Working Paper

TWO PROGRAM PACKAGES FOR DERIVING MULTISTATE-MULTIREGION LIFE TABLES AND TWO-SEX (FEMALE DOMINANT) POPULATION PROJECTIONS

Peer Just

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International Institute for Applied Systems Analysis
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FOREWORD

An important element of research on population at IIASA has been the development of computer programs for demographic analysis. Programs for spatial (multiregional) analysis, for multistate analysis, and for the estimation of model schedules and flow tables are some of the more widely used programs published by IIASA in the past years. To this collection we now add the programs described in this paper by Peer Just. Originally designed to carry out life table analyses and projections of a national population disaggregated by age, sex, marital status, and region, these programs also may be used to study other transitions, e.g., labor force transitions. They are being published to disseminate to a wider audience some of the analytical tools of multistate/multiregional demography developed at IIASA.

Andrei Rogers
Leader
Population Program

ABSTRACT

This paper describes two program packages for carrying out multistate/multiregion life table analyses and a female dominant two-sex projection by states and regions. The computer programs are adaptations of those published earlier for multistate life tables (Willekens 1979b) and for multiregional population projections (Willekens and Rogers 1978). Users not familiar with all the details of the theory of multistate demography nevertheless should be able to analyze populations disaggregated by age, sex, states, and regions, using these computer programs.

CONTENTS

TWO PROGRAM PACKAGES FOR DERIVING MULTISTATE-MULTIREGION LIFE TABLES AND TWO-SEX (FEMALE DOMINANT) POPULATION PROJECTIONS

1. INTRODUCTION

Soon after the framework of multiregional population analysis was developed by Rogers (1973, 1975), its generalization to other kinds of "regions" logically followed the previous research. The general case of a population disaggregated by states was studied by Keyfitz (1980), Krishnamoorthy (1977), Ledent (1978, 1979), Schoen (1975), Schoen and Land (1977), Rees (1978), and Willekens (1978, 1979a) among others.

After their publication, IIASA's computer programs for spatial demographic analysis (Willekens and Rogers 1978) were subsequently adapted to include the possibility of calculating increment-decrement life tables, which later became commonly used in multistate demographic analysis (Willekens 1979b). This program enables users to compute multistate life tables for a population disaggregated by states, but it does not take the regional dimension into account. To overcome this limitation the computer program presented here integrates transitions from one state to another, migration between regions, and multiple events into the existing increment-decrement life table framework.

A computer program to project a population by sex, states, and regions was still lacking, however, since the widely used multiregional projection program by Willekens and Rogers (1978) did not handle disaggregations by states or sex. The projection facility presented in this paper, was developed to allow for the projection of a population disaggregated by regions, by states, or by states and regions, as well as by sex using the so-called female dominant solution (see Keyfitz 1968, chapter 13).

The program packages set out in this paper are written in a way that allows them to be implemented by users not familiar with the theory of multistate population analysis. A single data file can be used as an input for the projection and life table calculations, provided that all age intervals are of equal length. In this case only a few parameters need to be specified. If the population is given by unequal age groups, then the projection program cannot be used. The application of the life table program, however, is not constrained by the character of the age disaggregation.

These two program packages were first applied to Australian data using two regions disaggregated by four marital states. Some numerical results are published in Rogers and Williams (1982).

1.1. Increment-Decrement Life Tables for Mixed States

In recent years demographers have given increased attention to the development of complex increment-decrement life tables. For example, the German demographic literature has focused on tables of working life (Linke 1976; Schaich and Schweitzer 1980). Recently several more general approaches can be distinguished. Schoen (1975) and Schoen and Nelson (1974) developed a uniradix multistate life table, which was applied to marital status patterns. Rogers (1975) and Rogers and Ledent (1976) considered the multiradix situation. Finally Willekens (1979b, 1980) reformulated and recalculated the working life table developed by Hoem

(1970, 1977) and Hoem and Fong (1976) using matrix notation. Rees (1978), Schoen and Land (1977), and Krishnamoorthy (1977) contributed further theoretical reflections.

The first program package presented here is an adaptation of the increment-decrement life table program described by Willekens (1979b). For details about the methodology the reader is referred to Willekens (1980) and Willekens and Rogers (1978).

Let us recall the distinction between population-based and status-based life tables (Willekens 1979b). A population-based life table is calculated for a particular age at which all states except one are empty. An example of such a uniradix situation is a marital status table based on age 0. All states except the state of never married are empty by definition at age 0. A status-based life table can be calculated for any age at which all states are nonempty. In such a case the number of cohorts has to equal the number of states.

If, however, mixed states (that is, regions and conventional states) are used, we are principally facing a multiradix situation where the number of cohorts is not necessarily equal to the number of states. Analogous to the previously defined population- and status-based life tables, therefore, are the region- and status-based tables. A region-based life table can be calculated for any age x for which exactly one state in each region will be nonempty. For a two-region working life table, for example, region-based calculations can be performed for any age between 0 and 15 since only the states "region 1, inactive" and "region 2, inactive" are nonempty for these ages. From age 16 up to the last age groups, various status-based life tables can be calculated.

As input data for a single-region increment-decrement life table, only transition rates between states are required. Introducing a spatial dimension means that migration also has to be taken into account as well as multiple events. One can now identify three types of rates

1. *Transitions from one state to another within a region*, for example, from "region 1, inactive" to "region 1, active"
2. *Migration from one region to another without changing state*, for example, migration from "region 1, inactive" to "region 2, inactive" (Note that migration data by states are required.)
3. *Simultaneous transitions*, for example, from "region 1, inactive" to "region 2, active"

If data are not available, model schedules can be used. Under the restrictive assumption that certain transitions are not possible, these rates can also be set to zero. Zero transition rates from region 1/state 1 to region 2/state 2, for example, do not mean that the probability of being in region 2/state 2 at age x + 1, having been in region 1/state 1 at age x is also zero. This is because the Option 3 method of estimating probabilities (Willekens and Rogers 1978) takes multiple transitions into account. A person may move from region 1/state 1 to region 2/state 1 and then to region 2/state 2 within the same interval.

In addition to computing multistate life tables, the extended life table program package presented here also performs multiple contingency calculations. A detailed description of the methodology and some numerical results can be found in Keyfitz and Rogers (1981).

1.2. Two-Sex Population Projection by States and Regions

Rogers (1975) has shown that a population projection by regions is an extension of the single region projection of Leslie (1945) and may be described by

$$\underline{K}(t+1) = \underset{\sim}{G}(t)\underline{K}(t) \qquad (1)$$

where the vectors $\underline{K}$ are the population by age and region at time t and t + 1, and $\underset{\sim}{G}$ represents the growth matrix of the multiregional system:

$$\underset{\sim}{G} = \begin{bmatrix} \underset{\sim}{0} & \underset{\sim}{0} & \underset{\sim}{B}(\alpha - 5) \ldots \underset{\sim}{B}(\beta - 5) \ldots & \underset{\sim}{0} & \underset{\sim}{0} \\ \underset{\sim}{S}(0) & 0 & & \vdots & \vdots \\ \underset{\sim}{0} & \underset{\sim}{S}(5) & \ddots & \vdots & \vdots \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ \underset{\sim}{0} & \underset{\sim}{0} & \cdot \; . & \underset{\sim}{S}(z - 5) & \underset{\sim}{0} \end{bmatrix}$$

The first row of $\underset{\sim}{G}$ is composed of matrices $\underset{\sim}{B}(x)$, where

$$\underset{\sim}{B}(x) = \frac{h}{4} [\underset{\sim}{P}(0) + \underset{\sim}{I}] [\underset{\sim}{F}(x) + \underset{\sim}{F}(x + h) \underset{\sim}{S}(x)] \tag{2}$$

$\underset{\sim}{F}(x)$ is a diagonal matrix of regional birth rates, and the matrix $\underset{\sim}{P}$ contains the probabilities of survival from exact age x to x + h. The sub-diagonal elements of $\underset{\sim}{G}$ denote the survivorship proportions calculated by

$$\underset{\sim}{S}(x) = [\underset{\sim}{I} + \underset{\sim}{P}(x + h)] \; \underset{\sim}{P}(x) \; [\underset{\sim}{I} + \underset{\sim}{P}(x)]^{-1} \tag{3}$$

The calculation of the transition probabilities is identical for the increment-decrement life table and the multistate projection. First the observed death and transition rates are arranged into a matrix

$$\underset{\sim}{M}(x) = \begin{bmatrix} \left[M_{1\delta}(x) + \sum\limits_{j \neq 1} M_{1j}(x)\right] & - M_{21}(x) & \ldots\ldots & - M_{n1}(x) \\ - M_{12}(x) & \left[M_{2\delta}(x) + \sum\limits_{j \neq 2} M_{2j}(x)\right] & \ldots\ldots & - M_{n2}(x) \\ \vdots & \vdots & & \vdots \\ - M_{1n}(x) & - M_{2n}(x) & \ldots & \left[M_{n\delta}(x) + \sum\limits_{j \neq n} M_{nj}(x)\right] \end{bmatrix}$$

According to Option 3, the probability matrix is calculated by (Willekens and Rogers 1978)

$$\underset{\sim}{P}(x) = [\underset{\sim}{I} + \frac{h}{2}\underset{\sim}{M}(x)]^{-1}\ [\underset{\sim}{I} - \frac{h}{2}\underset{\sim}{M}(x)]$$

In the case of a two-sex female dominant projection by states and regions, equation (1) and the calculation of the survivorship proportions remain unchanged. The elements of the first row of the growth matrix, however, have to be modified. This is because the state in which births appear is now not always identical with the state of the mother. In most multiregional projections, births are allocated to the state of the mother. In a multistate projection, however, some states may be empty by definition for certain age groups. Population projection by marital status is an example of this. Births can be borne by women in any of the four states: never married, married, divorced, or widowed. The children, on the other hand, can only be born into the never married state.

In order to perform a consistent projection by states and regions, two aspects have to be taken into account: the survival of children through the first age group, noting possible transitions, and the allocation of births into states at exact age 0. To this end a matrix $\underset{\sim}{C}$ can be defined that determines the allocation. The rows of $\underset{\sim}{C}$ denote the states into which children are born and the columns specify the states of mothers. A typical element C_{ij} is set to 1 if children born to mothers in state j are to be allocated in state i. For example

$$\underset{\sim}{C} = \begin{bmatrix} 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

State 1 receives births from 1 and 2 and State 3 will gather births from 3 and 4. This implies that the first age groups of states 2 and 4 will be empty. In the case of a two region projection by labor force status, state 1 could be "region 1, unemployed" and state 2, "region 2, employed". State 3 and 4 representing region 2 can be defined analogously.

The surviving of the births can easily be achieved by replacing matrix $\underset{\sim}{P}(0)$ in equation (2) by a matrix $\underset{\sim}{\overset{*}{P}}(0)$, which ensures that the probabilities of the states into which births appear will be applied independently from the states of mothers. Premultiplying equation (2) by $\underset{\sim}{C}$ and replacing $\underset{\sim}{P}(0)$ leads to

$$\underset{\sim}{B}(x) = \left(\frac{h}{4}\right)\underset{\sim}{C}\ [\underset{\sim}{\overset{*}{P}}(0) + \underset{\sim}{I}][\underset{\sim}{F}(x) + \underset{\sim}{F}(x + h)\underset{\sim}{S}(x)] \qquad (4)$$

Equations (3) and (4) are the elements of the growth matrix for a projection by age, states, and regions. It is now a straightforward exercise to complete the female dominant two-sex model. First a diagonal matrix $\underset{\sim}{X}^f$ has to be defined. Its elements are the ratios of males to females born to a woman in each state. Usually these ratios are identical. Thus

$$\underset{\sim}{X}^f = \begin{bmatrix} \bar{s}_1^f & \cdots & 0 \\ \vdots & \ddots & \vdots \\ & \bar{s}_j^f & \\ \vdots & \ddots & \vdots \\ 0 & \cdots & \bar{s}_n^f \end{bmatrix}$$

where

$$\bar{s}_j^f = 1/[1 + (b_j^m/b_j^f)] \qquad (5)$$

and b_j^m and b_j^f denote the number of male and female births. For the female projection the first row of the growth matrix is given by the elements

$$\underset{\sim}{B}^{f}(x) = (\tfrac{h}{4})\underset{\sim}{C}\ \underset{\sim}{X}^{f}\ [\overset{*}{\underset{\sim}{P}}{}^{f}(0) + \underset{\sim}{I})]\ [\underset{\sim}{F}(x) + \underset{\sim}{F}(x + h)\underset{\sim}{S}^{f}(x)] \tag{6}$$

The superscript f indicates that the survivorship proportions and probabilities of the female population are used. The projection of the male population is performed in two steps. First the total (male and female) population at exact age 0 is calculated by

$$\overset{*}{\underline{K}}(0) = \sum_{x} [\underset{\sim}{F}(x) + \underset{\sim}{F}(x + h)\ \ \underset{\sim}{S}^{f}(x)]\ \ {}^{t}\underline{K}^{f}(x) \tag{7}$$

$\overset{*}{\underline{K}}(0)$ is now input to the projection of males. The male population in the first age group at time t + 1 can easily be derived by means of

$${}^{t+1}\underline{K}(0)^{m} = \underset{\sim}{C}\ \underset{\sim}{X}^{m}\ \ [\overset{*}{\underset{\sim}{P}}(0)^{m} + \underset{\sim}{I}]\ \ \overset{*}{\underline{K}}(0) \tag{8}$$

where the elements $\bar{s}_{j}^{m}$ of $\underset{\sim}{X}^{m}$ are $1 - \bar{s}_{j}^{f}$. The other age groups are carried forward by

$${}^{t+1}\underline{K}^{m}(x + h) = \underset{\sim}{S}^{m}(x)\ \ {}^{t}\underline{K}^{m}(x) \tag{9}$$

for $h \leq X \leq n - h$, when n stands for the last age group.

The projection program package was designed to produce a total population projection (males and females) or a female dominant two-sex projection for

I. a population disaggregated by regions

II. a population disaggregated by states

III. a disaggregation by states and regions

This enables the user to study, for example, the projected active and inactive population on a national level (case II) or, by introducing an additional regional dimension (case III), disparities in the future labor force population among regions can be identified. The version of the program presented here projects the population at a constant rate. The user, however, can easily add subroutines to change the rates over time and recalculate the growth matrix at each stage of projection.

As far as the transition rates are concerned, the same applies for the projection as for the multistate-multiregion life table discussed in section 1.1. In addition to transition and death rates, the number of births in each state or the corresponding rates also need to be entered. Note that the program requires birth data by region and state of mother.

2. DESCRIPTION OF THE TWO PROGRAM PACKAGES

The program packages are designed as a modular system. Two general purpose subroutines are used in the projection and the life table packages; special purpose subroutines are called by the two main programs. The main programs are kept very short and consist mainly of call statements. Information is passed from one subroutine to the other by

arrays : labeled COMMON blocks
parameters : arguments of the CALL statements

The FORTRAN source code is presented in Appendix A.

2.1. General Purpose Subroutines

The two general purpose subroutines (a) MULTIP (matrix multiplication), and (b) INVERT (matrix inversion) have the following descriptions.

a. MULTIP: SUBROUTINE MULTIP (N,K,L)

Task: multiplication of two matrices $\underset{\sim}{A1}$ and $\underset{\sim}{B}$
$\underset{\sim}{C} = \underset{\sim}{A1} * \underset{\sim}{B}$

Parameters: N: number of rows of $\underset{\sim}{A1}$
K: number of columns of $\underset{\sim}{A1}$ (and consequently, number of rows of $\underset{\sim}{B}$)

	L: number of columns of $\underset{\sim}{B}$
Input:	— parameters in the CALL statement — matrices $\underset{\sim}{A1}$ and $\underset{\sim}{B}$ in a labeled COMMON: COMMON/CMUL/A1(N,K) B(K,L), C(N,L)
Output:	the result of the matrix multiplication stored in the N x L matrix $\underset{\sim}{C}$
Printing:	none
b. INVERT:	SUBROUTINE INVERT (NR, NRADIX)
Task:	inversion of the matrix $\underset{\sim}{CC}$
Parameters:	NR: rank of $\underset{\sim}{CC}$ NRADIX: see Section 3.1
Input:	— parameter NR in the CALL statement (the subroutine assumes that $\underset{\sim}{CC}$ is nonsingular and that all the diagonal elements are nonzero) — matrix $\underset{\sim}{CC}$ in labeled COMMON: COMMON/CINV/CC(NR, NR)
Output:	the original matrix $\underset{\sim}{CC}$ replaced by the inverted matrix
Printing:	none

2.2. Special Purpose Subroutines

2.2.1. Life Table Program Package

DATINCR:	reads and prints the data as they are read in; computes the observed rates if necessary
PROBSC:	computes and prints the transition probabilities
HIST:	computes and prints the complete life histories of the cohorts
LIFE:	computes and prints the increment-decrement life table

TAB:	prints a summary table in case the number of states equals 2

Additional subroutines for multiple contingency calculations include:

PROBN:	computes transition probabilities, mortality excluded (for subroutine RES)
LINS:	calculates present value of an insurance
RES:	calculates reserve needed

DATINCR: SUBROUTINE DATINCR (NA,NOPEN,NY,ZFNY,NR,NRADX, NDAT)

Task:	— reads data and prints them as they are read in (for details, see Section 3 on preparation of data deck) — computes observed rates
Parameters:	see Section 3.1
Input:	see Section 3.1
Output:	data as they are read in, data stored in labeled COMMON

PROBSC: SUBROUTINE PROBSC (NA,NR,NOPEN,IPROB,NRADIX)

Task:	computes and prints the transition probabilities following Option 3
Parameters:	NA,NR,NOPEN,NRADIX: see Section 3.1 IPROB is equal to 3
Input:	DATINCR must precede PROBSC
Output:	tables
Algorithm:	see Willekens and Rogers (1978, Section 2.7)

HIST: SUBROUTINE HIST (NA,NR,NRADIX,IHIST)

Task:	computes and prints the complete life histories of each cohort

Parameters: NA,NR,NRADIX: see Section 3.1

IHIST: parameter indicating that life histories are computed (If subroutine HIST is called, IHIST takes the value of one and the computation of the matrices $\underset{\sim}{\ell}(x)$ is skipped in the subroutine LIFE. If HIST is not called before LIFE, then IHIST is zero and $\underset{\sim}{\ell}(x)$ is computed in LIFE.)

Input: PROBSC must precede HIST

Output: tables

Algorithm: see Willekens and Rogers (1978, Section 2.1)

LIFE: SUBROUTINE LIFE (NA,ZFNY,NR,NRADIX,IHIST,ILIF,NOPEN)

Task: computes and prints the multiregional life table

Parameters: NA,ZFNY,NR,NRADIX,NOPEN: see Section 3

IHIST: see HIST

ILIF: parameter indicating that life table is computed (If subroutine LIFE is called, ILIF takes the value of one.)

Input: PROBSC must precede LIFE
HIST may precede LIFE but not necessarily

Output: increment-decrement life table

Algorithm: see Sections 2.2 to 2.6 of Willekens and Rogers (1978)

TAB: SUBROUTINE TAB (NA,NR,NRADIX)

Task: prints summary table if the number of regions equals 2

Parameters: NA,NR,NRADIX: see Section 3.1

Input: subroutine LIFE must precede TAB

Output: tables

PROBN: SUBROUTINE PROBN (NA,NR,NOPEN,IROB,NRADIX)

Task:	computes transition probabilities following Option 3, only used to calculate reserve
Parameters:	NA,NR,NOPEN,NRADIX: see Section 3.1
Input:	DATINCR must precede PROBN
Output:	none
Algorithm	adapted from Willekens and Rogers (1978, Section 2.7)

LINS: SUBROUTINE LINS (NA,ZFNY,NR,NRADIX,IHIST,ILIF,NOPEN,E)

Task:	presents value on insurance of unity by status at age x
Parameters:	NA,ZFNY,NR,NRADIX,NOPEN,E: see Section 3.1 IHIST: see HIST ILIF: see LIFE
Input:	PROBSC must precede LINS
Output:	tables
Algorithm:	see Keyfitz and Rogers (1981, p17)

RES: SUBROUTINE RES (NA,NR,NRADIX,E,IC)

Task:	calculates and prints tables for reserve and life insurance
Parameters:	NA,NR,NRADIX,E: see Section 3.1 IC: 0 calculates and prints reserve 1 calculates and prints life insurance
Input:	PROBN must precede RES
Output:	tables
Algorithm:	see Keyfitz and Rogers (1981, p17)

2.2.2. *Projection Program Package*

DATASB:	reads parameters and input data; calculates rates and matrix $\underset{\sim}{C}$
GROWTH:	calculates growth matrix
PROBSC:	computes and prints probabilities
PROJEC:	projects the population towards stability

DATAS: SUBROUTINE DATAS (NPR,NA,NY,ZFNY,NR,XZB,XZD,XZO, IPROB,NEIG)

Task	— reads and prints input data — calculates rates — computes matrix $\underset{\sim}{C}$ — stores input in labeled COMMON
Parameters:	see Section 3.2
Input:	parameters and input file
Output:	prints input file
Algorithm:	equation (3)

GROWTH: SUBROUTINE GROWTH (NA,ZFNY,NR,ILIF)

Task:	— computes survivorship proportions — calculates growth matrix — prints growth matrix — calculates $\overset{*}{\underline{K}}(0)$, see Section 1.2
Parameters:	ILIF: 0, $\underset{\sim}{S}(x)$ calculated in GROWTH
Input:	PROBSC must precede GROWTH
Output:	first row and diagonal elements of $\underset{\sim}{G}$
Algorithm:	see Willekens and Rogers (1978) and Section 1.2

PROBSC: SUBROUTINE PROBSC (NA,AFNY,NR,IPROB)

See Section 2.2.1.

PROJEC: SUBROUTINE PROJEC (NA,ZFNY,NR,ZLAMDA,IPOJ)

Task:	— projects total population or male and female population — calculates stable equivalent population
Parameters:	see Section 3.2
Input:	GROWTH must precede PROJEC
Output:	— projected population — percentage distribution — stable equivalent

2.3. Main Programs

MAININCR:	— calls subroutines for multistate-multiregion life table — defines default values for parameters
MAINPROJ:	— calls subroutines for multistate-multiregion projection — defines default values for parameters

3. INPUT PARAMETERS AND DATA

3.1. Input File for Life Table Calculations

All input data are read by subroutine DATINCR which is the first subroutine to be called by the main program. To make the program as flexible as possible the data can either be absolute numbers or rates. By specifying some additional parameters, the same data file as for the projection program can be used. The birth rates, or absolute numbers, needed for the projection are then skipped for the life table calculations. Two units are used for I/O

unit 5	input
unit 6	output

The arrangement of the input data file follows Willekens (1979):

a. Identification line
b. Parameter line
c. Title lines
d. Age composition (optional)
e. Names of states and regions
f. Sizes of cohorts
g. Data
h. "END" line

Appendix B gives an example of the composition of the parameter cards.

a. Identification Line

This line is used to label the input file. Since it is not used by the program it may contain any information.

Read and write FORMAT (25A4).

b. Parameter Line

The parameter line contains instructions to the program concerning the way the data are to be read and the desired computations. The parameter names, their interpretation, default values and formats are presented in Table 1.

c. Title Lines

The NU title lines are printed out as they are read in. The number of title lines has to be greater than zero.

Read and write FORMAT 25A4.

d. Age Composition

The program can handle any sequence of age intervals. Willekens (1979b) considers three types:

i. *Fixed intervals.* If all age groups are of the same length, then the length is given by the parameter NY and an age composition card is not needed.

Table 1. Parameter specification for multistate/multiregion life table.

Columns	Format	Name	Interpretation	Default Value	Maximum Value
1-2	I2	NAS	Starting (lowest) age for which data are available	0	-
3-5	I3	NAE	Highest age of population considered (NAE is the first age of the last interval)	-	100
6-7	I2	NASS	Lowest age of population considered in life table calculation (the life table is computed for cohorts of exact age NASS) In general NAS = NASS = 0 for life tables yielding population based measures; and NAS ≠ NASS for life tables giving state specific measures (except in multiradix case)	NAS	-
8-9	I2	NOPEN	Character of last age interval NOPEN = 1: last age interval is open-ended NOPEN = 2: last age interval is not open-ended but is of a given interval (this may be the case in working life tables with highest age being some advanced age of retirement, age 70 say. In this case the life expectancy at age x denotes the expected number of years lived up to the age of 70 + NY)	0	-
10-11	I2	NR	Number of states	-	8
12-13	I2	NRADX	Number of cohorts (i.e., number of nonempty states at age NASS)	1	8
14-15	I2	NY	Age interval: usually NY =1 or 5 - if NY = 98: fixed intervals of 5 years except for the first age groups which are 0 and 1-4 - if NY = 99: variable age intervals	-	-
16-17	I2	NU	Number of title cards	-	-
18-21	I4	INIT	Base year (year to which data refer)	-	-
22-23	I2	NDAT	Specification of the transition data NDAT = 1: absolute numbers NDAT = 2: occurrence/exposure rates	-	-
24	I1	IP	Skip population if input and NDAT = 2; IP = 1	0	-
25	I1	IB	Skip birth if input; IB = 1	0	-
26-33	8I1	IR(K)	Choose cohorts at age NASS - if state K empty, IR(K) = 0 - if state K nonempty, IR(K) = 1	0	-
34	F8.6	R	Discount rate for multiple contingency calculations	0	-

ii. *Fixed intervals, except for the first age group.* It frequently happens in demographic analysis that all age groups consist of a 5-year interval except for the first two age groups which are 0 and 1-4. If this is the case, i.e., if the data are supplied for this age structure, then NY must be given the value of 98 and the subroutine DATINCR generates the desired age structure. Consequently, the age composition card is not needed.

iii. *Variable intervals.* If the age groups are of variable lengths, the number of age groups and the age structure must be read in. Two cards are required:

1. number of age groups (NA)

COLS	FORMAT	VAR. NAME
1-2	I2	NA

2. age composition (age at beginning of each interval):

COLS	FORMAT	VAR. NAME
1-72	40I2	NAGE(X), X = 1, NA

If variable intervals are used (the age composition cards must be read) NY must be given a value of 99.

e. *Names of States and Regions*

To identify each state or region in the output it is labeled with a name. This name may consist of up to eight characters. Any character can be used. The last name in the sequence is that of the total system. So, NR + 1 names have to be specified.

COLS	FORMAT	VAR. NAME
1-72	9A8	REG(I), I = 1,NR + 1

f. *Size of Cohorts*

For each state the size of the cohort has to be defined. The cohorts which are actually chosen for the calculations are determined by IR.

COLS	FORMAT	VAR. NAME
1-72	9F8.0	RADIX(I), I = 1,NR

g. Data

Data related to each state are given sequentially:

- observation for state 1
- observation for state 2

:

- observation for state NR

Note that all transitions should refer to the same time period. Two types of data can be used:

- absolute numbers (NDAT = 1)
- occurrence/exposure rates (NDAT = 2)

The general composition of the data set for each state is given by:

i. *Population*

- must be input if transitions are absolute numbers (NDAT = 1)
- optional if transitions are rates (NDAT = 2). In this case IP = 1.

ii. *Birth*

- optional, if input IB = 1

iii. *Death*

- for absolute numbers, NDAT = 1 and IP = 0
- for rates, NDAT = 2, if population is also input IP = 1

iv. *Transitions from the given state to the various other states*

- for absolute numbers NDAT = 1 and IP = 0
- for rates NDAT = 2, if population is input IP = 1

DATA	COLS	FORMAT	VAR. NAME
population	1-100	10F10.0	HUP(X,I), X = 1,NA
birth	1-100	10A10	not stored
death	1-100	10F10.0	HUD(X,I), X = 1,NA
or	1-100	10F10.6	RATD(X,I), X = 1,NA
transitions	1-100	10F10.0	HUD(X,I,J), X = 1,NA
or	1-100	10F10.6	RATM (X,I,J), X = 1,NA

If more than 10 age groups are used, the same FORMAT is repeated. The maximum number of age groups is 101. Up to 8 states can be used.

h. "END" Line

COLS	FORMAT	VAR. NAME
1-4	A4	TIT (1)

3.2. Input File for Population Projection

The input file is read by subroutine DATAS called from the main program. Three I/O units are used

- unit 4 input/output (intermediate data storage)
- unit 5 input
- unit 6 output

For a total population projection, unit 4 is not used. In the case of a female dominant two-sex projection this unit stores the total number of births [$\overset{*}{K}(0)$] calculated by the female projection and used as input by the projection run for the male population.

The input file (unit 5) consists of parameter lines, identification lines, and the data set:

a. Identification line
b. Parameter lines
c. Names of states and regions

d. Size of cohorts
e. Data
f. "END" line

a. Identification line

Arbitrary text to be printed as page heading.
Read and write FORMAT (25A4).

b. Parameter Lines

Line 1:	instructions for the program concerning input and output and the kind of projection to be performed. Table 2 exhibits the interpretation of the parameters, formats, and default values.
Line 2:	Only used for the projection of female and total population. This line specifies those states into which births are allocated.
Line 3:	Female projection only. For each state defined in the second parameter line, those states are specified which contribute births. See also Table 2.

c. Names of States and Regions

The output identification of the states and regions may consist of up to 8 arbitrary characters. NR + 1 names have to be given where the last name is that of the total system.

COLS	FORMAT	VAR. NAME
1-72	9A8	REG(I), I = NR+1

d. Size of Cohorts

Instead of the sequence of cohorts also blanks can be input. In this case the program takes a default value of 100.000 for each nonempty state at age 0. Otherwise use

COLS	FORMAT	VAR. NAME
1-72	9F8.0	RADIX(I), I = 1,NR

Table 2. Parameter specification for a female dominant two-sex projection by states and regions.

Line	Columns	Format	Name	Interpretation	Default Value	Maximum Value
I	1-3	I3	NA	Number of age groups	-	101
	4-5	I2	NR	Number of regions	-	12
	6-7	I2	NY	Width of age group (e.g., 5 years) ZFNY = real value of NY: ZFNY = FLOAT(NY)	-	-
	8-9	I2	NU	Number of title cards	-	-
	10-11	I2	NZB	Time interval for which birth data are given, e.g., NZB = 1: one-year birth data NZB = 5: five-year birth data	1	-
	12-13	I2	NZD	Time interval of death data	1	-
	14-15	I2	NZO	Time interval of migration data	1	-
	16-17	I2	IRPOB	Option for estimating death and outmigration probabilities IPROB = 1: Option 1 method (PROBR) IPROB = 3: Option 3 method (PROBSC)	3	-
	18-21	I4	INIT	Base (initial) year	-	-
	22-25	I4	NHORIZ	Time horizon of short-term projections: year until which the detailed projection output is given at each time period	INIT	-
	26-29	I4	INTV	Time interval in years, for long-term projection output, e.g., INTV = 100 - detailed projection output is given every 100 years (starting from base year)	200	9999
	30-31	I2	ITOLX	Choice of stopping criterion for stable population analysis ITOLX = 2: criterion is difference in growth ratio between the first and the last region ITOLX = 3: criterion is difference in growth ratio of the first region between the actual and the previous time period	2	-

Table 2. Continued.

Line	Columns	Format	Name	Interpretation	Default Value	Maximum Value
I	32-33	I2	NTOLL	Tolerance level for stopping criterion	7	-
	34-35	I2	NEIG	Not used	0	-
	36-37	I2	NDAT	Specification of input NDAT = 1 absolute numbers NDAT = 2 rates	-	-
	38-39	I2	NBS	Number of states into which births are allocated	-	12
	40-41	I2	NSX	Kind of projection NSX = 1 projection of males NSX = 2 projection of females NSX = 3 projection of total population	-	-
	42-43	I2	IB	Only used for projection of males (otherwise IB = 0) IB = 0 if no male birth data are input IB = 1 if male birth data are input (this input is skipped)	0	-
	44-45	I2	IS	IS = 1 do not print growth matrix IS = 2 print growth matrix	-	-
				Tolerance level = 10^{-NTOLL}		
II	1-2*NBS	I2	LH(I)	For total and female population projections only. This vector holds the sequence numbers of those NBS states into which births are allocated.	0	12
III ⋮ III+NBS	1-8*NR	F8.5	DF(K,J)	For total and female population projections only. For each of the states defined by LH(I) one line has to be specified (K = 1,NBS). This line specifies whether a state J (J = 1,NR) contributes birth to a state K. Projection of females: DF(K,J) = 0.0; state J is not contributing birth to state K DF(K,J) = sex ratio of birth of state J; children born to mothers in state J will be allocated into state K. Projection of total population: DF(K,J) = 0.0; state J is not contributing birth to state K DF(K,J) = 1.0; children born to mothers in state J will be allocated into state K.	0	-

e. Data

As for the life table the data set is organized by states. Rates as well as absolute numbers are accepted by the program. A typical set for a state is arranged as follows:

i. *Population*

ii. *Birth*

- optional for projection of males, but not used for the computation. To skip these data IB has to be 1
- NDAT = 1 for absolute numbers
- NDAT = 2 for rates

iii. *Death*

- NDAT = 1 for absolute numbers
- NDAT = 2 for rates

iv. *Transitions from the given state to the various other states*

- if birth and death *rates* are input, the transition *rates* have to be used
- if *absolute numbers* of birth or death are used, *absolute numbers* for the transitions are required.

DATA	COLS	FORMAT	VAR. NAME
population	1-100	10F10.0	POP(X,I), X = 1,NA
birth	1-100	10F10.0	ZHU(X), X = 1,NA
or	1-100	10F10.6	FATF(X,I), X = 1,NA
death	1-100	10F10.0	ZHU(X), X = 1,NA
or	1-100	10F10.6	RATD(X,I), X = 1,NA
transitions	1-100	10F10.0	ZHU(X), X = 1,NA
or	1-100	10F10.6	RATM(X,I), X = 1,NA

The number of states and regions is limited to 12. Up to 101 age groups of equal length can be used.

f. "END" Line

Since the data file is read twice the "END" life is used to initiate the rewinding of the input file.

COLS	FORMAT	VAR. NAME
1-4	A4	TIT(1)

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APPENDIX A: LISTING OF SOURCE CODES

1. GENERAL PURPOSE SUBROUTINES

Subroutine INVERT (NR)

```
    subroutine invert (nr)
c nr : dimension of matrix cc to be inverted
    dimension pivot(12)
    common /cinv/ cc(12,12)
    do 606 i=1,nr
    pivot(i)=cc(i,i)
    cc(i,i)=1.0
    do 607 j=1,nr
    cc(i,j)=cc(i,j)/pivot(i)
 607 continue
    if (nr.eq.1) go to 10
    do 608 k=1,nr
    if (k.eq.i) go to 608
    h=cc(k,i)
    cc(k,i)=0.
    do 609 l=1,nr
    cc(k,l)=cc(k,l)-cc(i,l)*h
 609 continue
 608 continue
 606 continue
 10 continue
    return
     end
```

Subroutine MULTIP (N, K, L)

```
    subroutine multip (n,k,l)
c  al * b = c
c n : number of rows of al
c k : number of columns of al = number of rows of b
c l : number of columns of b
    common /cmul/ al(12,12),b(12,12),c(12,12)
    do 3 i=1,n
    do 3 j=1,l
    c(i,j)=0.
    do 3 jj=1,k
    c(i,j)=c(i,j)+al(i,jj)*b(jj,j)
  3 continue
     return
    end
```

2. LIFE TABLE SUBROUTINES

Subroutine DATINC (NA, NOPEN, NY, ZFNY, NR, NRADX, NDAT)

```
      subroutine datinc (na,nopen,ny,zfny,nr,nradx,ndat)
      dimension hup(105),hud(105)
      dimension title(25)
      common /cx/ ir(8)
      common /cnag/ nage(106)
      common /crate/ ratd(105,8),ratm(105,8,8)
      common /crad/ radix(8),radixt
      common /creg/ reg(13)
      common /ctit/ tit(25)
      common /cs/ r,nys
      double precision reg
      integer x
      data dy/4hend /
c
c -------------------------------------------------------------
c
c read input file as it is and rewind
c
c -------------------------------------------------------------
c
  100 continue
      read (5,3) (tit(j),j=1,25)
      print 50, (tit(j),j=1,25)
   50 format (1x,25a4)      .
      if (tit(1).ne.dy) go to 100
      rewind 5
c
c ---------------------------------------------------------------
c
c  read page heading and parameter card
c
c ----------------------------------------------------------------
c
      read (5,3) (tit(j),j=1,25)
    3 format (25a4)
      read (5,4) nas,nae,nass,nopen,nr,nradx,ny,nu,init,ndat,
     1ip,ib,(ir(j),j=1,8),r
    4 format (i2,i3,6i2,i4,i2,2i1,8i1,f8.6)
      nys=ny
      nh=nae-nas+1
      l1=nh/10
      h2=float(l1)
      h1=float(nh)/10.0
      if(h1.gt.h2)le=l1+1
      if(h1.eq.h2)le=l1
c
c ----------------------------------------------------------------------
c
c  read and print title
c
c -----------------------------------------------------------------------
c
      print 64
   64 format (1h1,1x)
      do 66 i=1,10
   66 print 65
   65 format (1x)
      do 67 i=1,nu
      read (5,3) (title(j),j=1,25)
      print 69, (title(j),j=1,25)
```

```
  69   format (10x,25a4)
  67   continue
       print 64
       if (ny.ge.90) go to 30
       na=(nae-nas)/ny+1
       nage(1)=nas
       naa=na-1
       do 654 x=1,na
 654   nage(x+1)=nage(x)+ny
       go to 33
  30   continue
       if (ny.ne.98) go to 34
       nage(1)=0
       nage(2)=1
       nage(3)=5
       nze=nae/5+2
       do 32 x=4,nze
  32   nage(x)=nage(x-1)+5
       na=nze
       go to 33
  34   continue
c
c read number of age groups and nage(x)
c
       if (ny.ne.99) go to 33
       read (5,35) na
       read (5,35) (nage(x),x=1,na)
  35   format (40i2)
  33   continue
c
c  if nopen=2 the last age groups is closed; the value
c  of nage(na+1) must therefore be known
c
c      !      nage(na+1)=nage(na)-nage(na-1)
       naa=na-1
       zfny=float(ny)
       nr1=nr+1
       read (5,14) (reg(j),j=1,nr1)
  14   format (9a8)
       read (5,15) (radix(j),j=1,nr)
  15   format (9f8.0)
       radixt=0.
       do 16 j=1,nr
  16   radixt=radixt+radix(j)
c
c -------------------------------------------------------------
c
       do 10 i=1,nr
       if(ip.eq.0)goto 112
       do 111 lh=1,le
 111   read(5,222)help
 222   format(a4)
 112   continue
       if (ndat.ne.1) go to 250
       read (5,17) (hup(j),j=1,na)
  17   format (10f10.0)
       if(ib.eq.0)goto 1001
       do 1002 lh=1,le
1002   read(5,222)help
1001   continue
```

```
      read (5,17) (hud(j),j=1,na)
      do 18 x=1,na
      ratd(x,i)=0.
      if (hup(x).ne.0.) ratd(x,i)=hud(x)/hup(x)
c
c  if ratd(na,i)=0, then the death rate in the last age group is
c  set equal to 0.4 (to avoid rmla(j,i) to be zero and to enable the
c  calculation of l(na,i,j)
c
      if (x.eq.na.and.ratd(x,i).eq.0.) ratd(x,i)=0.4
   18 continue
      do 19 j=1,nr
      read (5,17) (hud(x),x=1,na)
      do 19 x=1,na
      ratm(x,j,i)=0.
      if (hup(x).ne.0.) ratm(x,j,i)=hud(x)/hup(x)
   19 continue
      go to 251
  250 continue
      if(ib.eq.0)goto 2001
      do 2002 lh=1,le
 2002 read(5,222)help
 2001 continue
      read (5,27) (ratd(x,i),x=1,na)
   27 format (10f10.6)
      do 28 j=1,nr
      read (5,27) (ratm(x,j,i),x=1,na)
   28 continue
  251 continue
   10 continue
c
c
      na9=na
      if (nas.eq.nass) go to 720
c which age group is nass ?
      do 721 x=1,na
      if (nage(x).ne.nass) go to 721
      nassx=x
  721 continue
      na9=na-nassx+1
       na1=na+1
       do 723 x=nassx,na1
      ix=x-nassx+1
      nage(ix)=nage(x)
      if (x.eq.na1) go to 723
      do 722 i=1,nr
      ratd(ix,i)=ratd(x,i)
      do 722 j=1,nr
  722 ratm(ix,j,i)=ratm(x,j,i)
  723 continue
  720 continue
c
c  write rates
c
      na=na9
      print 64
      print 29
   29 format (1h0,5x,34hobserved occurrence/exposure rates/
     16x,34(1h*)/)
      do 25 i=1,nr
      print 23, reg(i)
   23 format (1h0,20x,a8/21x,8(1h*)//)
      print 24, (reg(j),j=1,nr)
   24 format (5x,3hage,3x,9hmortality,2x,8(2x,a8)/)
      do 25 x=1,na
      print 26, nage(x),ratd(x,i),(ratm(x,j,i),j=1,nr)
   26 format (5x,i3,2x,f10.6,2x,8f10.6)
   25 continue
      return
      end
```

Subroutine HIST (NA, NR, NRADIX, IHIST)

```
      subroutine hist (na,nr,nradix,ihist)
      dimension hulp(8),rm(8)
      common /cnag/ nage(106)
      common /ccl/ cl(105,8,8)
      common /cmul/ al(8,8),b(8,8),c(8,8)
      common /cpq/ p(105,8,8)
      common /crad/ radix(8),radixt
      common /creg/ reg(13)
      common /ctit/ tit(25)
      common /cs/ r,nys
      double precision reg
      integer x,xx
   66 format (1x)
      ihist=1
c -------------------------------------------------------
c compute the number of survivors at exact age x
c -------------------------------------------------------
      do 5 i=1,nradix
      cl(1,i,i)=1.
      do 5 j=1,nr
      if (i.ne.j) cl(1,i,j)=0.
    5 continue
      naa=na-1
      do 14 x=1,naa
      xx=x+1
      z=float(nage(xx)-nage(x))
      do 15 i=1,nr
      do 15 j=1,nr
      al(j,i)=p(x,j,i)
   15 b(j,i)=cl(x,i,j)
      call multip (nr,nr,nr)
      do 16 i=1,nr
      do 16 j=1,nr
   16 cl(xx,i,j)=c(j,i)
   14 continue
c -----------------------------------------------------
c compute and print the life history of the initial cohort
c -----------------------------------------------------
      print 1, (tit(j),j=1,25)
    1 format (1h1,50x,25a4)
      print 9201, nage(1)
 9201  format (1h0/20x,30hlife history of initial cohort,
     17h of age,i3/20x,40(1h*))
      do 250 io=1,nradix
       if (io.ne.1) print 9211
 9211 format (1h1,1x)
      print 9202, reg(io)
 9202 format (1h0,20x,24hinitial status of cohort,2x,a8/21x,
     134(1h*)/)
      iskip=3
       if (na.gt.18) iskip=2
      do 20 i=1,nr
      if (iskip.ne.i) go to 29
      print 9211
      if (na.le.18) iskip=iskip+2
      if (na.gt.18) iskip=iskip+1
   29 continue
      print 21, i,reg(i)
   21 format (10x,i2,2h.-,1x,15hstatus at age x,2x,a8/)
      print 22
```

```
 22  format (9x,6hdeaths,5x,14htransitions to)
     print 23, (reg(j),j=1,nr)
 23  format (1x,3hage,11x,12(1x,a8))
     print 66
     cdrt=0.
     do 6 j=1,nr
  6  hulp(j)=0.
     do 230 x=1,na
     zz=0.
     do 119 j=1,nr
119  zz=zz+p(x,j,i)
     zq=1.-zz
     zz=cl(x,io,i)*zq
     cdr=zz*radix(io)
     cdrt=cdrt+cdr
     do 24 j=1,nr
     zz=cl(x,io,i)*p(x,j,i)
     rm(j)=zz*radix(io)
 24  hulp(j)=hulp(j)+rm(j)
     print 25, nage(x),cdr,(rm(j),j=1,nr)
 25  format (1x,i3,2x,13f9.0)
230  continue
     print 26, cdrt,(hulp(j),j=1,nr)
 26  format (/1x,5htotal,13f9.0)
     print 66
     print 66
 20  continue
250  continue
     return
     end
```

Subroutine LIFE (NA, ZFNY, NR, NRADIX, IHIST, ILIF, NOPEN)

```
      subroutine life (na,zfny,nr,nradix,ihist,ilif,nopen)
      dimension cm(8),cme(106,8)
      dimension e(106,8,8),t(8),tr(8)
      common /clx/ lx(106,8,8)
      common /cx/ ir(8)
      common /cnag/ nage(106)
      common /ccl/ cl(105,8,8)
      common /cinv/ cc(8,8)
      common /cl/ l(105,8,8)
      common /cmul/ al(8,8),b(8,8),c(8,8)
      common /cpq/ p(105,8,8)
      common /crate/ ratd(105,8),ratm(105,8,8)
      common /crad/ radix(8),radixt
      common /creg/ reg(13)
      common /crmla/ rmla(8,8)
      common /ctit/ tit(25)
      common /csu/ su(105,8,8)
      common /cs/ r,nys
      double precision reg
      real l,lx
      integer x,xx,xy
      ilif=1
      naa=na-1
      iprex=1
  66  format (1x)
 9103 format (1x,i3,1x,f10.5,12f9.5)
 9020 format (15x,12(1x,a8))
 9001 format (//20x,6hstatus,2x,a8/20x,16(1h*)/)
 9999 format (1h1//1x)
 9011 format (1x,3hage,6x,5hdeath,5x,15htransition from,1x,a8,1x,2hto)
c --------------------------------------------------
c expected number of survivors at exact age x
c --------------------------------------------------
c compute number of survivors
c
      na4=naa
      if (nopen.eq.2) na4=na
      na5=na4+1
c
      if (ihist.ne.0) go to 5
      do 761 ih=1,nr
      if(ir(ih).ne.1)go to 762
      i=ih
      cl(1,i,i)=1.
      do 76 j=1,nr
      if (i.ne.j) cl(1,i,j)=0.
  76  continue
 762  continue
 761  continue
      do 77 x=1,na4
      xx=x+1
      z=float(nage(xx)-nage(x))
      do 6 i=1,nr
      do 6 j=1,nr
      al(j,i)=p(x,j,i)
    6 b(j,i)=cl(x,i,j)
      call multip (nr,nr,nradix)
      do 71 ih=1,nr
      if(ir(ih).ne.1)goto 71
      i=ih
```

```
      do 7 j=1,nr
    7 cl(xx,i,j)=c(j,i)
   71 continue
   77 continue
    5 continue
c print number of survivors
      print 1, (tit(j),j=1,25)
    1 format (1h1,50x,25a4)
      print 66
      print 66
      print 4831
 4831 format (20x,51hexpected number of survivors at exact age x in each
     17h status,/20x,58(1h*))
      iskip=3
      do 601 ih=1,nr
      if(ir(ih).ne.1)goto 601
      io=ih
      if (iskip.ne.io) go to 123
      print 9999
      iskip=iskip+2
  123 continue
      print 9502,reg(io)
 9502 format (//1x,3hage,6x,24hinitial status of cohort,2x,a8/1x,
     13(1h*),6x,34(1h*)/)
      print 9100, (reg(j),j=1,nr)
 9100  format (10x,5htotal,10(1x,a8))
       print 66
c
      do 60 x=1,na
      clt=0.
      do 8 j=1,nr
      cm(j)=cl(x,io,j)*radix(io)
    8 clt=clt+cm(j)
      print 9101, nage(x),clt,(cm(j),j=1,nr)
 9101 format (1x,i3,1x,f10.0,12f9.0)
   60 continue
  601 continue
c -------------------------------------------
c number of years lived between x and x+ny
c -------------------------------------------
c           - by status at age nass
c -------------------------------------------
      do 101 ih=1,nr
      if(ir(ih).ne.1)goto 101
      io=ih
      d=(nage(1)-nage(2))*0.5
      zi=d
      d=-d
      do 10 x=1,na4
      iz=nage(x+1)-nage(x)
      if (x.eq.na) iz=nage(x)-nage(x-1)
      zz=0.5*float(iz)
      xx=x+1
      do 9 i=1,nr
    9 l(x,io,i)=zz*(cl(x,io,i)+cl(xx,io,i))
   10 continue
  101 continue
   18 continue
      if (nopen.eq.2) go to 120
c number of years lived in last age group
      do 2 i=1,nr
      do 2 j=1,nr
    2 cc(j,i)=rmla(j,i)
      call invert (nr,nr)
      do 3 i=1,nr
      do 3 j=1,nr
      al(j,i)=cc(j,i)
    3 b(j,i)=cl(na,i,j)
      call multip (nr,nr,nr)
      do 4 i=1,nr
      do 4 j=1,nr
    4 l(na,i,j)=c(j,i)
  120 continue
   50 continue
      print 9999
      print 4832
```

```
 4832 format(10x,39hnumber of years lived in each status by
     1,14h a unit cohort/10x53(1h*))
      iskip=3
      do 34 ih=1,nr
      if(ir(ih).ne.1)goto 34
      io=ih
      if (io.ne.iskip) go to 124
      print 9999
      iskip=iskip+2
  124 continue
      print 9502, reg(io)
      print 9100, (reg(j),j=1,nr)
      print 66
      do 58 x=1,na
      cllt=0.
      do 11 j=1,nr
   11 cllt=cllt+l(x,io,j)
      print 9103, nage(x),cllt,(l(x,io,j),j=1,nr)
   58 continue
   34 continue
c ---------------------------------------------------
c            - by status at age x
c ---------------------------------------------------
      print 9999
      print 80
   80 format (10x,39hnumber of years lived in each status by
     1,16h person of age x/10x,55(1h*))
      iskip=3
      do 85 ih=1,nr
      if(ir(ih).ne.1)goto 85
      i=ih
      if (i.ne.iskip) go to 82
      print 9999
      iskip=iskip+2
   82 continue
      print 83, reg(i)
   83 format (//1x,3hage,6x,15hstatus at age x,
     12x,a8/1x,3(1h*),6x,25(1h*)/)
      print 9100, (reg(j),j=1,nr)
      print 66
      do 81 x=1,na
      iz=nage(x+1)-nage(x)
      if (x.eq.na) iz=nage(x)-nage(x-1)
      zfny2=0.5*float(iz)
      cmt=0.
      do 84 j=1,nr
      if (i.eq.j) cme(x,j)=zfny2*(1.+p(x,j,i))
      if (i.ne.j) cme(x,j)=zfny2*p(x,j,i)
      if (x.eq.na) cme(x,j)=cc(j,i)
c      if (x.eq.na)d=float(na)+0.5*float(nage(na)-nage(na-1))
c      if ((x.eq.na).and.(r.ne.0.0))cme(x,j)=cc(j,i)*exp(-r*d)
      cmt=cmt+cme(x,j)
      lx(x,i,j)=cme(x,j)
   84 continue
      print 9103, nage(x),cmt,(lx(x,i,j),j=1,nr)
   81 continue
   85 continue
c -----------------------------------------------------
c  number of years lived beyond age x and life expectancy by
c     status at age x
c ----------------------------------------------------------
      print 9999
      print 4835
 4835 format (10x,40htotal number of years lived beyond age x/
     110x,40(1h*))
       iskip=3
      do 51 ih=1,nr
      if(ir(ih).ne.1)goto 51
      io=ih
        if (iskip.ne.io) go to 126
         print 9999
         iskip=iskip+2
  126  continue
      print 9502, reg(io)
      print 9100, (reg(j),j=1,nr)
      print 66
```

```
      do 14 x=1,na
      tt=0.
      do 17 i=1,nr
      t(i)=0.
      tr(i)=0.0
      do 12 xy=x,na
      tr(i)=tr(i)+l(xy,io,i)
   12 t(i)=t(i)+l(xy,io,i)
   17 tt=tt+tr(i)
      print 9103, nage(x),tt,(tr(j),j=1,nr)
      clt=0.
      do 333 j=1,nr
  333 clt=clt+cl(x,io,j)
      do 13 j=1,nr
      e(x,io,j)=0.
      if (clt.eq.0.) go to 13
      e(x,io,j)=t(j)/clt
   13 continue
   14 continue
   51 continue
c
c  print life expectancy
c
      print 9999
      print 4830, nage(1)
 4830 format (30x,37hexpectations of life by status at age ,
     1i3/30x,40(1h*))
  876 iskip=3

      do 651 ih=1,nr
      if(ir(ih).ne.1)goto 651
      io=ih
        if (iskip.ne.io) go to 127
        print 9999
       iskip=iskip+2
  127 continue
      if (iprex.eq.1) print 9502, reg(io)
      if (iprex.eq.25) print 83, reg(io)
      print 9100, (reg(j),j=1,nr)
      print 66
      do 65 x=1,na
      eex=0.0
      ee=0.
      do 15 j=1,nr
   15 ee=ee+e(x,io,j)
      print 9103, nage(x),ee,(e(x,io,j),j=1,nr)
   65 continue
  651 continue
      if (iprex.eq.25.and.r.ne.0.0)call res(na,nr,nradix,e,0)
      if (iprex.eq.25) go to 877
c -------------------------------------------------------
c life expectancy by status at age x
c --------------------------------------------------
      if (nradix.ne.nr) return
c
      print 9999
      if(r.ne.0.0)print 156, r
  156 format(20x,71hpresent value of a annuity of 1$ by status at age
     1x , interest rate :,f5.2/20x,76(1h*))
      if(r.eq.0.0)print 56
   56 format (30x,39hexpectations of life by status at age x/
     130x,39(1h*))
      iprex=25
      d=float(nage(na)-nage(na-1))
      do 130 i=1,nr
      do 130 j=1,nr
  130 e(na,i,j)=p(na,j,i)*exp(-r*d)*d*0.5
      do 769 j=1,nr
      e(na,j,j)=e(na,j,j)+d*0.5
  769 continue
      if(nopen.eq.2)goto 299
      do 288 i=1,nr
      do 288 j=1,nr
      e(na,i,j)=lx(na,i,j)
  288 continue
  299 continue
      d=0.0
```

```
      do 140 ix=1,na-1
      x=na-ix
      d=float(nage(x+1)-nage(x))
      do 393 i=1,nr
      do 393 j=1,nr
      a1(i,j)=e(x+1,j,i)
      b(i,j)=p(x,i,j)
  393 continue
      call multip (nr,nr,nr)
      do 394 i=1,nr
      do 394 j=1,nr
  394 e(x,i,j)=c(j,i)*exp(-r*d)+p(x,j,i)*exp(-r*d)*d*0.5
      do 538 j=1,nr
      e(x,j,j)=e(x,j,j)+d*0.5
  538 continue
  140 continue
      go to 876
 877  if(r.ne.0.0)call lins(na,zfny,nr,nradix,ihist,ilif,nopen,e)
      if(r.ne.0.0)call res(na,nr,nradix,e,1)
      return
      end
```

Subroutine LINS (NA, ZFNY, NR, NRADIX, IHIST, ILIF, NOPEN, E)

```
      subroutine lins (na,zfny,nr,nradix,ihist,ilif,nopen,e)
c
c     only called to calculate A(x) for r
c
      dimension e(106,8,8)
      common /clx/ lx(106,8,8)
      common /cnag/ nage(106)
      common /ccl/ cl(105,8,8)
      common /cinv/ cc(8,8)
      common /cl/ l(105,8,8)
      common /cmul/ al(8,8),b(8,8),c(8,8)
      common /cpq/ p(105,8,8)
      common /crate/ ratd(105,8),ratm(105,8,8)
      common /crad/ radix(8),radixt
      common /creg/ reg(13)
      common /crmla/ rmla(8,8)
      common /ctit/ tit(25)
      common /csu/ su(105,8,8)
      common /cs/ r,nys
      double precision reg
      real l,lx
      integer x
c  print life expectancy
      goto 1111
 876  iskip=3
      do 65 io=1,nradix
        if (iskip.ne.io) go to 127
        print 9999
       iskip=iskip+2
  127 continue
      print.83, reg(io)
      print 9100, (reg(j),j=1,nr)
      print 66
      do 65 x=1,na
      eex=0.0
      ee=0.
      do 15 j=1,nr
  15  ee=ee+e(x,io,j)
      print 9103, nage(x),ee,(e(x,io,j),j=1,nr)
  65  continue
      go to 877
c -------------------------------------------------------
c life expectancy by status at age x
c ------------------------------------------------
 1111 print 9999
      print 156, r
 156  format(20x,76hpresent value of a life insurance of 1$ by status at
     1 age x , interest rate :,f5.2,/20x,81(1h*))
      if(r.eq.0.0)print 56
  56  format (30x,31hpresent value by status at age x /
     130x,31(1h*))
      d=float(nage(na)-nage(na-1))
      do 130 i=1,nr
      do 130 j=1,nr
      if(i.eq.j)da=d*0.5
      if(i.ne.j)da=0.0
  130 e(na,i,j)=(p(na,j,i)*exp(-r*d)*d*0.5+da)*ratd(na,i)
c     i or j in ratd
      d=0.0
      do 140 ix=1,na-1
```

```
      x=na-ix
      d=float(nage(x+1)-nage(x))
      do 393 i=1,nr
      do 393 j=1,nr
      al(i,j)=e(x+1,j,i)
      b(i,j)=p(x,i,j)
  393 continue
      call multip (nr,nr,nr)
      do 394 i=1,nr
      do 394 j=1,nr
      if(i.eq.j)da=d*0.5
      if(i.ne.j)da=0.0
  394 e(x,i,j)=c(j,i)*exp(-r*d)+(p(x,j,i)*exp(-r*d)*d*0.5+da)
     1*ratd(x,i)
  140 continue
      go to 876
 877  continue
 9502 format (//1x,3hage,6x,24hinitial status of cohort,2x,a8/1x,
     13(1h*),6x,34(1h*)/)
  83  format (//1x,3hage,6x,15hstatus at age x,
     12x,a8/1x,3(1h*),6x,25(1h*)/)
 9100  format (10x,5htotal,10(1x,a8))
 9999 format (1h1//1x)
 9103 format (1x,i3,1x,f10.5,12f9.5)
   66 format (1x)
      return
      end
```

Subroutine PROBN (NA, NR, NOPEN, IPROB, NRADIX)

```
      subroutine probn (na,nr,nopen,iprob,nradix)
      dimension rm(8,8),p(105,8,8),rmla(8,8)
      common /cnag/ nage(106)
      common /cinv/ cc(8,8)
      common /cmul/ al(8,8),b(8,8),c(8,8)
      common /cnn/ cn(105,8,8)
      common /crate/ ratd(105,8),ratm(105,8,8)
      common /creg/ reg(13)
      common /ctit/ tit(25)
      common /cs/ r,nys
      double precision reg
      integer x
c ---------------------------------------
c   matrix of observed rates  m(x)
c ---------------------------------------
      d=0.0
      do 100 x=1,na
      iz=nage(x+1)-nage(x)
      if (x.eq.na) iz=nage(x)-nage(x-1)
      d=d+float(iz)
      zzz=0.5*float(iz)
      do 5 i=1,nr
      z=0.0
      do 4 j=1,nr
      if (i.eq.j) go to 4
      z=z+ratm(x,j,i)
    4 continue
      rm(i,i)=z
      do 6 j=1,nr
      if (j.eq.i) go to 6
      rm(j,i)=-ratm(x,j,i)
    6 continue
    5 continue
      if (x.ne.na) go to 13
      do 14 i=1,nr
      do 14 j=1,nr
   14 rmla(j,i)=rm(j,i)
      if (nopen.ne.2) go to 100
   13 continue
c ---------------------------------------------
c  probability matrices
c ---------------------------------------------
      do 7 i=1,nr
      do 7 j=1,nr
      if (i.eq.j) cc(j,i)=1.+zzz*rm(j,i)
    7 if (i.ne.j) cc(j,i)=zzz*rm(j,i)
      call invert (nr,nr)
      do 8 i=1,nr
      do 8 j=1,nr
      al(j,i)=cc(j,i)
      if (j.eq.i) b(j,i)=1.-zzz*rm(j,i)
    8 if (j.ne.i) b(j,i)=-zzz*rm(j,i)
      call multip (nr,nr,nr)
      do 9 i=1,nr
      do 9 j=1,nr
    9 p(x,j,i)=c(j,i)
  100 continue
      if (nopen.eq.2) go to 140
      do 10 i=1,nr
      do 10 j=1,nr
```

```
 10  p(na,j,i)=0.
140  continue
     do 51 i=1,nradix
     cn(1,i,i)=1.
     do 51 j=1,nr
     if (i.ne.j) cn(1,i,j)=0.
  51 continue
     naa=na-1
     do 141 x=1,naa
     xx=x+1
     z=float(nage(xx)-nage(x))
     do 151 i=1,nr
     do 151 j=1,nr
     a1(j,i)=p(x,j,i)
 151 b(j,i)=cn(x,i,j)
     call multip (nr,nr,nr)
     do 161 i=1,nr
     do 161 j=1,nr
 161 cn(xx,i,j)=c(j,i)
 141 continue
     return
     end
```

Subroutine PROBSC (NA, NR, NOPEN, IPROB, NRADIX)

```
      subroutine probsc (na,nr,nopen,iprob,nradix)
      dimension rm(8,8)
      common /cnag/ nage(106)
      common /cinv/ cc(8,8)
      common /cmul/ al(8,8),b(8,8),c(8,8)
      common /cpq/ p(105,8,8)
      common /crate/ ratd(105,8),ratm(105,8,8)
      common /creg/ reg(13)
      common /crmla/ rmla(8,8)
      common /ctit/ tit(25)
      common /cs/ r,nys
      double precision reg
      integer x
c -------------------------------------
c   matrix of observed rates  m(x)
c -------------------------------------
      d=0.0
      do 100 x=1,na
      iz=nage(x+1)-nage(x)
      if (x.eq.na) iz=nage(x)-nage(x-1)
      d=d+float(iz)
      zzz=0.5*float(iz)
      do 5 i=1,nr
      z=ratd(x,i)
      do 4 j=1,nr
      if (i.eq.j) go to 4
      z=z+ratm(x,j,i)
    4 continue
      rm(i,i)=z
      do 6 j=1,nr
      if (j.eq.i) go to 6
      rm(j,i)=-ratm(x,j,i)
    6 continue
    5 continue
      if (x.ne.na) go to 13
      do 14 i=1,nr
      do 14 j=1,nr
   14 rmla(j,i)=rm(j,i)
      if (nopen.ne.2) go to 100
   13 continue
c --------------------------------------------
c  probability matrices
c --------------------------------------------
      do 7 i=1,nr
      do 7 j=1,nr
      if (i.eq.j) cc(j,i)=1.+zzz*rm(j,i)
    7 if (i.ne.j) cc(j,i)=zzz*rm(j,i)
      call invert (nr,nr)
      do 8 i=1,nr
      do 8 j=1,nr
      al(j,i)=cc(j,i)
      if (j.eq.i) b(j,i)=1.-zzz*rm(j,i)
    8 if (j.ne.i) b(j,i)=-zzz*rm(j,i)
      call multip (nr,nr,nr)
      do 9 i=1,nr
      do 9 j=1,nr
      if((i.eq.j).and.(c(j,i).eq.1.0))c(j,i)=0.0
    9 p(x,j,i)=c(j,i)
  100 continue
      if (nopen.eq.2) go to 140
      do 10 i=1,nr
      do 10 j=1,nr
   10 p(na,j,i)=0.
  140 continue
```

```
e ---------------------------------------------
c print probabilities
c ---------------------------------------------
 9999  format (1h1,1x)
      print 9999
      print 1, (tit(j),j=1,25)
   1  format (50x,25a4//)
      print 4500
 4500 format (20x,24htransition probabilities/20x,24(1h*)/)
       iskip=3
      if (na.gt.18) iskip=2
      do 726 i=1,nr
      if (iskip.ne.i) go to 121
      print 9999
       if (na.le.18) iskip=iskip+2
       if (na.gt.18) iskip=iskip+1
 121  continue
      print 9001, reg(i)
 9001 format (//20x,6hstatus,2x,a8,1x/20x,16(1h*)/)
      print 9011, reg(i)
 9011 format (5x,3hage,5x,5hdeath,5x,15htransition from,1x,a8,1x,2hto)
      print 9020, (reg(j),j=1,nr)
 9020 format (18x,12(1x,a8))
      print 66
  66  format (1x)
      do 726 x=1,na
      zz=0.
      do 11 j=1,nr
      zz=zz+p(x,j,i)
  11  continue
      zq=1.-zz
      if(zq.eq.1.0)zq=0.0
      if(x.eq.na)zq=1.0
      print 9103, nage(x),zq,(p(x,j,i),j=1,nr)
 9103 format (5x,i3,1x,13f9.6)
  726 continue
       return
      end
```

Subroutine RES (NA, NR, NRADIX, E, IC)

```
      subroutine res (na,nr,nradix,e,ic)
      dimension e(106,8,8),ex(8)
      common /cinv/ cc(8,8)
      common /cnag/ nage(106)
      common /cnn/ cn(105,8,8)
      common /creg/ reg(13)
      common /cs/ r,nys
      double precision reg
      integer x
      print 9999
      if(ic.eq.0)print 156, nage(1),r
      if(ic.eq.1)print 158, nage(1),r
      do 65 io=1,nradix
      print 83, nage(1),reg(io)
      print 9100, (reg(j),j=1,nr)
      print 66
      do 65 x=1,na
      do 5 l=1,nr
    5 ex(l)=0.0
      ee=0.
      do 15 j=1,nr
      do 6 l=1,nr
    6 ex(j)=ex(j)+e(x,l,j)*cn(x,io,l)
   15 ee=ee+ex(j)
      print 9103, nage(x),ee,(ex(j),j=1,nr)
   65 continue
  156 format(20x,53hreserve needed for a annuity of 1$ by status at age
     1 ,i2,17h, interest rate :,f5.2/20x,77(1h*))
  158 format(20x,57hreserve needed for life insurance of 1$ by status at
     1 age ,i2,17h, interest rate :,f5.2/20x,81(1h*))
 9999 format (1h1//1x)
   66 format (1x)
 9103 format (1x,i3,1x,f10.5,12f9.5)
 9100 format (10x,5htotal,10(1x,a8))
   83 format (//1x,3hage,6x,14hstatus at age ,i2,
     12x,a8/1x,3(1h*),6x,26(1h*)/)
      return
      end
```

Subroutine TAB (NA, NR, NRADIX)

```
      subroutine tab (na,nr,nradix)
c
c this program prints the summary tables
c
      dimension hu(105),hup(4,4),hul(4)
      dimension zex(4),hut(4)
      common /cnag/ nage(106)
      common /ccl/ cl(105,8,8)
      common /cl/ l(105,8,8)
      common /cpq/ p(105,8,8)
      common /crate/ ratd(105,8),ratm(105,8,8)
      common /crad/ radix(8),radixt
      common /creg/ reg(13)
      common /ctit/ tit(25)
      double precision reg
      real l
       integer x
      write (7,4) (tit(j),j=1,25)
    4 format (1h1,50x,25a4)
      write (7,12)
   12 format (1h0,16x,18hage-specific rates,14x,
     124htransition probabilities/11x,30(1h-),2x,40(1h-))
      write (7,64)
   64 format (1x)
      write (7,13)
   13 format (5x,3hage,3x,9hmortality,4x,6h1 to 2,4x,6h2 to 1,
     16x,6h1 to 1,4x,6h1 to 2,4x,6h2 to 1,4x,6h2 to 2/)
      do 15 x=1,na
   15 write (7,14) nage(x),ratd(x,1),ratm(x,2,1),ratm(x,1,2)
     1,((p(x,i,j),i=1,nr),j=1,nr)
   14 format (5x,i3,2x,3f10.6,2x,4f10.6)
      if (nradix.eq.1) write (7,33)
   33 format (1h1,30x,38hpopulation-based life-table statistics/
     131x,38(1h*))
      if (nradix.eq.nr) write (7,34) nage(1)
   34 format (1h1,30x,34hstatus-based life table statistics,
     118h (by status at age,i3,1x,1h) /31x,57(1h*))
c
       do 500 io=1,nradix
c
      if (io.ne.1) write (7,66)
   66 format (1h1,1x)
      write (7,17)
   17 format (1h0,10x,30hlife history of initial cohort )
      if (nradix.eq.1) write (7,37)
   37 format (11x,30(1h-))
      if (nradix.eq.nr) write (7,38)reg(io)
   38 format (11x,10(1h-),1x,a8,1x,10(1h-))
      write (7,64)
      write (7,16)
   16 format (16x,6hdeaths,22x,11htransitions,20x,
     131hnumber of people at exact age x/10x,
     120(1h-),2x,40(1h-),2x,32(1h-)/)
       write (7,18) (reg(j),j=1,nr),(reg(j),j=1,nr)
   18 format (5x,3hage,4x,a8,2x,a8,6x,6h1 to 1,4x,6h2 to 1,
     14x,6h1 to 2,4x,6h2 to 2,4x,a8,2x,a8,7x,5htotal/)
      do 19 x=1,na
      hu(x)=0.
      pmig=0.
      do 3 j=1,2
```

```
      hu(x)=hu(x)+cl(x,io,j)*radix(io)
    3 pmig=pmig+p(x,j,1)
      do 20 i=1,2
      hul(i)=cl(x,io,i)*(1.-pmig)*radix(io)
      hut(i)=cl(x,io,i)*radix(io)
      do 20 j=1,2
   20 hup(j,i)=cl(x,io,i)*p(x,j,i)*radix(io)
      hutt=hu(x)
   19 write (7,21) nage(x),(hul(j),j=1,2),((hup(j,i),i=1,2),
     1j=1,2),(hut(j),j=1,2),hutt
   21 format (5x,i3,2x,2f10.0,2x,4f10.0,2x,2f10.0,
     12x,f10.0)
      write (7,23)
   23 format (1h1,10x,30hexpected number of years lived,
     128h by member of initial cohort/11x,58(1h-)/)
      write (7,24)
   24 format (11x,28hwithin age interval x to x+1,6x,
     124hlife expectancy at age x/)
      write (7,25) (reg(j),j=1,nr),(reg(j),j=1,nr)
   25 format (5x,3hage,2(4x,a8,2x,a8,5x,5htotal)/)
      do 27 x=1,na
      cllt=0.
      zext=0.
      hu(x)=hu(x)/radix(io)
      do 30 j=1,nr
      zex(j)=0.
      if (hu(x).eq.0.) go to 30
      tt=0.
      do 32 ix=x,na
   32 tt=tt+l(ix,io,j)
      zex(j)=tt/hu(x)
      zext=zext+zex(j)
      cllt=cllt+l(x,io,j)
   30 continue
   27 write (7,26) nage(x),(l(x,io,j),j=1,2),cllt,
     1(zex(j),j=1,2),zext
   26 format (5x,i3,2(2x,3f10.6))
  550 continue
  500 continue
      return
      end
```

3. PROJECTION SUBROUTINES

Subroutine DATAS (NPR, NA, NY, ZFNY, NR, XZB, XZD, XZO, IPROB, LNEIG)

```
      subroutine datas (npr,na,ny,zfny,nr,xzb,xzd,xzo,iprob,
     1neig)
      dimension zhu(105)
      common /cis/ is
      common /cx/ df(12,12),dm(12,12),nbs,nsx,lh(12)
      common /cpar/ init,nhoriz,intv,itolx,ntoll
      common /cl/ pop(105,12)
      common /cnag/ nage(105)
      common /crad/ radix(12),radixt
      common /crate/ ratd(105,12),ratm(105,12,12),ratf(105,12)
      common /creg/ reg(13)
      common /ctit/ tit(25)
      double precision reg
      integer x
      data end/3hend/
      goto 2222
  301 read (5,302) (tit(j),j=1,25)
  302 format (25a4)
      print 303, (tit(j),j=1,25)
  303 format (1x,25a4)
      if (tit(1).eq.end) go to 305
      go to 301
  305 continue
      rewind 5
 2222 continue
c ---------------------------------------------------------------
c read parameter card
c ---------------------------------------------------------------
      read (5,222) (tit(j),j=1,20)
  222 format (20a4)
      read (5,2) na,nr,ny,nu,nzb,nzd,nzo,iprob,init,nhoriz,
     1intv,itolx,ntoll,neig,ndat,nbs,nsx,ib,is
    2 format (i3,7i2,3i4,8i2)
      if(nsx.eq.1)goto 92
      read(5,81)(lh(i),i=1,nbs)
      do 91 i=1,nbs
      k=lh(i)
      read(5,82)(df(k,j),j=1,nr)
   91 continue
   81 format(12i2)
   82 format(12f8.5)
      if(nsx.eq.3) goto 93
      do 94 i=1,nr
      do 94 j=1,nr
      dm(i,j)=0.0
      if(df(i,j).eq.0.0)goto 96
      df(i,j)=1.0/(1.0+df(i,j))
      dm(i,j)=1.0-df(i,j)
   96 continue
   94 continue
      goto 92
   93 continue
      do 99 i=1,nr
      do 99 j=1,nr
      if(df(i,j).ne.0.0)df(i,j)=1.0
   99 continue
      goto 97
   92 continue
      do 98 i=1,nr
      if(nsx.eq.2)write(4,898)(dm(i,j),j=1,nr)
      if(nsx.eq.1)read(4,898)(df(i,j),j=1,nr)
   98 continue
  898 format(12f10.6)
   97 continue
```

```
c ------------------------------------------------------------
c define default values for parameters
c ------------------------------------------------------------
      do 6 x=1,na
    6 nage(x)=(x-1)*ny
       if (nzb.eq.0) nzb=1
       if (nzd.eq.0) nzd=1
       if (nzo.eq.0) nzo=1
      if (itolx.ne.2) itolx=2
      if (ntoll.eq.0) ntoll=7
      if (intv.eq.0) intv=200
      xzb=float(nzb)
      xzd=float(nzd)
      xzo=float(nzo)
      zfny=float(ny)
      do 45 i=1,nr
   45 if (radix(i).eq.0.) radix(i)=100000.
      do 4 i=1,nu
    4 read (5,114)
  114 format (1x)
      nr1=nr+1
      read (5,14) (reg(j),j=1,nr1)
   14 format (9a8)
c read radices  radix(j)
      read (5,13) (radix(j),j=1,nr)
   13 format (9f8.0)
      radixt=0.
      do 66 i=1,nr
   66 radixt=radixt+radix(i)
      if(ndat.eq.2)goto 70
c read population, births, deaths, migrants
      do 10 i=1,nr
      read (5,3) (pop(x,i),x=1,na)
    3 format (10f10.0)
      if((nsx.eq.1).and.(ib.eq.0))goto 69
      read (5,31) (zhu(x),x=1,na)
   31 format (10f10.0)
      do 44 x=1,na
   44 ratf(x,i)=zhu(x)/pop(x,i)
   69 continue
      read (5,31) (zhu(x),x=1,na)
      do 48 x=1,na
   48 ratd(x,i)=zhu(x)/pop(x,i)
      do 32 j=1,nr
      read (5,31) (zhu(x),x=1,na)
      do 46  x=1,na
   46 ratm(x,j,i)=zhu(x)/pop(x,i)
   32 continue
   33 continue
   10 continue
      go to 71
   70 continue
c read population birth death and transition rates
      do 72 i=1,nr
      read(5,3)(pop(x,i),x=1,na)
      if((nsx.eq.1).and.(ib.eq.0))goto 73
      read(5,85)(ratf(x,i),x=1,na)
   73 continue
   85 format(10f10.6)
      read(5,85)(ratd(x,i),x=1,na)
      do 72 j=1,nr
      read(5,85)(ratm(x,j,i),x=1,na)
   72 continue
   71 continue
      return
      end
```

Subroutine GROWTH (NA, ZFNY, NR, ILIF)

```
      subroutine growth (na,zfny,nr,ilif)
      dimension bs(12,12)
      common /cis/ is
      common /cbs/ bs(105,12,12),hm(12,12)
      common /cx/ df(12,12),dm(12,12),nbs,nsx,lh(12)
      common /cnag/ nage(105)
      common /cgrow/ br(105,12,12),popr(105,12)
      common /cinv/ cc(12,12)
      common /cmul/ al(12,12),b(12,12),c(12,12)
      common /cpq/ p(105,12,12)
      common /crate/ ratd(105,12),ratm(105,12,12),ratf(105,12)
      common /creg/ reg(13)
      common /crmla/ rmla(12,12)
      common /ctit/ tit(25)
      common /csu/ su(105,12,12)
      double precision reg
      integer x,xx
      naa=na-1
      zz=zfny*0.25
      zfny2=zfny*0.5
c --------------------------------------------------------
c compute survivorship proportions if ilif=0
c --------------------------------------------------------
      if (ilif.ne.0) go to 50
      do 30 x=1,naa
      xx=x+1
      do 21 i=1,nr
      cc(i,i)=1.+p(x,i,i)
      do 21 j=1,nr
      if (i.ne.j) cc(j,i)=p(x,j,i)
 21   continue
      call invert (nr)
      do 22 i=1,nr
      do 22 j=1,nr
      al(j,i)=p(x,j,i)
 22   b(j,i)=cc(j,i)
      call multip (nr,nr,nr)
      if (x.eq.naa) go to 44
      do 23 i=1,nr
      al(i,i)=1.+p(xx,i,i)
      do 23 j=1,nr
      if (i.ne.j) al(j,i)=p(xx,j,i)
 23   b(j,i)=c(j,i)
      call multip (nr,nr,nr)
      go to 25
 44   do 26 i=1,nr
      do 26 j=1,nr
 26   cc(j,i)=rmla(j,i)
      call invert (nr)
      do 27 i=1,nr
      do 27 j=1,nr
      al(j,i)=cc(j,i)/zfny2
 27   b(j,i)=c(j,i)
      call multip (nr,nr,nr)
 25   do 28 i=1,nr
      do 28 j=1,nr
 28   su(x,i,j)=c(j,i)
      do 68 i=1,nr
      do 68 j=1,nr
      if(su(x,i,j).lt.0.0)su(x,i,j)=0.0
 68   continue
 30   continue
 50   continue
```

```
c -----------------------------------------------------------
c compute first row of generalized leslie matrix
c -----------------------------------------------------------
      do 4 x=1,naa
      xx=x+1
      do 3 i=1,nr
      do 3 j=1,nr
      if(i.eq.j) al(j,i)=ratf(xx,i)
      if(i.ne.j) al(j,i)=0.
    3 b(j,i)=su(x,i,j)
      call multip (nr,nr,nr)
      do 5 i=1,nr
      do 5 j=1,nr
      if (i.eq.j) bs(x,j,i)=ratf(x,i)+c(j,i)
    5 if (i.ne.j) bs(x,j,i)=c(j,i)
      do 7 i=1,nr
      do 55 k=1,nr
      if(df(k,i).gt.0.0)k1=k
   55 continue
      do 7 j=1,nr
      if (i.eq.j) b(j,i)=zz*(p(1,j,k1)+1.)
      if (i.ne.j) b(j,i)=zz*p(1,j,k1)
    7 continue
      do 71 k1=1,nr
      do 71 k2=1,nr
   71 al(k1,k2)=df(k1,k2)
      call multip (nr,nr,nr)
      do 73 k1=1,nr
      do 73 k2=1,nr
      al(k1,k2)=c(k1,k2)
      if(nsx.eq.1)hm(k1,k2)=c(k1,k2)
   73 b(k1,k2)=bs(x,k1,k2)
      if(nsx.eq.1)goto 111
      call multip (nr,nr,nr)
      do 8 i=1,nr
      do 8 j=1,nr
    8 br(x,j,i)=c(j,i)
    4 continue
  111 continue
      if(is.eq.1)goto 1111
c -------------------------------------------------------------
c  print growth matrix (first row and subdiagonal elements)
c -------------------------------------------------------------
      print 1, (tit(j),j=1,25)
    1 format (1h1,50x,25a4)
      print 10
   10 format (1h0,5x,48hthe discrete model of multiregional demographic
     1,6hgrowth/6x,54(1h*)/6x,54(1h*)/)
      print 11
   11 format (/5x,31hmultiregional projection matrix/5x,31(1h*))
      do 20 i=1,nr
       if (i.ne.1) print 120
  120 format (1h1,1x)
      print 12, reg(i)
   12 format (//20x,6hregion,2x,a8/20x,16(1h*))
      print 13
   13 format (/5x,3hage,8x,9hfirst row)
      print 14, (reg(j),j=1,nr)
   14 format (11x,12(2x,a8))
      print 15
   15 format (1x)
      do 16 x=1,naa
   16 print 17, nage(x),(br(x,j,i),j=1,nr)
   17 format (5x,i3,3x,12f10.6)
      print 18
   18 format (/5x,3hage,8x,24hsurvivorship proportions)
      print 14, (reg(j),j=1,nr)
      print 15
      do 19 x=1,naa
   19 print 17, nage(x),(su(x,i,j),j=1,nr)
   20 continue
 1111 continue
      return
      end
```

Subroutine PROBSC (NA, ZFNY, NR, IPROB)

```
      subroutine probsc (na,zfny,nr,iprob)
      dimension rm(12,12)
      common /cis/ is
      common /cnag/ nage(105)
      common /cinv/ cc(12,12)
      common /cmul/ al(12,12),b(12,12),c(12,12)
      common /cpq/ p(105,12,12)
      common /crate/ ratd(105,12),ratm(105,12,12),ratf(105,12)
      common /creg/ reg(13)
      common /crmla/ rmla(12,12)
      common /ctit/ tit(25)
      double precision reg
      integer x
c ----------------------------------------
c    matrix of observed rates   m(x)
c ----------------------------------------
      naa=na-1
      zzz=zfny*0.5
      do 100 x=1,na
      do 5 i=1,nr
      z=ratd(x,i)
      do 4 j=1,nr
      if (i.eq.j) go to 4
      z=z+ratm(x,j,i)
    4 continue
      rm(i,i)=z
      do 6 j=1,nr
      if (j.eq.i) go to 6
      rm(j,i)=-ratm(x,j,i)
    6 continue
    5 continue
      if (x.ne.na) go to 13
      do 14 i=1,nr
      do 14 j=1,nr
   14 rmla(j,i)=rm(j,i)
      go to 100
   13 continue
c ----------------------------------------------------
c  probability matrices
c ----------------------------------------------------
      do 7 i=1,nr
      do 7 j=1,nr
      if (i.eq.j) cc(j,i)=1.+zzz*rm(j,i)
    7 if (i.ne.j) cc(j,i)=zzz*rm(j,i)
      call invert (nr)
      do 8 i=1,nr
      do 8 j=1,nr
       al(j,i)=cc(j,i)
      if (j.eq.i) b(j,i)=1.-zzz*rm(j,i)
    8 if (j.ne.i) b(j,i)=-zzz*rm(j,i)
      call multip (nr,nr,nr)
      do 9 i=1,nr
      do 9 j=1,nr
      if((i.eq.j).and.(c(j,i).eq.1.0))c(j,i)=0.0
    9 p(x,j,i)=c(j,i)
  100 continue
      do 10 i=1,nr
      do 10 j=1,nr
   10 p(na,j,i)=0.
      if(is.eq.1)goto 1111
```

```
c ---------------------------------------------
c print probabilities
c ---------------------------------------------
 9999  format (1h1,1x)
      print 9999
      print 1, (tit(j),j=1,25)
    1 format (50x,25a4//)
      print 4500, iprob
 4500 format (20x,36hprobabilities of dying and migrating/
     120x,13(1h*),7h option,i2,1x,13(1h*)/33x,10(1h*))
       iskip=3
      do 726 i=1,nr
      if (iskip.ne.i) go to 121
      print 9999
       iskip=iskip+2
 121  continue
      print 9001, reg(i)
 9001 format (//20x,6hregion,2x,a8,1x/20x,16(1h*)/)
      print 9011, reg(i)
 9011 format (5x,3hage,5x,5hdeath,5x,14hmigration from,1x,a8,1x,2hto)
      print 9020, (reg(j),j=1,nr)
 9020 format (18x,12(1x,a8))
      print 66
  66  format (1x)
      do 726 x=1,na
      zz=0.
      do 11 j=1,nr
      zz=zz+p(x,j,i)
   11 continue
      zq=1.-zz
      if(zq.eq.1.0)zq=0.0
      if(x.eq.na)zq=1.0
      print 9103, nage(x),zq,(p(x,j,i),j=1,nr)
 9103 format (5x,i3,1x,13f9.6)
  726 continue
 1111 continue
      return
      end
```

Subroutine PROJEC (NA, NY, ZFNY, NR, ZLAMDA, IPROJ)

```
      subroutine projec (na,ny,zfny,nr,zlamda,iproj)
      dimension zmin1(12),hup(12),zlamb(12),agem(12)
      dimension perc(12),hu(12)
      dimension poptot(12)
      common /cih/ ihm,ihf,hp(12),rlam
      common /cbs/ bs(105,12,12),hm(12,12)
      common /cx/ df(12,12),dm(12,12),nbs,nsx,lh(12)
      common /cpar/ init,nhoriz,intv,itolx,ntol1
      common /cnag/ nage(105)
      common /cgrow/ br(105,12,12),popr(105,12)
      common /cmul/ al(12,12),b(12,12),c(12,12)
      common /crate/ ratd(105,12),ratm(105,12,12),ratf(105,12)
      common /creg/ reg(13)
      common /ctit/ tit(25)
      common /csu/ su(105,12,12)
      common /ctotra/ pct(105),ratdt(105),ratft(105),ratmt(105)
      double precision reg
      integer x,x1,x2
      data zdat1/5hm.age/,zdat2/5hsha  /,zdat3/5hlam  /,zdat4/5h   r  /
      ihf=0
      iproj=1
      jgo=0
      iproj=0
      zl1=(-1)*ntol1
      tolx=10.**(zl1)
      naa=na-1
       zlam1=10.
      nyear1=init
      nyeapr=init+intv
      print 1876, (tit(j),j=1,25)
 1876 format (1h1,50x,25a4)
      print 1
    1 format (1h0,5x,35hmultiregional population projection/6x,
     135(1h*)/)
      if(nsx.eq.1)read(3,887)ihm,rlam
  887 format(i5,f10.6)
      go to 509
c -----------------------------------------------------------
c project population ny years
c ------------------------------------------------------------
 500  continue
c iproj = iteration number
c nyear1=projection year (=init + iproj*ny )
c zmin1(i) = population of region i at time t-1
c zmint    = population of total system at time t-1
      iproj=iproj+1
      nyear1=nyear1+ny
      do 3 i=1,nr
    3 zmin1(i)=poptot(i)
      zmint=ptota
      if((nsx.eq.1).and.(ihf.lt.ihm))read(4,889)(hp(j),j=1,nr)
      if(nsx.gt.1)goto 999
      if(ihf.lt.ihm)goto 999
      do 998 j=1,nr
      hp(j)=hp(j)*rlam
  998 continue
  999 continue
      iz=0
   92 continue
      do 689 i=1,nr
```

```
  689 hup(i)=0.0
      iz=iz+1
c first age group
      do 2 x=1,na
      do 4 j=1,nr
      b(j,1)=popr(x,j)
      if(nsx.eq.1)b(j,1)=hp(j)
      do 4 i=1,nr
      al(j,i)=br(x,j,i)
      if(nsx.eq.1)al(j,i)=hm(j,i)
      if((nsx.eq.2).and.(iz.eq.1))al(j,i)=bs(x,j,i)
    4 continue
      call multip (nr,nr,1)
      do 5 j=1,nr
    5 hup(j)=hup(j)+c(j,1)
      if(nsx.eq.1)goto 93
    2 continue
   93 continue
      if(iz.eq.1)ihf=ihf+1
      if((nsx.eq.2).and.(iz.eq.1))write(4,889)(hup(j),j=1,nr)
      if((nsx.eq.2).and.(iz.eq.1))goto 92
  889 format(12f10.1)
c other age groups
      do 6 x=1,naa
      x1=na-x
      x2=x1+1
      do 7 j=1,nr
      b(j,1)=popr(x1,j)
      do 7 i=1,nr
    7 al(j,i)=su(x1,i,j)
      call multip (nr,nr,1)
      do 8 j=1,nr
    8 popr(x2,j)=c(j,1)
    6 continue
      do 9 j=1,nr
    9 popr(1,j)=hup(j)
  509 continue
c  compute total popul ation
      do 11 x=1,na
      pct(x)=0.
      do 11 j=1,nr
   11 pct(x)=pct(x)+popr(x,j)
      do 13 j=1,nr
      poptot(j)=0.
      do 13 x=1,na
   13 poptot(j)=poptot(j)+popr(x,j)
      ptota=0.
      do 17 j=1,nr
   17 ptota=ptota+poptot(j)
c ------------------------------------------------------------
c check whether output must be printed
c -------------------------------------------------------------
      if ((nyearl.gt.nhoriz).and.(nyearl.ne.nyeapr)) go to 501
c -------------------------------------------------------------
c print projected population
c ---------------------------------------------------------------
      if (iproj.gt.0) print 51
   51 format (1h1,1x)
      print 52, nyearl
   52 format (5x,4hyear,1x,i5/5x,10(1h-)/)
```

```
        print 253
  253  format (10x,10hpopulation/10x,5(2h- )/)
  578  if (nr.le.10) print 53, (reg(j),j=1,nr)
   53  format (1x,3hage,2x,6x,5htotal,10(3x,a8))
       if (nr.gt.10) print 80, (reg(j),j=1,nr)
   80  format (1x,3hage,2x,6x,5htotal,12(1x,a8))
       print 54
   54  format (1x)
       do 55 x=1,na
       if (nr.le.10) print 56, nage(x),pct(x),(popr(x,j),j=1,nr)
   56  format (1x,i3,2x,11f11.0)
   55  if (nr.gt.10) print 81, nage(x),pct(x),(popr(x,j),j=1,nr)
   81  format (1x,i3,2x,f11.0,12f9.0)
        print 54
       if (nr.le.10) print 57, ptota,(poptot(j),j=1,nr)
   57  format (1x,5htotal,11f11.0)
       if (nr.gt.10) print 82, ptota,(poptot(j),j=1,nr)
   82  format (1x,5htotal,f11.0,12f9.0)
c  percentage distribution
       print 58
   58  format (//10x,23hpercentage distribution/10x,12(2h- )/)
       if (nr.le.10) print 53, (reg(j),j=1,nr)
       if (nr.gt.10) print 80, (reg(j),j=1,nr)
       print 54
       zhu=0.
       do 23 j=1,nr
   23  hu(j)=0.
       do 59 x=1,na
       prct=100.*pct(x)/ptota
       zhu=zhu+prct
       do 14 j=1,nr
       perc(j)=100.*popr(x,j)/poptot(j)
   14  hu(j)=hu(j)+perc(j)
       if (nr.le.10) print 60, nage(x),prct,(perc(j),j=1,nr)
   60  format (1x,i3,2x,11f11.4)
   59  if (nr.gt.10) print 84, nage(x),prct,(perc(j),j=1,nr)
   84  format (1x,i3,2x,f11.2,12f9.2)
       if (nr.le.10) print 761, zhu, (hu(j),j=1,nr)
  761  format (/1x,5htotal,11f11.4)
       if (nr.gt.10) print 85, zhu,(hu(j),j=1,nr)
   85  format (/1x,5htotal,f11.2,12f9.2)
c  mean age
       agemt=0.
        do 21 j=1,nr
   21  agem(j)=0.
       do 20 x=1,na
       n9=nage(x)
       a9=float(n9)+zfny*0.5
       agemt=agemt+a9*pct(x)/ptota
       do 20 j=1,nr
   20  agem(j)=agem(j)+a9*popr(x,j)/poptot(j)
       if (nr.le.10) print 22, zdatl,agemt,(agem(j),j=1,nr)
   22  format (1x,a5,11f11.4)
       if (nr.gt.10) print 86, zdatl,agemt,(agem(j),j=1,nr)
   86  format (1x,a5,f11.4,12f9.4)
c  regional share
       z=0.
       do 16 j=1,nr
       hup(j)=(poptot(j)/ptota)*100.
   16  z=z+hup(j)
```

```
      if (nr.le.10) print 22, zdat2,z,(hup(j),j=1,nr)
      if (nr.gt.10) print 86, zdat2,z,(hup(j),j=1,nr)
 501  continue
c growth ratio  (lam)
      if (iproj.eq.0) go to 500
      if (jgo.ge.1) go to 505
      do 62 j=1,nr
  62  zlamb(j)=poptot(j)/zmin1(j)
       zz=ptota/zmint
      if ((nyear1.gt.nhoriz).and.(nyear1.ne.nyeapr)) go to 502
      if (nyear1.gt.nhoriz) nyeapr=nyeapr+intv
 505  continue
      if (nr.le.10) print 64, zdat3,zz,(zlamb(j),j=1,nr)
  64  format (1x,a5,11f11.6)
      if (nr.gt.10) print 88, zdat3,zz,(zlamb(j),j=1,nr)
  88  format (1x,a5,f11.6,12f9.6)
c annual growth rate
      rstab=alog(zz)/zfny
      do 27 j=1,nr
  27  hup(j)=alog(zlamb(j))/zfny
      if (nr.le.10) print 64, zdat4,rstab,(hup(j),j=1,nr)
      if (nr.gt.10) print 88, zdat4,rstab,(hup(j),j=1,nr)
 502  continue
      if((nsx.eq.1).and.(ihf.lt.ihm))goto 500
      if (jgo.ge.1) go to 504
c ---------------------------------------------------------------
c compare growth ratio with tolerance level
c ---------------------------------------------------------------
      if (itolx.eq.3) ztolx=zlamb(1)-zlam1
      if (itolx.eq.3) zlam1=zlamb(1)
      if (itolx.eq.2) ztolx=zlamb(nr)-zlamb(1)
      ttolx=-tolx
      if ((ztolx.gt.tolx).or.(ztolx.lt.ttolx)) go to 500
      jgo=jgo+1
c zlamda = stable growth ratio
      zlamda=zz
      print 18, tolx
  18  format (1h0,1x,30htolerance level for eigenvalue,e14.4)
      print 65, iproj
  65  format (2x,39hnumber of iterations to reach stability,i7)
c --------------------------------------------------------------
c  stable equivalent
c --------------------------------------------------------------
      zs=zlamda**iproj
      do 66 j=1,nr
      poptot(j)=poptot(j)/zs
      do 66 x=1,na
  66  popr(x,j)=popr(x,j)/zs
      do 68 x=1,na
  68  pct(x)=pct(x)/zs
      ptota=ptota/zs
      print 69
  69  format (1h1,1x,40hstable equivalent to original population/2x,
     140(1h*)/)
      go to 578
 504  continue
      if(nsx.eq.2)write(3,887)ihf,zz
      return
      end
```

4. MAIN PROGRAMS

Program MAININCR

```
      call datinc (na,nopen,ny,zfny,nr,nradx,ndat)
      na5=na
      if (nopen.eq.2) na5=na+1
c
      call probn (na,nr,nopen,3,nradx)
      call probsc (na,nr,nopen,3,nradx)
      ilif=0
      ihist=0
c     call hist (na5,nr,nradx,ihist)
      call life (na,zfny,nr,nradx,ihist,ilif,nopen)
      if (nr.eq.2) call tab (na,nr,nradx)
      stop
      end
```

Program MAINPROJ

```
      common /c1/ pop(105,12)
      common /cnag/ nage(105)
      common /cgrow/ br(105,12,12),popr(105,12)
      common /crate/ ratd(105,12),ratm(105,12,12),ratf(105,12)
      integer x
      npr=1
      ihist=0
      ilif=0
      iproj=0
      call datas (npr,na,ny,zfny,nr,xzb,xzd,xzo,iprob,
     1neig)
      call probsc (na,zfny,nr,iprob)
      call growth (na,zfny,nr,ilif)
      do 10 i=1,nr
      do 10 x=1,na
   10 popr(x,i)=pop(x,i)
      call projec (na,ny,zfny,nr,zlamdk,iproj)
      print 33
   33 format (1x//)
      stop
      end
```

APPENDIX B: EXAMPLE OF PARAMETER CARDS

The five sets of parameter cards presented here consider a data set with the following specifications:

a. 2 regions, 4 marital states. The input for each of these 8 states are population data, birth, death, and transition rates. These data are available for male, female, and total populations.

b. Data are given in one year age groups, age 0 to 100+.

c. State 1 (region 1 - never married) receives birth born to mothers in states 1 to 4. These states are:

region 1 - never married
region 1 - married
region 1 - divorced
region 1 - widowed

State 5 (region 2 - never married) takes the births from states 5 to 8.

1. LIFE TABLE

Region based increment-decrement life table

```
region based life table
0010100010802010319800201011000 1000
 increment-decrement life table
 8 states/regions , 2 cohorts
  region based
1-n.mar.1-marri.1-divor.1-widow.2-n.mar.2-marri.2-divor.2-widow.
 100000. 100000. 100000. 100000. 100000. 100000. 100000. 100000.
```

Status based increment-decrement life table

```
status based life table
001012001080801031980020101111111111
 increment-decrement life table
 8 states/regions , 8 cohorts
  status based , age 20
1-n.mar.1-marri.1-divor.1-widow.2-n.mar.2-marri.2-divor.2-widow.
 100000. 100000. 100000. 100000. 100000. 100000. 100000. 100000.
```

2. PROJECTION

Two-sex female dominant projection: females

```
two-sex female dominant projection : females
101080103010101031980200099990207000202020001
0105
1.0534,1.0534,1.0534,1.0534,0.0,0.0,0.0,0.0,
0.0,0.0,0.0,0.0,1.0534,1.0534,1.0534,1.0534,
 two-sex female dominant projection
       8 states/regions
        females 1980
1-n.mar.1-marri.1-divor.1-widow.2-n.mar.2-marri.2-divor.2-widow.
 100000. 100000. 100000. 100000. 100000. 100000. 100000. 100000.
```

Two-sex female dominant projection: males

```
two-sex female dominant projection : males
101080103010101031980200099990207000202010101
two- sex female dominant projection
    states/regions
        males
1-n.mar.1-marri.1-divor.1-widow.2-n.mar.2-marri.2-divor.2-widow.
 100000. 100000. 100000. 100000. 100000. 100000. 100000. 100000.
```

Total population projection

```
total population projection
101080103010101031980200099990207000202030001
0105
1.0,1.0,1.0,1.0,0.0,0.0,0.0,0.0,
0.0,0.0,0.0,0.0,1.0,1.0,1.0,1.0,
 total population projection
       8 states/regions
        females + males
1-n.mar.1-marri.1-divor.1-widow.2-n.mar.2-marri.2-divor.2-widow.
 100000. 100000. 100000. 100000. 100000. 100000. 100000. 100000.
```