Working Paper

A DYNAMIC APPROACH TO THE ESTIMATION OF MORBIDITY

P. Kitsul

May 1980
WP-80-71

International Institute for Applied Systems Analysis
A-2361 Laxenburg, Austria

A DYNAMIC APPROACH TO THE ESTIMATION OF MORBIDITY

P. Kitsul

May 1980
WP-80-71

INTERNATIONAL INSTITUTE FOR APPLIED SYSTEMS ANALYSIS
A-2361 Laxenburg, Austria

THE AUTHOR

Dr. Pavel Kitsul has been a research scholar at IIASA since December 1977. He came from the Institute of Control Sciences of the USSR Academy of Sciences and has a Ph.D. in physics and mathematics from the Moscow Institute of Physics and Technology.

FOREWORD

The prinicpal aim of health care research at IIASA has been to develop a family of submodels of national health care systems for use by health service planners. The modeling work is proceeding along the lines proposed in the Institute's current Research Plan. It involves the construction of linked submodels dealing with population, disease prevalence, resource need, resource allocation, and resource supply.

This paper presents the outlines of a Dynamic Morbidity Model (DYMOD) that has been developed as a part of the Health Care Systems modeling activities carried out at IIASA. The purpose of this model is to help resolve the problem of estimating age-specific morbidity rates for degenerative diseases experienced by populations with a nonstable structure.

Related publications in the Health Care Systems Task are listed at the end of this report.

Andrei Rogers
Chairman
Human Settlements
and Services Area

ACKNOWLEDGMENTS

The author would like to acknowledge the work carried out by members of the South West Health Authority, to provide the cancer data through Richard Gibbs for this modeling. Similar data from Frans Rutten (Netherland Ministry of Health and Environment) were also very useful.

This data supply was necessary to begin the modeling, however, this paper would never have been finished without the substantial support of Maria Rogers. The author is very grateful for her comments and valuable editorial suggestions to improve the paper.

ABSTRACT

Degenerative diseases are inherent in human beings. They are caused by the aging process, and the morbidity rate in these diseases usually increases with age.

Unfortunately, the routine morbidity statistics in all countries record only some of the cases of degenerative diseases, and it is necessary to estimate the true number of cases on the basis of other indirect statistics - in particular, mortality data.

The development of the morbidity models at IIASA is directed toward reducing the restrictions on the changes in population structure and disease. For example, the assumption that population structure is stable and stationary implies that this type of model can be applied only to populations with a monotonic-like age structure. In addition, it is necessary to adapt these models to use comprehensive health study data about a specific region, in order to avoid extending clinical survival data to the latent sick individuals.

One way to overcome these difficulties is to use the state-space approach to describe disease dynamics. This approach is used in the model developed for the estimation of morbidity rates in the case of unstable and unstationary population structures (DYMOD). The application of this model has required corresponding medical and demographic statistics for several consecutive years; and data collected from the South West Region of the UK and the Netherlands were used in testing the DYMOD model.

CONTENTS

A DYNAMIC APPROACH TO THE ESTIMATION OF MORBIDITY

1. INTRODUCTION

The aim of the IIASA Health Care System Modeling (HCS) Task is to develop a large-scale national HCS model and apply it in collaboration with national research centers as an aid to the health service planner. The main methodological problems of the creation of such a model were discussed at the IIASA-WHO conference (Moscow-Laxenburg, 1975, Venedictov, 1977) where a conceptual scheme for health care systems was proposed.

This conference defined the main directions of the HCS Task to be the creation of a suite of interrelated submodels oriented to a mathematical description of the main "blocks" of the HCS and to the usage of these submodels in the decision-making process on various levels of health care management.

During the first steps, the main attention of our work was given to the modeling of resource demands, allocation, and supply. The current state of IIASA health care modeling activity is expressed in Figure 1. As shown in this figure, models for resource demands assume as a prerequisite the estimation of health indices for a population, because of the problem of insufficient data in many countries. Alternative approaches to the estimation

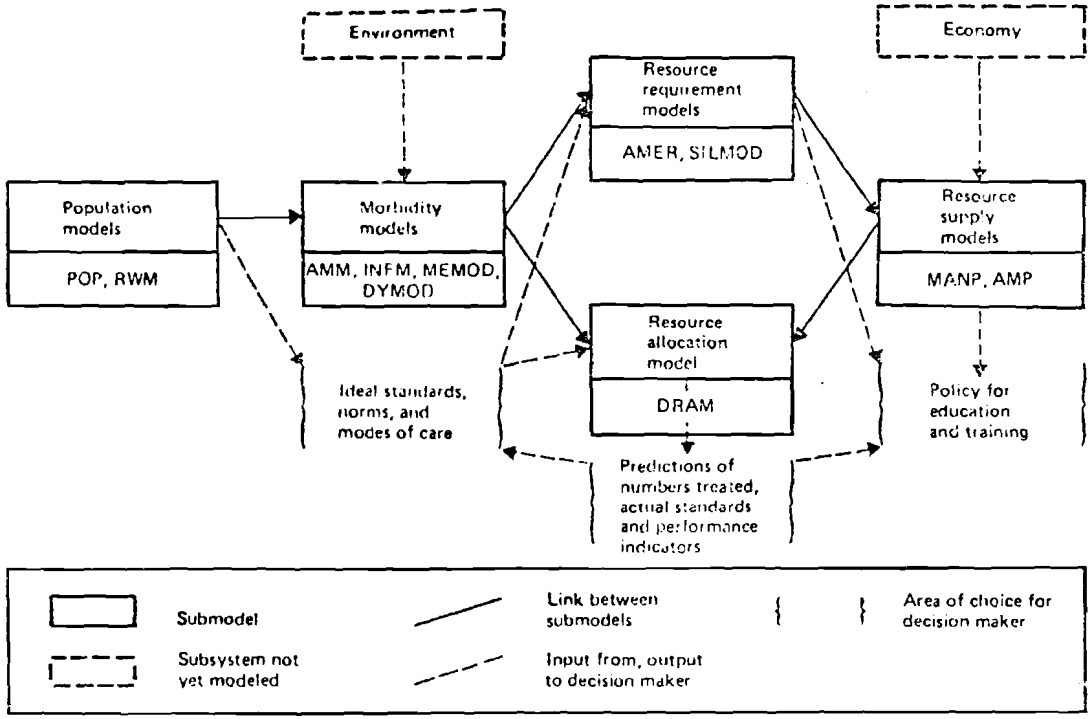

FIGURE 1. Family of HCS submodels constructed at IIASA. (Source: Shigan et al. 1979:11).

of morbidity indices (rates) on the basis of information available in different countries have been described by Shigan (1977).

Morbidity estimation models can be divided into the following types:

a. *Aggregative morbidity models*, for estimating and forecasting "crude" general morbidity rates without specification of the group of diseases or specific disease
b. *Group morbidity models*, for modeling groups of diseases, e.g. the classes in the International Classification of Diseases (ICD), or groups used in several IIASA publications (degenerative diseases, infections, accidents, etc.)
c. *Specific morbidity models*, oriented to specific diseases, such as cancer, cholera, tuberculosis, etc.
d. *Stage of disease models*, oriented not only to a specific disease, but also to the different stages of the development process or risk-group estimation and classification.

At the present time IIASA morbidity models include in various degrees the first three types of models, in particular those for degenerative diseases* (Kaihara et al., 1977 and Klementiev, 1977). The main peculiarity of these morbidity models for degenerative diseases is the use of the mortality data and population age structure for the estimation of morbidity for a given group of diseases.

The natural evolution of morbidity models has tended to reduce the number of restrictions on the dynamics of population age structure and disease. In Kaihara et al. (1977), for example, it is assumed that the population structure is stable and stationary for the duration of an illness, the duration of illness is the same for each person, and that the sick individual eventually dies from the given disease after some fixed time.

The final restrictions are not proposed in the work of Klementiev (1977). Instead, it is assumed that persons who became ill at time t die at time θ with the known probability $P(t,\theta) = P(t-\theta)$ and that the probability of dying due to other

*Sick people suffering from degenerative disease are considered as sick for the duration of their lives.

other causes is not equal to zero. On the other hand, the first assumption concerning the unchangeability of the population structure for the duration of illness is highly significant when used in building a morbidity model. Due to this assumption, the estimation of morbidity and prevalence rates can be done only for a monotonic population structure. However, the consideration of data for several consecutive years becomes necessary in the case of an unstable population.

The present approach is a continuation of the work done at IIASA on morbidity modeling for degenerative diseases. In the case of the estimation of morbidity rates for an unstable, unstationary population age structure, it is necessary to describe the "destiny" of sick individuals from the beginning of illness to their death in a similar way as in demographic models. In demography, the situation is complicated and more data are required. In the modeling of degenerative diseases, however, there only exist three states: survival, illness, and death. Further, we assume that degenerative diseases have no interaction between cohorts, and therefore, if we have data for both survival and death, we can estimate morbidity rates. With these rates we can then estimate and predict the size and age structure of the sick population. The model discussed below and described further in the Appendix is based on the dynamics of the population age structure. If we are able to obtain data from registered morbidity statistics for a certain year, this model can also incorporate this information (Shigan, 1977).

2. THE DYNAMIC MORBIDITY MODEL (DYMOD): ASSUMPTIONS, NOTATIONS, AND PROBLEM STATEMENT

We begin with a formulation of the different morbidity estimation problems in terms of available statistics.

a. Let us assume that only survival probabilities $s(n,\tau)$ and mortality statistics $d(n,t)$ are known (n = age, t = time, τ = time from the beginning of the illness).

b. Let us assume that survival probability $s_t(n,\tau)$ is known and that we can measure not only mortality

d(n,t) but also for some time t* the age structure of the sick population C(t*,x) (special investigation). How is it possible to incorporate these data to estimate the age-specific morbidity rate, $\mu(n,t)$?

c. Let us assume we have the possibility to measure the mortality d(n,t) and age structure of a sick population C(n,t) in a certain region.
How is it possible to use this information in another, similar region in which only mortality data d(n,t) are available?

We do not pretend to solve all these porblems. Instead, we will concentrate our attention on the solution of the first two problems and just discuss the last one. To achieve this aim, we will need to introduce more precise definitions.

Let $P_t = \{P_{1,t}, \ldots p_{N,t}\}$ be the population age structure vector* for some region at time t, where N is the number of age groups.

Let us assume that an individual is afflicted at a certain time with a given type of disease having a maximal duration of illness m (years) and consider the sick part of the population as a vector

$$C_t = \{c^0_{1,t}, \ldots, c^0_{n,t}, c^1_{1,t}, \ldots, c^1_{N,t}, \ldots, c^m_{1,t}, \ldots, c^m_{N,t}\},$$

where $c^k_{j,t}$ is the number of individuals in the j-th age group at time t, afflicted with a given type of disease k years age.

Let $\mu(n,t)$ be the age-specific morbidity rate, e.g. the ratio of the number of sick individuals in the initial stage of illness to the number of the "healthy" individuals in the previous year

$$\mu(n,t) = C^0_{n+1,t+1} / (P_{n,t} - \sum_{k=0}^{m} C^k_{n,t})$$

Further, let $s^k(n,t)$ be the age-specific survival rate for sick individuals in stage k

*All vectors are column-vectors.

$$s^k(n,t) = C^{k+1}_{n+1,t+1}/C^k_{n,t}$$

and $s^k(n,t)$ be the age-specific mortality rate, e.g. the ratio of the decrement of sick individuals in stage (k+1) in comparison with stage k one year age over the number of sick individuals in stage k:

$$s^k(n,t) = (C^k_{n,t} - C^{k+1}_{n+1,t+1})/C^k_{n,t}$$

It is possible to show that the dynamics of the sick part of the population can be described in the following recurrent matrix equation:

$$C_{t+1} = \underset{\sim}{S}C_t + \underset{\sim}{\mu}[P_t - (\underset{\sim}{E},\underset{\sim}{E},\ldots,\underset{\sim}{E})C_t],$$

where $\underset{\sim}{S}$ is the survival matrix for sick individuals, which has the usual block structure

$$\underset{\sim}{S} = \begin{pmatrix} \underset{\sim}{0} & \cdots & \underset{\sim}{\mu} \\ \underset{\sim}{s}_{0,1} & \underset{\sim}{0} & \underset{\sim}{0} \\ \underset{\sim}{0} & & \underset{\sim}{0} \\ \underset{\sim}{0} & \underset{\sim}{s}_{k-1,k} & \underset{\sim}{0} \\ & & \\ \underset{\sim}{0} & \underset{\sim}{s}_{m-1,m} & \underset{\sim}{0} \end{pmatrix}$$

where the blocks $\underset{\sim}{s}_{k-1,k}$ have the form

$$\underset{\sim}{s}_{k-1,k} = \begin{pmatrix} 0 & \cdots & 0 \\ s^{k-1}_{1,2} & & 0 \\ 0 & s^{k-1}_{n-1,n} & 0 \end{pmatrix}, \quad k = \overline{1,m} \quad ;$$

$\underset{\sim}{\mu}$ is morbidity matrix

$$\underset{\sim}{\mu} = \begin{pmatrix} \mu_{1,t} & 0 \cdots\cdots 0 \\ & \ddots \\ 0 \cdots 0 & \mu_{n,t} \\ \underset{\sim}{0} & \\ \underset{\sim}{0} & \end{pmatrix},$$

$\underset{\sim}{E}$ is $(n \times n)$ identity matrix and $\underset{\sim}{0}$ is $(n \times n)$ zero matrix.

Let us introduce vector d_t

$$d_t = (d_{1,t}, \ldots, d_{N,t})$$

where $d_{l,t}$ is the number of individuals in l-th age groups, who died from a given disease at time t.

Next, let us introduce the mortality block matrix

$$\underset{\sim}{\delta}_t = [\underset{\sim}{\delta}^1(t), \underset{\sim}{\delta}^2(t), \ldots, \underset{\sim}{\delta}^m(t)]$$

where

$$\underset{\sim}{\delta}^i(t) = \begin{bmatrix} \delta^i(1,t), 0 \cdots\cdots 0 \\ \vdots \quad \ddots \\ \vdots \qquad \ddots \\ \vdots \qquad\quad \ddots \\ 0 \cdots\cdots 0 \quad \delta^i(N,t) \end{bmatrix}, \qquad i=\overline{1,m}$$

and $\delta^i(n,t)$ is the mortality rate of sick individuals in the i-th stage of diseases, at age n, time t.
Then, after simple transformation, we obtain

$$d_{t+1} = \underset{\sim}{\delta}_t C_t$$

Hence, we have the equations

$$C_{t+1} = \underset{\sim}{S} C_t + \underset{\sim}{\mu}[P_t - (\underset{\sim}{E}, \underset{\sim}{E}, \ldots, \underset{\sim}{E}) C_t]$$
$$d_{t+1} = \underset{\sim}{\delta}_t C_t$$

which describes the dynamic evolution of the sick part of the population C_t and the mortality rate d_t.

Vector C_t and matrix $\underset{\sim}{\mu}$ are unobservable and our aim consists of estimating these vectors and this matrix by the observed mortality statistic

$$d_0^t = \{d_0, d_1, \ldots d_t\}$$

From a mathematical point of view, the problem under consideration is the estimation of the state (C_t) and parameters ($\underset{\sim}{\mu}$) of the nonlinear, dynamic nonstationary system according to indirect observations. If the sequence of observation is sufficiently long (t>>m), this problem can be solved by using some extensions of the Kalman-Bucy recurrence estimation [see Liptser and Shiryayev (1974)].

Unfortunately, in the real situation the sequence of the available data for many diseases is not sufficient for a reliable estimation by standard techniques of morbidity and prevalence rates. Because of this it is necessary to perform a more detailed investigation taking into account the dynamics of the disease within the population cohorts.

3. COHORT APPROACH

It is easy to see that the dynamics of the sick part of the population within a cohort can be described by the following equations

$$\begin{aligned}
c^0_{n+1,t+1} &= \mu(n,t) H_{n,t} \\
c^1_{n+1,t+1} &= s^0(n,t) C^0_{n,t} \\
&\cdots\cdots\cdots\cdots\cdots\cdots \\
c^{i+1}_{n+1,t+1} &= s^i(n,t) C^i_{n,t} \\
&\cdots\cdots\cdots\cdots\cdots\cdots \\
c^m_{n+1,t+1} &= s^{m-1}(n,t) C^{m-1}_{n,t}
\end{aligned} \qquad (1)$$

here

$$H_{n,t} = P_{n,t} - \sum_{i=1}^{m} C^{i}_{n,t}$$

is the number of "healthy" individuals, $H_{n,t}$ who are not afflicted with a given disease, $\mu(n,t)$ and $s^{i}(n,t)$ are the morbidity and survival rates defined above. The number of individuals who died of a given disease at time (t+1) and age (n+1) is

$$d_{n+1,\ t+1} = \sum_{i=1}^{m} \delta^{i}(n,t) C^{i}_{n,t} \qquad (2)$$

where $\delta^{i}(n,t)$ is mortality rate for sick individuals at age n, time t, and stage of disease i.

Let us assume from the beginning that survival probabilities $S^{i}(n,t)$ and mortality rates $\delta^{i}(n,t)$ are given. The problem now consists of the estimation of morbidity rates $\mu(n,t)$ and the number of sick individuals $\sum_{i=1}^{m} C^{i}_{n,t} = C_{(n,t)}$ from the mortality data

$$d(n,t),\ n=\overline{1,N},\ t=\overline{t_0,t_M},$$

where N is the number of age groups and M is the total number of years of available data.

4. SOLUTION

To solve the problem it is necessary to find the relation between mortality data d(n,t) and unknown morbidity rates $\mu(n,t)$. To achieve this aim, let us transform equation (2) in the following way

$$d(n+1,t+1) = \delta^{1}(n,t) C^{1}_{n,t} + \sum_{i=2}^{m} \delta^{i}(n,t) C^{i}_{n,t}$$

and using equation (1) we obtain

$$d(n+1,t+1) = \delta^{1}(n,t)\ \mu(n-1,t-1) H_{n-1,t-1}$$

$$+ \sum_{i=2}^{m} \delta^{i}(n,t)\ s^{i-1}(n-1,t-1) C^{i-1}_{n-1,t-1}$$

and

$$\mu(n-1,t-1) = \frac{d(n+1,t+1)-F(n-1,t-1)}{\delta^1(n,t)\ H_{n-1,t-1}} \tag{3}$$

where

$$F(n-1,t-1) = \sum_{i=2}^{m} \delta^i(n,t)s^{i-1}(n-1,t-1)C^{i-1}_{n-1,t-1}$$

and finally

$$\mu(n,t) = \frac{d(n+1,t+1)-F(n,t)}{\delta^1(n+1,t+1)H_{n,t}}$$

The general equations will be

$$\bar{C}(n+1,t+1) = f[\mu(n,t),\bar{C}(n,t),P_{n,t}] \tag{4}$$

$$\mu(n,t) = \phi[d(n+2,t+2),\bar{C}(n,t)] \tag{5}$$

where

$$\bar{C}(n,t) = \{C^i{}_{n,t}\}, \quad i=\overline{1,m}$$

and functions f and ϕ were specified above [see (1) and (3)].

It is easy to see that if for the initial year the t_0 vector $\bar{C}(n,t_0)$ is given, we can calculate morbidity rates

$$\mu(n,t),\ t\geq t_0$$

and the structure of the sick part of the population

$$\bar{C}(n,t) = \{C^1{}_{n,t},\ldots,C^m{}_{n,t}\}, \quad t\geq t_0$$

as well.

This way of morbidity estimation can be used if for a certain year, we have the results of detailed investigations on the health of a population in a given region. Here we assume that $\bar{C}(1,t)=0$.

Unfortunately in general, the structure of the sick part of the population $\bar{C}(n,t_0)$ is also unknown.

Nevertheless, taking into account that $\bar{C}(1,t)=0$ we can find from equations (4) and (5) the values of $\mu(n,t)$ and $\bar{C}(n,t)$ under the line and including the line $n = t-t_0$ (see Figure 2).

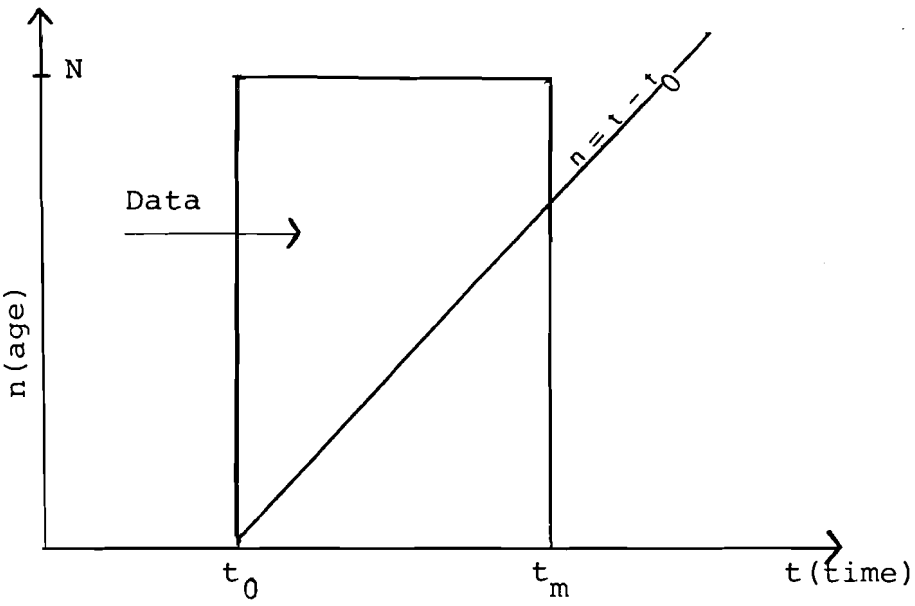

Figure 2. Illustration of the morbidity estimation for cohorts with incomplete data.

To define the value of $\mu(n,t)$ on the line $n = t-t_0+1$, we have to take into account that for two consecutive years of the same age groups the ratios

$$\frac{\bar{C}(n,t)}{P(n,t)} \quad \text{and} \quad \frac{\bar{C}(n+1,t)}{P(n+1,t)}$$

are almost equal.

This fact allows us to define an approximation for $\bar{C}(2,t_0)$ and, hence, $\mu(n,t)$ and $\bar{C}(n,t)$ on the $n = t-t_0+1$ line. After that we can use the same approach to define $\mu(n,t)$ and $\bar{C}(n,t)$ on the line $n = t-t_0+2$, etc. Obviously for such an approximate solution to be valid, it is necessary to provide certain sensitivity analyses for equations (4) and (5).

The sensitivity analyses should be carried out with two sets of variables. The first one is the prevalence $\bar{C}(n,t_0)$ in initial years t_0. We should measure this sensitivity to the "point" $\bar{C}^*(n,t_0)$ which can be obtained by the method proposed above. The second one is the survival rates $s^i(n,t)$ and related with these survival rates, specific mortality rates $\delta^i(n,t)$. We will now focus our attention on the calculation of survival and specific mortality rates [the parameters of equations (4), (5)] from the available data.

The relation between survival and mortality rates can be obtained from the equality

$$s^i(n,t) + \delta^i(n,t) + \varepsilon^i\Delta(n,t) = 1$$

where $\varepsilon^i\Delta(n,t)$ is the probability of dying from something other than the given disease (accident, etc.) for sick individuals in stage i, $\Delta(n,t)$ is the same probability for healthy people

$$\Delta(n,t) = d(n,t) - \delta^c(n,t)$$

Here $d(n,t)$ is the general mortality rate and $\delta^c(n,t)$ is the specific mortality rate per 1000 population (sick or not).

Survival rate $s^i(n,t)$ can be obtained from clinical data but only in aggregate form ($s^i(n,t) = s^i$). The mortality rate $\Delta(n,t)$ can be easily obtained from routine statistics, and ε^i can be obtained either from routine statistics or, if impossible, from the opinions of experts.

In conclusion, the solution of our estimation problem can be divided into the following steps:

1. Preparation of population dynamics $\{P_t\}$ (see for example Willekens and Rogers, 1976)
2. Preparation of specific mortality statistics $\{d_t\}$ (Emmanuel and Evseenko 1970,and Kapadia and McInnis 1977)
3. Preparation of survival rates for the sick part of population

4. Estimation of $\mu(n,t)$ and $\bar{C}_{(n,t)}$ by using the proposed algorithm

The block-scheme of this model is represented in Figure 3 (see also Shigan, 1977, Figure 2).

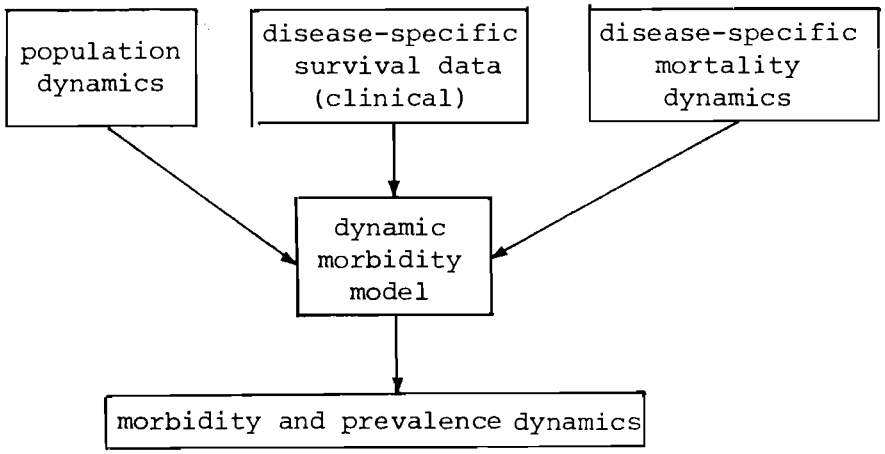

Figure 3. General scheme of the dynamic morbidity model.

In addition, it is sometimes necessary to estimate survival probabilities in order to avoid the inevitable error that will occur when clinical survival data is extended to the latent sick individuals and also to compensate for the uncertainty of the time of the beginning of the disease. This can be done by introducing a new survival rate (estimated by doctors) to satisfy the equality of the number of sick individuals in the first stage of a disease and the number of individuals dying of a particular disease after a specified time (e.g., after four of five years for stomach cancer)

$$\left(\sum_{n=1}^{m} C^{0}_{n,t} = \sum_{n=1}^{m} d_{n+m,t+m} \right), \qquad m = 4 \sim 5$$

5. CONCLUSION

In this paper, we have attempted to find a solution to the problem of estimating age-specific morbidity rates and estimating the prevalence of degenerative diseases such as cancer. Indeed, we have solved problems (a) and (b) which were formulated in section 2.

The recursive algorithm (4), (5) proposed in section 3 allows us to estimate the age-structure of a sick population and the age specific morbidity rates if mortality statistics for consecutive years and survival probabilities are given. The outputs of the model can be obtained more straightforwardly when, for some fixed year (for example t_0), the age structure of the sick population is given [problem (b)]. The model can also be used to adjust the initial survival probability by taking into account the equality between the total number of individuals in the first stage of disease and the total number of individuals dying of this disease. Because the morbidity rates and survival probabilities are relatively constant in different regions, it is possible to use the estimation of the morbidity rates and/or survival probabilities in one region in order to estimate prevalence for a given disease in another region in which only the mortality data are available [problem (c)].

APPENDIX: HOW TO USE THE HCS PROGRAM DYMOD

1. Model Description

The Dynamic Morbidity Model is one of the submodels of IIASA's Health Care Systems model. The purpose of DYMOD is to estimate the morbidity and/or prevalence of degenerative diseases for an unstationary and unstable population structure using age-specific survival rates for a general and specific mortality age structure over time. The output shows an age-specific risk (morbidity/mortality) ratio for given diseases as a function of survival probabilities.

2. Files

2.1. Storage of files

All files necessary to run DYMOD are stored on the tape FS. Models which are available from the Health Care Systems Modeling Task. To get these files, mount the tape on one of the tape drives, login and type:

```
mkdir dymod (to create the directory if it does not exist,
otherwise start with the next command)
fs x (x is either 0 or 1 according to the tape drive used)
e dymod/* (to extract the files)
```

st (stop)

To be sure that this procedure has worked try

cd dymod (to change to directory dymod)
f (the content of the directory is listed)

2.2. Types of Files

There are four kinds of files: source files, object files, input and output (I/O) files. Only the object files and the I/O files are necessary for a normal run of the model.

2.2.1. Source Code

The model is programmed in Fortran (with no unusual features). There is a single main program which allows for the introduction of the arbitrary (meaningful) survival probability in an interactive mode of operation. The file containing the source code is TOL.F.

2.2.2. Object Code

The files containing the object code are:

File Name
TOL
DYMOD - SWF
DYMOD - SWM
DYMOD - NL

File TOL contains the object code of the main program. Three other files are shell files which hold the command to execute the object file for the following cases:

a. SWF - South West Region of Great Britain (female population)
b. SWM - South West Region of Great Britain (male population)
c. NL - Netherlands(female population)

2.2.3. Input Files

For each case (a,b,c) there are three input files:

	File Name				
a.	SWF:	b.	SWM:	c.	NL:
	PFSW		PMSW		PFN
	CFSW		CMSW		PFN
	DFSW		DMSW		DNFN

All changes of these files have to be made by means of the editor. "Unix Programmer's Manual" explains how to use the text editor.

2.2.4. Output Files

The program writes to the terminal and to three output files (for each case):

	File Name				
a.	SWF	b.	SWM	c.	NL
	MRFSW		MRMSW		MRN
	PRFSW		PRMSW		PRN
	OUTFSW		OUTMSW		OUTN

The terminal display gives the aggregate result of modeling for certain survival probabilities.
All files can be printed by the command: p File Name

3. Performing a Run

3.1. Change of Data

After the first running of DYMOD, the user is invited to change the survival probabilities if it is necessary. Therefore, type the new probabilities under the old ones as indicated on the terminal display. The program DYMOD will produce a new result. To stop the program type "carriage return". Before it terminates, the last result will be in the "output" file.

3.1.1. Explanation of Input

Figure A1 shows the input files which contain the dynamics of the population age-structure over time (PFSW), the dynamics of age-specific mortality rates over time for stomach cancer, ICD 151 (CFSW) and similar data for general mortality rates (DFSW). The terminal input is shown in Figure A2 and represents the aggregate survival probabilities.

3.2. Execution

To run the model, type one of the following commands:

DYMOD - SWF
DYMOD - SWM
DYMOD - NL

The program now performs the calculation, displays the results on the terminal and invites the user to change the survival probabilities. If it is necessary, type new survival probabilities under the old ones and after that "carriage return". If it is not, type "carriage return" only.

3.2.1. Explanation of Output

Figure A2 shows an example of the aggregate output which contains the ratio between the number of individuals who are ill to the number of individuals who have died at the same time and age. This figure is contained in the "output" file. The disaggregated prevalence and mortality rates (per 1000 population) are contained in the files PRFSW and MRFSW. Disaggregation is in one year brackets from age 1 to age 80 for 16 consecutive years beginning in 1960.

4. General Use of DYMOD

The procedure as explained above is designed to run DYMOD on the IIASA PDP 11/70 computer. For use outside IIASA a special tape containing the Fortran source file and the data files can be created. This tape is 800 bpi, 9 track, unlabeled, EBCDIC, upper case, files are separated by two end of the file

marks. It is readable by nearly every computer. Other tapes can be prepared on request.

To run the model the files have to be compiled one by one to trace errors, and then linked. For the execution of the load-and-go code some preparation is necessary to define the input and output channels.

DYMOD requires 8 I/O channels:

Channel Number	FSW Case:
2	input, data file PFSW
3	input, data file CFSW
4	input, data file DFSW
5	input, terminal
6	output, terminal
8	output, data file MRSW
9	output, data file PRSW
10	output, table file OUTFSW

(1)

YEARS :	AGE GROUPS									
	1	2-4	5-14	15-24	25-34	35-44	45-54	55-64	65-74	75+
1960	25,80	96,20	249,00	206,00	200,00	222,00	240,00	220,00	167,00	116,00
1961	26,50	98,50	249,00	213,00	198,00	223,00	240,00	224,00	170,00	119,00
1962	27,30	101,70	244,00	224,00	200,00	224,00	237,00	228,00	172,00	121,00
1963	28,30	105,30	243,20	231,70	199,50	225,10	231,50	228,80	175,30	124,20
1964	29,10	109,70	245,90	239,50	202,10	229,50	227,30	232,20	181,60	121,00
1965	29,60	113,30	248,70	244,00	203,10	225,60	229,20	235,30	185,50	124,50
1966	29,40	118,60	254,00	248,10	202,10	220,10	231,30	237,40	187,60	126,50
1967	28,90	119,90	259,10	251,30	203,00	216,10	232,30	239,00	190,40	129,90
1968	28,00	120,40	265,90	261,80	211,70	219,40	235,00	241,90	196,50	132,40
1969	28,10	119,20	272,60	262,90	216,00	216,70	233,80	243,90	200,50	135,70
1970	26,90	117,10	280,80	263,60	220,40	214,80	232,80	245,10	203,90	138,60
1971	27,60	114,30	284,20	258,10	224,10	213,10	235,90	250,70	213,60	140,80
1972	26,60	112,10	288,80	255,70	233,00	211,90	238,20	247,50	216,20	148,20
1973	25,40	111,00	291,80	256,00	241,80	211,70	249,40	245,40	220,30	151,10
1974	18,90	84,10	232,50	207,00	195,70	168,90	205,00	198,10	184,20	128,10
1975	18,60	82,50	234,00	209,20	201,10	168,50	199,20	201,50	186,30	130,70

(2)

YEARS :	AGE GROUPS									
	1	2-4	5-14	15-24	25-34	35-44	45-54	55-64	65-74	75+
1960	0,00	0,00	0,00	0,00	1,00	5,00	15,00	48,00	117,00	247,00
1961	0,00	0,00	0,00	0,00	3,00	6,00	19,00	66,00	132,00	230,00
1962	0,00	0,00	0,00	0,00	2,00	3,00	15,00	58,00	132,00	233,00
1963	0,00	0,00	0,00	0,00	2,00	5,00	26,00	65,00	131,00	214,00
1964	0,00	0,00	0,00	0,00	1,00	7,00	14,00	71,00	120,00	199,00
1965	0,00	0,00	0,00	0,00	2,00	4,00	18,00	55,00	103,00	195,00
1966	0,00	0,00	0,00	0,00	1,00	3,00	23,00	57,00	104,00	179,00
1967	0,00	0,00	0,00	0,00	3,00	5,00	18,00	56,00	121,00	226,00
1968	0,00	0,00	0,00	0,00	1,00	6,00	15,00	60,00	112,00	203,00
1969	0,00	0,00	0,00	0,00	1,00	7,00	10,00	60,00	129,00	208,00
1970	0,00	0,00	0,00	0,00	1,00	7,00	14,00	56,00	139,00	221,00
1971	0,00	0,00	0,00	0,00	1,00	2,00	14,00	52,00	136,00	205,00
1972	0,00	0,00	0,00	0,00	1,00	5,00	14,00	36,00	126,00	247,00
1973	0,00	0,00	0,00	0,00	2,00	4,00	13,00	50,00	96,00	196,00
1974	0,00	0,00	0,00	0,00	1,00	3,00	12,00	35,00	75,00	172,00
1975	0,00	0,00	0,00	0,00	1,00	3,00	13,00	30,00	99,00	183,00

(3)

YEARS :	AGE GROUPS									
	1	2-4	5-14	15-24	25-34	35-44	45-54	55-64	65-74	75+
1960	16,40	0,79	0,27	0,47	0,69	1,43	4,23	9,70	28,20	101,28
1961	17,21	0,89	0,31	0,46	0,80	1,65	4,18	10,20	29,70	102,47
1962	17,73	0,95	0,28	0,33	0,81	1,63	4,23	10,29	29,11	101,36
1963	16,71	0,77	0,26	0,42	0,82	1,67	4,48	10,49	30,21	105,98
1964	15,64	0,66	0,28	0,40	0,68	1,70	4,14	10,37	26,92	95,43
1965	14,46	0,80	0,28	0,43	0,59	1,53	4,11	9,35	26,57	97,45
1966	14,63	0,76	0,23	0,44	0,68	1,68	4,01	9,50	27,15	102,96
1967	13,56	0,66	0,29	0,41	0,50	1,64	3,89	9,54	25,50	95,26
1968	14,25	0,73	0,25	0,39	0,62	1,58	4,09	9,86	25,84	105,08
1969	14,41	0,58	0,25	0,37	0,54	1,62	4,08	9,91	25,78	99,13
1970	14,87	0,54	0,21	0,32	0,57	1,41	3,80	9,79	26,50	99,05
1971	12,79	0,66	0,26	0,38	0,65	1,49	4,00	9,32	24,34	99,30
1972	14,89	0,59	0,25	0,42	0,52	1,43	4,15	9,73	25,44	98,08
1973	13,62	0,57	0,23	0,42	0,53	1,48	3,92	9,20	25,30	98,67
1974	11,32	0,48	0,22	0,37	0,57	1,34	3,77	9,34	23,74	96,01
1975	11,94	0,34	0,20	0,40	0,49	1,29	3,69	8,60	23,69	95,17

Figure A1. Example of Output: (1) PFSW, (2) CFSW, (3) DFSW.

THE RATIO: MORBIDITY/MORTALITY

YEARS	AGE GROUPS									
	1	2-4	5-14	15-24	25-34	35-44	45-54	55-64	65-74	75+
1965	0,00	0.00	0,00	0,00	3,06	3,10	2,82	2,91	2,58	1,96
1966	0,00	0.00	0,00	0,00	3,36	2,75	3,15	2,75	2,66	1,94
1967	0,00	0.00	0,00	0,00	2,19	4,24	2,90	2,63	2,78	1,93
1968	0,00	0.00	0,00	0,00	3,27	2,87	2,73	2,93	2,60	1,94
1969	0,00	0.00	0,00	0,00	2,92	2,59	2,95	2,73	2,71	1,95
1970	0,00	0.00	0,00	0,00	2,75	3,32	2,85	2,83	2,62	1,95
1971	0,00	0,00	0,00	0,00	3,33	3,03	3,17	2,84	2,74	1,92
1972	0,00	0.00	0,00	0,00	2,85	2,18	2,58	2,91	2,68	1,93
1973	0,00	0.00	0,00	0,00	2,95	3,05	2,95	2,82	2,71	2,05
1974	0,00	0.00	0,00	0,00	2,31	2,95	2,70	2,65	2,75	1,98
1975	0,00	0.00	0,00	0,00	3,13	3,20	2,28	2,61	3,11	2,25

UNREGISTERED IN SPECIFIC MORTALITY DATA
18,%
PRINT NEW SURVIVAL PROBABILITIES UNDER OLD ONES
SRV1=0,676 SRV2=0,676 SRV3=0,676 SRV4=0,676

Figure A2. Example of Output.

REFERENCES

Emmanuel', N.M., and L.S. Evseenko (1970) *Kolichestvennye osnoy Klinicheskoi onkologii (Quantative Aspects of Clinical Oncology)*. Meditsina, Moscow.

Kaihara, S., I. Fujimasa, K. Atsumi, and A.A. Klementiev (1977) *An Approach to Building a Universal Health Care Model: Morbidity Model of Degenerative Diseases.* RM-77-6. International Institute for Applied Systems Analaysis. Laxenburg, Austria.

Kapadia, A.S., and B.C. McInnis (1977) Stochastic Compartmental Modeling, Parameter Estimation and Analysis of Cancer Treatment Systems, in D.D. Venedictov, ed. *Health System Modeling and the Information System for the Coordination of Research in Oncology.* CP-77-4. International Institute for Applied Systems Analysis. Laxenburg, Austria.

Klementiev, A.A. (1977) *On the Estimation of Morbidity.* RM-77-43. International Institute for Applied Systems Analysis. Laxenburg, Austria.

Liptser, R.S., and A.N. Shiryayev (1974) *Statistika Sluchainyk protsessov (Statistics of Random Processes II)* Springer Verlag, New York 1977. Nauka, Moscow.

Shigan, E.N. (1977) *Alternative Analysis of Different Methods for Estimation Prevalence Rate.* RM-77-40. International Institute for Applied Systems Analysis. Laxenburg, Austria.

Venedictov, D.D., et al. (1977) Health Care: A Systems Approach, in D.D. Venedictov, ed. *Health System Modeling and the Information System for the Coordination of Research in Oncology*. CP-77-4. International Institute for Applied Systems Analysis. Laxenburg, Austria.

Willekens, F., and A. Rogers (1976) *Computer Programs for Spatial Demographic Analysis*. RM-76-58. International Institute for Applied Systems Analysis. Laxenburg, Austria.

LIST OF RECENT PUBLICATIONS IN THE HEALTH CARE SYSTEMS TASK

Shigan, E.N., ed. (1978) Systems Modeling in Health Care. Proceedings of an IIASA Conference, November 22-24, 1977 (CP-78-12).

Gibbs, R.J. (1978) The IIASA Health Care Resources Allocation Sub-Models: Mark 1 (RR-78-08).

Gibbs, R.J. (1978) A Disaggregated Health Care Resource Allocation Model (RM-78-01).

Kaihara, S., N. Kawamura, K. Atsumi, and I. Fujimasa (1978) Analysis and Future Estimation of Medical Demands Using A Health Care Simulation Model: A Case Study of Japan (RM-78-03).

Fujimasa, I., S. Kaihara, and K. Atsumi (1978) A Morbidity Submodel of Infectious Diseases (RM-78-10).

Propoi, A. (1978) Models for Educational and Manpower Planning: A Dynamic Linear Programming Approach (RM-78-20).

Klementiev, A.A., and E.N. Shigan (1978) Aggregate Model for Estimating Health Care System Resource Requirements (AMER) (RM-78-21).

Hughes, D.J. (1978) The IIASA Health Care Resource Allocation Sub-Model Mark 2: The Allocation of Many Different Resources (RM-78-50).

Hughes, D.J. (1978) The IIASA Health Care Resource Allocation Submodel: Estimation of Parameters (RM-78-67).

Hughes, D.J. (1979) A Model of the Equilibrium Between Different Levels of Treatment in the Health Care System: Pilot Version (WP-79-15).

Fleissner, P. (1979) Chronic Illnesses and Socio-Economic Conditions: The Finland Case 1964 and 1968 (WP-79-29).

Shigan, E.N., D.J. Hughes, P. Kitsul (1979) Health Care System Modeling at IIASA: A Status Report (SR-79-4).

Rutten F.F.H. (1979) Physician Behavior: The Key to Modeling Health Care Systems for Government Planning (WP-79-60).

A Committee Report (1979) to IIASA by the Participants in an Informal Meeting on Health Delivery Systems in Developing Countries (CP-79-10).

Shigan, E.N., P. Aspden, and P. Kitsul (1979) Modeling Health Care Systems: June 1979 Workshop Proceedings (CP-79-15).

Hughes, D.J., E. Nurminski, and G. Royston (1979) Nondifferentiable Optimization Promotes Health Care (WP-79-90).

Rousseau, J.M., R.J. Gibbs (1980) A Model to Assist Planning the Provision of Hospital Services (CP-80-3).

Fleissner, P., K. Fuchs-Kittowski, and D.J. Hughes (1980) A Simple Sick-Leave Model used for International Comparison (WP-80-42).

Aspden, P., R.J. Gibbs, and T. Bowen (1980) DRAM Balances Care (WP-80-43)

Aspden, P., M. Rusnak (1980) The IIASA Health Care Resource Allocation Submodel: Model Calibration for Data from Czechoslovakia (WP-80-53).