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ON THE ESTIMATION OF MORBIDITY

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Preface

Health care system (HCS) managers need quantitative tools to assist them in their planning and management activities. The main task of the health care systems team of IIASA's Human Settlements and Services Area is to construct one of these analytic tools--a HCS model. While the prevalence estimation model presented here forms a part of the HCS model, it can also be used independently.

Knowledge about the prevalence of a disease (needs) gives the health care decision maker the opportunity to allocate resources better than he could using only incidence data (demands). For this reason, special investigations have been carried out to find out disease prevalence in some countries (see for example [10], [11], [12]). The method presented here is not as universal as the mentioned investigations, but for some diseases it allows one to estimate the true figures of prevalence. In these particular cases, the method allows for saving time and money and for answering questions about prevalence estimation.

Abstract

A mathematical model of a degenerative type disease is discussed in this paper. The model allows the user to estimate the number of new morbidity episodes and the prevalence of the disease, provided data on population age structure and age specific deaths are available. To verify the model some experiments with its computer version were carried out. The computer program listing and results of the experiments are presented.

On the Estimation of Morbidity

1. INTRODUCTION

The development of a health care system model is the main task of the health care systems team of the Human Settlements and Services Area at IIASA. The main concepts and results of the team's activities have been published in [1-4]. This work is a continuation of modeling the morbidity of degenerative diseases [2]. Available data used for experimenting with the model are:

a) population by age [5];
b) all causes death rates specified by age [5];
c) cause-specific death rates by age [5]; and
d) survival of sick individuals [6,7].

The approach presented here provides the possibility for estimating the prevalence of a given type of degenerative disease from indirect data.

2. PREVALENCE MODEL

Prevalence of a given disease at time t is defined to be the number of individuals afflicted with this disease at time t. It is specified by sex and age, per 100,000 population. *Morbidity rate*, or *incidence*, refers to the rate at which people contract the disease: the number per year per 100,000 people, specified by age and sex. *Death rates from all causes* and *death rates according to cause* are used here as they are defined in [5].

Let us consider a given degenerative type disease. An individual is considered *healthy* if he has not contracted the disease under consideration; otherwise, he is considered to be *sick*. The population is divided into N age strata. In addition:

p_i is the number of individuals in the i-th stratum, $i = \overline{1,N}$;

h_i is the number of healthy individuals;

μ_i is the incidence, specified by sex, per 100,000 healthy individuals from the i-th stratum;

$\tilde{D}_i$ is the death rate from all causes, specified by sex, per 100,000 population;

D_i^* is the death rate according to cause (given disease), specified by sex, per 100,000 population;

d_{ij} is the *specific death rate* and is defined to be the number of deaths per 100,000 sick individuals who contracted the disease in the i-th stratum j years ago.

$$D_i = \tilde{D}_i - D_i^* \tag{1}$$

$$\beta_{ij} = D_{i+j} + d_{ij} \tag{2}$$

The flow diagram for the prevalence is presented in Figure 1.

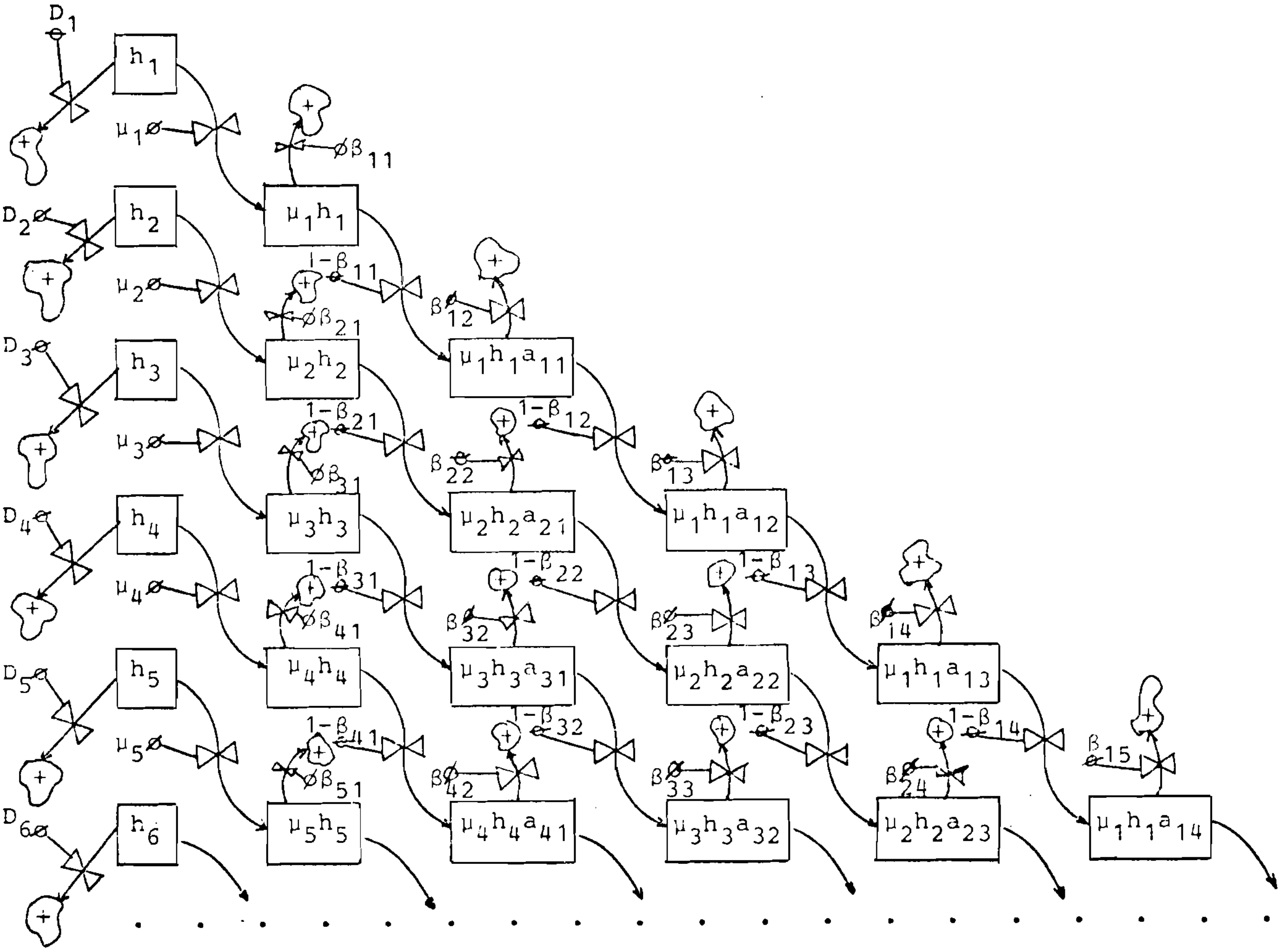

Figure 1

It can be seen from the diagram that the number of healthy people in the first stratum is equal to h_1. During one year, $\mu_1 h_1$ healthy people contract the disease. In the following year, $\mu_1 h_1 (1 - \beta_{11})$ are still alive, and so forth. Thus, one can see that for each stratum, balance equations, describing that the number of individuals in the i-th stratum is equal to the sum of healthy and sick individuals, can be written as follows:

$$p_1 = h_1 \tag{3.1}$$

$$p_2 = h_2 + \mu_1 h_1 \tag{3.2}$$

$$p_3 = h_3 + \mu_2 h_2 + \mu_1 h_1 (1 - \beta_{11}) \tag{3.3}$$

$$p_4 = h_4 + \mu_3 h_3 + \mu_2 h_2 (1 - \beta_{21}) + \mu_1 h_1 (1 - \beta_{11})(1 - \beta_{12}) \tag{3.4}$$

$$\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots$$

$$p_i = h_i + \mu_{i-1} h_{i-1} + \sum_{j=2}^{i-1} \mu_{i-j} h_{i-j} a_{i-j,j-1} \quad , \qquad i = \overline{3,N} \tag{3.i}$$

$$\cdots\cdots\cdots\cdots\cdots\cdots\cdots\cdots$$

where

$$a_{ij} = \prod_{k=1}^{j} (1 - \beta_{ik}) \quad , \qquad i = \overline{1,N-2} \quad ; \quad j = \overline{1,N-2} \quad . \tag{4}$$

In addition to (3), balance equations for the number of deaths in each stratum can be written as follows:

$$p_1 \tilde{D}_1 = h_1 D_1 \tag{5.1}$$

$$p_2 \tilde{D}_2 = h_2 D_2 + \mu_1 h_1 \beta_{11} \tag{5.2}$$

$$p_3 \tilde{D}_3 = h_3 D_3 + \mu_2 h_2 \beta_{21} + \mu_1 h_1 a_{11} \beta_{12} \tag{5.3}$$

$$p_4\tilde{D}_4 = h_4D_4 + \mu_3h_3\beta_{31} + \mu_2h_2a_{21}\beta_{22} + \mu_1h_1a_{12}\beta_{13} \tag{5.4}$$

. . . .

$$p_i\tilde{D}_i = h_iD_i + \mu_{i-1}h_{i-1}\beta_{i-1,1} + \sum_{j=2}^{i-1} \mu_{i-j}h_{i-j}a_{i-j,j-1}\beta_{i-j,j} \quad , \tag{5.i}$$

$$i = \overline{3,N}$$

. . . .

Systems (3) and (5) can be solved with respect to the unknown variables μ_i and h_i in the following way. From (3.1):

$$h_1 = p_1 \quad ; \tag{6}$$

then, from (3.2) and (5.2):

$$\mu_1 = \frac{p_2(\tilde{D}_2 - D_2)}{p_1(\beta_{11} - D_2)} \quad , \tag{7}$$

and

$$h_2 = p_2 \cdot \frac{\beta_{11} - \tilde{D}_2}{\beta_{11} - D_2} \quad . \tag{8}$$

Let us designate the last term in (3.i) as

$$F_i = \sum_{j=2}^{i-1} \mu_{i-j}h_{i-j}a_{i-j,j-1} \quad , \tag{9}$$

and the last term in (5.i) as

$$G_i = \sum_{j=2}^{i-1} \mu_{i-j}h_{i-j}a_{i-j,j-1}\beta_{i-j,j} \quad . \tag{10}$$

With one more auxiliary variable:

$$U_i = G_i - F_i D_i \quad , \tag{11}$$

with (9)-(11) taken into consideration, we now have from (3.i) and (5.i):

$$\mu_{i-1} = \frac{p_i(\tilde{D}_i - D_i) - U_i}{h_{i-1}(\beta_{i-1,1} - D_i)} \tag{12}$$

and

$$h_i = \frac{p_i(\tilde{D}_i - \beta_{i-1,1}) - G_i + F_i \cdot \beta_{i-1,1}}{D_i - \beta_{i-1,1}} \quad , \tag{13}$$

$$i = \overline{3,N} \quad .$$

The same description can be presented in matrix form. Let the number of sick individuals in the i-th stratum be designated as:

$$S_i = p_i - h_i \quad ; \tag{14}$$

then, matrix A can be written as:

$$A = \begin{bmatrix} 0 & 1 & a_{11} & a_{12} & a_{13} & a_{14} & a_{15} & \cdots & a_{1,N-4} & a_{1,N-3} & a_{1,N-2} \\ 0 & 0 & 1 & a_{21} & a_{22} & a_{23} & a_{24} & \cdots & a_{2,N-5} & a_{2,N-4} & a_{2,N-3} \\ 0 & 0 & 0 & 1 & a_{31} & a_{32} & a_{33} & \cdots & a_{3,N-6} & a_{3,N-5} & a_{3,N-4} \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdots & \cdot & \cdot & \cdot \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \cdots & 0 & 1 & a_{N-2,1} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \cdots & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \cdots & 0 & 0 & 0 \end{bmatrix}$$

Now systems (3) and (5) may be rewritten as:

$$\underline{S} = (\underline{\mu}H)' \cdot A \quad , \tag{3'}$$

and

$$P\tilde{\underline{D}} - H\underline{D} = (\underline{\mu}H)' \cdot B \quad , \tag{5'}$$

respectively, where:

$$H = \begin{bmatrix} h_1 & 0 & 0 & \cdots & 0 \\ 0 & h_2 & 0 & \cdots & 0 \\ 0 & 0 & h_3 & \cdots & 0 \\ \cdot & \cdot & \cdot & \cdots & \cdot \\ 0 & 0 & 0 & \cdots & h_n \end{bmatrix} ; \qquad P = \begin{bmatrix} p_1 & 0 & 0 & \cdots & 0 \\ 0 & p_2 & 0 & \cdots & 0 \\ 0 & 0 & p_3 & \cdots & 0 \\ \cdot & \cdot & \cdot & \cdots & \cdot \\ 0 & 0 & 0 & \cdots & p_N \end{bmatrix} ;$$

and:

$$B = \begin{bmatrix} 0 & \beta_{11} & a_{11}\beta_{12} & a_{12}\beta_{13} & \cdots & a_{1,N-2}\beta_{1,N-1} \\ 0 & 0 & \beta_{21} & a_{21}\beta_{22} & \cdots & a_{2,N-3}\beta_{2,N-2} \\ 0 & 0 & 0 & \beta_{31} & \cdots & a_{3,N-4}\beta_{3,N-3} \\ 0 & 0 & 0 & 0 & \cdots & a_{4,N-5}\beta_{4,N-4} \\ \cdot\;\cdot & \cdot\;\cdot & \cdot\;\cdot\;\cdot & \cdot\;\cdot\;\cdot & \cdots & \cdot\;\cdot\;\cdot\;\cdot\;\cdot \\ 0 & 0 & 0 & 0 & \cdots & a_{N-2,1}\beta_{N-2,2} \\ 0 & 0 & 0 & 0 & \cdots & \beta_{N-1,1} \\ 0 & 0 & 0 & 0 & \cdots & 0 \end{bmatrix} .$$

3. FURTHER DEVELOPMENT OF THE MODEL

It can be observed that the type of survival curve of sick individuals is dependent on the type of disease. For example, in Figure 2 [6] the survival of patients with inoperable stomach cancer is shown. The survival curve is approximately exponential: $\sigma(t) - 100e^{-\gamma t}(\%)$. It is shown in [6] that for most types of cancer, the survival curve is approximately the same as that of the exponential function, the difference between them being determined only by the parameter γ.

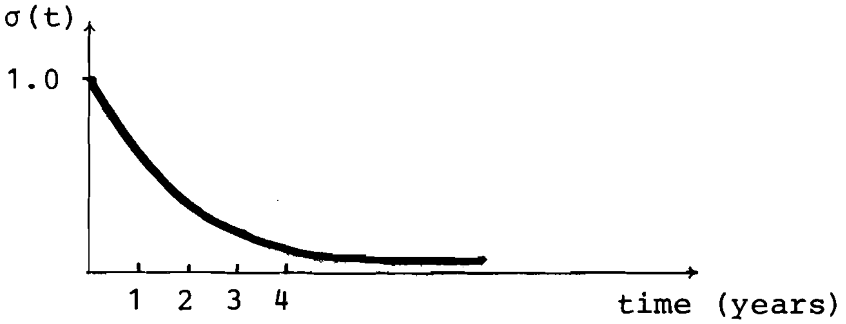

Figure 2

In the case of cardiovascular diseases, the survival curve would be of the shape shown in Figure 3.

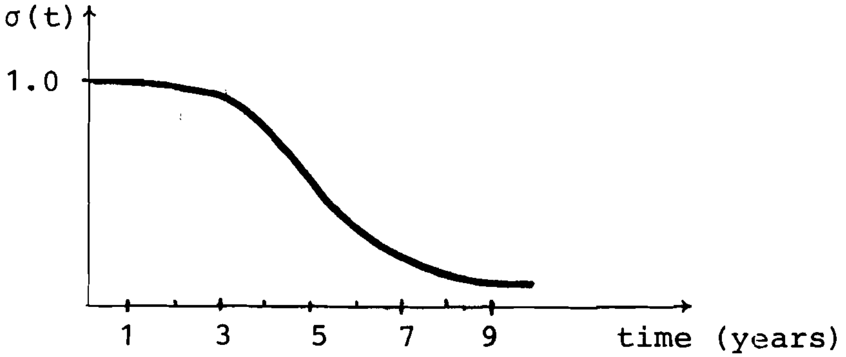

Figure 3

Both curve types (Figures 2 and 3) can be described by the general formula:

$$\sigma(j) = \frac{1}{1 + \alpha(e^{j\gamma} - 1)} , \qquad (15)$$

with $0 < \alpha < 1$ and discrete time $j = 0,1,2,\ldots$

So, with the help of (15), the survival curve for every degenerative type of disease can be presented by a pair of parameters $\underline{\alpha}$ and $\underline{\gamma}$. The parameters are vectors if the shape of the curve is dependent on the initial age. In this case, the survival should be specified by the age:

$$\sigma_i(j) = \frac{1}{1 + \alpha_i(e^{j\gamma_i} - 1)} \quad . \tag{15a}$$

The above-determined death rate d_{ij} can now be designated as:

$$d_{ij} = \sigma_i(j + 1) - \sigma_i(j) \quad . \tag{16}$$

Taking into account the above-mentioned considerations, a special catalogue of survival curves for degenerative type diseases (and their vector-parameters $\underline{\alpha}$ and $\underline{\gamma}$) can be prepared and then the tables for d_{ij} can be calculated in accordance with the given diseases.

Also, the computer program for morbidity estimation can be supplemented by an interpolation subroutine. This is necessary because the initial data (death rates, population age structure) are usually aggregated.

This method is to be extended for the cases when treatment alters the survival curve. In other words, the influence of HCS resource consumption on prevalence will be taken into account. But as usual, the more accurate initial data we have (about mortality, population structure and survival), the more likely estimation of prevalence can be provided. This is the reason why the method cannot be implemented successfully for the prevalence estimation of psychiatric diseases.

4. RESULTS OF COMPUTER EXPERIMENTS

Estimation of malignant neoplasm* prevalence was carried out for Austria, Bulgaria and France. [5] and [6] were used

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*ICD, A-List: A45-A57.

as sources of the initial data. d_{ij} was considered as independent of i (we still need survival data) and was set equal to 0.2.

The input data derived from [5] is listed in Appendix 2. The results of calculations are presented in Appendix 3. To simplify the comparison of the number of deaths, according to disease, with the prevalence figures for the same age group, these figures are presented in a double column.

APPENDIX 1

Computer Program Listing

```
APR 12 14:19 1977  MORA,F PAGE 1
C      THIS IS THE NEW VERSION
        DIMENSION P(80),BETA(71,71),DTIL(80),AMU(80),XAA(80),XAB(80),
     1XAU(80),A(71,71),H(80),D(80),SI(80)
         N=71
      READ(5,22) (P(I),I=1,N)
   22 FORMAT(1X,7F10.2)
      READ(4,23) (DTIL(I),I=1,N+2)
   23 FORMAT(1X,7F10.6)
      READ(8,23) (D(I),I=1,N+2)
C FILE P(I),NAME 'POPUL', NO 5, AGE STRUCTURE
C FILE DTIL(I), NAME 'ALCODE', NO 4, ALL CAUSES DEATH RATE
C FILE D(I),NAME 'ELIDE', NO 8, AL CAU DE RA WITH SPEC ONE ELIMIN
C    BETA FILE IS CREATED
      DO 91 I=1,N
      DO 91 J=1,N-I+2
      BETA(I,J)=D(I+J)+0.2
C     BETA(I,J)=D(I+J)+0.07*(3.*EXP(FLOAT(J))/10000000.)
C    1/(1.+(3./10000000.)*(EXP(FLOAT(J))-1.))+0.008
   91 CONTINUE
C A FILE IS CREATED
      DO 29 I=1,N
      A(I,1)=1.-BETA(I,1)
      DO 29 J=2,N-I
      A(I,J)=A(I,J-1)*(1.-BETA(I,J))
   29 CONTINUE
        H(1)=P(1)
        H(2)=P(2)*(BETA(1,1)-DTIL(2))/(BETA(1,1)-D(2))
      SICKY=.0
        AMU(1)=(P(2)*(DTIL(2)-D(2)))/(P(1)*(BETA(1,1)-D(2)))
        DO 2 I=3,N
        XAB(I)=0.
        XAA(I)=0.
        DO 1 J=2,I-1
        XAA(I)=XAA(I)+AMU(I-J)*H(I-J)*A(I-J,J-1)
        XAB(I)=XAB(I)+AMU(I-J)*H(I-J)*BETA(I-J,J)*A(I-J,J-1)
    1 CONTINUE
      XAU(I)=XAB(I)-XAA(I)*D(I)
      UPP=P(I)*(DTIL(I)-D(I))-XAU(I)
      DOW=H(I-1)*(BETA(I-1,1)-D(I))
      AMU(I-1)=UPP/DOW
      UPE=P(I)*(DTIL(1)-BETA(I-1,1))-XAB(I)+XAA(I)*BETA(I-1,1)
      DWN=D(I)-BETA(I-1,1)
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APR 12 14:19 1977  MORA.F PAGE 2

      H(I)=UPE/DWN
      SI(I)=P(I)-H(I)

      SICKY=SICKY+SI(I)
    2 CONTINUE
         WRITE(6,3)
    3 FORMAT(4X,'AGE',8X,'POPUL',7X,'PREVALENCE',3X,'HEALTHY',3X,
     1'MORBIDITY',3X,'ALCODE',7X,'ELIDE'7X,'XAA',7X,'XAB',7X,'XAU',
     13X,'BETA',5X,'A(1,J)')
         DO 5 I=1,N
         WRITE(6,4) I,P(I),SI(I),H(I),AMU(I),DTIL(I),D(I),XAA(I),XAB(I),
     1XAU(I),BETA(1,I),A(1,I)
    4 FORMAT(3X,I3,5X,F10.2,3X,F10.2,3X,F10.2,2X,F9.6,3X,F10.7,2X,F10.7
     1,3(F10.4),2F10.7)
    5 CONTINUE
      WRITE(6,25) SICKY
   25 FORMAT(///,5X,'PREVALENCE IS',2X,F10.2)
       STOP
      END
```

APPENDIX 2

Initial Data

	AUSTRIA			BULGARIA			FRANCE		
File / Age	P(I)	D(I)	DTIL(I)	P(I)	D(I)	DTIL(I)	P(I)	D(I)	DTIL(I)
1	111.4	0.026100	0.026101	132.0	0.024922	0.024922	854.0	0.01419	0.01419
2	120.1	.018200	.018201	131.6	.017017	.017017	848.8	.00500	.00500
3	126.8	.010200	.010201	131.1	.009112	.009112	843.6	.00175	.00175
4	126.1	.002205	.002201	130.7	.001208	.001208	838.4	.00079	.00079
5	125.3	.001700	.001701	130.2	.001102	.001102	833.2	.00068	.00068
6	125.0	.001300	.001301	129.8	.000996	.000996	828.0	.00062	.00062
7	124.0	.001050	.001051	129.3	.000890	.000890	822.8	.00056	.00056
8	123.5	.000850	.000851	128.9	.000784	.000784	817.6	.00050	.00050
9	123.0	.000750	.000751	128.4	.000678	.000678	812.4	.00046	.00046
10	122.5	.000540	.000541	128.0	.000572	.000572	807.2	.00041	.00041
11	122.0	.000440	.000441	127.5	.000466	.000466	802.0	.00038	.00038
12	120.0	.000529	.000541	128.5	.000503	.000506	805.3	.00042	.00042
13	116.0	.000529	.000541	129.4	.000540	.000545	808.6	.00046	.00046
14	114.0	.000638	.000651	130.4	.000578	.000851	811.9	.00050	.00050
15	112.5	.000642	.000655	131.3	.000615	.000625	815.2	.00056	.00056
16	111.3	.000711	.000725	132.3	.000652	.000665	818.5	.00063	.00063
17	110.0	.000840	.000855	133.2	.000689	.000704	821.8	.00072	.00070
18	107.5	.000939	.000955	134.2	.000727	.000745	825.1	.00075	.00075
19	105.0	.001037	.001055	135.1	.000764	.000784	828.4	.00085	.00085
20	104.0	.001137	.001155	136.1	.000802	.000823	831.7	.00093	.00093
21	103.3	.001235	.001255	137.0	.000839	.000863	835.0	.00102	.00102
22	102.7	.001238	.001260	134.9	.000866	.000898	814.6	.00103	.00104
23	102.1	.001255	.001280	132.7	.000893	.000933	794.2	.00104	.00105
24	101.5	.001262	.001290	130.6	.000920	.000968	773.8	.00105	.00107
25	101.0	.001278	.001310	128.4	.000947	.001003	753.4	.00109	.00111
26	100.6	.001284	.001320	126.3	.000974	.001037	733.0	.00112	.00115
27	100.2	.001300	.001340	124.2	.001002	.001072	712.6	.00113	.00117
28	99.8	.001304	.001350	122.0	.001029	.001107	692.2	.00115	.00119
29	99.4	.001318	.001370	119.9	.001056	.001142	671.8	.00116	.00120
30	99.0	.001322	.001380	117.7	.001083	.001177	651.4	.00117	.00122
31	97.7	.001334	.001400	115.6	.001110	.001212	631.1	.00119	.00124
32	96.4	.001460	.001540	116.9	.001188	.001314	636.3	.00124	.00132
33	95.2	.001577	.001670	118.1	.001267	.001415	639.0	.00126	.00140
34	94.0	.001702	.001810	119.4	.001346	.001517	641.8	.00132	.00152
35	93.7	.001825	.001950	120.6	.001424	.001619	644.5	.00143	.00175
36	92.4	.001920	.002090	121.9	.001503	.001721	647.3	.00156	.00181
37	91.1	.002060	.002230	123.2	.001582	.001823	650.1	.00167	.00200
38	89.8	.002160	.002360	124.4	.001660	.001925	652.8	.00178	.00205
39	88.5	.002270	.002500	125.7	.001739	.002026	655.6	.00195	.00217
40	87.2	.002370	.002640	126.9	.001817	.002128	658.3	.00212	.00250
41	86.7	.002478	.002780	128.2	.001896	.002230	661.1	.00228	.00265
42	86.2	.002720	.003060	126.0	.002110	.002504	653.0	.00241	.00270
43	85.7	.002960	.003340	123.7	.002324	.002778	644.9	.00259	.00305
44	85.1	.003210	.003630	121.5	.002538	.003052	636.8	.00278	.00350
45	84.6	.003440	.003910	119.2	.002752	.003326	628.7	.00300	.00365
46	84.1	.003665	.004190	117.0	.002966	.003600	620.6	.00322	.00393
47	83.6	.003900	.004480	114.8	.003180	.003874	612.4	.00338	.00420
48	83.1	.004110	.004760	112.5	.003394	.004148	604.3	.00350	.00460
49	82.6	.004300	.005040	110.3	.003608	.004422	596.2	.00373	.00500
50	82.1	.004490	.005320	108.0	.003822	.004696	588.1	.00398	.00550
51	82.5	.004668	.005610	105.8	.004036	.004970	580.0	.00457	.00579
52	82.9	.005480	.006510	104.2	.004772	.005878	572.0	.00488	.00649
53	83.3	.006260	.007410	102.6	.005509	.006786	564.0	.00543	.00700
54	83.7	.007000	.008300	101.0	.006245	.007694	556.0	.00585	.00750
55	84.1	.007800	.009200	99.4	.006982	.008602	548.0	.00631	.00805
56	84.5	.008500	.010100	97.8	.007718	.009510	540.0	.00670	.00900
57	84.9	.009200	.011000	96.2	.008454	.010418	532.0	.00742	.00960
58	85.3	.009900	.011900	94.6	.009191	.011326	524.0	.00800	.01050
59	85.7	.010600	.012800	93.0	.009927	.012234	516.0	.00860	.01125
60	86.1	.011300	.013700	91.4	.010663	.013142	508.0	.00955	.01250
61	84.6	.011950	.014600	89.8	.011400	.014050	500.0	.01061	.01375
62	83.1	.014120	.017120	86.7	.013681	.016608	492.5	.01100	.01500
63	81.6	.01644	.019640	83.6	.015963	.019166	485.0	.01200	.01600
64	80.1	.018760	.022190	80.5	.018244	.021724	477.5	.01305	.01750
65	78.6	.020960	.024710	77.4	.020526	.024282	470.0	.01450	.01900
66	77.1	.023180	.027230	74.3	.022807	.026840	462.5	.01600	.02100
67	75.6	.025350	.029750	71.2	.025089	.029398	455.0	.01700	.02250
68	74.1	.027470	.032270	68.1	.027370	.031956	447.5	.01900	.02450
69	72.6	.029590	.034790	65.0	.029652	.034514	440.0	.02125	.02700
70	71.1	.03176	.037310	61.9	.031933	.037072	432.5	.02200	.02900
71	67.4	.033633	.039830	58.8	.034215	.039630	425.0	.02544	.03157
72	63.7	.039220	.045820	55.7	.036496	.042188	410.3	.02750	.03500
73	60.0	.044840	.051840	52,6	.038778	.044746	395.5	.03125	.03875
74	56.3	.050360	.057860	49.5	.041059	.047304	380.8	.03600	.04250
75	52.6	.055880	.063880	46.4	.043341	.049862	366.0	.03900	.04580

APPENDIX 3

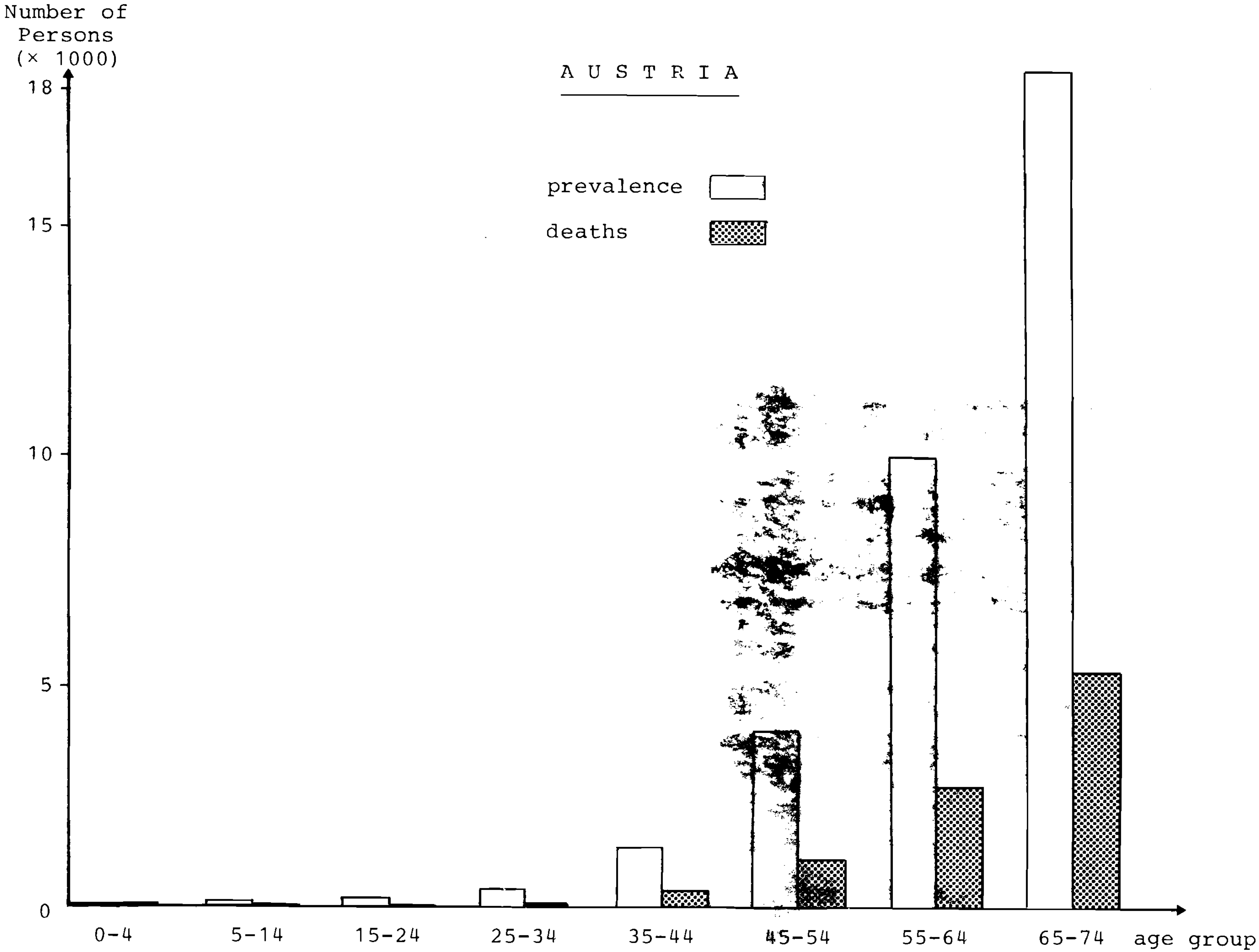
Results of Calculations

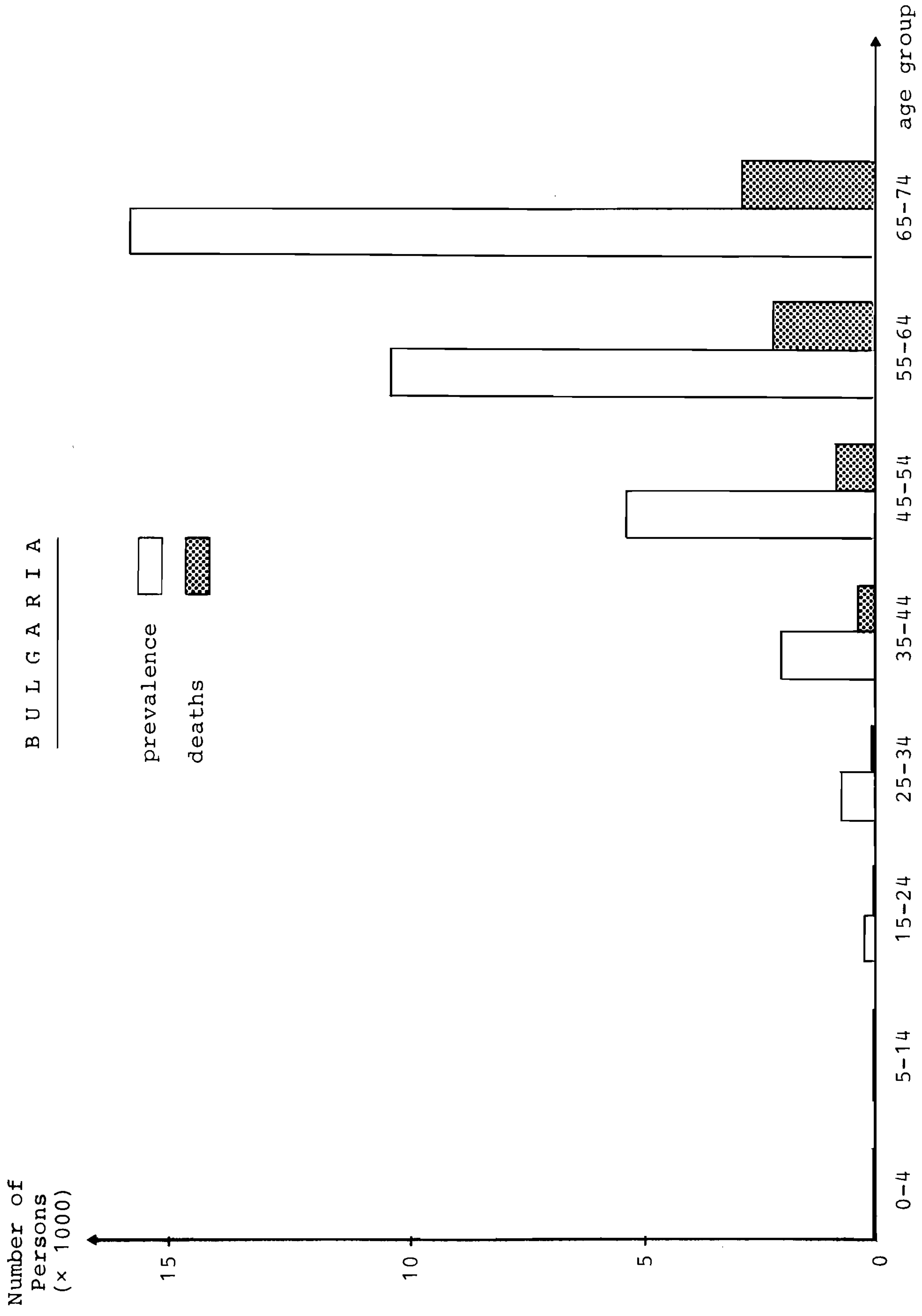
	AUSTRIA		BULGARIA		FRANCE	
Age	Prevalence*)	Deaths**)	Prevalence*)	Deaths**)	Prevalence*)	Deaths**)
0-4	0	0	0	6***)	0	19***)
5-14	40	10	20	12	0	64***)
15-24	110	22	190	32	210	121
25-34	340	78	680	104	3 210	312
35-44	1 290	332	2 210	392	12 690	2 186
45-54	3 810	950	5 380	907	38 210	6 314
55-64	10 780	2 600	10 410	2 214	81 480	14 346
65-74	18 200	5 028	15 950	2 923	153 400	23 165

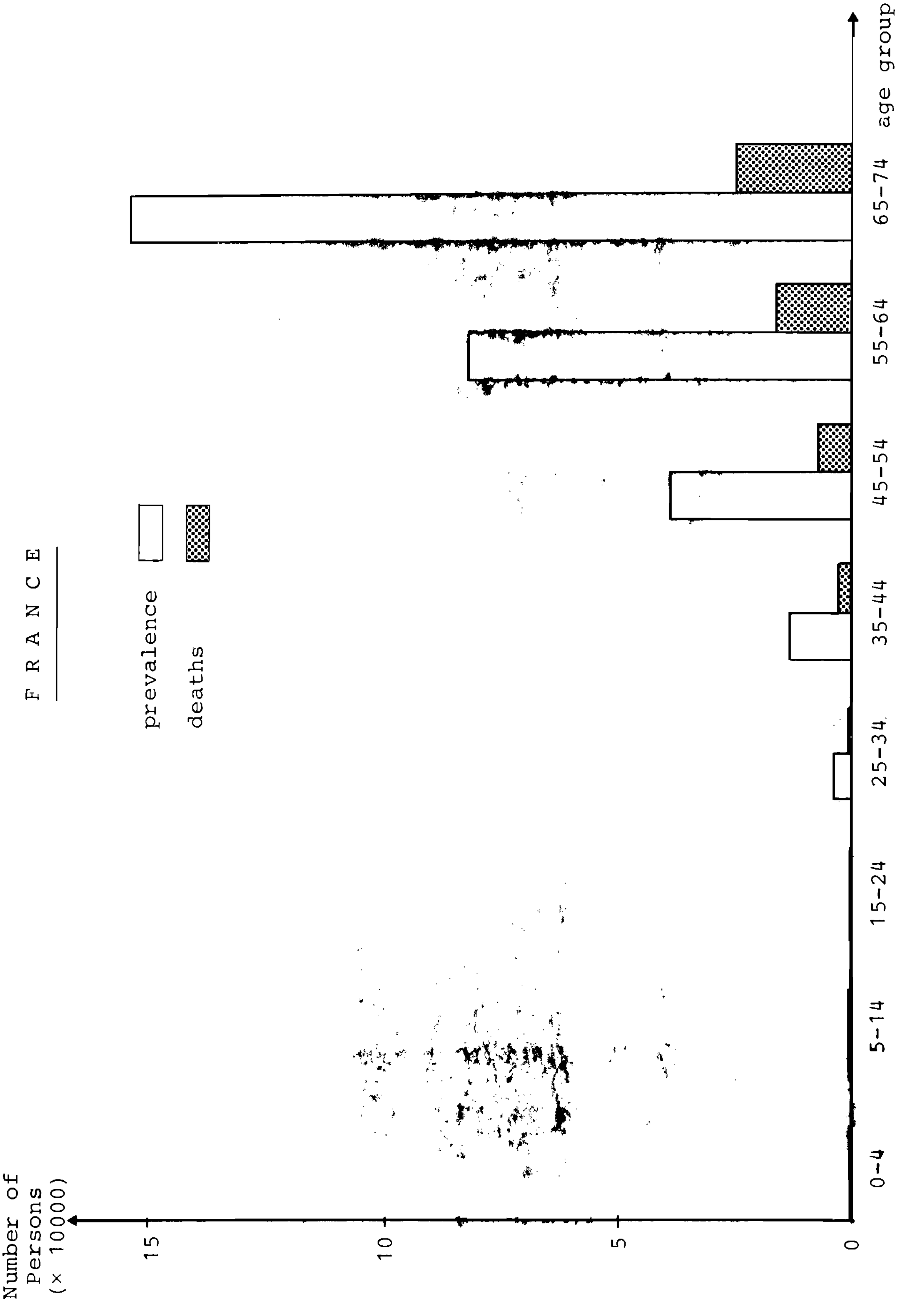
*) Absolute numbers, using estimation method.

**) Absolute numbers, from [6].

***) Figure neglected as input data (in corresponding death rate).


A U S T R I A
prevalence
deaths
Number of Persons (× 1000)
18
15
10
5
0
0-4
5-14
15-24
25-34
35-44
45-54
55-64
65-74
age group


B U L G A R I A
prevalence
deaths
Number of Persons (× 1000)
15
10
5
0
0-4
5-14
15-24
25-34
35-44
45-54
55-64
65-74
age group


F R A N C E
prevalence
deaths
Number of Persons (× 10000)
15
10
5
0
0-4
5-14
15-24
25-34
35-44
45-54
55-64
65-74
age group

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