

Online Resource 1

Disease Incidence and Mortality Among Older Americans and Europeans

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Evaluation of Survey Mortality Reports

In order to evaluate the mortality data in both surveys, we follow these steps: 1) we compared mortality rates estimated from survey data to life-tables mortality rates from the Human Mortality Data Base (HMD) in 2004 for nine European countries (SHARE baseline) and the U.S.; 2) we selected into our analysis the five European countries and the U.S. for which survey estimates are relatively close to life table estimates between ages 50 and 80, with high response rates and 3) we pooled the European data and computed partial life expectancy to see how closely they represent the entire set of SHARE countries in terms of life expectancy.

Mortality for the 5 countries we use in our analysis is quite close to that in the HMD, with the exception of some ages for the Netherlands and Italy where survey-based estimates are slightly below the life-table estimates. Average probability of dying at age 50 (q_{50}) in 2004 in the HMD for the set of 9 European countries in SHARE (excluding Greece and Switzerland) is 0.0035; while the average probability of dying for our subset 5 European countries is 0.0029. The probability of dying for the U.S. is 0.0044. In 2004, average life expectancy at age 50 in the HMD for the set of 9 European countries is 31.7 years; while life expectancy in our 5-country subsample is 31.8. At the same date, life expectancy in the U.S. is a year lower or 30.8 years.

Partial life expectancies between age 50 and 80 estimated from both the surveys and the HMD in 2004 indicating that partial life expectancies are slightly higher from the survey estimates for four of the selected SHARE countries, but similar to the HMD for the U.S. and Spain.

Partial life expectancy between ages 50-80, 2004

Country	Human Mortality Database	Survey Estimates (SHARE and HRS)
Denmark	25.4	26.2
France	26.5	27.0
Italy	26.8	27.2
Netherlands	26.2	27.1
Spain	26.6	26.3
United States	25.6	25.4

Source: SHARE and HRS (2004) and HMD (2004)

Effect of Differential Response Rates

Because of high levels of nonresponse in SHARE, we analyzed the determinants of nonresponse for the selected SHARE countries using multinomial logit models for the outcomes of responded, died and status unknown, with baseline sociodemographic variables (age, sex, foreign born, marital status, and years of education), health covariates (health behaviors and health conditions) and home ownership for those individuals aged 50 to 79 (Table A.1). We replicated the same analysis for the U.S.

Overall, we found no consistent pattern across countries in the association of the observed characteristics with being in the unknown status, although some health conditions are negatively associated with nonresponse which would suggest that sicker individuals are more likely to have responded rather than be lost from SHARE; and in some cases for HRS, too. To measure how much these associations matter for our calculations, we constructed inverse probability weights to correct for selection on those observables following the strategy outlined by Michaud et al. (2011). We multiplied the SHARE baseline weight, which corrects for differential baseline nonresponse based on age and sociodemographics using census information, by this inverse probability weight, which now corrects for differential nonresponse in the follow-up, to obtain a new weight for the follow-up sample. When we compared the distribution of this new weight to the weight provided by SHARE, we concluded that the distributions were similar and that our

approach was similar to the SHARE approach in developing the weights. We also compared the incidence rates reported in our analysis based on SHARE weights with incidence rates based on our version of the weights and found them to be very similar. Therefore, we conclude that differential nonresponse is accounted for in the SHARE weights and unlikely to bias the inferences we make on the two populations. In our analysis, we use the SHARE/HRS weights for prevalence and mortality and the inverse probability weights for incidence to account for non-follow-up.

To measure the extent of bias introduced by non-follow-up, we used the refreshment sample entering in wave 2. We compare prevalence by age in wave 2 for respondents who answered in wave 1 (the follow-up sample) and the refreshment sample. If non follow-up is not a problem, prevalence rates should be similar. If it is a problem but the missing at random assumption is sufficient, then the weighted prevalence should line up with prevalence in the refreshment sample. Results are presented in the table A.2, weighted for those in the follow-up using inverse probability weights and un-weighted. First, differences are generally small between the un-weighted follow-up sample and the refreshment sample. Second, the weights do very little to change the prevalence numbers obtained in the follow-up sample. Taken together, these results suggest that non follow-up is unlikely to distort the comparisons we make between both surveys, HRS and SHARE.

Table S1
Multinomial Logit Results: Characteristics associated with Death and Unknown Status
Relative to Alive Status, aged 50-79

Panel A: Died				
Variables	U.S.		Europe	
<i>Socio-demographic</i>				
Age	0.06	***	0.07	***
Male	0.47	***	1.05	***
Foreign	-		-0.41	
Marriage	-0.17	***	-0.50	**
Years of education	0.00		-0.04	**
<i>Health behaviors</i>				
Smoking	0.17	***	0.24	***
Obese	-0.43	***	-0.45	*
<i>Health Conditions</i>				
Cancer	0.90	***	1.13	***
Hypertension	0.22	*	0.14	
Heart disease	0.52	***	0.28	
Stroke	0.51	***	0.91	***
Diabetes	0.79	***	0.69	***
Lung disease	0.76	***	0.46	*
<i>Home ownership</i>	-0.64	***	-0.14	
<i>Any missing</i>	-	-	-0.07	
<i>Constant</i>	-8.00	***	-8.72	***
Panel B: Status Unknown				
	U.S.		Europe	
<i>Socio-demographic</i>				
Age	-0.05	***	0.00	
Male	0.30	***	0.13	**
Foreign	-		0.32	***
Marriage	-0.21	**	-0.32	***
Years of education	-0.04	***	0.00	
<i>Health behaviors</i>				
Smoking	0.01		-0.11	***
Obese	-0.06		-0.27	***
<i>Health Conditions</i>				
Cancer	-0.38	**	-0.13	
Hypertension	-0.11		-0.13	**
Heart disease	-0.29	*	-0.02	
Stroke	-0.14		-0.09	
Diabetes	-0.05		0.10	
Lung disease	-0.53	**	-0.35	***
<i>Home ownership</i>	-0.25	**	0.02	
<i>Any missing</i>	-		0.26	**
<i>Constant</i>	1.07	**	-0.25	

Source: SHARE (2004) and HRS (2004). Europe includes: Denmark, France, Italy, the Netherlands, and Spain.

Table S2
Comparison of the follow-up and refreshment sample by health conditions

Health conditions	Follow-up	Refreshment	Difference	z
Heart Disease	0.099	0.096	0.003	0.43
Hypertension	0.334	0.300	0.034	3.90
Stroke	0.029	0.025	0.004	1.1
Diabetes	0.112	0.090	0.022	3.81
Lung Disease	0.060	0.054	0.006	1.33
Cancer	0.033	0.045	-0.012	-3.30

Notes: Prevalence at wave 2 is weighted using SHARE wave 2 weights for the refreshment sample and with inverse probability weights for the follow-up sample. The z-statistic from an independent sample test for the equality of proportions with unequal sample size is also reported.

Estimation of Incidence and Mortality models

For estimating both incidence and mortality, the metric for time is the age of the respondent, t , and T is the random variable that denotes the age at which the event occurs. We observe each respondent at two possible ages: (t_1, t_2) . The gap between observation times is irregular, not constant, and we know if the event occurred during the age interval.

Let $d = 1$ denote that the health event (incidence or mortality) occurred during the time interval and $d = 0$ does not. We also observe a vector of age-invariant characteristics x . Our estimation procedure will account for the partial observation of the age of onset of diseases or mortality using a grouped duration model (Sueyoshi, 1995).

We assume a proportional continuous time hazard model of the following form:

$$h(t) = h_0(t) \exp(x\beta)$$

where x includes a constant.

We use two specific models of the baseline hazard ($h_0(t)$) for incidence and mortality. First, the baseline hazard takes the Weibull form for the incidence models:

$$h_0(t) = \alpha t^{\alpha-1}$$

The Weibull distribution is used in our incidence analysis (hazard models) to address the nonmonotonic pattern of onset with age observed in the descriptive data. Second, we take the standard Gompertz baseline hazard for mortality:

$$h_0(t) = \exp(\alpha t)$$

For an individual observed at ages (t_1, t_2) , we derive the probability that the event occurs between these two ages using the continuous hazard. We do this for both incidence of disease and mortality. The probability that the event occurs (incidence or mortality) is given by:

$$P(t_2 > T > t_1 | T > t_1, x) = 1 - \exp(-H_0_{t_1}^{t_2} \exp(x\beta))$$

where the integrated baseline hazard from age t_1 to t_2 is given by

$$HO_{t_1}^{t_2} = \int_{t_1}^{t_2} h_0(s) ds$$

Denoting the probability of onset:

$$p_1(x, t_1, t_2) = P(t_2 > T > t_1 | T > t_1, x)$$

Therefore, the probability that the health event does not occur during the age interval is given by:

$$p_0(x, t_1, t_2) = 1 - p_1(x, t_1, t_2)$$

Then the probability of observing the health event (d) given x and age t is given by:

$$p(d_i | x_i, t_{i,1}, t_{i,2}) = p_1(x_i, t_{i,1}, t_{i,2})^{d_i} p_0(x_i, t_{i,1}, t_{i,2})^{1-d_i}$$

The maximum likelihood estimator for $\theta = (\alpha, \beta)$ maximizes

$$\frac{1}{N} \sum_i \log p(d_i | x_i, t_{i,1}, t_{i,2})$$

Reconstructing Prevalence

For the follow-up sample, we reconstructed wave 2 prevalences by age from wave 1 prevalence, and wave 1 to 2 predicted incidences and survival for each condition. Denoting $s(t,d)$ the two-year survival rate at age t conditional on having the disease $d=1$ or not $d=0$, $i(t)$ the two-year incidence rate at age t , and $p(t)$ the prevalence at age t , we have that prevalence at age $t+2$ is given by:

$$p(t+2) = s(t,1)p(t) + i(t) s(t,0) (1-p(t)).$$

To do this, we used the incidence and mortality models estimated in Table 3 and 5 to compute $s(t,d)$ and $i(t)$. We smooth rates as a function of age using a lowess filter. We used inverse probability weights for incidence rates to correct for non-follow-up and use life table survival rates to correct for the overestimation of survival rates. Because of differences in question design, actual SHARE prevalence in wave 2 is lower than predicted by incidence and survival. Some respondents report not being bothered by the condition in wave 2. Since we did not allow for recovery in our definition of prevalence, in order to compare with U.S., we correct wave 2 prevalence in SHARE by assigning automatically prevalence in wave 2 for those who had the condition in wave 1. Figure A.1 and A.2 report actual and predicted prevalence in wave 2 for SHARE and HRS. Not surprisingly, we conclude that actual wave 2 prevalence and predicted wave 2 prevalence line up very well in both HRS and SHARE. This method for reconstructing prevalence is used in Figure 4, 5 and 6.

Figure S1
Comparison of predicted wave 2 (2006) prevalence and actual wave 2 prevalence in the follow-up sample for the U.S.

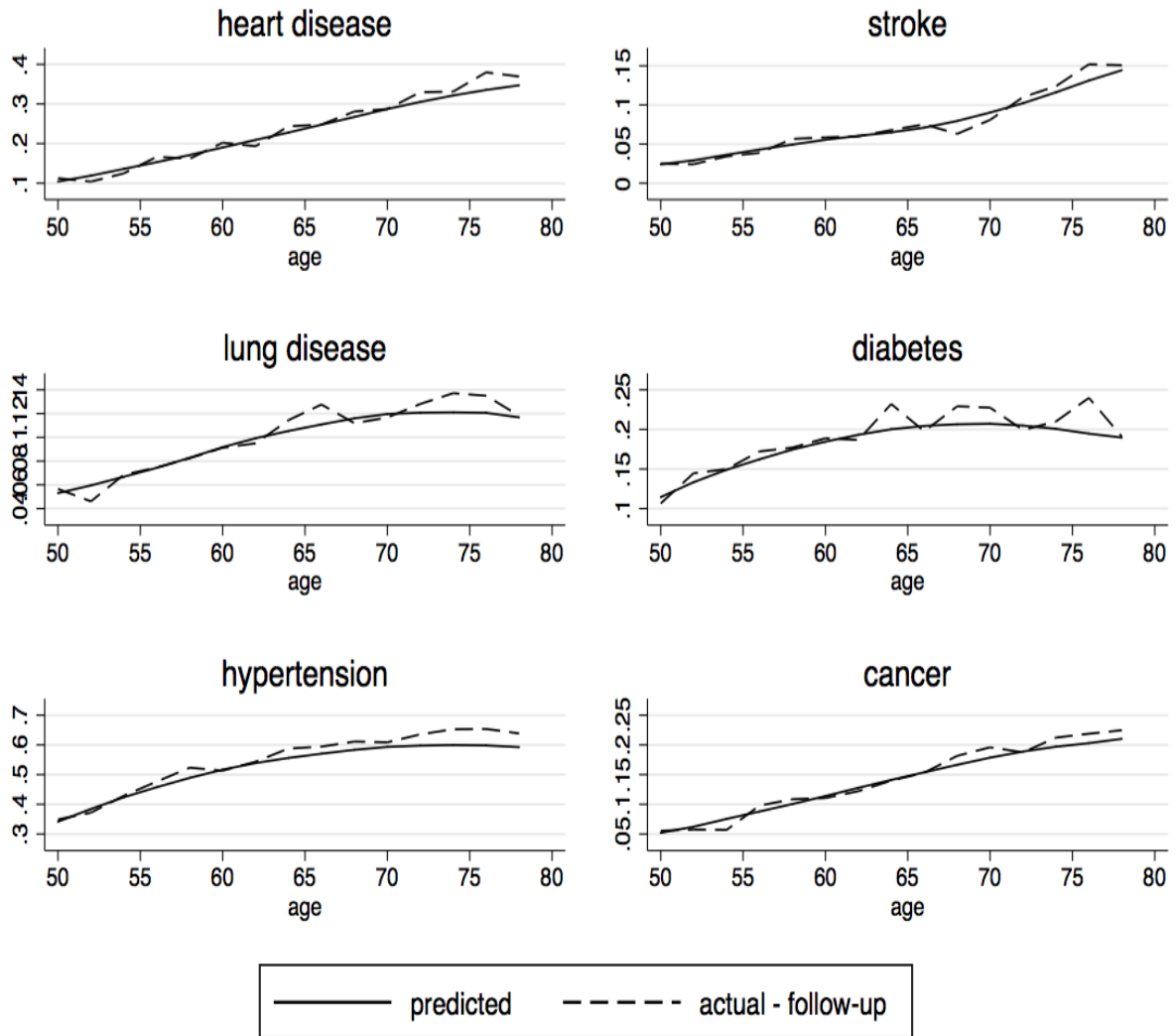


Figure S2
Comparison of predicted wave 2 (2006) prevalence and actual wave 2 prevalence in the follow-up sample for Europe

