that all demographic flows are systematically and correctly specified, so rates can be correctly defined and estimated.
The definition of occurrence-exposure demographic rates takes into account the length of time that a population is exposed to various population processes of birth, death and migration. In a one year period, the population that survives has a exposure time of one year while the population that dies only has an exposure time of an half year on average. Therefore, the deceased population is given a weight of 0.5 and the surviving population a weight of one in the denominators of occurrence-exposure demographic rates
definitions. However, population projections are usually carried out from the population of previous years. An iterative procedure is needed to use occurrence-exposure demographic rates for population projection ( Rees and Wilson, 1977 ). Survival rates are often used for population projections. It has been found that survival rates can be derived from occurrence-exposure rates via matrix inversion although an approximate definition of occurrenceexposure rates needs to be used (Rogers and Willekens, 1986a; Rees, 1989 ).
More recently, a set of more detailed multiregional population accounts has been used by Shen ( 1994a) to develop a forward demographic rates-based multiregional population model. More realistic demographic rates can be defined on the basis of these expanded population accounts. The definition of forward demographic rates based on a starting population was introduced. It has been found that there is a unique relation between forward demographic rates and occurrence-exposure rates. One main advantage of forward demographic rates is that they can be used directly in population projection
models so that neither an iterative procedure nor a matrix inversion procedure is needed for population projection. The discussions in this monograph are developed on the basis of this forward demographic rates-based approach.

### 1.3 Organization of the text

The case of single-region population systems will be discussed first in section 2. The notations of age-group and period-cohort and their relationship will be discussed in section 2.1. These notations are often used in population models and will also be used in this monograph. The concept of population accounts as a form to record population change will be introduced for the case of singleregion population systems in section 2.2. The definitions of mortality and fertility rates are the basis of any population analysis. The various ways to define these demographic rates will be discussed in section 2.3.

The discussion in section 2 will be extended to the case of multiregional population systems in section 3. Multiregional population accounts and accounts equations will be used to describe a general n-region population system in section 3.1. Those data generally available and those not will be identified. Populations at risk and exposure times will be discussed to define occurrence-exposure rates in section 3.2. In section 3.3, the definition of forward demographic rates will be introduced and their relations with occurrence-exposure rates will be discussed. Section 4 will discuss the estimation of population accounts and forward demographic rates from the population data available. An estimation procedure will be presented. Section 5 will discuss a forward demographic rates-based population projection model. The problem is to estimate an end population from a starting population using forward demographic rates. A brief summary of this volume will be given in section 6 .

## 2 DYNAMIC ANALYSIS OF SINGLE-REGION POPULATION SYSTEMS

### 2.1 Age group and period-cohort notations

In section 2, we will discuss the description and analysis of single-region population systems. In demographic analysis, it is often inadequate to analyze a regional population just in terms of its total population though the size of its total population is what is of most concern in many practical applications. To make a precise projection of the total population, a regional population needs to be disaggregated into various sectors by age and gender. This is obvious as populations with different ages have different demographic behaviours. The mortality rate tends to be low among the young but high among the elderly. The disaggregation of a population into male and female populations is also important. Fertility rate is often defined on the basis of female population.
The categorisation of population by gender is clear. More discussions are needed about the categorisation of population by age. Age is a continuous variable rather than a discrete one. At a specific time such as the midnight of December 31, 1992, the exact age may be ten years for some people and two years and three months for some other people, and so on. It means that we cannot disaggregate a real population by exact age. Instead, we use various ranges of exact age to disaggregate a real population similar to procedures in the frequency analysis of the distribution of a geographical variable. The most commonly used ranges of exact age to disaggregate a population are by oneyear or five year intervals. In the case of one year intervals, these ranges are as follows (inclusive at the lower limit of an age range but exclusive at the higher limit of an age range ): 0-1, 1-2, 2-3, and so on. The populations in these age ranges are called age groups and are often named respectively as age group one, age group two, age group three and so on. Thus the population in age group one ( 0-1 ) includes all persons whose exact ages are just below one year. Indeed, the population in age group one consists of all those infants produced in the previous one year period. The population in age group two (1-2) includes all persons whose exact ages are equal to or over one year but below two years, and so on. In many cases in real life, the meaning of ages refers to age-groups of one year interval. If someone is 20 years old, it actually means that his or her exact age is equal to or over 20 years but below 21 years. Thus the concept of ages in real life is not a precise one and this is one reason that actual dates of birth are more commonly used for administrative purposes.

It should be noted that the concept of age-groups is related to a specific time. Our aim is to analyze the change of population in time. For simplicity, time intervals (or periods) of one year or five years are often used in demographic analysis. In the case of one year age and time intervals, the
population in age group one at a specific time (e.g. December 31, 1991 ) will be in age group two at a time one year late ( December 31, 1992 in this case). The same intervals for age group and time are often used so that the shift of one period of time will result in exactly a shift of one age group for the same population group concerned. This will greatly simplify calculations in population projection. Thus for age groups of one year interval, periods of one year interval are often used. For age groups of five year interval, periods of five year interval are often used.

So far, we have disaggregated a population into age groups of one or five year intervals. We have also disaggregated time into periods of one or five year intervals. We assume the one year interval for age groups and periods in the following discussions. It is noted that the population in an age group will shift to the next age group after a period of time. This can be shown in a Lexis diagram in Figure 1. There are two axes --- age and time in a Lexis diagram. A lifeline of an individual such as the line starting from the point of age zero at time $t$ shows the increase of age with time. A Lexis diagram is often used to show the relation between age and time. In the Lexis diagram shown in Figure 1, age group one at time $t$ will become age group two at time $t+1$ after the first period, and age group three at time $t+2$ after the second period. The infants produced in the first period t to $\mathrm{t}+1$ will become age group one at time $t+1$, age group two at time $t+2$ after the second period, and age group three at time $t+3$ after the third period.
Age group one at time $t$ and age group two at time $t+1$ refers actually to the same group of population. It is convenient to use just one label to refer to this group of population in the period from $t$ to $t+1$. The concept of period-cohort


Fig. 1 Lexis diagram showing the notations of age group and period-cohort.
is introduced (Rees and Wilson, 1977; Rees, 1989 ). Thus period-cohort one refers to the same population in the period $t$ to $t+1$ who are in age group one at time $t$ ( beginning of the period $t$ to $t+1$ ) and age group two at time $t+1$ ( end of the period $t$ to $t+1$ ). Period-cohort two refers to the same population in the period $t$ to $t+l$ who are in age group two at time $t$ and age group three at time $t+1$, and so on. Period-cohort zero refers to the infants produced in the period $t$ to $t+1$ who are in age group one at time $t+1$.

It is noted that the notation of period-cohorts is related to the period of time concerned while the notation of age group is related to a specific time, often the beginning or the end of a period. Generally, period-cohort a in period $t$ to $t+1$ refers to age group a at the beginning of period $t$ to $t+1$ and age group $a+1$ at the end of period $t$ to $t+1$. The exact age of period-cohort a in period $t$ to $t+1$ will be equal to or over a- 1 but below a at time $t$, and equal to or over a but below a+l at time $t+1$.

Assume that period-cohort A is the last and open-ended period-cohort concerned. Period-cohort A in period to tor refers to age group A at the beginning of period to to $t+1$ and part of age group $A$ at the end of period to $t+1$. Age-group A is the last open-ended age group including persons whose ages are equal or over A-1 years. It is noted that the population in age group A at the end of period $t$ to $t+1$ comes from two age-groups A- 1 and A at the beginning of period $t$ to $t+1$. For example, if age group 101 is the last age group which includes all persons with ages of 100 years and over, then the population in age group 100 and 101 at a specific time ( e.g. December 31, 1991 ) will be in just one age-group 101 one-year later ( December 31, 1992 in this case ).

So far, we have disaggregated population into age groups. We have also defined age groups one, two ,..., A at a specific time and period-cohorts zero, one, two , ..., A during a specific period $t$ to $t+1$. The notation of age groups is useful in describing the age composition of a population at a specific time. The notation of period-cohorts is most useful in the analysis of population change in a period $t$ to $t+1$. Essentially, these two kinds of notations are closely related as mentioned above.

### 2.2 Single-region population accounts

In the case of single-region population systems, we assume that there is no external migration between the region concerned and the rest of the world. The two components of population change are birth and death. It is noted that the amount of population change is related to the length of time. One year age and time intervals are used here. Therefore, what we need to know are the counts of birth and death in a one year period. As the population is disaggregated by age and gender, the death counts should be recorded for each gender and period-cohort (or by age at death ) and the birth counts should be recorded for each period-cohort of the female population who
produce births. To calculate rates of population change, we also need to know the population in each period-cohort at the begining or at the end of each one year period. These population data can be conveniently recorded in forms of population accounts.

Table 1 presents the population accounts of the female population from period-cohorts zero to ten for the one year period 1986-1987 in China. These are single-region, closed system accounts and external migration is ignored. Those data available from the Department of Population Statistics (DPS, 1988), State Statistical Bureau of China are printed in bold. It is noted that the death counts for various period-cohorts are not directly available. The available data for deaths are recorded by age at death as shown in Table 1. Figure 2 shows the meaning of these two kinds of mortality data via a Lexis diagram. Area ABCD is the population who died at age zero (or more exactly, equal to or over zero but less than one ) in the period $t$ to $t+1$. Area CDEF is the population who died at age one (or more exactly, equal to or over one but less than two ) in the period $t$ to $t+1$. Area ABD is the deaths of

Table 1
Population accounts for China 1986-1987 (females, thousands )

| Periodcohort | 987 |  |  | Deaths by age at death |
| :---: | :---: | :---: | :---: | :---: |
|  | Population | Survived population | Deaths by period-cohort |  |
| 0 | 11083.0 | 10839.0 | 244.0 | 283.0 |
| 1 ( 0-1 )a | 9563.0 | 9502.4 | 60.6 | 43.2 |
| 2 (1-2) | 8855.6 | 8822.3 | 33.3 | 23.3 |
| 3 (2-3) | 8671.2 | 8651.6 | 19.6 | 15.8 |
| 4 (3-4) | 9481.8 | 9466.6 | 15.2 | 14.5 |
| 5 ( 4-5) | 10552.1 | 10540.2 | 11.9 | 9.3 |
| 6 ( 5-6) | 8740.2 | 8731.8 | 8.4 | 7.5 |
| 7 ( 6-7) | 9112.1, | 9105.7 | 6.4 | 5.3 |
| 8 (7-8) | 9433.2 | 9428.4 | 4.8 | 4.3 |
| 9 ( 8-9) | 8971.1 | 8966.5 | 4.6 | 4.8 |
| 10 (9-10) | 9407.9 | 9403.0 | 4.9 | 5.0 |

Notes:
(a) These are exact age ranges for each period-cohort at the beginning of period 1986-1987.
(b) Those data available from DPS ( 1988 ) are printed in bold, from which other data in the population accounts are calculated.
(c) Population accounts for period-cohort 11 and over are omitted here.
period-cohort zero ( infants-cohort ) in the period t to $\mathrm{t}+1$, i.e., those infants produced in the period $t$ to $t+l$ and died in the same period. It is clear that the deaths of period-cohort zero ( area ABD ) are just part of the population who died at age zero ( area ABCD ). Area ACDF is the deaths of period-cohort one in the period $\mathbf{t}$ to $\mathbf{t + 1}$. The deaths of period-cohort one ( area ACDF ) include two parts: a part of the population who died at age zero (area ABCD) and a part of the population who died at age one ( area CDEF ). Similarly, the deaths of period-cohort two ( area CEFH ) also consist of two parts: a part of the population who died at age one ( area CDEF) and a part of the population who died at age two ( area EFGH), and so on.
A simple and convenient procedure is often adopted. The number of deaths in a period-cohort is estimated as the average number of deaths at the two ages involved. In Figure 2, area CEFH is estimated as the average of areas CDEF and EFGH.


Exact age
ABCD: Population who died at age zero in the period $t$ to $t+1$
CDEF: Population who died at age one in the period $t$ to $t+1$
ABD: Deaths of period-cohort zero ( infants-cohort ) in the period $t$ to $t+1$ ACDF: Deaths of period-cohort one in the period $t$ to $t+1$

Fig. 2 Relation of death data by period-cohort and by age at death
If we define $\mathrm{Pd}_{\text {ag }}$ as the deaths of period-cohort a of gender g ( $\mathrm{g}=\mathrm{m}$, male; f , female ) and $\mathrm{D}_{\mathrm{ag}}$ as the population who died at age a , then we have the following equation:

$$
\mathrm{Pd}_{\mathrm{ag}}=0.5 \mathrm{D}_{\mathrm{a} \cdot 1 \mathrm{~g}}+0.5 \mathrm{D}_{\mathrm{M}} \quad \mathrm{a}=2,3, \ldots, \mathrm{~A}-\mathrm{l} ; \mathrm{g}=\mathrm{m}, \mathrm{f} \quad \text { (1) }
$$

Thus for the female population of period-cohort two in Table I, the number
of deaths in the period 1986 to 1987 is:

$$
\begin{equation*}
\mathrm{Pd}_{2 f}=0.5 \mathrm{D}_{1 \mathrm{f}}+0.5 \mathrm{D}_{2 \mathrm{l}}=0.5 \times 43.2+0.5 \times 23.3=33.3 \tag{2}
\end{equation*}
$$

The deaths in the last open-ended period-cohort A should include all the deaths who died at age A and over, thus we have the following equation:

$$
\begin{equation*}
\mathrm{Pd}_{\mathrm{Ag}}=0.5 \mathrm{D}_{\mathrm{A}-\mathrm{lg}}+\mathrm{D}_{\mathrm{Ag}} \tag{3}
\end{equation*}
$$

$$
\mathrm{g}=\mathrm{m}, \mathrm{f}
$$

The population who died at age zero cannot be equally divided for periodcohorts zero and one as the deaths in period-cohort zero are much greater than in period-cohort one. Fortunately, we can calculate the number of deaths of period-cohort zero from the number of total births and those infants who are alive at the end of period 1986 to 1987.
If we define $\mathrm{Pb}_{\mathrm{g}}$ as the total births of gender g in period $t$ to $\mathrm{t}+1$ and $\mathrm{Pag}_{\mathrm{ag}}$ as the survived population of period-cohort a of gender $g$ at the end of period $t$ to $t+l$, then $\mathrm{Pb}_{\mathrm{g}}$ and $\mathrm{P}_{\mathrm{Og}}$ are the starting and end population of period-cohort zero respectively. We have the following equation to estimate the deaths of period-cohort zero:

$$
\begin{equation*}
\mathrm{Pd}_{0 \mathrm{~g}}=\mathrm{Pb}_{\mathrm{g}}-\mathrm{P}_{0 \mathrm{~g}} \quad \mathrm{~g}=\mathrm{m}, \mathrm{f} \tag{4}
\end{equation*}
$$

Thus in Table 1, the number of deaths of the female population of periodcohort zero is:

$$
\begin{equation*}
\mathrm{Pd}_{\mathrm{Of}}=\mathrm{Pb}_{\mathrm{f}}-\mathrm{P}_{\mathrm{Df}}=11083.0-10839.0=244.0 \tag{5}
\end{equation*}
$$

The rest of deceased population who died at age zero belongs to periodcohort one. Thus the number of deaths of period-cohort one should be calculated as follows:

$$
\begin{aligned}
\mathrm{Pd}_{1 \mathrm{~g}}= & \text { a part of the population who died at age zero }+ \text { a part of the } \\
& \text { population who died at age one }
\end{aligned}
$$

$$
\begin{equation*}
=D_{0 g}-P_{(0)}+0.5 P_{i g} \quad g=m, f \tag{6}
\end{equation*}
$$

In Table 1, the number of deaths of the female population of period-cohort one is:

$$
\mathrm{Pd}_{1 \mathrm{f}}=\mathrm{D}_{0 \mathrm{f}}-\mathrm{Pd}_{\mathrm{Of}}+0.5 \mathrm{D}_{\mathrm{U}}=283.0-244.0+0.5 \times 43.2
$$

$$
\begin{equation*}
=39.0+21.6=60.6 \tag{7}
\end{equation*}
$$

So far, we have calculated the deceased populations of various period-
cohorts in Table 1. Now, starting populations of various period-cohorts in the period 1986 to 1987 can be calculated from survived and deceased populations. We have defined $P_{\text {itg }}$ as the survived population of period-cohort a of gender $g$ at the end of period : to $t+I$. We further define $P^{*}{ }_{a g}$ as the starting population of period-cohort a of gender $g$ at the beginning of period $t$ to $\mathbf{t + 1}$. It is straightforward to find out that:

## Starting population $=$ Survived population + deceased population

$$
\mathrm{P}^{*} \mathrm{ag}_{\mathrm{g}}=\mathrm{P}_{\mathrm{ag}}+\mathrm{Pd}_{\mathrm{ag}} \quad \mathrm{a}=0,1,2, \ldots, \mathrm{~A} ; \mathrm{g}=\mathrm{m}, \mathrm{f}(8)
$$

For the female population of period-cohort one in Table 1, its starting population is:

$$
\begin{equation*}
\mathrm{P}_{1 \mathrm{f}}=\mathrm{P}_{1 \mathrm{f}}+\mathrm{Pd}_{1 \mathrm{f}}=9502.4+60.6=9563.0 \tag{9}
\end{equation*}
$$

All other data in Table 1 can be calculated using the procedures discussed above. Thus population accounts for the female population of China are constructed. Similarly, population accounts for the male population of China can be constructed.
We also need to construct birth accounts for fertility analysis in the next section. The task is much easier. The births produced by various periodcohorts of the female population are often available. Table 2 presents the birth accounts of China in the period 1986 to 1987. In this table, births include both male and female. Population accounts of the female population of various period-cohorts who produced these births are also presented. These population accounts are actually part of Table 1 .

### 2.3 Definitions of mortality and fertility rates

In the previous section, we have developed population accounts and birth accounts to describe the states and changes of a single-region population system in a period $\mathbf{t}$ to $\mathrm{t}+1$. In a further step of demographic analysis, it is convenient to use a set of rates of population changes, i.e., mortality and fertility rates, to describe the dynamics of a population system. These rates are useful for the purposes of population projections and can also be used to compare mortality and fertility levels among various countries or regions.

Generally, the mortality ( or fertility ) rate is defined by dividing the amount of population change, deaths ( or births ) in this case, by a suitable denominator, usually the population base which produces this population change. There are at least two kinds of population base that can be used to define mortality or fertility rates. Thus there are two ways to define these demographic rates.

Table 2
Birth accounts for China 1986-1987 (thousands )

Period-
cohort

| Female population |  |  |  |
| :--- | :--- | :--- | :---: |
| Starting state | Ending state in period 1986-1987 |  |  |
| Population | Survived <br> population | Deaths by <br> period-cohort |  |

Births

| 15 (14-15) a | 12215.6 | 12204.9 | 10.8 | 2.3 |
| :---: | :---: | :---: | :---: | :---: |
| 16 (15-16) | 13240.7 | 13228.4 | 12.3 | 22.0 |
| 17 (16-17) | 12636.9 | 12623.4 | 13.6 | 96.4 |
| 18 (17-18) | 13367.0 | 13353.0 | 13.9 | 277.7 |
| 19 (18-19) | 11489.2 | 11475.8 | 13.4 | 629.3 |
| 20 (19-20) | 11110.5 | 11096.2 | 14.3 | 1294.4 |
| 21 (20-21) | 12013.5 | 11999.0 | 14.5 | 2069.1 |
| 22 (21-22) | 11904.8 | 11890.6 | 14.2 | 2701.3 |
| 23 (22-23) | 12394.2 | 12380.1 | 14.1 | 3308.0 |
| 24 (23-24) | 13345.6 | 13334.2 | 11.4 | 2691.8 |
| 25 (24-25) | 7947.8 | 7938.8 | 9.0 | 1593.8 |
| 26 (25-26) | 5732.6 | 5724.7 | 7.9 | 1225.9 |
| 27 (26-27) | 6769.4 | 6761.7 | 7.8 | 1129.0 |
| 28 (27-28) | 6930.1 | 6920.0 | 10.1 | 1142.7 |
| 29 (28-29) | 6995.0 | 6982.8 | 12.1 | 1070.4 |
| 30 (29-30) | 8980.4 | 8968.7 | 11.6 | 878.1 |
| 31 (30-31) | 8431.8 | 8421.2 | 10.6 | 727.8 |
| 32 (31-32) | 9325.4 | 9314.1 | 11.3 | 625.0 |
| 33 (32-33) | 8827.4 | 8815.2 | 12.1 | 454.6 |
| 34 (33-34) | 8409.8 | 8396.9 | 12.9 | 346.4 |
| 35 (34-35) | 8260.6 | 8248.3 | 12.3 | 251.1 |
| 36 (35-36) | 7103.9 | 7092.3 | 11.6 | 171.1 |
| 37 (36-37) | 7190.2 | 7179.2 | 11.0 | 141.4 |
| 38 (37-38) | 6370.0 | 6360.0 | 10.1 | 97.2 |
| 39 (38-39) | 5925.5 | 5914.6 | 10.9 | 76.5 |
| 40 (39-40) | 5946.4 | 5934.9 | 11.5 | 61.0 |
| 41 (40-41) | 5294.9 | 5284.6 | 102 | 43.0 |
| 42 (41-42) | 5027.4 | 5015.8 | 11.5 | 33.5 |
| 43 (42-43) | 4731.8 | 4718.5 | 13.2 | 21.0 |
| 44 (43-44) | 4536.1 | 4523.1 | 13.0 | 21.0 |
| 45 (44-45) | 4728.8 | 4714.1 | 14.7 | 12.8 |
| 46 (45-46) | 4586.6 | 4571.5 | 15.1 | 6.7 |
| 47 (46-47) | 4387.2 | 4371.0 | 16.2 | 3.9 |
| 48 (47-48) | 4456.2 | 4438.4 | 17.9 | 4.4 |
| 49 (48-49) | 4450.6 | 4431.1 | 19.5 | 1.8 |

Notes:
(a) These are exact age ranges for each period-cohort at the beginning of period 1986-1987.
(b) Those data available from DI'S ( 1988 ) are printed in bold. Other data have been calculated in the female population accounts in Table 1.

A few concepts will be discussed first which will be useful to define demographic rates for the case of single-region population systems, and even more useful for the case of multiregional population systems.
First, the population who produce the amount of population change (births or deaths ) is called the population at risk. For the deaths $\mathrm{Pd}_{\mathrm{ag}}$ of periodcohort a of gender g in period t to $\mathrm{t}+1$, its population at risk consists of two parts, the survived population $\mathrm{P}_{\mathrm{ag}}$ and the deceased population $\mathrm{Pd}_{\mathrm{ag}}$ itself. Second, it is noted that the amount of population change (deaths or births ) is also related to the time that a population is exposed to the birth or death process. Thus we also need to find out the exposure time for populations at risk. The survived population $\mathrm{P}_{\text {ag }}$ is alive during the whole period and is exposed to the death process for one year. The exposure time of the population at risk $\mathrm{P}_{\mathrm{ag}}$ is one year. The deceased population Pdag is alive for half a year on average in the period $t$ to $t+1$ and is exposed to the death process for half a year. Thus the exposure time of the population at risk $\mathrm{Pd}_{\text {ag }}$ is half a year. Third, a further concept is population-time at risk which is obtained by multiplying populations at risk by their exposure time respectively and adding together. The term ' population at risk ', used by Rees and Wilson (1977), is termed population-time at risk here. As shown in Table 3, the population-time at risk PARdag of period-cohort a of gender $g$ for deaths $\mathrm{Pd}_{\mathrm{ag}}$ is as follows:

$$
\operatorname{PARd}_{\mathrm{ag}}=\mathrm{P}_{\mathrm{ag}}+0.5 \mathrm{Pd}_{\mathrm{ag}} \quad a=0,1,2, \ldots, \mathrm{~A} ; \mathrm{g}=\mathrm{m}, \mathrm{f}(10)
$$

Similarly, for the births Pbaf produced by the female population of periodcohort a in period $t$ to $t+1$, its populations at risk are $P a f$ and $\mathrm{Pd}_{\mathrm{a}} \mathrm{f}$. Their exposure times are one year and half a year respectively. It is straightforward to find out that the population-time at risk PAR $b_{a}$ f for the births $\mathrm{Pb}_{\mathrm{a}} \mathrm{f}$ produced by the female population of period-cohort $a$ is as follows:

$$
\begin{equation*}
\operatorname{PAR}_{\mathrm{af}}=\mathrm{P}_{\mathrm{af}}+0.5 \mathrm{Pd}_{\mathrm{ai}} \quad \mathrm{a}=0,1,2, \ldots, \mathrm{~A} \tag{11}
\end{equation*}
$$

Now, the occurrence-exposure mortality ( or fertility ) rate can be defined by the number of deaths (or births ) divided by the population-time at risk. The occurrence-exposure mortality rate $d_{a b}$ of the period-cohort a of gender $g$ is defined as follows:

$$
\begin{equation*}
\mathrm{d}_{\mathrm{ag}}=\mathrm{Pd}_{\mathrm{ag}} / \text { PARd }_{\mathrm{alg}}=P \mathrm{Pd}_{\mathrm{ag}} /\left(\mathrm{P}_{\mathrm{ag}}+0.5 \mathrm{Pd}_{\mathrm{ag}}\right) \quad \mathrm{g}=\mathrm{m}, \mathrm{f} \tag{12}
\end{equation*}
$$

For the female population of period-cohort one in China in Table 1, its occurrence-exposure mortality rate dif can be calculated as follows:

$$
\begin{align*}
& \mathrm{P}_{\mathrm{lf}}=9502.4 \\
& \mathrm{Pd}_{1 \mathrm{f}}=60.6 \\
& \operatorname{PARd}_{\mathrm{ff}}=\mathrm{P}_{1 \mathrm{f}}+0.5 \mathrm{Pd}_{\mathrm{if}}=9502.4+0.5 \times 60.6=9532.7  \tag{13}\\
& \mathrm{~d}_{1 \mathrm{f}}=\mathrm{Pd}_{1 \mathrm{f}} / \mathrm{PARd}_{1 \mathrm{f}}=60.6 / 9532.7=0.00636
\end{align*}
$$

The occurrence-exposure fertility rate $\mathrm{b}_{\mathrm{a}} \mathrm{r}$ of period-cohort a of the female population is defined as follows:

$$
\begin{equation*}
\mathrm{b}_{\mathrm{af}}=\mathrm{Pb}_{\mathrm{af}} / \mathrm{PARb}_{\mathrm{af}}=\mathrm{Pb}_{\mathrm{af}} /\left(\mathrm{P}_{\mathrm{af}}+0.5 \mathrm{Pd}_{\mathrm{af}}\right) \tag{14}
\end{equation*}
$$

For the female population of period-cohort 25 in China in Table 2, its occurrence-exposure fertility rate b251 can be calculated as follows:

| $\mathrm{P}_{25 \mathrm{f}}=7938.8$ | $\mathrm{PARb}_{25 \mathrm{~F}}=7943.3$ |
| :--- | :--- |
| $\mathrm{Pd}_{25 f}=9.0$ | $\mathrm{~Pb}_{25 \mathrm{f}}=1593.8$ |
| $\mathrm{~b}_{25 \mathrm{f}}=\mathrm{Pb}_{25 \mathrm{f}} / \mathrm{PARb}_{251}=1593.8 / 7943.3=0.20065$ |  |

Now, another way to define a mortality ( or fertility ) rate will be introduced. This second definition is based on the starting population, i.e., the population of a period-cohort at the beginning of a period $t$ to $t+1$. The rates defined in this way are called forward mortality or fertility rates. As shown in Table 3, the starting population PSTd $_{\text {ag }}$ of period-cohort a of gender $g$ for deaths $\mathrm{Pd}_{\text {ag }}$ is as follows:

$$
\begin{equation*}
\operatorname{PSTd}_{\mathrm{ag}}=\mathrm{P}_{\mathrm{ag}}+\mathrm{Pd}_{\mathrm{ag}}=\mathrm{P}_{\mathrm{igg}}^{*} \quad \mathrm{a}=0.1,2, \ldots, \mathrm{~A}: \mathrm{g}=\mathrm{m}, \mathrm{f} \tag{16}
\end{equation*}
$$

Table 3 Population-time at risk and starting populations for components of population change

| Population change | Poputation at risk | Population-time al risk | Starting population |
| :---: | :---: | :---: | :---: |
| Deaths $\mathrm{Pd}_{\text {ag }}$ | $\mathrm{P}_{\mathrm{ag}}, \mathrm{Pd}_{\text {ag }}$ | $\mathrm{Pab}_{\mathrm{ib}}+0.5 \mathrm{Pd}_{\text {ag }}$ | $P_{\text {ag }}+\mathrm{Pd}_{\text {ag }}$ |
| Births $\mathrm{Pb}_{\text {af }}$ | Par, $\mathrm{Pd}_{\text {af }}$ | $\mathrm{Pal}_{\text {al }}+0.5 \mathrm{Pd}_{\mathrm{af}}$ | $\mathrm{Paf}_{\mathrm{af}}+\mathrm{Pd}_{\text {af }}$ |

Similarly, for the births Pbaf produced by the female population of periodcohort a in period $t$ to its populations at risk are Pat and $\mathrm{Pd}_{\mathrm{a}} \mathrm{f}$. It is straightforward to deduce that the starting population $\mathrm{PSTb}_{\mathrm{a}} \mathrm{f}$ for the births t

$$
\mathrm{PSTb}_{\mathrm{af}}=\mathrm{P}_{\mathrm{af}}+\mathrm{Pd}_{\mathrm{alf}}
$$

$\mathrm{a}=0,1,2, \ldots, \mathrm{~A}$
(17)

Now, the forward mortality ( or fertility ) rate can be defined by the number of deaths ( or births ) divided by the starting population. The forward mortality rate $\mathrm{u}_{\mathrm{ag}}$ of the period-cohort a of gender g is defined as follows:

$$
\begin{equation*}
\mathrm{u}_{\mathrm{ag}}=\mathrm{Pd}_{\mathrm{ag}} / \mathrm{PST}_{\mathrm{ag}}=\mathrm{Pd}_{\mathrm{ag}} /\left(\mathrm{P}_{\mathrm{ag}}+\mathrm{Pd}_{\mathrm{ag}}\right) \quad \mathrm{g}=\mathrm{m}, \mathrm{f} \tag{18}
\end{equation*}
$$

It is noted that the population at risk $\mathrm{Pd}_{\mathrm{ag}}$ is given a time weight of one year in the calculation of a forward mortality rate rather than half a year in the calculation of an occurrence-exposure rate.

For the female population of period-cohort one in China in Table 1, its forward mortality rate $u_{1 i}$ can be calculated as follows:

$$
\begin{align*}
& \mathrm{P}_{1 \mathrm{f}}=9502.4 \\
& \mathrm{Pd}_{1 \mathrm{f}}=60.6 \\
& \mathrm{PSTd}_{1 \mathrm{f}}=\mathrm{P}_{1 \mathrm{f}}+\mathrm{Pd}_{1 \mathrm{f}}=9502.4+60.6=9563.0  \tag{19}\\
& \mathrm{u}_{1 \mathrm{f}}=\mathrm{Pd}_{1 \mathrm{f}} / \mathrm{PSTd}_{1 \mathrm{f}}=60.6 / 9563.0=0.00634
\end{align*}
$$

The forward fertility rate $f_{a r}$ of period-cohort a of the female population is defined as follows:

$$
\begin{equation*}
\mathrm{f}_{\mathrm{af}}=\mathrm{Pb}_{\mathrm{af}} / \mathrm{PSTb}_{\mathrm{af}}=\mathrm{Pb}_{\mathrm{al}} / /\left(\mathrm{Palif}+\mathrm{Pd}_{\mathrm{aff}}\right) \tag{20}
\end{equation*}
$$

For the female population of period-cohort 25 in China in Table 2, its forward fertility rate $f_{251}$ can be calculated as follows:

$$
\begin{array}{ll}
\mathrm{P}_{25 \mathrm{f}}=7938.8 & \mathrm{PSIb}_{25 i}=7947.8 \\
\mathrm{Pd}_{25 \mathrm{f}}=9.0 & \mathrm{~Pb}_{25 \mathrm{~F}}=1593.8 \\
\mathrm{f}_{25 \mathrm{f}}=\mathrm{Pb}_{25 \mathrm{f}} / \mathrm{PST}_{25 \mathrm{r}}=1593.8 / 7947.8=0.20054 \tag{21}
\end{array}
$$

There are unique relations between occurrence-exposure rates and forward rates. Substitute equation (16) into equation (12):

$$
\begin{align*}
d_{\mathrm{ag}}= & \mathrm{Pd}_{\mathrm{ag}} /\left(\mathrm{Pag}_{\mathrm{ag}}+0.5 \mathrm{Pd}_{\mathrm{ag}}\right)=\mathrm{Pd}_{\mathrm{ag}} /\left(\mathrm{P}_{\mathrm{igg}}+\mathrm{Pd}_{\mathrm{ag}}-0.5 \mathrm{Pd}_{\mathrm{ag}}\right) \\
& =\mathrm{Pd}_{\mathrm{ag}} /\left(\mathrm{PSTd} \mathrm{a}_{\mathrm{ag}}-0.5 \mathrm{Pd}_{\mathrm{ag}}\right) \tag{22}
\end{align*}
$$

Dividing the numerator and denominator of the right side of equation (22) by PSTd ag and using equation (18), the following equation can be obtained:

$$
\begin{equation*}
\mathrm{d}_{\mathrm{ag}}=u_{\mathrm{ag}} /\left(1-0.5 u_{\mathrm{ig}}\right) \tag{23}
\end{equation*}
$$

Substituting equation (17) into equation (14):

$$
\begin{align*}
\mathrm{b}_{\mathrm{af}}= & \mathrm{Pb}_{\mathrm{af}} /\left(\mathrm{Paf}_{\mathrm{af}}+0.5 \mathrm{Pd}_{\mathrm{af}}\right)=\mathrm{Pb}_{\mathrm{ar}} /\left(\mathrm{Paf}_{\mathrm{af}}+\mathrm{Pd}_{\mathrm{af}}-0.5 \mathrm{Pd}_{\mathrm{af}}\right) \\
& =\mathrm{Pb}_{\mathrm{af}} /\left(\mathrm{PSTb}_{\mathrm{af}}-0.5 \mathrm{Pd}_{\mathrm{af}}\right) \tag{24}
\end{align*}
$$

Dividing the numerator and denominator of the right side of equation (24) by $\mathrm{PSTb}_{\text {af }}$ and using equation (20), the following equation can be obtained:

$$
\begin{equation*}
b_{a f}=f_{a f} /\left(1-0.5 u_{a f}\right) \tag{25}
\end{equation*}
$$

Equations (23) and (25) express occurrence-exposure mortality and fertility rates in terms of forward mortality and fertility rates respectively. The forward mortality and fertility rates can also be expressed in terms of occurrence-exposure mortality and fertility rates as follows:

$$
\begin{align*}
& \mathbf{u}_{\mathrm{ag}}=\mathrm{d}_{\mathrm{ag}} /\left(\mathrm{l}+0.5 \mathrm{~d}_{\mathrm{ag}}\right)  \tag{26}\\
& \mathrm{f}_{\mathrm{af}}=\mathrm{b}_{\mathrm{af}} /\left(1+0.5 \mathrm{dal}^{1}\right) \tag{27}
\end{align*}
$$

Equations (23), (25), (26) and (27) show the unique relations between the occurrence-exposure mortality and fertility rates and forward mortality and fertility rates respectively. According to equations (26) and (27), forward rates are a little smaller than occurrence-exposure rates. This is because the starting population is greater than the population-time at risk, as the deceased population is given a time weight of one year in the calculation of the starting population and a time weight of half a year in the calculation of the populationtime at risk. It is noted that a forward fertility rate is related to both the occurrence-exposure fertility rate and occurrence-exposure mortality rate. One main advantage of forward rates is that they can be used directly for population projections. Given the base year population (i.e., starting population ) the number of births in the next one year period and the population by the end of the one year period can be straightforwardly calculated using forward fertility and mortality rates.

Table 4 presents the occurrence-exposure and forward mortality and fertility rates of the female population in China 1986-1987. It is clear that the occurrence-exposure and forward mortality rates are increasing with age for the female populations of period-cohort 32 and over in China. The occurrenceexposure and forward fertility rates have a peak around period-cohort 23. It has been found that there are remarkably persistent regularities in age-specific fertility and mortality rates (Rogers, 1984 ). It is convenient to separate the level of fertility from its distribution across the ages. Total fertility rate TFR is often used to express the level of fertility of a population. It is the sum of age-specific occurrence-exposure fertility rates:

Mortality and fertility rates of the female population in China 1986-1987

$$
\begin{equation*}
\mathrm{TFR}=\sum 2_{\mathrm{a}=\mathrm{a} 1} \mathrm{~b}_{\mathrm{af}} \tag{28}
\end{equation*}
$$

Here al and a2 are the first and last period-cohorts of the fertile female population. In our example, $\mathrm{al}=15, \mathrm{a} 2=49$. It can be calculated from Table 4 that '11-1 ( is 2.457 for China in 1986-1987. It means that an average Chinese woman, at the fertility level in 1986-1987, will produce 2.457 children in her life. In population projections, various trends of TFR can be assumed to make low, medium and high scenarios of population projections.

Normal fertility rates can be defined as fertility rates divided by the total fertility rates to express the distribution of fertility across the ages as follows:

$$
\begin{array}{lll}
\text { Normal occurrence-exposure fertility rate } & \mathrm{bn}_{\mathrm{af}}=\mathrm{b}_{\mathrm{af}} / \text { TFR } \\
\text { Normal forward fertility rate } & \mathrm{fn}_{\mathrm{af}}=\mathrm{f}_{\text {af }} / \mathrm{TFR} \tag{30}
\end{array}
$$

These normal fertility ( N-fertility ) rates are also presented in Table 4 for the female population of China in the period 1986-1987. In population projections, it is often assumed that normal fertility rates are constant over the projection period.

## 3 MULTIREGIONAL POPULATION ACCOUNTS AND DEMOGRAPHIC RATE DEFINITIONS

### 3.1 Multiregional population accounts

In this section, we attempt to describe and analyze spatial population systems We assume that the spatial population system of interest consists of N regions. These N regions are interrelated via population migration. We further assume that these N regions are not interrelated with the rest of the world. This means that there is no external migration. In practice, this assumption is acceptable for some countries such as China where the scale of international migration, compared with the scale of her population, is negligibly small and, can be ignored. However, this assumption can be easily relaxed if we include the rest of the world as one of the N regions. Thus all populations in the world are included.

We assume that the population is disaggregated by age and gender as we have done for the case of a single-region population in section 2. Many concepts such as period-cohorts and age-groups can be used here. But we add one more dimension into our analysis, i.e., the spatial dimension. The whole population is disaggregated by space. The populations in various regions are interrelated via interregional migration. Thus in any region, there are three components of population change: birth, death and migration. As the amount of population change is related to time, we need to specify the length of time
of a period. One year time and age intervals are used here. As in the case of single-region population systems, there are similar notations and derivations for male and female populations except that births and fertility rates are only associated with the female population. So gender label g is omitted in most discussions, but will be added back in the multiregional population model in section 5 to project female and male populations separately.
The spatial-dynamic population system, being a type of space-time system, needs to be described in space-time dimensions. A most straightforward description of the system is via multiregional population accounts. Table 5 presents an example of multiregional population accounts for a system of two regions i and j . Only the population transitions for period-cohort a ( $\mathrm{a}=1,2$, ... A) and infants-cohort ( period-cohort zero ) are presented. Here A is the last period-cohort. The birth accounts in Table 6 show the births produced by the female population of period-cohort a in each region. In this case, the system consists of two regions and migrations only take place between region i and region j. Similar population accounts for a general case of N regions can be obtained. A notation system has been used here: ' e ' means ' existence ', ' s ' means 'survival', ' d ' means 'death', ' b ' means ' birth '. For example, Peisj ${ }_{a}$ is the population of period-cohort a who exist in region i at the beginning of period t.to $t+1$ and survive in region $j$ at the end of period $t$ to $t+1$. Notation * indicates summation over a variable.
In Table 5, we have region $i$ and region $j$. For region $i$, the population of period-cohort a at the beginning of the period $t$ to $t+1$ is $\mathrm{Pi}^{*}$ a. This population has been divided into five items according to their states at the end of period $t$ to $t+1$. These five items belong to two basic population categories: nonmigrating population and migrating population.

Table 5 Population accounts (a) for period-cohort a (b) for infants-cohort

| Starting state | Ending state in period t to $\mathrm{t}+1$ |  |  |  |  |  | Total |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Survived in <br> Region i Region j |  | Deaths in |  |  |  |  |
|  |  |  | Regio |  | egion j |  |  |
| (a) Period-cohort a |  |  |  |  |  |  |  |
| Region i | Peisi ${ }_{\text {a }}$ | Peisj ${ }_{\text {a }}$ | Peidi ${ }_{\text {a }}$ | Peidi ${ }_{\text {aj }}$ |  | Peidj $_{\text {aj }}$ | $\mathrm{Pi}^{*}{ }^{\text {a }}$ |
| Region j | Pejsia | $\mathrm{Pejsj}_{\mathrm{a}}$ | Pejidi ${ }_{\text {a }}$ |  | $\mathrm{Pejdj}_{\text {ai }}$ | Pejdj ${ }_{\text {aj }}$ | $\mathrm{Pj}^{4}{ }^{\text {a }}$ |
| Total | $\mathrm{P}^{*} \mathrm{i}_{\mathrm{a}}$ | $\mathrm{P}^{*} \mathrm{j}_{\mathrm{a}}$ | $\mathrm{P}^{* \text { di }_{\text {a }}}$ |  |  | $\mathrm{P} * \mathrm{dj}_{\mathrm{a}}$ | $\mathrm{P}^{* *}{ }^{\text {a }}$ |
| (b) Infants-cohort |  |  |  |  |  |  |  |
| Region i | Pbisi | Pbisj | Pbidi ${ }_{\text {i }}$ | Pbidi $_{j}$ |  | $\mathrm{Pbidj}_{j}$ | Pbi* |
| Region j | Pbjisi | Pbjs | Pbjdi ${ }_{\text {i }}$ |  | $\mathrm{Pbjdj}_{i}$ | $\mathrm{Pbjdj}_{\mathrm{j}}$ | Pbj* |
| Total | $\mathrm{Pb}{ }^{\text {i }}$ | $\mathrm{Pb}{ }^{*}$ | $\mathrm{Pb}{ }^{*} \mathrm{di}$ |  |  | $\mathrm{Pb}^{*} \mathrm{dj}$ | $\mathrm{Pb} * *$ |

[^0]Table 6 Population accounts for birth

| Starting state | Ending state in period to t+1 |  |  |  |
| :---: | :---: | :---: | :---: | :---: |
|  | Births in Region i | Region |  | Total |
| Region i | Peibi ${ }_{\text {ai }}$ Peibi ${ }_{\text {aj }}$ |  | Peibj ${ }_{\text {aj }}$ | $\mathrm{Pib}^{*}{ }_{\text {a }}$ |
| Region j | Pejbi ${ }_{\text {a }}$ | $\mathrm{Pejbj}_{\text {ai }}$ | $\mathrm{Pej}^{\text {bj }}{ }_{\text {aj }}$ | $\mathrm{Pjb}^{*}{ }_{\text {a }}$ |
| Total | $\mathrm{P}^{*} \mathrm{bi}_{\mathrm{a}}$ |  | $\mathrm{P}^{*} \mathrm{bj}_{\mathrm{a}}$ | $\mathrm{P}^{*}{ }^{*}{ }_{\text {a }}$ |

## Note: See text for explanations.

There are two non-migrating population items. Population Peisia is the surviving non-migrating population which remains in region $i$ in the period $t$ to $t+1$. Population Peidiai is the non-surviving, non-migrating population who lived only in region i and died there in the period t to $\mathrm{t}+1$.

There are three migrating population items. Population Peisj $j_{a}$ is the surviving, migrating population who migrated from region $i$ to region $j$ in the period $t$ to $t+1$. Population Peid ${ }_{a j}$ is the non-surviving, migrating population who are potential migrants but died in the origin region i before migration actually took place in the period $t$ to $t+1$. Population Peidj ${ }_{a j}$ is the nonsurviving, migrating population who migrated from region $i$ to region $j$ and then died in region $j$ in the period $t$ to $t+1$. Here, subscript ' $j$ ' beside subscript ' a ' indicates the destination region of migration.

Similarly, the starting population $\mathrm{Pj}^{*}$ of period-cohort a in region j at the beginning of the period $t$ to $t+1$ is also divided into five items according to their states at the end of period $t$ to $t+1$ : surviving, non-migrating population Pejsj $_{a}$, non-surviving, non-migrating population Peidj $\mathrm{j}_{\mathrm{aj}}$, surviving, migrating population Pejsia, and non-surviving, migrating populations Pejdjaid and Pejdiai in origin and destination regions respectively.
At the end of period $t$ to $t+1$, the population in region $i$ is $P^{*} i_{a}$. It consists of the surviving, non-migrating population in its own region Peisia and the surviving, migrating population from region j Pejsia. Similarly, the population in region $\mathrm{P}^{*} \mathrm{j}_{\mathrm{a}}$ at the end of period t to $\mathrm{t}+\mathrm{l}$ consists of the surviving, nonmigrating population in its own region $\mathrm{Pejsj}_{\mathrm{a}}$ and the surviving, migrating population from region $i$ Peisj ${ }_{a}$.
In the period to to $t+1$, the total number of deaths occurring in region $i$ is $p * d i a$. It consists of three parts: the non-surviving, non-migrating population Peidi ${ }_{a i}$ in region $i$, the non-surviving, migrating population Peidi ${ }_{a j}$ who died in region i before migration actual took place, and the non-surviving, migrating population Pejdiai who migrated from region $j$ and died in region i . Similarly,
the total number of deaths occurring in region $\mathrm{j}^{*} \mathrm{dj}_{\mathrm{a}}$ also consists of three parts: the non-surviving, non-migrating population Pejdj ${ }_{a j}$ in region $j$, the nonsurviving, migrating population Pejd ${ }_{\text {ai }}$ who died in region j before migration actual took place, and the non-surviving, migrating population Peidj ${ }_{\text {aj }}$ who migrated from region i and died in region j .

The meanings of the population accounts for the infants-cohort ( periodcohort zero ) are similar to those of period-cohort a. The notations use ' $b$ ' to indicate the infants-cohort.

The birth accounts parallel the death accounts in the population accounts of period-cohort a . The notations use ' b ' to refer to births in the birth accounts while ' d ' is used to refer to deaths in the death accounts. The total number of births produced by the female population of period-cohort a who were in region $i$ at the beginning of the period $t$ to $t+1$ is Pib*. It consists of three parts: births Peitidid produced by the non-migrating populations (Peisia and Peidi ${ }_{\text {ai }}$ ) in region i, births Peitiaj produced by migrating populations ( Peisj $_{\text {a }}$, Peidi $_{\mathrm{aj}}$ and Peidj $\mathrm{aj}_{j}$ ) in region i , and births Peibiaj produced by migrating populations ( Peisj $_{\mathrm{a}}$ and Peidj $_{\mathrm{aj}}$ ) in region j . Similarly, the total number of births produced by the female population of period-cohort a who were in region $j$ at the beginning of the period $t$ to $t+1$ is $\mathrm{Pj}^{*}$ and also consists of three parts: births $\mathrm{Pejbj}_{\mathrm{aj}}$ produced by the non-migrating populations ( $\mathrm{Pejsj}_{\mathrm{a}}$ and $P^{e j d j}{ }_{a j}$ ) in region $j$, births $P^{e j b j} j_{a i}$ produced by migrating populations ( $\mathrm{Pejsi}_{\mathrm{a}}$, Pejdjai and Pejdi ${ }_{\mathrm{a}}$ ) in region j , and births Pejbia produced by migrating populations ( $\mathrm{Pejsi}_{\mathrm{a}}$ and $\mathrm{Pejdi}_{\mathrm{ai}}$ ) in region i .

The total number of births produced by the female population of periodcohort a in region i is $\mathrm{P}^{*} \mathrm{bi}_{\mathrm{a}}$. It consists of three parts: births Peibiai produced by the non-migrating populations ( Peisi $_{3}$ and Peidiai ) in region i, bitths Peibi ${ }_{\text {aj }}$ produced by migrating populations ( Peisj $_{\mathrm{a}}$, Peidi $_{\mathrm{aj}}$ and Peidj $_{\mathrm{aj}}$ ) in region i , and births Pejbiai produced by migrating populations from region $j$ ( Pejsia and Pejdiai ) in region i. Similariy, the total number of births produced by the female population of period-cohort a in region j is $\mathrm{P}^{*}$ bj and also consists of three parts: births Pejbjaj produced by the non-migrating populations ( $\mathrm{Pejsj}_{\mathrm{a}}$ and Pejdj ${ }_{a j}$ ) in region j , births $\mathrm{Pejbj}_{\mathrm{ai}}$ produced by migrating populations ( $\mathrm{Pej}_{\mathrm{j}}^{\mathrm{a}} \mathrm{a}_{\mathrm{a}}$, $P^{P e j d j}{ }_{j i}$ and $\mathrm{Pejdi}_{a i}$ ) in region j , and births $\mathrm{Peibj}_{\text {aj }}$ produced by migrating populations from region $\mathrm{i}\left(\right.$ Peisj $_{\mathrm{a}}$ and Peidj $_{\mathrm{aj}}$ ) in region j .
So far, we have described the movement or transition of population in a two region system by a set of multiregional population accounts. We found that an individual in region $i$ at the beginning of period $t$ to $t+l$ may remain in region $i$ or migrate to region $j$, and may die in region $i$ or region j. Furthermore, a female in region $i$ at the beginning of period $t$ to $t+1$ may produce births in region $i$ or region $j$. The total number of deaths occurring in region in the period $t$ to $t+1$ is not solely from the population in region i at the beginning of
period $t$ to $t+1$. The total number of births produced in region $i$ in the period $t$ to $t+l$ is again not solely produced by the female population in region $i$ at the beginning of period to to $t+l$. These phenomena make it more difficult and complicated to define and calculate mortality, fertility and migration rates correctly for multiregional population systems than for single-region population systems. Multiregional population accounts discussed above provide a framework to define these demographic rates correctly.

Table 7 presents the population accounts of the male population of periodcohort 20 in China in the period 1986-1987. The country is divided into two regions: urban (cities and towns) and rural (counties ). International migration is ignored here. Only those data generally available are shown in Table 7. For the case of China, one year migration data shown in this table were estimated from five year migration data using a special procedure (Shen, 1991).

Table 7 Population accounts of period-cohort 20 of the urban and rural population systems of China 1986-1987 ( male population, thousands )

| Starting <br> state | Ending state in period 1986 to 1987 |  |  |  | Total |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  | Survival in |  | Death in |  |  |
|  | Urban | Rural | Urban | Rural |  |
| Urban | 4653.16 | 2.72 | * * | * |  |
| Rural | 98.88 | 6085.50 | * | ** |  |
| Total | 4752.04 | 6088.22 | 6.24 | 8.09 | 10854.60 |

According to Table 7, for the male population of period-cohort 20, there were 4752.04 thousand males in the urban region at the end of period 1986-1987. These consist of 4653.16 thousand surviving, non-migrating males in the urban region and 98.88 thousand surviving, migrating males from the rural region. There were 6088.22 thousand males in the rural region at the end of period 1986-1987. These consist of 6085.50 thousand surviving, nonmigrating males in the rural region and 2.72 thousand surviving, migrating males from the urban region. In the period 1986-1987, there were 6.24 thousand deaths in the urban region and 8.09 thousand deaths in the rural region. Adding together all surviving and deceased populations in the urban and rural regions, there were 10854.60 thousand males in period-cohort 20 at the beginning of period 1986-1987. Many detailed items of the deceased populations in the population accounts in Table 7 are not known. The six asterisks in Table 7 represent six death items which are not available. These include the non-surviving, non-migrating population and non-surviving, migrating population who died in origin and destination regions. These data
need to be estimated from the available data. The estimation procedure will be discussed in section 4 following the discussions of demographic rate defmitions in sections 3.2 and 3.3.
In the rest of this section, we need to introduce notations for the genera case of multiregional population systems consisting of N regions. Region k or region z will refer to a general region instead of specific region i and region j in the previous discussions on the two region case. These notations are as follows. They are similar to those used for region i and region j .
$\mathrm{Pk}_{\mathrm{a}} \quad$ is the starting population of region k in period t to $\mathrm{t}+1$ in periodcohort $\mathrm{a}, \mathrm{k}=1,2, \ldots, \mathrm{~N}$. Period-cohort a refers to the same population group in the period $t$ to $t+1$ that belongs to age group a at time $t$.
$\mathrm{P}^{*} \mathrm{k}_{\mathrm{a}}$
$P^{*} d_{k} \quad$ is the population in period-cohort a who died in period $t$ to $t+1$ in region $\mathrm{k}, \mathrm{k}=1,2, \ldots, \mathrm{~N}$.
Peiss $z_{a} \quad$ is the population of period-cohort a who exist in region $k$ at time $t$ and survive in region $z$ in period $t$ to $t+1, k, z=1,2, \ldots, N$. is the population of period-cohort a who died in region $k$ in period to $t+1$ corresponding to non-migrating population in region $\mathrm{k}, \mathrm{k}=1,2, \ldots, \mathrm{~N}$.
Pekdk ${ }_{a z}$ is the population of period-cohort a who died in region k in period $t$ to $t+1$ corresponding to migrating population from region $k$ to region $z, k, z=1,2, \ldots, N ; k \neq z$.
Pexdzaz is the population of period-cohort a who died in region $z$ in period $t$ to $t+1$ corresponding to migrating population from region $k$ to region $z, k, z=1,2, \ldots, N ; k \neq z$.
Pbk* is the number of infants born in region k in period t to $\mathrm{t}+1, \mathrm{k}=1$, $2, \ldots, N$.
Ptiksz is the number of infants born in region k who survive in region z in period $t$ to $t+1, k, z=1,2, \ldots, N$.
Pbkdk $\quad$ is the number of infants who died in region $k$ in period $t$ to $t+1$ corresponding to non-migrating infants in region $k, k=1,2, \ldots$, N .
Pbkdk $\quad$ is the number of infants who died in region $k$ in period to $t+1$ corresponding to migrating infants from region k to region z , $k, z=1 ; 2, \ldots, N ; k \neq z$.
Pbkdz $z_{z} \quad$ is the number of infants who died in region $z$ in period to $t+1$ corresponding to migrating infants from region k to region z , $\mathrm{k}, \mathrm{z}=1,2, \ldots, \mathrm{~N} ; \mathrm{k} \neq \mathrm{z}$.
is the number of infants at the end of period $t$ to $t+1$ in region $k$, $\mathrm{k}=1,2, \ldots, \mathrm{~N}$. is the number of infants who die in region $k$ in period $t$ to $t+1$, $\mathrm{k}=1,2, \ldots, \mathrm{~N}$.
is the births in region $k$ in period $t$ to $t+1$ given by non-migrating population of period-cohort a in region $k, k=1,2, \ldots, N$.
is the births in region $k$ in period $t$ to $t+1$ given by migrating population of period-cohort a from region $k$ to region $z, k, z=1$, $2, \ldots, N ; k \neq z$.
Pekbz $a_{z} \quad$ is the births in region z in period t to $\mathrm{t}+1$ given by migrating population of period-cohort a from region $k$ to region $z, k, z=1$, $2, \ldots, \mathrm{~N} ; \mathrm{k} \neq \mathrm{z}$.
is the number of births in period to $t+1$ given in all regions by population of period-cohort a who are in region k at time $\mathrm{t}, \mathrm{k}=1$, $2, \ldots, N$.
is the number of births in period $t$ to $t+1$ given in region $k$ by population of period-cohort a in all regions, $k=1,2, \ldots, N$.

Here, population is also divided into two categories: migrating population and non-migrating population. Each category may have surviving and nonsurviving populations. Some populations may produce births. A general population accounts for a general case of N regions can be obtained based on these notations.

It is useful to derive some account equations here. The population at the beginning of period $t$ to $t+1 \mathrm{Pk}^{*}{ }_{\mathrm{a}}$ of period-cohort a in region k consists of five types of populations: surviving, non-migrating population Peksk ${ }_{a}$, surviving, migrating population Peksza ( $z=1,2, \ldots, N, z \neq k$ ), non-surviving, non-migrating population Pekdk $_{\mathrm{ak}}$, non-surviving, migrating population who died in region $k P^{e k d k}{ }_{a z}(z=1,2, \ldots, N, z \neq k)$, and non-surviving, migrating population who died in region $z P_{e k d z} z_{z}(z=1,2, \ldots, N, z \neq k)$. Thus, we have the following equation:

The population at the end of period $t$ to $t+1 \mathrm{P}^{*} \mathrm{k}_{\mathrm{a}}$ of period-cohort a in region $k$ consists of two types of populations: surviving, non-migrating population Peksk ${ }_{\mathrm{a}}$ in region k , and surviving, migrating population Pezsk $\mathrm{a}_{\mathrm{a}}$ from region $\mathrm{z}(\mathrm{z}=1,2, \ldots, \mathrm{~N}, \mathrm{z} \neq \mathrm{k})$ to region k . Thus we have the following equation:

$$
\mathrm{P}^{*} \mathrm{k}_{\mathrm{a}}=\sum \mathrm{N}_{\mathrm{z}=1} \text { Pezsk }_{\mathrm{a}} \quad \mathrm{k}=1,2, \ldots, \mathrm{~N}
$$

The total number of deaths $\mathrm{P}^{*} \mathrm{dk}_{\mathrm{a}}$ in region k in period t to $\mathrm{t}+1$ consists of three types of death; non-surviving, non-migrating population Pekdk ${ }_{\text {ak }}$ in region $k$, non-surviving, migrating population Pekdk ${ }_{a z}(z=1,2, \ldots, N, z \neq k$ ) who died in region $k$, and non-surviving, migrating population from region $z$ to region $k$ Pezdk $_{a k}(z=1,2, \ldots, N, z \neq k)$ who died in region $k$. Thus we have the following equation:

$$
\begin{equation*}
\mathrm{P}^{*} \mathrm{~d} k_{\mathrm{a}}=\Sigma \mathrm{N}_{\mathrm{z}=1} \text { Pekdik }_{\mathrm{az}}+\sum \mathrm{N}_{\mathrm{z}=1: \mathrm{i} \neq \mathrm{k}} \text { Peadk }_{\mathrm{ak}} \quad \mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{33}
\end{equation*}
$$

There are similar accounting equations for the infants-cohort.
The total number of births $\mathrm{P}^{\mathrm{bb}}{ }^{*}{ }_{a}$ produced by the female population in period $t$ to $t+1$ who were in region $k$ at the beginning of period $t$ to $t+1$ consists of three types of birth: births produced by the non-migrating population in region k Pekbk $\mathrm{a}_{\mathrm{ak}}$, births produced by the migrating population in region k Pekbk $_{\mathrm{az}}(\mathrm{z}=1,2, \ldots, \mathrm{~N}, \mathrm{z} \neq \mathrm{k})$, and births produced by the migrating population in region $z$ Pekbz $_{a z}(z=1,2, \ldots, N, z \neq k)$. Thus we have the following equation:

$$
\begin{equation*}
P k b^{*}{ }_{a}=\sum N_{z=1} \text { Pekb }_{a z}+\sum N_{z=1 ; z \neq k} \text { Pekbz }_{a z} \quad k=1,2, \ldots, N \tag{34}
\end{equation*}
$$

The total number of births $\mathrm{P}^{*}$ bika produced in region $k$ in period $t$ to $t+1$ consists of three types of birth: births produced by the non-migrating population in region k Pekbk $_{\mathrm{ak}}$, births produced by the migrating population in region $k$ Pekbk $\mathrm{a}_{\mathrm{a}}(\mathrm{z}=1,2, \ldots, \mathrm{~N}, \mathrm{z} \neq \mathrm{k})$, and births produced by the migrating population from region $z$ in region $k \operatorname{Pezbk}_{a k}(z=1,2, \ldots, N, z \neq k)$.Thus we have the following equation:

$$
\mathrm{P}^{*} \mathrm{bk}_{\mathrm{a}}=\sum \mathrm{N}_{z=1} \text { Pekbk }_{\mathrm{az}}+\sum \mathrm{N}_{\mathrm{z}=\mathrm{I} ; \mathrm{z} \neq \mathrm{k}} \text { Pezbk }_{\mathrm{ak}} \quad \mathrm{k}=1,2, \ldots, \mathrm{~N}
$$

### 3.2 Population at risk and occurrence-exposure rates

In the previous section, we have discussed multiregional population accounts to describe the states and changes of multiregional population systems in a period $t$ to $t+1$. As in the case of single-region population systems, a further step of demographic analysis is to use a set of rates of population changes to describe the dynamics of multiregional population systems. In addition to fertility and mortality rates discussed in the case of single-region population systems, we also need to introduce migration rates to describe the spatial interaction in multiregional population systems.

There are three components of population change here: deaths, births and migration. These components have been further divided into several types in multiregional population accounts. For the component of death, there are
basically three types of death in region k : the non-surviving, non-migrating population Pekdk ${ }_{\text {ak }}$, the non + surviving, migrating population Pekdk ${ }_{a z}$ who died in region $k$, and the non-surviving, migrating population from region $z$ Pezdk ${ }_{\text {ak }}$ who died in region k . The population which produces a population change is called the population at risk. The population at risk producing the population change, non-surviving, non-migrating population Pekdk ak, consists of two parts: surviving and non-surviving, non-migrating populations Peksk ${ }_{a}$ and Pekdkak. The population at risk who produce the population change, nonsurviving, migrating population Pexdk ${ }_{a z}$ who died in region $k$,consists of three parts: surviving and non-surviving, migrating populations Pekz $_{3}$, Pekdk $_{\text {az }}$ and Perdz $_{\text {az }}$. The population at risk who produce the population change, nonsurviving, migrating population Pezdk $_{\text {ak }}$ who died in region $k$, consists of two parts: surviving and non-surviving, migrating populations Pezska and Pezdk $\mathrm{ak}_{\mathrm{ak}}$. It is noted that various populations at risk involve only five basic population items in the multiregional population accounts.

It is noted that the non-surviving migrating population Pezdzak ${ }_{\text {ak }}$ who died in region z is not included in the population at risk for the population change, non-surviving, migrating population Peadk ${ }_{a k}$ who died in region $k$, as these people died in region $z$ before migration actually took place and were not relevant to deaths occurring in region $k$ after migration.
Similarly, for the component of births, there are three basic types of birth in region k : births Pektk ak produced by the non-migrating population of periodcohort a in region $k$, births Pekbk ${ }_{\text {az }}$ produced in region $k$ by the migrating population of period-cohort a from region $k$ to region $z$, births Pezbkak produced in region $k$ by the migrating population of period-cohort a from region $z$ to region $k$. It is noted again that births Pekbk $z_{z}$ are produced by the migrating population in the origin region before they migrate to the destination region. The population at risk for each of these three basic types of birth is the same as the population at risk for each of three basic types of death respectively.

For the component of migration, the population at risk for the migrating population from region k is the population in region k at the beginning of a period. Table 8 summarizes the populations at risk for various death, birth and migration items. For total births or deaths in region k, its population at risk is obtained by adding up all the populations at risk of various birth or death items.

To calculate occurrence-exposure mortality, fertility and migration rates, we need to specify the exposure time of various populations at risk to calculate population-time at risk. There are only five basic population items involved as pointed out earlier. We need only to specify the exposure time for these five population items. Figure 3 and Table 9 show the average exposure time of populations at risk in different regions. In Figure 3, the states of life in region

| Items | Population at risk |
| :---: | :---: |
| Death or birth item |  |
| Pekdk $_{\text {ak }}$, Pekbk ${ }_{\text {ak }}$ | Peksk ${ }_{\text {a }}$, Pekdk ${ }_{\text {ak }}$ |
| Pekdk ${ }_{\text {az }}$, Pekbk ${ }_{\text {az }}$ | Peksz $_{\text {a }}$, Pekdz $_{\text {az }}$, Pekdk ${ }_{\text {a }}$ |
| Pezdk $_{\text {ak }}$, Pezbk $_{\text {ak }}$ | Pezsk $_{\text {a }}$, Pezdk ${ }_{\text {ak }}$ |
| Pekdk $_{\mathrm{a}}=\Sigma \mathrm{N}_{\mathrm{z}=1}$ Pekdk $_{\text {az }}$, | $\begin{aligned} & \Sigma N_{\mathrm{z}=1} \text { Peksz }_{\mathrm{a}}, \Sigma \mathrm{~N}_{\mathrm{z}=1, \mathrm{z} \neq \mathrm{k}} \text { Pekdz }{ }_{\mathrm{a} z}, \\ & \Sigma \mathrm{~N}_{\mathrm{z}=1} \text { Pekdk }_{\mathrm{a} \mathrm{z}} \end{aligned}$ |
| $\mathrm{Pekbk}_{\mathfrak{a}}=\Sigma \mathrm{N}_{z=1}$ Pekbk $_{\text {az }}$ |  |
| $\mathrm{P}^{*} \mathrm{dk}_{\mathrm{a}}=\Sigma \mathrm{N}_{2=1,2 \pm k} \mathrm{Pezdk}_{\mathrm{ak}}+$ Pekdk $_{\text {a }}$, | $\begin{aligned} & \Sigma N_{z=1} \text { Peksz }_{\mathrm{a}}, \Sigma \mathrm{~N}_{\mathrm{z}=1, \mathrm{zzk}} \text { Pekdz }_{\mathrm{az}}, \\ & \Sigma N_{\mathrm{z}=1} \text { Pexdk }_{\mathrm{az}}, \Sigma N_{\mathrm{z}=1, z \neq \mathrm{k}} \text { Pezsk }_{\mathrm{a}}, \\ & \Sigma \mathrm{~N}_{\mathrm{z}=1, \mathrm{z} \neq \mathrm{k}} \text { Pezdk }_{\mathrm{ak}} \end{aligned}$ |
| $\mathrm{P}^{*} \mathrm{bk}_{\mathrm{a}}=\Sigma \mathrm{N}_{\mathrm{z}=1, \mathrm{z} \neq \mathrm{k}} \mathrm{Pezbk}_{\text {ak }}+$ Pekbk $_{\text {a }}$ |  |


| Migration item |  |
| :---: | :---: |
| Peksz $_{\text {a }}$, Pekdr $_{\text {az }}$, Pekdk ${ }_{\text {az }}$ | $\begin{aligned} & \sum \mathrm{N}_{\mathrm{z}=1} \text { Peksz }_{\mathrm{a}}, \Sigma \mathrm{~N}_{\mathrm{z}=1} \text { Pekdk } \\ & \sum \mathrm{N}_{\mathrm{z}=1, \mathrm{z}, \mathrm{k}}, \end{aligned}$ |

Note: See text for explanations.
Table 9 Exposure times of various populations at risk

| Item | Region k Region z |  |  |  | death |
| :---: | :---: | :---: | :---: | :---: | :---: |
| Survival non-migrating population | Pekska | 1 | 0 | 0 | 0 |
| Non-survival non-migrating population | Pekdk ${ }_{\text {ak }}$ | 0.5 | 0 | 0 | 0.5 |
| Survival migrating population | Peksza | 0.5 | 0.5 | 0 | 0 |
| Non-survival migrating poptulation died in region k | Pekdk ${ }_{\text {az }}$ | 0.25 | 0 | 0 | 0.75 |
| Non-survival migrating population died in region z | Pekdz ${ }_{\text {az }}$ | 0.5 | 0.25 | 0 | 0.25 |

Note: See text for explanations.
k and region z , and the state of death are presented for various populations at risk respectively. It is assumed that all events are uniformly distributed over the period. Population item Peksk ${ }_{a}$ is the surviving, non-migrating population spending the whole period of time in region $k$, so its exposure time is one in region $k$ and zero in other regions ( Figure 3(a)). The non-surviving, nonmigrating population Pexdk ${ }_{\text {ak }}$ will spend on average half the time in region $k$,

(a) Suviving nom-migrating population (b)Non-surviving non-migrating population

Exposure time:
0.5 in each recion

(c) Surving migrating population
(d) Migrating population died in region $k$

$\rightarrow$ life in region $k$
$\cdots>$ life in region 2
(e) Migrating population died in rgion 2

Fig. 3 Exposure times of the population in region k at the beginning of period $t$ to $t+1$
so its exposure time is 0.5 in region k and zero in other regions ( Figure 3(b)). The surviving, migrating population Peksza will spend half of the period in the origin and destination regions, so its exposure time is 0.5 in regions k and z , and zero in other regions ( Figure $3(\mathrm{c})$ ). The non-surviving, potential migrating population Pekdx ${ }_{\text {az }}$ is subjected to a double process of losing population by migrating and dying in region k , so its exposure time is 0.25 in region k and zero in other regions (Figure 3(d)). The non-surviving, migrating population Pekdz ${ }_{a z}$ is subjected to one process of losing population by migrating in region $k$ and one further process of losing population by dying in region z , so its exposure time is 0.5 in region k and 0.25 in region z , and zero in other regions (Figure 3(e)). It is noted that the exposure time specified for Pekdk ${ }_{a} z$ and Pekdz $_{\text {az }}$ here is implicitly different from Rees and Wilson (1977) as a set of more detailed multiregional population accounts is used.
Similarly, exposure times can be specified for population items of an infantscohort. On average, infants can live at most one half period in one whole period. Therefore, the exposure time for an infants-cohort is half the exposure time for period-cohort a. If one whole period is used as the time unit for period-cohort a and one half period is used as the time unit for an infantscohort, the units of exposure time for period-cohort a and the infants-cohort will become the same. This assumption will essentially lead to the same formulas and calculations for period-cohort a and the infants-cohort.

Therefore, the infants-cohort can be treated in the same way as the general period-cohort a and be labelled as period-cohort zero.

Now, population-time at risk for deaths and births of period-cohort a in region k can be calculated by multiplying various populations at risk by their exposure time respectively and then adding up. Population-time at risk $P^{2} R^{* d k_{a}}$ and PAR $^{*} b k_{a}$ for the total deaths $\mathrm{P}^{*} \mathrm{dk}_{\mathrm{a}}$ and the total births $\mathrm{P}^{*} \mathrm{bk}_{\mathrm{a}}$ of period-cohort a in region $k$ respectively are the same and are as follows:

$$
\begin{align*}
& \text { PAR }^{*} \mathrm{dk}_{a}=\operatorname{PAR}^{*} \mathrm{bk}_{\mathrm{a}}=\text { Peksk }_{\mathrm{a}}+0.5 \sum \mathrm{~N}_{\mathrm{z}=1 ; \mathrm{z} \pm \mathrm{k}}\left(\text { Peksz }_{\mathrm{a}}+\text { Pezsk }_{\mathrm{a}}\right) \\
& +0.5 \text { Pekdk }_{a k}+0.25 \sum \mathrm{~N}_{\mathrm{z}=1 ; \mathrm{z} \neq \mathrm{k}}\left(\text { Pekdk }_{\mathrm{az}}+\text { Pezdk }_{\mathrm{ak}}\right) \\
& +0.5 \sum \mathrm{~N}_{\mathrm{z}=1 \mathrm{i} \mathrm{z} \neq \mathrm{k}} \mathrm{Pekdz}_{\mathrm{az}} \\
& \mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{3}
\end{align*}
$$

Occurrence-exposure mortality rate $\mathrm{dk}_{\mathrm{a}}$ and fertility rate $\mathrm{b}_{\mathrm{a}}$ are calculated by dividing the total deaths and total births by population-time at risk respectively.
$\mathrm{d} \mathrm{k}_{\mathrm{a}}=$ Total deaths of period-cohort a in region $\mathrm{k} /$ Population-time at risk

$$
\begin{equation*}
=\left(\text { Pekdk }_{\mathrm{ak}}+\sum \mathrm{N}_{z=1 ; z \neq k}\left(\text { Pekdk }_{\mathrm{az}}+\mathrm{Pezdk}_{\mathrm{ak}}\right)\right) / \mathrm{PAR}^{* \mathrm{dk}_{\mathrm{a}}} \tag{37}
\end{equation*}
$$

$\mathrm{b}_{\mathrm{a}}=$ Total births of period-cohort a in region $\mathrm{k} /$ Population-time at risk

$$
\begin{gather*}
=\left(\text { Pekbk }_{a k}+\sum N_{z=1 ; z \neq k}\left(\text { Pekbk }_{a z}+\text { Pezbk }_{a k}\right)\right) / P_{A R}^{*} \mathrm{Pk}_{\mathbf{a}}  \tag{38}\\
k=1,2, \ldots, N
\end{gather*}
$$

Three occurrence-exposure, destination-specific migration rates will be defined. These are the potential migration rate ${ }^{w} \mathrm{kz}_{1 \mathrm{a}}$, the actual migration rate $\mathrm{w}^{\mathrm{kz}} 2_{2 \mathrm{a}}$ and the survival migration rate $\mathrm{wkz}_{3 \mathrm{a}}$. All migrants, including potential migrants who fail to realize migration because of death in the accounting period, are accounted for in the potential migration rate $\mathrm{wkz}_{1 \mathrm{a}}$. Only migrants that actually make migrations are accounted for in the actual migration rate $w k z_{2 a}$. Only survived migrants are accounted for in the survival migration rate $w \mathrm{kz}_{3}$.

Population-time at risk PARk $_{a}$ for migrations from region $k$ can be calculated by multiplying various populations at risk by their exposure-time and adding together.

$$
\begin{array}{r}
\text { PARk }_{\mathrm{a}}=\text { Peksk }_{\mathrm{a}}+0.5 \sum \mathrm{~N}_{\mathrm{z}=1 ; z \neq \mathrm{k}} \text { Peksz }_{\mathrm{a}}+0.5 \text { Pekdk }{ }_{\mathrm{ak}} \\
+0.25 \sum \mathrm{~N}_{\mathrm{z}=1 ; \mathrm{z} \neq \mathrm{k}} \text { Pekdk }_{\mathrm{az}}+0.5 \sum_{\mathrm{z}}+1 ; z \neq \mathrm{k} \text { Pekdz} \mathrm{P}_{\mathrm{az}} \\
\mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{39}
\end{array}
$$

The three occurrence-exposure migration rates $\mathrm{wkz}_{1 \mathrm{a}}, \mathrm{wkz}_{2 \mathrm{a}}, \mathrm{wkz}_{3 \mathrm{a}}$ can be calculated by dividing the numbers of migrants by population-time at risk respectively as follows:

| Potential migration rate $\mathrm{w}^{\mathrm{k} z_{1 \mathrm{a}}}=\left(\mathrm{Peksz}_{\mathrm{a}}+\mathrm{Pekdz}_{\mathrm{az}}+\mathrm{Pekdk}_{\mathrm{az}}\right) / \mathrm{PARk}_{\mathrm{a}}$ |  |
| :---: | :---: |
|  | (40) |
| Actual migration rate $w k z_{2 a}=\left(\right.$ Peksz $_{a}+$ Pekdz $\left._{\text {az }}\right) / \mathrm{PARk}_{\mathrm{a}}$ | (41) |
| Strivival migration rate $\mathrm{wk}_{3}{ }_{3 \mathrm{a}}=\mathrm{Peksz}_{\mathrm{a}} /$ PARk ${ }_{\mathrm{a}}$ | (42) |

For the purpose of population projections, forward demographic rates are often used so that step by step projections can proceed from the starting population. In the next section, forward demographic rates will be defined and their relations with occurrence-exposure demographic rates discussed.

### 3.3 Forward demographic rates and their relationships with occurrence-exposure demographic rates

This section will define forward demographic rates for multiregional population systems. Forward demographic rates for a single-region population system have already been discussed in section 2.3. In that case, it has been found that there are unique relations between the forward and occurrenceexposure mortality and fertility rates respectively. Their relations are expressed by equations (23), (25-27).
For the general case of a spatial population system consisting of N regions, it can be proved that the same relations between the occurrence-exposure mortality rate ( $\mathrm{dk}_{\mathrm{a}}$ ) and fertility rate ( $\mathrm{bk}_{\mathrm{a}}$ ) and the forward mortality rate ( $\mathrm{u}_{\mathrm{a}}$ ) and fertility rate ( $\mathrm{fk} \mathrm{k}_{\mathrm{a}}$ ) still bold as long as starting populations for death items and birth iterns are correctly specified. Therefore:

$$
\begin{array}{ll}
u k_{a}=d k_{a}\left(1-0.5 u k_{a}\right)=d k_{a} /\left(1+0.5 d k_{a}\right) & k=1,2, \ldots, N(43) \\
f k_{a}=b k_{a}\left(1-0.5 u k_{a}\right)=b k_{a} /\left(1+0.5 d k_{a}\right) & k=1,2, \ldots, N(44)
\end{array}
$$

It seems clear that forward mortality and fertility rates are less than occurrence-exposure mortality and fertility rates respectively because population-time at risk is generally less than the starting population due to the loss of exposure-time of the deceased population. Their differences are determined by the mortality rate in the region concerned as shown in equations (43) and (44).
It can be proved that correct starting populations PST*dk and PST* ${ }^{*} k_{a}$ for the total deaths $\mathrm{P}^{*} \mathrm{dk}_{\mathrm{7}}$ and the total births $\mathrm{P}^{*} h \mathrm{k}_{\mathrm{a}}$ of period-cohort a in region k
respectively are the same, and are as follows:

$$
\begin{gathered}
\text { PST }^{*} \mathrm{dk}_{\mathrm{a}}=\text { PST* }^{*} \mathrm{bk}_{\mathrm{a}}=\text { Peksk }_{a}+0.5 \sum \mathrm{~N}_{z=1 ; z \neq k}\left(\text { Peksz }_{a}+\text { Pezsk }_{a}\right)+\text { Pekdk }_{\mathrm{ak}} \\
+0.75 \sum \mathrm{~N}_{z=1 ; z \neq k}\left(\text { Pekdk }_{a z}+\text { Pezdk }_{\mathrm{ak}}\right)+0.5 \sum \mathrm{~N}_{\mathrm{z}=1 ; z \neq \mathrm{k}} \text { Pekdz }_{a z} \\
\mathrm{k}=1,2, \ldots, \mathrm{~N}
\end{gathered}
$$

Similar to exposure-time specified for population-time at risk calculations, different time-weights are applied to various populations at risk in starting population calculations as shown in Table 10. Starting population is calculated by multiplying various populations at risk by their time-weights respectively and then adding up. Derivation of equation (45) is lengthy and is omitted here.

Table 10 Time-weights of various populations at risk

| Item | Region k Region z Other regions |  |  |  |
| :---: | :---: | :---: | :---: | :---: |
| Surviving non-migrating population | Pekska | 1 | 0 | 0 |
| Non-surviving non-migrating population | Pekdk ${ }_{\text {ak }}$ | 1 | 0 | 0 |
| Surviving migrating population | Peksza | 0.5 | 0.5 | 0 |
| Non-surviving migrating population died in region k | Pekdk ${ }_{\text {az }}$ | 0.75 | 0 | 0 |
| Non-surviving migrating population died in region $z$ | Pekdz ${ }_{\text {az }}$ | 0.5 | 0.75 | 0 |

Note: See text for explanations.
A straightforward explanation for various time-weights used is as follows. On average, surviving migrating populations spend one-half period in origin and destination regions, so their time-weight is 0.5 in regions k and z . Population item Pekdz ${ }_{a z}$ is subjected to only one process of losing population by migrating from region $k$ and can be treated in region $k$ as a surviving migrating population item like Peksza. Therefore, the time-weight in region $k$ for Pekdzaz is also 0.5. Population item Peksk $\mathrm{a}_{\mathrm{a}}$ spends the whole period of time in region k , so its time-weight is one in region k . As in the non-spatial case of the starting population given in equation (18), the non-surviving, non-migrating population Pekdk ${ }_{\text {ak }}$ also has a time-weight of one in region K. Population items Pekdk ${ }_{a z}$ and Pezdk ${ }_{a k}$ have characteristics of both a migration population item and a deceased population item in region k . Their time-weight is 0.75 in region $k$, which is the average of time weights for a migration population item (0.5) and a deceased population item (one).

Now the forward mortality rate, $\mathrm{u}_{\mathrm{a}}$, and fertility rate, $\mathrm{fk}_{\mathrm{a}}$, can be defined in terms of population items in multiregional population accounts:
$\mathbf{u k}_{\mathbf{a}}=$ Total deaths of period-cohort $\mathbf{a}$ in region $\mathbf{k} /$ Starting population

$$
\begin{equation*}
=\mathrm{P}^{*} \mathrm{dk}_{\mathrm{a}} / \mathrm{PST}^{*} \mathrm{dk}_{\mathrm{a}} \quad \mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{46}
\end{equation*}
$$

$\mathrm{fk}_{\mathrm{a}}=$ Total births of period-cohort a in region $\mathrm{k} /$ Starting population

$$
\begin{equation*}
=\mathrm{P}^{*} b \mathrm{k}_{\mathrm{a}} / \mathrm{PST}^{*} b k_{\mathbf{a}} \quad \mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{47}
\end{equation*}
$$

The starting population $\mathrm{PSTk}_{\mathbf{a}}$ for migrations from region k can be defined as the population in region k at the beginning of the period t to $\mathrm{t}+1$ :

$$
\begin{gather*}
\operatorname{PSTk}_{\mathrm{a}}=\sum \mathrm{N}_{\mathrm{z}=1} \text { Peksz }_{\mathrm{a}}+\sum \mathrm{N}_{\mathrm{z}=1} \text { Pekdk }_{\mathrm{az}}+\sum_{\mathrm{z}=1 ; \mathrm{zzk}} \mathrm{Pekdz}_{\mathrm{az}}=\mathrm{Pk}^{*}{ }_{\mathrm{a}} \\
\mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{48}
\end{gather*}
$$

It should be pointed out that the starting population PSTk ${ }_{\mathrm{a}}$ in equation (48) is subjected to a double process of losing population by migrating and dying in one period. By the end of period, the end population PEDk ${ }_{a}$ is:

$$
\text { PEDk }_{\mathrm{a}}=\text { Peksk }_{\mathrm{a}} \quad \mathrm{k}=1,2, \ldots, \mathrm{~N}
$$

All other population items in the starting population have been lost via migration and death. It is noted that the population-time at risk in equation (39) is less than the average of starting population and end population in equations (48) and (49). Due to the interaction of the migration process and the death process, the starting population will decrease by migrating and dying at a decreasing rate. This fact is reflected by the much shorter exposure-time of population item Pekdkaz experiencing the double process of losing population by migration and death.

The forward potential migration rate $\mathrm{m}^{\mathrm{kz}} 1_{2}$, the actual migration rate $\mathrm{mk}_{2 \mathrm{a}}$ and the survival migration rate $\mathrm{mkz}_{3_{\mathrm{a}}}$ can be defined:

$$
\begin{align*}
& \mathrm{mkz}_{1 \mathrm{a}}=\left(\text { Peksz }_{\mathrm{a}}+\text { Pekdz }_{\mathrm{az}}+\text { Pekdk }_{\mathrm{az}}\right) / \text { PSTx }_{\mathrm{a}}  \tag{150}\\
& m^{k} z_{2 a}=\left(\text { Peksz }_{a}+\text { Pekdz }_{\mathrm{az}}\right) / \text { PSTk }_{\mathrm{a}}  \tag{51}\\
& k, z=1,2, \ldots, N ; k \neq z \tag{52}
\end{align*}
$$

The following relations between occurrence-exposure migration rates and forward migration rates can be obtained:

$$
\begin{align*}
& \mathrm{m}^{\mathrm{kz}}{ }_{\mathrm{la}}=\mathrm{wkz}_{1 \mathrm{a}} / \mathrm{ck}_{\mathrm{a}}  \tag{53}\\
& \begin{array}{l}
m k z_{2 a}=w k z_{2 a} / c k_{a} \\
m k z_{3 a}=w k z_{3 a} / c k_{a}
\end{array}  \tag{54}\\
& \begin{array}{l}
m k z_{2 a}=w k z_{2 a} / \mathrm{ck}_{a} \\
\mathrm{~m}^{k z_{3 \mathrm{a}}}=\mathrm{wkz}_{3 \mathrm{a}} / \mathrm{ck}_{\mathrm{a}}
\end{array} \tag{55}
\end{align*}
$$

Here $c k_{a}$ is the ratio of the occurrence-exposure migration rates to the forward migration rates of the period-cohort a in region $k$.

$$
\begin{align*}
\mathrm{c}_{\mathrm{a}}= & 1+0.5 \sum \mathrm{~N}_{z=1 ; z \neq \mathrm{k}} w \mathrm{kz}_{1 \mathrm{a}}+0.5 \mathrm{~d}_{\mathrm{a}} \\
& +0.125 \sum \mathrm{~N}_{\mathrm{z}=1 ; z * k} w \mathrm{kz} 1_{1 \mathrm{a}} \mathrm{dk}_{2} /\left(1+0.25 \mathrm{~d} \mathrm{k}_{\mathrm{a}}\right) \quad \mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{56}
\end{align*}
$$

The derivation of equation (56) is again omitted here. It is clear that forward migration rates are less than occurrence-exposure migration rates. This is because the population-time at risk is generally less than the starting population due to the loss of exposure-time of the deceased and migrating populations. Their differences are determined by the mortality rate and total migration rate to all destinations of the region concerned as shown in equation (56).

The relations between forward demographic rates and occurrence-exposure demographic rates have now been established in equations (43), (44), and (53)(56).

Now we will use the urban-rural population system of China as an example to illustrate these relations. In the case of China, international migration is relatively small and is ignored in this analysis. Three coefficients will be used to express the relations of various demographic rates.
Coefficient $\mathrm{ok}_{\mathrm{a}}$ is defined as the ratio of the occurrence-exposure mortality (or fertility) rate to the forward mortality (or fertility ) rate of the periodcohort a in region k . The following equation can be obtained from equations (43) and (44):

$$
\begin{equation*}
\mathbf{o k}_{\mathrm{a}}=\mathrm{d} \mathbf{k}_{\mathrm{a}} / \mathrm{u} \mathbf{k}_{\mathrm{a}}=\mathrm{b} \mathbf{k}_{\mathrm{a}} / \mathrm{f} \mathbf{k}_{\mathrm{a}}=1 /\left(1-0.5 u \mathrm{k}_{\mathrm{a}}\right) \tag{57}
\end{equation*}
$$

Coefficient $c_{a}$ is defined as the ratio of the occurrence-exposure migration rates to the forward migration rates of the period-cohort a in region k . The following equation can be obtained from equations (53)-(56):

$$
\begin{align*}
& =1 /\left(1-0.5 \sum N_{z=1 ; z \neq k} \mathrm{mkz}_{1 \mathrm{a}} /\left(\mathrm{I}-0.25 \mathrm{uk}_{\mathrm{a}}\right)\right. \\
& -0.5 \mathrm{uk}_{\mathrm{a}}\left(1-\sum \mathrm{N}_{\mathrm{z}=1 ; \mathrm{z} \neq \mathrm{k}} \mathrm{mkz}_{1 \mathrm{a}}\right) \text { ) } \tag{58}
\end{align*}
$$

Coefficient $\mathrm{c}_{\mathrm{mk}}^{a}$ is defined as the ratio of the potential migration rate $\mathrm{mkz}_{1 \mathrm{a}}$ (or $w k z_{1 a}$ ) to the actual migration rate $m^{\mathrm{k}} z_{2 \mathrm{a}}$ (or $w \mathrm{k} z_{2 \mathrm{a}}$ ) of the period-cohort a in region k . It can be proved that $\mathrm{cmz}_{\mathrm{a}}$ is the ratio of the actual migration rate $\mathrm{mkz}_{2 \mathrm{a}}$ (or $w k z_{2 \mathrm{a}}$ ) to the survival migration rate $\mathrm{mkz} \mathcal{3 a b}$ (or $w k z_{3 a}$ ) of the period-cohort a in region k . It can be deduced that:

$$
\begin{align*}
& \mathrm{cmk}_{\mathrm{a}}=\mathrm{mkz}_{1 \mathrm{a}} / \mathrm{m}^{\mathrm{k}} 2_{2 \mathrm{a}}=\mathrm{wkz}_{1 \mathrm{a}} / \mathrm{wk} z_{2 \mathrm{a}}=\left(1-0.25 \mathrm{uk}_{\mathrm{a}}\right) /\left(1-0.75 \mathrm{uk}_{\mathrm{a}}\right) \\
& \mathrm{crz}_{\mathrm{a}}=\mathrm{mkz}_{2 \mathrm{a}} / \mathrm{mkz}_{3 \mathrm{a}}=\mathrm{wkz}_{2 \mathrm{a}} / \mathrm{wkz}_{\mathrm{ya}_{\mathrm{a}}}=\left(\mathrm{i}-0.25 \mathrm{uz}_{\mathrm{a}}\right) /\left(1-0.75 \mathrm{ukz}_{\mathrm{a}}\right) \tag{59}
\end{align*}
$$

The forward mortality rate, the fertility rate and the survival migration rate of the urban-rural population systems of China have been estimated in previous research ( Shen, 1991 ). Various coefficients, the forward actual and potential migration rates, and all occurrence-exposure demographic rates can be calculated using equations (57)-(60). This section presents the results for

Table 11 Ratios of occurrence-exposure demographic rates to forward demographic rates ( female populations, China)

| Period- Jrban |  |  |  | Rural |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| cohor | - 0 | c | cm | 0 | c | cm |
| 1 | 1.00148 | 1.00191 | 1.00148 | 1.00420 | 1.00593 | 1.00421 |
| 6 | 1.00038 | 1.00053 | 1.00038 | 1.00053 | 1.00212 | 1.00053 |
| 11 | 1.00028 | 1.00037 | 1.00028 | 1.00021 | 1.00220 | 1.00021 |
| 16 | 1.00026 | 1.00034 | 1.00026 | 1.00042 | 1.00374 | 1.00042 |
| 21 | 1.00051 | 1.00232 | 1.00051 | 1.00064 | 1.01106 | 1.00064 |
| 26 | 1.00061 | 1.00181 | 1.00061 | 1.00090 | 1.00978 | 1.00090 |
| 31 | 1.00063 | 1.00084 | 1.00063 | 1.00074 | 1.00385 | 1.00074 |
| 36 | 1.00075 | 1.00087 | 1.00075 | 1.00093 | 1.00358 | 1.00093 |
| 41 | 1.00093 | 1.00103 | 1.00093 | 1.00116 | 1.00368 | 1.00116 |
| 46 | 1.00141 | 1.00148 | 1.00141 | 1.00173 | 1.00379 | 1.00173 |
| 51 | 1.00188 | 1.00196 | 1.00188 | 1.00262 | 1.00416 | 1.00263 |
| 56 | 1.00445 | 1.00454 | 1.00446 | 1.00398 | 1.00538 | 1.00399 |
| 61 | 1.00664 | 1.00671 | 1.00666 | 1.00708 | 1.00835 | 1.00710 |
| 66 | 1.00919 | 1.00925 | 1.00923 | 1.01037 | 1.01196 | 1.01042 |
| 71 | 1.01683 | 1.01697 | 1.01697 | 1.01611 | 1.01767 | 1.01624 |
| 76 | 1.02684 | 1.02694 | 1.02721 | 1.02742 | 1.02932 | 1.02780 |
| 81 | 1.04914 | 1.04954 | 1.05037 | 1.04619 | 1.04897 | 1.04729 |
| 86 | 1.07747 | 1.07799 | 1.08059 | 1.06693 | 1.06871 | 1.06925 |
| 91 | 1.12627 | 1.12686 | 1.13477 | 1.11997 | 1.12268 | 1.12763 |

Note: o: ratio of occurrence-exposure mortality ( or fertility ) rate to forward mortality ( or fertility ) rate;
c: ratio of occurrence-exposure migration rate to forward migration rate;
cm : ratio of potential migration rate to actual migration rate of the region or the ratio of actual migration rate to survival migration rate of the other region.
the female population of the urban-rural population system of China. Table 11 shows the various ratios of occurrence-exposure demographic rates to forward demographic rates, and the ratios among potential, actual and survival migration rates of female populations. Figure 4 presents three

According to equations (57)-(60), the greater the mortality rate and migration rate, the greater these ratios will be. All these ratios are close to one below age 50 and increase with age due to the increase of the mortality rate. The ratio of the occurrence-exposure migration rates to the forward migration rates has a peak around period-cohort 21 due to the high migration rate.
Figure 5 presents the occurrence-exposure and forward mortality rates of the urban female population. Figure 6 presents the occurrence-exposure and forward potential migration rates of the rural female population. It can be seen that the forward demographic rates are close to the occurrence-exposure demographic rates. However, their differences do become relatively large for ages over 80 . For example, the occurrence-exposure mortality rate of periodcohort 81 of the urban female population is 0.09827 while the forward mortality rate is 0.09367 .

o: ratio of occurrence-exposure mortality ( or fertility ) rate to forward mortality ( or fertility ) rate;
c: ratio of occurrence-exposure migration rate to forward migration rate; cm : ratio of potential migration rate to actual migration rate of the region or the ratio of the actual migration rate to the survival migration rate of the other region.


Urban u: forward mortality rate; Urban d: occurrence-exposure mortality rate
Fig. 5 Mortality rates of the female population ( Urban China )


Rural ml : forward potential migration rate;
Rural wt : occurrence-exposure potential migration rate.
Fig. 6 Potential migration rates of the female population (rural China )

Fig. 4 Coefficients of the female population ( urban China )

## 4 ESTIMATION OF FORWARD DEMOGRAPHIC RATES

Forward mortality, fertility and migration rates have been defined in the previous section on the basis of multiregional population accounts. The next step is to estimate three demographic rates and multiregional population accounts from the population data available. These demographic rates can then be used for multiregional population projections. As will be shown in the next section, forward mortality, fertility and migration rates can be used straightforwardly for population projections. However, an iterative procedure is needed to estimate these forward demographic rates and multiregional population accounts.
It is assumed that the following population data are available: the ending population of period-cohort a $\mathrm{P}^{*} \mathrm{k}_{\mathrm{a}}$; the surviving, migrating population Pexsza the population $D k_{a}$ who died at age a in region $k$ in period $t$ to $t+1$; the birth population $\mathrm{Bk}_{\mathrm{a}}$ produced by the female population at age a in region k in period $t$ to $t+1$; the total births in region $k$, i.e., the population of the infantscohort (period-cohort zero) $\mathrm{Pk}^{*}{ }_{0}$ at the beginning of period t to $\mathrm{t}+1$. The estimation procedure for the infants-cohort and the other period-cohorts are slightly different as both the populations of the infants-cohort at the beginning and end of period $t$ to $t+1$ are known. The estimation of the mortality rate of the infants-cohort will be discussed first. Then the estimation of the mortality rates of other period-cohorts, of fertility rates and of migration rates will be discussed.

Two key equations used in the following estimation procedure express the non-surviving, migrating populations who died in origin (region k ) and destination ( region $z$ ) regions respectively in terms of the surviving, migrating population from region k to region z . These two equations are as follows for the infants-cohort which is labelled as period-cohort zero:

$$
\begin{array}{r}
\text { Pekdz }_{0 z}=0.5 \text { Peksz }_{0} \mathrm{uz}_{0} /\left(1-0.75 \mathrm{u}_{0}\right) \quad \mathrm{k}, \mathrm{z}=1,2, \ldots, \mathrm{~N} ; \mathrm{k} \neq \mathrm{z}(61) \\
\text { Pekdk }_{0 \mathrm{z}}=0.5 \mathrm{Peksz}_{0} \mathrm{uk}_{0}\left(1-0.25 \mathrm{uz}_{0}\right) /\left(1-0.75 \mathrm{uk}_{0}\right) /\left(1-0.75 \mathrm{uz}_{0}\right) \\
\mathrm{k}, \mathrm{z}=1,2, \ldots, \mathrm{~N} ; \mathrm{k} \neq \mathrm{z} \quad(62)
\end{array}
$$

The derivation of equations (61) and (62) is based on the definition of forward mortality rates and is omitted here.
The following equations can be obtained from equations (31)-(33) as both the populations of the infants-cohort at the beginning and end of period $t$ to t+ I are known:

Non-surviving, non-migrating population:

Surviving, non-migrating population:

$$
\begin{equation*}
\text { Peksk }_{0}=\mathrm{P}^{*} \mathbf{k}_{0}-\sum \mathrm{N}_{z=1 ; z \neq k} \text { Pezsk }_{0} \quad \mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{64}
\end{equation*}
$$

Total deaths in region k :

$$
\begin{align*}
\mathrm{P}^{*} \mathrm{dk}_{0} & =\mathrm{Pk}^{*} 0-\Sigma \mathrm{N}_{\mathrm{z}=1} \text { Peksz }_{0}-\Sigma \mathrm{N}_{\mathrm{z}=1 ; \mathrm{z} \neq \mathrm{k}} \text { Pekdzz }_{0 \mathrm{z}}+\Sigma \mathrm{N}_{\mathrm{z}=1 ; \mathrm{z} \neq \mathrm{k}} \text { Pezdk }_{0 k} \\
= & \mathrm{Pk}^{*} 0-\mathrm{P}^{*} \mathrm{k}_{0}+\Sigma \mathrm{N}_{z=1 ; z \neq \mathrm{k}}\binom{\text { Pezsk } \left._{0}-\text { Peksz }_{0}+\text { Pezdk }_{0 k}-\text { Pekdz }_{0 z}\right)}{\mathrm{k}=1,2, \ldots, \mathrm{~N}}
\end{align*}
$$

The forward mortality rate of the infants-cohort can be calculated using equation (46):

$$
\begin{equation*}
\mathrm{uk}_{0}=\mathrm{P}^{*} \mathrm{dk}_{0} / \mathrm{PST}^{*} \mathrm{dk}_{0} \quad \mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{66}
\end{equation*}
$$

An iterative procedure is necessary to estimate the mortality rate of the infants-cohort as unknown mortality rates appear in the right-hand side of equations (61)-(63) and (65). An initial forward mortality rate can be estimated using the following equation derived by assuming the same mortality rates in all regions and using equations (31) and (32):

The estimation procedure can be carried out by repeating calculations using equations (61)-(63), (65) and (66). Equations (64) and (67) will be used in the first step. Then new estimation of the mortality rate of the infants-cohort in equation (66) can be used in the next iteration. Unknown items in the population accounts of the infants-cohort are estimated by equations (61)-(64).

The deceased population $\mathrm{P}^{*} \mathrm{dk}_{0}$ of the infants-cohort in region k wa estimated by the equation (65). As in the case of single-region population systems, the population $\mathrm{Dk}_{\mathrm{a}}$ who died in region k in period t to $\mathrm{t}+1$ involves period-cohorts a and $a+1$. For simplicity, they are evenly allocated to the two period-cohorts involved. The deceased population $P^{*} \mathrm{dk}_{\mathrm{a}}$ of the remaining period-cohorts in the region $k$ can be estimated using following equation:

$$
\begin{equation*}
\mathrm{P}^{*} \mathrm{dk}_{1}=\mathrm{Dk}_{0}-\mathrm{P}^{*} \mathrm{dk}_{0}+0.5 \mathrm{Dk}_{1} \tag{68}
\end{equation*}
$$

$$
k=1,2, \ldots, N
$$

$$
\begin{align*}
& =\left(\mathrm{Pk}^{*}{ }_{0}-\text { Peksk }_{0}-\sum \mathrm{N}_{\mathrm{z}=1 ; \mathrm{z} \neq \mathrm{k}} \text { Peksz }_{0}\right) / \mathrm{Pk}^{\mathrm{k}^{*}} 0 \\
& =\left(\mathrm{Pk}_{0}{ }_{0}-\mathrm{P}^{* k_{0}}+\Sigma \mathrm{N}_{\mathrm{z}=1: Z \neq k}\left(\mathrm{Pezsk}_{0}-\mathrm{Pexsz}_{0}\right)\right) / \mathrm{Pk}_{0} \\
& k=1,2, \ldots, N \tag{67}
\end{align*}
$$

$$
\begin{align*}
& \text { Pekdk }_{0 k}=P{ }^{*}{ }_{0}-P^{*} k_{0}+\Sigma N_{z=1 ; z \neq k}\left(\text { Pezsk }_{0}-\text { Peksz }_{0}-\text { Pekdk }_{0 z}-\text { Pekdz }_{0 z}\right) \\
& k=1,2, \ldots, N \tag{63}
\end{align*}
$$

$$
\begin{array}{rr}
P^{*} d k_{a}=0.5\left(D k_{a-1}+D k_{a}\right) & \mathrm{a}=2,3, \ldots, \mathrm{~A}-1 ; \mathrm{k}=1,2, \ldots, \mathrm{~N}(69) \\
\mathrm{P}^{*} \mathrm{dk}_{\mathrm{A}}=0.5 \mathrm{D} k_{\mathrm{A}-1} & \mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{70}
\end{array}
$$

Now the estimation of the forward mortality rate of period-cohort a ( $a=1$, $2, \ldots$, A) will be discussed. The ending population $P^{*} x_{a}$ and deceased population $P^{*} \mathrm{dk}_{\mathbf{a}}$ are known. Similar to the infants-cohort, the following equations can be obtained for period-cohort a:

Non-surviving, migrating population who died in region z :

$$
\operatorname{Pekdz}_{\mathrm{az}}=0.5 \text { Peksz }_{\mathrm{a}} \mathrm{uz}_{\mathrm{a}} /\left(1-0.75 \mathrm{uz}_{\mathrm{a}}\right) \quad \mathrm{k}, \mathrm{z}=1,2, \ldots, \mathrm{~N} ; \mathrm{k} \neq \mathrm{z}(71)
$$

Non-surviving, migrating population who died in region k :

$$
\begin{array}{r}
\text { Pekdk }_{a z}=0.5 \text { Peksz }_{a} u_{\mathrm{a}}\left(1-0.25 u z_{a}\right) /\left(1-0.75 u k_{a}\right) /\left(1-0.75 u z_{a}\right) \\
k, z=1,2, \ldots, N ; k \neq z(72)
\end{array}
$$

Non-surviving, non-migrating population who died in region k :

$$
\text { Pekdk }_{\mathrm{ak}}=\mathrm{P}^{\star} \mathrm{dk}_{\mathbf{a}}-\Sigma \mathrm{N}_{\mathrm{z}=1 ; z \neq \mathbf{k}}\left(\text { Pekdk }_{\mathrm{az}}+\text { Pezdk }_{\mathrm{ak}}\right) \quad \mathrm{k}=1,2, \ldots, \mathrm{~N}(73)
$$

Surviving, non-migrating population:

$$
\text { Peksk }_{\mathrm{a}}=\mathrm{P}^{* k_{a}}-\Sigma \mathrm{N}_{2=1: 2 \neq \mathrm{k}} \text { Pezsk }_{\mathrm{a}} \quad \mathrm{k} \neq 1,2, \ldots, \mathrm{~N}
$$

The population at the beginning of a period in region k :

$$
\begin{align*}
\mathrm{Pk}_{\mathrm{a}}^{*}= & \sum \mathrm{N}_{\mathrm{z}=1} \text { Peksz }_{\mathrm{a}}+\Sigma \mathrm{N}_{\mathrm{z}=1} \text { Pekdk }_{\mathrm{az}}+\Sigma \mathrm{N}_{\mathrm{z}=1 ; \mathrm{z} \neq \mathrm{k}} \text { Pekdz }_{\mathrm{az}} \\
= & \mathrm{P}^{*} \mathrm{k}_{\mathrm{a}}+\Sigma \mathrm{N}_{\mathrm{z}=1 ; \mathrm{z} \neq k}\left(\text { Peksz }_{\mathrm{a}}-\text { Pezsk }_{\mathrm{a}}\right)+\mathrm{P}^{*} \mathrm{dk}_{\mathrm{a}} \\
& +\sum \mathrm{N}_{\mathrm{z}=1 ; \mathrm{z} \neq \mathrm{k}}\left(\text { Pekdz }_{\mathrm{az}}-\text { Pezdk }_{\mathrm{ak}}\right) \quad \mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{75}
\end{align*}
$$

The forward mortality rate of period-cohort a can be calculated using equation (46):

$$
\mathrm{uk}_{\mathrm{a}}=\mathrm{P}^{*} \mathrm{dk}_{\mathrm{a}} / \mathrm{PST}^{*} \mathrm{dk}_{\mathrm{a}} \quad \mathrm{a}=1,2, \ldots, \mathrm{~A} ; \mathrm{k}=1,2, \ldots, \mathrm{~N}(76)
$$

An iterative procedure is necessary to estimate the mortality rate of periodcohort a as unknown mortality rates appear in the right-hand side of equations (71)-(73), (75) and, (76). To estimate an initial forward mortality rate of period-cohort a, the following equation can be obtained from equations (31)(33) by assuming the same mortality rate in all regions:

$$
\left.\begin{array}{rl}
\mathrm{P}^{*} \mathrm{dk}_{\mathrm{a}} & +\sum \mathrm{N}_{z=1: z \neq \mathrm{k}}\left(\mathrm{Pekdz}_{\mathrm{az}}-\mathrm{Pe}_{2 \mathrm{dk}}^{\mathrm{ak}}\right.
\end{array}\right)=\mathrm{uk}_{\mathrm{a}}\left(\mathrm{P}^{*} \mathrm{k}_{\mathrm{a}}+\Sigma \mathrm{N}_{\mathrm{z}=1: z \neq \mathrm{k}}\left(\mathrm{Peksz}_{\mathrm{a}}\right)\right.
$$

Substitute equation (71) into (77) assuming the same mortality rates in all regions, and rearrange:

$$
\begin{align*}
& P^{*} d k_{a}=u k_{a}\left(P^{*} k_{a}+P^{*} d k_{a}+\left(0.5+0.125 u k_{a} /\left(1-0.75 u k_{a}\right)\right)\right. \\
&\left.\sum N_{z=1 ; z \neq k}\left(P c k s z_{a}-P^{2} z s k_{a}\right)\right) \\
&= u k_{a}\left(P^{*} k_{a}+P^{*} d k_{a}+0.5 \sum N_{z=1: z \neq k}\left(\text { Peksz }_{a}-P_{e z s k_{a}}\right)\right) \\
& \quad k=1,2, \ldots, N \tag{78}
\end{align*}
$$

The small item $0.125 \mathrm{uk}_{\mathrm{a}} /\left(1-0.75 \mathrm{u}_{\mathrm{a}}\right.$ ) in equation (78) was disregarded. The initial mortality rate of period-cohort a can be estimated as follows:

$$
\begin{array}{r}
\mathrm{u}_{\mathrm{a}}=\mathrm{P}^{*} \mathrm{dk}_{\mathrm{a}} /\left(\mathrm{P}^{* k_{\mathrm{a}}}+\mathrm{P}^{*} \mathrm{dk}_{\mathrm{a}}+0.5 \Sigma \mathrm{~N}_{z=1 ; z \neq \mathrm{k}}\left(\mathrm{Peksz}_{\mathrm{a}}-\mathrm{Pezsk}_{\mathrm{a}}\right)\right) \\
\mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{79}
\end{array}
$$

Now, the estimation procedure can be carried out by repeating calculations using equations (71)-(73) and (76). Equations (74) and (79) will be used in the first step. Then new estimates of the mortality rate of period-cohort a in equation (76) can be used in the next iteration. Unknown items in the population accounts of period-cohort a are estimated by equations (71)-(75).

As an example, the estimation procedures discussed above will be used to construct the population accounts of period-cohort $20(\mathrm{a}=20)$ of the urban and rural population systems of China. We consider the male population only. The data available have been presented in Table 7. Here region one refers to the urban region and region two the rural region. There are two regions in total ( $\mathrm{N}=2$ ).
In the first step, the data available are collected as follows.
Populations at the end of period 1986 to 1987 in urban and rural regions:

$$
\begin{aligned}
& \mathrm{P}^{*} \mathrm{I}_{20}=4752.04 \\
& \mathrm{P}^{*} 2_{20}=6088.22
\end{aligned}
$$

Total deaths in period 1986 to 1987 in urban and rural regions:

$$
\begin{aligned}
& \mathrm{P}^{*} \mathrm{~d} 1_{20}=6.24 \\
& \mathrm{P}^{*} \mathrm{~d} 2_{20}=8.09
\end{aligned}
$$

Surviving migrants from the urban region to the rural region:

$$
\mathrm{Pe} 1 \mathrm{~s} 2_{20}=2.72
$$

Surviving migrants from the rural region to the urban region:

$$
\mathrm{Pe} 2 \mathrm{~s}_{20}=98.88
$$

In the second step, the surviving non-migrating populations in the urban and rural regions can be calculated using equation (74):

$$
\begin{aligned}
& \mathrm{Pels} 1_{20}=\mathrm{P}^{*} 1_{20}-\mathrm{Pe} 2 \mathrm{sl}_{20}=4752.04-98.88=4653.16 \\
& \mathrm{Pe} 2 \mathrm{~s} 2_{20}=\mathrm{P}^{*} 2_{20}-\mathrm{Pe} 1 \mathrm{~s} 2_{20}=6088.22-2.72=6085.50
\end{aligned}
$$

In the third step, the initial forward mortality rates can be estimated for the urban and rural regions using equation (79):

$$
\begin{aligned}
& \mathrm{ul}_{20}=\mathrm{P}^{*} \mathrm{dl}_{20} /\left(\mathrm{P}^{*} \mathrm{l}_{20}+\mathrm{P}^{*} \mathrm{dl}_{20}+0.5 \mathrm{x}\left(\mathrm{Pels}_{20}-\mathrm{Pe}^{2 \mathrm{~s} 1_{20}}\right)\right) \\
& =6.24 /(4752.04+6.24+0.5 \times(2.72-98.88))=0.00132 \\
& \mathrm{u}^{2}{ }_{20}=\mathrm{P}^{*} \mathrm{~d} 2_{20} /\left(\mathrm{P}^{*} 2_{20}+\mathrm{P}^{*} \mathrm{~d} 2_{20}+0.5 \mathrm{x}\left(\mathrm{Pe} 2 \mathrm{~s} 1_{20}-\mathrm{Pe} 1 \mathrm{~s} 2_{20}\right)\right) \\
& =8.09 /(6088.22+8.09+0.5 \times(98.88-2.72))=0.00132
\end{aligned}
$$

In the forth step, the unknown items in the population accounts are estimated using equations (71)-(73):

The non-surviving, migrating population from the urban region who died in the rural region:

$$
\begin{aligned}
\text { Peld }_{20.2} & =0.5 \text { Pels }_{20} 20 \mathrm{u}^{2} 20 /\left(1-0.75 \mathrm{u}^{2} 20\right) \\
& =0.5 \times 2.72 \times 0.00132 /(1-0.75 \times 0.00132)=0.0018
\end{aligned}
$$

The non-surviving, migrating population from the rural region who died in the urban region:


```
    =0.5 < 98.88 \times 0.00132/(1-0.75 \times 0.00132 )=0.0653
```

The non-surviving, migrating population who died in the urban region before migration:

$$
\begin{aligned}
& \text { Peld }_{20.2}=0.5 \mathrm{Pe} 1 \mathrm{~s}_{20} \mathrm{ul}_{20}\left(1-0.25 \mathrm{u}^{2} 20\right) /\left(1-0.75 \mathrm{ul}_{20}\right) /\left(\mathrm{l}-0.75 \mathrm{u}^{2} 20\right) \\
& \quad=0.5 \times 2.72 \times 0.00132 \times(1-0.25 \times 0.00132) \\
& \quad /(1-0.75 \times 0.00132)^{2}=0.0018
\end{aligned}
$$

The non-surviving, migrating population who died in the rural region before migration

```
\(\mathrm{Pe} 2 \mathrm{~d}_{20.1}=0.5 \mathrm{Pe}_{2 \mathrm{~s}} \mathrm{I}_{20} \mathrm{u}^{2} 20\left(1-0.25 \mathrm{ul}_{20}\right) /\left(1-0.75 \mathrm{u}^{2} 20\right) /\left(1-0.75 \mathrm{u}^{20}\right)\)
    \(=0.5 \times 98.88 \times 0.00132 \times(1-0.25 \times 0.00132)\)
    \(/(1-0.75 \times 0.00132)^{2}=0.0654\)
```

The non-surviving, non-migrating population who died in the urban region:

$$
\begin{aligned}
\mathrm{Peld}_{20, \mathrm{l}} & =\mathrm{P}^{*} \mathrm{~d}_{20}-\mathrm{Pe} 1 \mathrm{~d} 1_{20.2}-{\mathrm{Pe} 2 \mathrm{~d} 1_{20.1}}=6.24-0.0018-0.0653 \\
& =6.1729
\end{aligned}
$$

The non-surviving, non-migrating population who died in the rural region:

$$
\begin{aligned}
\mathrm{Pe} 2 \mathrm{~d} 20.2 & =\mathrm{P}^{*} \mathrm{~d}_{20}-\mathrm{Pe} 2 \mathrm{~d}_{20,1}-\mathrm{Pe} 1 \mathrm{~d} 2_{20,2}=8.09-0.0654-0.0018 \\
& =8.0228
\end{aligned}
$$

In the fifth step, the starting populations for the forward mortality rates of period-cohort 20 in the urban and rural regions can be calculated using equation (45):

```
PST*d120 = Pe1s120}+0.5\times(Pels\mp@subsup{2}{20}{*}+\mp@subsup{\textrm{Pe}2\textrm{s1}}{20}{})+\mp@subsup{\textrm{Peld1}}{20,1}{
    +0.75 x ( Peldl 20,2 + Pe2dl 20,1 ) + 0.5 Peld2 20,2
    =4653.16+0.5 x (2.72+98.88)+6.1729
    +0.75 x (0.0018+0.0653)+0.5 x 0.0018
    = 4710.1841
PST**d2}20=Pe2s\mp@subsup{2}{20}{}+0.5\times(\mp@subsup{\textrm{Pe}2\textrm{sI}}{20}{}+\textrm{Pels}\mp@subsup{2}{20}{})+\textrm{Pe2d}220.
    +0.75 x ( Pe2d220.1 + Peld220.2 ) +0.5 Pe2d120,1
    =6085.50+0.5 x (98.88+2.72)+8.0228
    +0.75\times(0.0654+0.0018)+0.5 x 0.0653
    =6144.4058
```

In the sixth step, the forward mortality rates for the urban and rural regions can be updated using equation (76):

$$
\begin{aligned}
& \mathrm{u}^{1}{ }_{20}=\mathrm{P}^{*} \mathrm{~d} 1_{20} / \mathrm{PST}^{*} \mathrm{~d}_{20}=6.24 / 4710.1841=0.00132 \\
& \mathrm{u}^{2} 20=\mathrm{P}^{*} \mathrm{~d} 2_{20} / \mathrm{PST}^{*} \mathrm{~d}_{20}=8.09 / 6144.4058=0.00132
\end{aligned}
$$

Now, steps four to six will be repeated to update unknown items in the population accounts and step three again to update forward mortality rates. This procedure will be repeated until a specified iterative standard is satisfied.
In this example, it can be noted that the same estimates of forward mortality rates as the initial estimates in the third step have been obtained. We do not need to continue the iterative procedure.

A multiregional population account for the male population of periodcohort 20 has also been constructed in the calculations above and is presented in Table 12. The populations at the beginning of the period 1986 to 1987 in both regions are calculated using equation (75):

$$
\begin{aligned}
\mathrm{P}^{*}{ }_{20} & =\Sigma 2_{\mathrm{k}=1} \mathrm{Pe} 1 \mathrm{sk}_{20}+\Sigma 2_{\mathrm{k}=1} \text { Peldk }{ }_{20 \mathrm{k}}+\mathrm{Pe} 1 \mathrm{~d} 2_{20.2} \\
& =4653.16+2.72+6.17+0.0018+0.0018=4662.05 \\
\mathrm{P}^{2}{ }_{20} & =\Sigma 2_{\mathrm{k}=1}{\mathrm{Pe} 2 \mathrm{sk}_{20}}+\Sigma 2_{\mathrm{k}=1} \text { Pe2dk }_{20 \mathrm{k}}+\mathrm{Pe} 2 \mathrm{d1}_{20,1} \\
& =98.88+6085.50+0.0654+0.0653+8.0228=6192.54
\end{aligned}
$$

Table 12 Estimated population accounts of period-cohort 20 of the urban and rural population systems of China 1986-1987 ( male population, thousands )

| Starting <br> state | Ending state in period 1986 to 1987 |  |  |  |  |  | Total |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Survived in |  | Deaths in |  |  |  |  |
|  | Urban | Rural | Urban |  | Rural |  |  |
| Urban | 4653.16 | 2.72 | 6.17 | 0 | 0 |  | 4662.05 |
| Rural | 98.88 | 6085.50 | 0.07 |  | 0.07 | 8.02 | 6192.54 |
| Total | 4752.04 | 6088.22 | 6.24 |  | 8.09 |  | 10854.60 |

It is straightforward to estimate the forward fertility rates and migration rates as the multiregional population accounts have been estimated above.

The birth population $\mathrm{P}^{*} \mathrm{bk}_{\mathrm{a}}$ can be estimated in the similar way as the deceased population $\mathrm{P}^{*} \mathrm{dk}_{\mathrm{a}}$ :

$$
P^{*} b k_{a}=0.5\left(B k_{a-1}+B k_{a}\right) \quad a=a_{1}, a_{1}+1, \ldots, a_{2} ; k=1,2, \ldots, N(80)
$$

Here $a_{1}$ and $a_{2}$ are the first and last period-cohorts of the fertile female population. The forward fertility rate $f k_{a}$ can be estimated using equation (47). Three forward migration rates can be estimated using equations (50) - (52).

## 5 MULTIREGIONAL POPULATION PROJECTION MODEL

One major task of spatial population analysis is to make consistent multiregional population projections. Regional population numbers in the future are often needed by central and local governments and various agencies for purposes of planning, resource allocation and marketing. This section will develop a multiregional population projection model based on forward
demographic rates. The model will be used to make a urban-rural population projections for China.

Given base year population, forward mortality rates, fertility rates and migration rates, multiregional population projections can be carried out using a multiregional population projection model proposed in this section. The gender label g ( m for male and f for female ) will be added back in this section. The time label $t$ is also added to variables. All demographic rates describe rates of population change in a period and are related to two time points at the beginning and end of a period concerned. For simplicity, we use the time point at the end of a period to label the demographic rates. For example, $\mathrm{uk}_{\mathrm{ag}}(\mathrm{t}+1)$ is the forward mortality rate of period-cohort a of gender g in region k in the period t to $\mathrm{t}+1$.
The total fertility rate $\operatorname{TFR} x(t+1)$ and normal forward fertility rate $f{ }^{n k} k_{a}(t+1)$ of period-cohort a of the female population in region $k$ in period $t$ to $t+1$ will be discussed first. Here, the total fertility rate is used to express the level of fertility of a regional population. Age-specific normal fertility rates are used to express the distribution of fertility across the ages.
As mentioned before, the forward fertility rate $f k_{a}$ is related to the mortality rate in region $k$. It is better to define the total fertility rate TFRk( $\mathrm{t}+1)$ in terms of the occurrence-exposure fertility rate $b^{k_{a}}$ so that it is independent of mortality rates in region k :

$$
\begin{gather*}
\operatorname{TFRk}(\mathrm{t}+1)=\sum \mathrm{a} 2_{\mathrm{a}=\mathrm{a}} 1^{\gamma} \mathrm{k}_{\mathrm{a}}(\mathrm{t}+1)=\sum \mathrm{a} 2_{\mathrm{a}=\mathrm{a} 1} \mathrm{fk}_{\mathrm{a}}(\mathrm{t}+1) /\left(1-0.5 \mathrm{u} \mathrm{k}_{\mathrm{af}}(\mathrm{t}+1)\right) \\
\mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{81}
\end{gather*}
$$

Here at and a2 are the first and last period-cohorts of the fertile female population. In equation (81), the total fertility rate is the sum of age-specific occurrence-exposure fertility rates and is also expressed in terms of forward fertility rates.
The normal occurrence-exposure fertility rate $b_{n k}(t+1)$ can be defined by dividing the occurrence-exposure fertility rate by the total fertility rate:

$$
\begin{equation*}
\mathrm{brk}_{\mathrm{a}}(\mathrm{t}+1)=\mathrm{bk} \mathrm{k}_{\mathrm{a}}(\mathrm{t}+1) / \mathrm{TFR} \mathrm{k}(\mathrm{t}+1) \quad \mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{82}
\end{equation*}
$$

Similarly, the normal forward fertility rate is defined as follows:

$$
\begin{equation*}
\mathrm{frk}_{3}(\mathrm{t}+1)=\mathrm{fk} \mathrm{k}_{\mathrm{a}}(\mathrm{t}+1) / \mathrm{TFRk}(\mathrm{t}+1) \quad \mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{83}
\end{equation*}
$$

According to the forward mortality and migration rate definitions, the following equations can be obtained. Here the time label is omitted for simplicity, but will be added back later.

$$
\begin{equation*}
\text { Pekdk }_{a g k}=\left(\text { Peksk }_{a_{g}}+\text { Pekdk }_{\text {agk }}\right) u_{a_{a g}} \tag{84}
\end{equation*}
$$

$$
\begin{align*}
& \text { Pekdk }_{a g z}=\left(0.5 \text { Peksz }_{a g}+0.75 \text { Pekdk }_{a g z}+0.5 \text { Pekdz }_{a g z}\right) u k_{a g}  \tag{85}\\
& \text { Pekdz }_{\mathrm{agz}}=\left(0.5 \text { Peksz }_{a g}+0.75 \text { Pekdz }_{\mathrm{agz}}\right) \mathrm{u}_{\mathrm{ag}}  \tag{86}\\
& \text { Peksz }_{\mathrm{ag}}+\text { Pekdk }_{\mathrm{agz}}+\text { Pekdz }_{\mathrm{agz}}=\mathrm{mkz}_{\mathrm{lag}} \text { Pk }_{\mathrm{ag}}^{*} \tag{87}
\end{align*}
$$

Here, we should refer back to the populations at risk for the components of population change concerned and their time-weights for the calculation of starting populations. The various death and migration components of population change are simply obtained by multiplying their starting populations by forward mortality or migration rates respectively.
Substituting equation (87) into equation (31), the following equation can be obtained:

$$
\begin{equation*}
\text { Peksk }_{\mathrm{ag}}+\text { Pexdk }_{\mathrm{agk}}=\left(1-\Sigma \mathrm{N}_{z=1, z \neq \mathrm{k}} \mathrm{mk} z_{1 \mathrm{lag}}\right) \mathrm{Pk}^{*}{ }_{\mathrm{ag}} \tag{88}
\end{equation*}
$$

In equation (88), the total non-migrating population is expressed as the population at the beginning of a period discounted by forward potential migration rates.
Substitute equation (88) into equation (84):

$$
\begin{equation*}
P_{e k d k}^{a g k}=\left(1-\Sigma N_{z=1, z \neq k} m^{k z}{ }_{1 a g}\right) P^{*}{ }_{a g u^{k}}{ }_{a g} \tag{89}
\end{equation*}
$$

In equation (89), the non-surviving, non-migrating population is expressed as the total non-migrating population multiplied by the forward mortality rate.
Substitute equation (89) into equation (88):

$$
\begin{equation*}
\text { Peksk }_{\mathrm{ag}}=\left(1-\Sigma N_{z=1, z \neq k} m^{k z}{ }_{l a g}\right) P k^{*}{ }_{a g}\left(1-u k_{a g}\right) \tag{90}
\end{equation*}
$$

In equation (90), the surviving, non-migrating population is expressed as the population at the beginning of a period discounted by forward migration and mortality rates.

The following equation can be obtained from equation (86):

$$
\begin{equation*}
\text { Pekdragz }_{\mathrm{agz}}=0.5 \text { Peksz }_{\mathrm{ag}^{\mathrm{g}} \mathrm{uz}_{\mathrm{ag}}} /\left(1-0.75 \mathrm{u}_{\mathrm{ag}}\right) \tag{91}
\end{equation*}
$$

Substitute into equation (85) and rearrange:

$$
\begin{equation*}
\text { Pckdk }_{\mathrm{ag}}=0.5 \text { Ṕeksz }_{\mathrm{ag}} u \mathrm{k}_{\mathrm{ag}}\left(1-0.25 \mathrm{uz}_{\mathrm{ag}}\right) /\left(I-0.75 \mathrm{uk}_{\mathrm{ag}}\right) /\left(1-0.75 \mathrm{u}_{\mathrm{ag}}\right) \tag{92}
\end{equation*}
$$

Substitute equations (91) and (92) into equation (87) and rearrange:

$$
\begin{equation*}
\text { Peks } z_{\mathrm{ag}}=\mathrm{Pk}^{*}{ }_{\mathrm{ag}} \mathrm{mkz}^{\mathrm{lag}}\left(1-0.75 \mathrm{uk}_{\mathrm{ag}}\right)\left(1-0.75 \mathrm{ux}_{\mathrm{ag}}\right) /\left(1-0.25 \mathrm{uk}_{\mathrm{ag}}\right) /\left(1-0.25 \mathrm{uz}_{\mathrm{ag}}\right) \tag{93}
\end{equation*}
$$

In equation (93), the surviving, migrating population is expressed in terms of the population at the beginning of a period and the migration rate discounted by mortality rates in origin and destination regions.

Substitute equation (93) into equations (91) and (92) and rearrange:

$$
\begin{align*}
& \text { Pexdz }_{\mathrm{agz}}=0.5 \mathrm{Pk}^{*}{ }_{{ }_{\mathrm{ag}} \mathrm{mkz}}^{1 \mathrm{ag}} \mathrm{uz}_{\mathrm{ag}}\left(1-0.75 \mathrm{uk}_{\mathrm{ag}}\right) /(1-0.25 \mathrm{uk} \mathrm{ag}) /\left(1-0.25 \mathrm{uz}_{\mathrm{ag}}\right) \\
& \text { Pekdk }_{\mathrm{agz}}=0.5 \mathrm{Pk}^{*}{ }_{\mathrm{ag}} \mathrm{mkz}_{\text {lag }} \mathrm{uk}_{\mathrm{ag}} /\left(1-0.25 \mathrm{uk}_{\mathrm{ag}}\right) \tag{94}
\end{align*}
$$

In equations (94) and (95), the non-surviving, migrating populations who died in origin and destination regions are expressed in terms of the population at the beginning of a period, migration and mortality rates.
Substitute equations (89), (90), (93)-(95) into equation (45) and rearrange:

$$
\begin{align*}
& \text { PST }^{* d k_{a g}}=\text { PST }^{*} \mathrm{bk}_{\mathrm{ag}}=\mathrm{Pk}^{*}{ }_{\mathrm{ag}}\left(1-0.5 \sum \mathrm{~N}_{z=1, z \neq \mathrm{k}} \mathrm{mkz}_{\mathrm{ag}}\left(1-0.5 \mathrm{uk}_{\mathrm{ag}}\right) /\right. \\
& \left.\left(1-0.25 \mathrm{uk}_{\mathrm{ag}}\right)\right)+0.5 \sum \mathrm{~N}_{\mathrm{z}=1, \mathrm{z} \mathrm{\neqk}} \mathrm{Pz}_{\mathrm{zag}^{*}} \mathrm{~m}^{2 k_{1 a g}}\left(1-0.75 \mathrm{uz}_{\mathrm{ag}}\right) / \\
& \left(1-0.25 \mathrm{uk}_{\mathrm{ag}}\right) /\left(1-0.25 \mathrm{uz}_{\mathrm{ag}}\right) \\
& =P \mathrm{Pk}^{*}{ }_{\mathrm{ag}}{ }^{2 k k_{a g}}+\sum \mathrm{N}_{\mathrm{z}=1,2 \neq \mathrm{k}} \mathrm{Pz}^{*}{ }_{\text {ag }} \mathrm{Vzk}_{\mathrm{ag}} \tag{96}
\end{align*}
$$

In equation (96), the starting population for total deaths and births in region k is expressed in terms of the populations at the beginning of the period in both regions and various migration and mortality rates. Here, special rates $\mathrm{vzk}_{\mathrm{ag}}(\mathrm{t}+1)$ are defined to calculate the starting population in equation (96) as follows:

$$
\begin{gather*}
\mathrm{vkk}_{\mathrm{ag}}(\mathrm{t}+1)=1-0.5 \quad \sum \mathrm{~N}_{z=1, z \neq \mathrm{k}} \mathrm{mkz}_{\mathrm{lag}}(\mathrm{t}+1)\left(1-0.5 \mathrm{uk}_{\mathrm{ag}}(\mathrm{t}+1)\right) \\
/\left(1-0.25 \mathrm{uk}_{\mathrm{ag}}(\mathrm{t}+1)\right) \quad \mathrm{k}=1,2, \ldots, \mathrm{~N}  \tag{97}\\
\mathrm{vzk}_{\mathrm{ag}}(\mathrm{t}+1)=0.5 \mathrm{~m}^{2 \mathrm{k}} \mathrm{lag}(\mathrm{t}+1)\left(1-0.75 \mathrm{u}_{\mathrm{ag}}(\mathrm{t}+1)\right) /\left(1-0.25 \mathrm{uk}_{\mathrm{ag}}(\mathrm{t}+1)\right) \\
/\left(1-0.25 \mathrm{uz}_{\mathrm{ag}}(\mathrm{t}+1)\right) \quad \mathrm{k}, \mathrm{z}=1,2, \ldots, \mathrm{~N} ; \mathrm{k} \neq \mathrm{z} \tag{98}
\end{gather*}
$$

Now, define survival rates ( transition probabilities) $\mathrm{skz}_{\mathrm{ag}}(\mathrm{t}+1)$ as follows:

$$
\begin{array}{r}
\mathrm{skk}_{\mathrm{ag}}(\mathrm{t}+\mathrm{l})=\left(1-\sum \mathrm{N}_{z=1, z \neq \mathrm{k}} \mathrm{mkz}_{\mathrm{iag}}(\mathrm{t}+\mathrm{l})\right)\left(1-\mathrm{uk}_{\mathrm{ag}}(\mathrm{t}+\mathrm{l})\right) \\
\mathrm{k}=1,2, \ldots, \mathrm{~N}
\end{array}
$$

The survival rate $s k k_{\mathrm{ag}}(\mathrm{t}+\mathrm{l})$ is the probability that the population at the beginning of a period in region k will not migrate and survive in the period t to $t+1$. It is determined by the total forward potential migration rates to all destinations and the forward mortality rate of the region.

$$
\begin{gather*}
\mathrm{skz}_{\mathrm{ag}}(\mathrm{t}+1)=\mathrm{m}^{\mathrm{kz}} 1_{\mathrm{ag}}(\mathrm{t}+1)\left(1-0.75 \mathrm{uk}_{\mathrm{ag}}(\mathrm{t}+1)\right)\left(1-0.75 \mathrm{uz}_{\mathrm{ag}}(\mathrm{t}+1)\right) \\
/\left(1-0.25 \mathrm{uk}_{\mathrm{ag}}(\mathrm{t}+1)\right) /\left(1-0.25 \mathrm{u}^{\mathrm{z}} \mathrm{ag}(\mathrm{t}+1)\right) \\
\mathrm{k}, \mathrm{z}=1,2, \ldots, \mathrm{~N} ; \mathrm{k} \neq \mathrm{z} \tag{100}
\end{gather*}
$$

The survival rate $\mathrm{skz}_{\mathrm{ag}}(t+1)$ is the probability that the population at the beginning of a period in region k will migrate to region z and survive in the period $t$ to $t+1$. It is determined by the forward potential migration rate from region k to region z and the forward mortality rates in origin and destination regions.

Finally, the following population projection model can be obtained. Births of gender g in region k can be projected using the following equation. Here Sexkg is the ratio of gender g in total births in region k .

$$
\begin{array}{r}
\mathrm{Pk}^{*} \mathrm{og}_{\mathrm{g}}(\mathrm{t})=\mathrm{P}^{*} \mathrm{bk}_{\mathrm{g}}(\mathrm{t}+1)=\mathrm{Sexk}_{\mathrm{g}} \operatorname{TFRk}(\mathrm{t}+1) \sum \mathrm{P}_{\mathrm{a}=\mathrm{a} 1} \text { fnk }_{\mathrm{a}}(\mathrm{t}+1) \\
\left(\mathrm{Pk}^{*}{ }_{\mathrm{af}}(\mathrm{t}) \mathrm{vkk}_{\mathrm{af}}(\mathrm{t}+1)+\sum \mathrm{N}_{\mathrm{z}=1,2 \neq k} \mathrm{Pz}^{*}{ }_{a f}(\mathrm{t}) \mathrm{v}^{\left.2 k_{a f}(\mathrm{t}+1)\right)}\right. \\
\mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{101}
\end{array}
$$

Equation (101) is obtained by multiplying forward fertility rates by starting populations in equation (96). Only the female population is involved. The total number of births is then divided into male and female infants by gender ratio Sexkg.
The end population in period $t$ to $t+1$ can be projected using the following equation:

$$
\begin{align*}
& P^{*} \mathrm{k}_{\mathrm{ag}}(\mathrm{t}+1)=\sum N_{z=1} P_{2^{*}}{ }_{\mathrm{ag}}(\mathrm{t}) \mathrm{sz}_{\mathrm{z}}^{\mathrm{ag}}(\mathrm{t}+1)  \tag{102}\\
& \quad \mathrm{a}=0,1, \ldots, \mathrm{~A} ; \mathrm{g}=\mathrm{m}, \mathrm{f} ; \mathrm{k}=1,2, \ldots, \mathrm{~N}
\end{align*}
$$

The populations of each period-cohort at the beginning and end of period $t$ to $t+1$ are linked by survival rates in equation (102).
The total deaths of gender g in region k can be projected using the following equation:

$$
\begin{aligned}
& \mathrm{P}^{*} \mathrm{dk}_{* g}(\mathrm{t}+1)=\sum \mathrm{A}_{\mathrm{a}=0} \mathrm{uk}_{\mathrm{ag}}(\mathrm{t}+1) \mathrm{PST}^{*} \mathrm{dk}_{\mathrm{ag}} \\
& =\sum \mathrm{A}_{\mathrm{a}=0} \mathrm{uk}_{\mathrm{ag}}(\mathrm{t}+1)\left(\mathrm{Pk}^{*}{ }_{\mathrm{ag}}(\mathrm{t}) \mathrm{vkk}_{\mathrm{ag}}(\mathrm{t}+1)+\sum \mathrm{N}_{\mathrm{z}=1, \mathrm{z} \mathrm{\neqk}} \mathrm{Pz}_{z^{*}}{ }_{\mathrm{ag}}(\mathrm{t}) \mathrm{vzk}_{\mathrm{ag}}(\mathrm{t}+1)\right) \\
& \quad \mathrm{g}=\mathrm{m}, \mathrm{f} ; \mathrm{k}=1,2, \ldots, \mathrm{~N}
\end{aligned}
$$

Equation (103) is obtained by multiplying forward mortality rates by starting populations In equation (96)

The population at the beginning of the next projection period is as follows:

$$
\mathrm{Pk}^{*}{ }_{a \mathrm{~g}}(\mathrm{t}+\mathrm{l})=\mathrm{P}^{*} \mathrm{k}_{\mathrm{a}-1 \mathrm{~g}}(\mathrm{t}+1) \quad \mathrm{a}=1, \ldots, \mathrm{~A}-1 ; \mathrm{g}=\mathrm{m}, \mathrm{f} ; \mathrm{k}=1,2, \ldots, \mathrm{~N}(104)
$$

In equation (104), the population of period-cohort a-1 at the end of period t to $t+1$ becomes the population of period-cohort a at the beginning of period $\mathrm{t}+1$ to $\mathrm{t}+2$.

$$
\mathrm{Pk}^{*}{ }_{\mathrm{Ag}}(\mathrm{t}+1)=\mathrm{P}^{*} \mathrm{k}_{\mathrm{A} \cdot} \cdot \lg (\mathrm{t}+1)+\mathrm{P}^{*} \mathrm{k}_{\mathrm{Ag}}(\mathrm{t}+1)
$$

$$
\begin{equation*}
\mathrm{g}=\mathrm{m}, \mathrm{f} ; \mathrm{k}=1,2, \ldots, \mathrm{~N} \tag{105}
\end{equation*}
$$

In equation (105), the population of period-cohort A at the beginning of period $t+1$ to $t+2$ consists of two parts, the population of period-cohorts A-1 and $A$ at the end of period $t$ to $t+1$ as the population of the last period-cohort will remain in the same period-cohort.

Equations (97)-(105) constitute a multiregional population projection model based on forward demographic rates. The main steps for multiregional population projections can be summarized as follows:

Step one, prepare forward fertility, mortality and migration rates.
Step two, calculate survival rates and special rates using equations(97)-(100).
Step three, prepare the base year population, i.e., age-specific population at the beginning of the first projection period.
Step four, project the birth population using equation (101).
Step five, project the population at the end of the period from the population at the beginning of period using survival rates by equation (102).
Step six, project the total number of deaths using equation (103)
Step seven, update and prepare the population of each period-cohort at the
beginning of the next period using equations (104) and (105).
Steps four to seven should be repeated until the target projection year is reached.
Now we consider the projection of the urban and rural populations of China for the period 1987-2040. Table 13 presents selected forward mortality and potential migration rates of the urban and rural female populations of China. Survival rates can be calculated using equations (98) and (99) and are presented in Table 14. Similarly, survival rates of the urban and rural male populations can be calculated and are omitted here. To make urban-rural population projections for China, we also need age-specific fertility rates of the urban and rural female populations and the age-specific populations in the base-year 1987.

A series of urban-rural population projections for China have been carried out (Shen, 1994b ). The major results of these projections will be briefly discussed here. In these projections, a further submodel of urban-rural migration has been used to project urban-rural migrations. Urban and rural migration rates and survival rates are recalculated each year on the basis of these migration projections in the projection period.

The total fertility rate is a key variable in population projection. The total fertility rate in China has declined significantly in the past two decades. It was 5.746 in 1970 and 2.618 in 1982 ( Coale and Chen, 1987). The total fertility

Table 13 Forward mortality and potential migration rates ( female populations, China )

| Age | Mortality rate |  | Potential migration rate |  |
| :---: | :---: | :---: | :---: | :---: |
|  | Urban | Rural | Urban | Rural |
| 0 | 0.00295 | 0.00836 | 0.00085 | 0.00339 |
| 5 | 0.00076 | 0.00105 | 0.00030 | 0.00318 |
| 10 | 0.00056 | 0.00042 | 0.00018 | 0.00396 |
| 15 | 0.00052 | 0.00083 | 0.00015 | 0.00662 |
| 20 | 0.00102 | 0.00128 | 0.00361 | 0.02056 |
| 25 | 0.00121 | 0.00180 | 0.00240 | 0.01754 |
| 30 | 0.00125 | 0.00147 | 0.00042 | 0.00619 |
| 35 | 0.00150 | 0.00185 | 0.00024 | 0.00528 |
| 40 | 0.00186 | 0.00232 | 0.00020 | 0.00500 |
| 45 | 0.00281 | 0.00346 | 0.00015 | 0.00407 |
| 50 | 0.00375 | 0.00523 | 0.00016 | 0.00304 |
| 55 | 0.00886 | 0.00793 | 0.00017 | 0.00274 |
| 60 | 0.01319 | 0.01406 | 0.00013 | 0.00246 |
| 65 | 0.01821 | 0.02053 | 0.00011 | 0.00304 |
| 70 | 0.03310 | 0.03171 | 0.00027 | 0.00290 |
| 75 | 0.05228 | 0.05338 | 0.00018 | 0.00336 |
| 80 | 0.09367 | 0.08831 | 0.00066 | 0.00455 |
| 85 | 0.14380 | 0.12546 | 0.00076 | 0.00270 |
| 90 | 0.22422 | 0.21424 | 0.00073 | 0.00339 |

rate of the urban population began to decline in the late 1950 s from 6.165 in 1957 to 1.499 in 1982 except for an abnormal downward and then upward fluctuation in the period 1961-1964. The fertility rate decline in the rural population was much later. The total fertility rate of the rural population began to decline in the early 1970s, from 6.313 in 1970 to 2.857 in 1982. The decline of the total fertility rate in China is associated with the overall level of socio-economic development and a series of government birth control campaigns. It seems that both of these have contributed to the dramatic decline of the fertility rate in the past two decades (Birdsail and Jamison, 1983 ). There has been a trend to intensify the birth control campaign from the early 1970s to the late 1980s. The most controversial "one-child campaign" was launched in 1978. However, the rigorous birth control policy has been somewhat relaxed since 1984 in that most rural couples are now allowed to have two children (Peng, 1991; Greenhalgh, 1986). Generally, however, the government is still strongly encouraging couples to have only one child. Most urban couples are still required to have only one child. The recent economic reforms and the introduction of the household production responsibility

Table 14 Survival rates ( female populations, China )

| Age | From urban to |  | From rural to |  |  |
| :--- | :--- | :--- | :--- | :--- | :--- |
|  | Urban |  | Rural |  | Urban |
|  |  |  | Rural |  |  |
| 0 | 0.99620 | 0.00085 |  | 0.00337 | 0.98828 |
| 5 | 0.99894 | 0.00030 |  | 0.00318 | 0.99577 |
| 10 | 0.99926 | 0.00018 |  | 0.00396 | 0.99562 |
| 15 | 0.99933 | 0.00015 |  | 0.00662 | 0.99255 |
| 20 | 0.99537 | 0.00361 |  | 0.02054 | 0.97818 |
| 25 | 0.99639 | 0.00240 | 0.01751 | 0.98070 |  |
| 30 | 0.99833 | 0.00042 | 0.00618 | 0.99235 |  |
| 35 | 0.99826 | 0.00024 | 0.00527 | 0.99288 |  |
| 40 | 0.99794 | 0.00020 | 0.00499 | 0.99269 |  |
| 45 | 0.99704 | 0.00015 | 0.00406 | 0.99248 |  |
| 50 | 0.99609 | 0.00016 |  | 0.00303 | 0.99174 |
| 55 | 0.99097 | 0.00017 |  | 0.00272 | 0.98935 |
| 60 | 0.98668 | 0.00013 |  | 0.00243 | 0.98351 |
| 65 | 0.98168 | 0.00011 |  | 0.00298 | 0.97650 |
| 70 | 0.96664 | 0.00026 |  | 0.00281 | 0.96548 |
| 75 | 0.94755 | 0.00017 |  | 0.00318 | 0.94344 |
| 80 | 0.90573 | 0.00060 |  | 0.00414 | 0.90754 |
| 85 | 0.85555 | 0.00066 |  | 0.00234 | 0.87218 |
| 90 | 0.77521 | 0.00057 |  | 0.00265 | 0.78310 |
|  |  |  |  |  |  |

system in rural areas may decrease the effect of government birth control efforts (Hull, 1990 ). Under this household production responsibility system, each rural household actually becomes an independent economic entity being able to produce and sell surplus agricultural products at a market price after selling a stipulated amount of staple such as rice or wheat to the state according to a contract. It means that each household is operating marginally on a market economy basis and is much less constrained by the state and its agencies. The overall implication is that socio-economic development and modernization may play a much greater role in the future trajectory of the fertility rate in China. Government birth control efforts of course will still have some effects, and there are arguments that they need to be maintained, if not intensified, if population growth in China is to be slowed down feasibly and quickly. In fact, the total fertility rate of China has been further reduced from 2.618 in 1982 to 2.374 by 1987.

For the purpose of urban-rural population projections, three sets of total fertility rate trends in China are assumed. In set (A), it is assumed that the total fertility rates of urban and rural populations will remain unchanged from the base year 1987. The projection (A) based on this assumption shows the
consequence of continuing population growth if fertility rates are not reduced in future.

Total fertility rates of urban and rural populations, however, are likely to decline in future because of population control policy and changes of social, economic and psychological factors. According to previous population projection research on China, it is recognized that a U-shaped total fertility rate trend is probably both desirable and feasible. A realistic long term target for the population control policy may be a zero population growth rate. The total fertility rate for a stable zero growth rate population can be calculated and turns out to be about 2.2 for both the urban and rural populations. Thus a total fertility rate of 2.2 is partly used in some of the assumptions of population projection sets (B) and (C).
In set (B), it is assumed that the total fertility rate of the urban population will gradually decline to 1.5 in 2000, remain unchanged until 2010, gradually increase to 2.2 in 2030, and then remain unchanged until 2040. A total fertility rate of 1.5 is used as the lower limit of fertility for the urban population. The population of China is about to enter a stable or declining stage in the 2030s and it is desirable that fertility will be returned to a replacement level. The total fertility rate of the rural population will decline more slowly and is assumed to decline gradually to 2.2 by the year 2020, then remain unchanged until 2040.

However there may be concern that once the total fertility rate of the urban population has declined to a low level, it may be difficult to reverse the trend and increase the total fertility rate unless the earlier decline is a forced one. In set (C), it is assumed that the total fertility rate of the urban population will decline to 1.5 by the year 2000, then remain unchanged until 2040. For this projection $(\mathrm{C})$ the total fertility rate trend of the rural population is assumed to be the same as in set (B).

The main results of the urban-rural population projections are presented in Table 15. Projection (A) assumes that the urban and rural total fertility rates will remain unchanged though the total fertility rate of China will decline because of the increasing urban population component. Under this assumption the model projects that the total population of China will continue to grow until 2040 as shown in Figure 7. It will increase from 1136 million in 1990 to 1312 million in 2000 and 1604 million in 2040 . The urban population will increase from 367 million in 1990 to 531 million in 2000 and reach 1123 million by 2040 . The rural population will slightly increase from 769 million in 1990 to 781 million in 2000 . Then it will gradually and significantly decline to 481 million by 2040 . The urban population component will steadily increase from $32 \%$ in 1990 to $40 \%$ in 2000 and reach $70 \%$ in 2040.

Projection (B) assumes that the total fertility rates of the urban and rural populations will decline in future, but that the total fertility rate of the urban population will have a U-shaped trend. This means that the urban and rural populations will have the same total fertility rate of 2.2 after 2030. The trend

Table 15 Urban and rural population projections ( millions )
Year $\frac{\text { Total Population }}{\mathrm{A} \quad \mathrm{B} \quad \mathrm{C}} \frac{}{l}$ Urban Proportion \%

| Urban China |  |  |  |  |  |  |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| 1990 | 367 | 367 | 367 |  |  |  |
| 1995 | 450 | 448 | 448 |  |  |  |
| 2000 | 531 | 525 | 525 |  |  |  |
| 2010 | 703 | 688 | 688 |  |  |  |
| 2020 | 876 | 851 | 842 |  |  |  |
| 2030 | 1016 | 986 | 950 |  |  |  |
| 2040 | 1123 | 1081 | 1011 |  |  |  |
| Rural China |  |  |  |  |  |  |
| 1990 | 769 | 768 | 768 |  |  |  |
| 1995 | 779 | 774 | 774 |  |  |  |
| 2000 | 781 | 771 | 771 |  |  |  |
| 2010 | 725 | 701 | 701 |  |  |  |
| 2020 | 655 | 614 | 612 |  |  |  |
| 2030 | 579 | 529 | 522 |  |  |  |
| 2040 | 481 | 435 | 419 |  |  |  |
| China total |  |  |  |  |  |  |
| 1990 | 1136 | 1135 | 1135 | 32 | 32 | 32 |
| 1995 | 1229 | 1223 | 1221 | 37 | 37 | 37 |
| 2000 | 1312 | 1296 | 1296 | 40 | 41 | 41 |
| 2010 | 1428 | 1388 | 1388 | 49 | 50 | 50 |
| 2020 | 1530 | 1466 | 1454 | 57 | 58 | 58 |
| 2030 | 1595 | 1515 | 1472 | 64 | 65 | 65 |
| 2040 | 1604 | 1516 | 1430 | 70 | 71 | 71 |

Note: See text for assumptions used in making the projections
in total population is similar to those in projection (A) though the figures are somewhat smaller. For this projection the total population of China will also continue to grow. It will increase to 1296 million in 2000 and 1519 million in 2035. It will decline slowly after 2035 to reach 1516 million by 2040 . The urban population will increase to 525 million in 2000 and then double to reach 1081 million by 2040 . The rural population will increase slowly to 774 million in 1995, then decrease gradually to 435 million in 2040 . The trend in the urban population component of this projection is similar to, if slightly higher than, that of projection (A).

Projection (C) assumes that the total fertility rates of urban and rural populations will decline in future, and that the former will remain at a level
lower than the replacement level. Under these conditions the total population of China will continue to grow until 2030. It will increase to 1296 million in 2000 and 1472 million by 2030. It will decrease after 2030 to 1430 million in 2040. The urban population will increase to 525 million in 2000 and then nearly double to reach 1011 million in 2040. The rural population will increase slowly to 774 million in 1995, then decrease gradually to 419 million by 2040. The trend in the urban population component of projection (C) is again similar to the previous projections.


Fig. 7 Population projections (A)

## 6 CONCLUSION

Dynamic analysis of spatial population systems has been discussed in this monograph using an accounts and demographic rates-based approach. The approach and model developed in this monograph are useful for making multiregional population projections.

Various fertility, mortality and migration rates have been defined to measure the rates of population changes of a spatial population system. These definitions are based on multiregional population accounts so that demographic rates can be correctly defined. The definitions of forward demographic rates based on the starting population have been introduced. One main advantage of forward demographic rates is that they can be used straightforwardly in population projection models while other approaches may need an iterative procedure or a matrix inversion procedure for population projections.
We discussed the case of single-region population systems in section two. Basic notations of age group and period-cohort and the definitions of occurrence-exposure and forward mortality and fertility rates were
introduced. These discussions provide a basis for the discussions of the complex case of multiregional population systems in subsequent sections. Single-region population accounts have been expanded to record the population transitions both in a region ( birth and death ) and between regions ( migration ) in section three. A further rate of population change, the migration rate, was introduced. Three kinds of migration rate, potential, actual and survival migration rates, were defined depending on whether or not the migrating population who died in their origin or destination regions were counted in the measure of a particular migration rate.

Section four discussed the ways that forward mortality, fertility and migration rates can be estimated from the population data available. An iterative procedure was presented. Section five developed a forward demographic rates-based multiregional population model. Some examples of the Chinese population and the urban-rural population system of China have been used to illustrate some procedures and calculations.
It is noted that a practical analysis of a particular spatial population system involves the collection and processing of a large amount of population data. A set of FORTRAN programms has been developed by the author based on the methods discussed here. Contact the author for details and the availability of these programms. Another important source of computer programs for spatial population analysis is in Willekens and Rogers ( 1978 ).
The discussions on the topic of spatial population analysis in this monograph were concerned with a relatively simple case of closed spatial population systems consisting of N regions. It was assumed that these regions have no interaction with the rest of the world. Recently various methods have been adopted to include the external migration in the multiregional population models ( Rees, 1989; 1991; Rogers, 1989; Willekens and Drewe, 1984; Shen 1994b ). Another important topic of spatial population analysis is the construction of multiregional population life tables which show the life expectations of individuals of various ages in a region. This topic is not covered here but has been discussed elsewhere ( Rees and Wilson, 1977; Rogers and Willekens,1986b; Shen, 1993 ).
Significant progress has been made on multiregional population analysis and modelling since the mid-1960's. A number of practical applications of these methods can be found in a comparative study of the multiregional population dynamics in the seventeen member nations of the International Institute for Applied Systems Analysis ( Rogers and Willekens, 1986b ) including the United Kingdom and Canada. More recently, the forward demographic ratesbased approach discussed in this monograph has been applied to the urbanrural and multiregional ( provincial level ) population analysis of China (Shen, 1991; 1994b).

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[^0]:    Note: See text for explanations.

