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Common mortality modelling and coherent forecasts. An empirical analysis of worldwide mortality data

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Abstract

A new common mortality modeling structure is presented for analyzing mortality dynamics for a pool of countries, under the framework of generalized linear models (GLM). The countries are first classified by fuzzy c-means cluster analysis in order to construct the *common sparse age-period model* structure for the mortality experience. Next, we propose a method to create the *common sex difference age-period model* structure and then use this to produce the *residual age-period* model structure for each country and sex. The time related principal components are extrapolated using dynamic linear regression (DLR) models and coherent mortality forecasts are investigated. We make use of mortality data from the "Human Mortality Database".

Keywords: Fuzzy c-Means Cluster; Generalized Linear Models; Sparse Principal Component Analysis; Dynamic Linear Regression; Mortality Forecasting; Residuals; Coherent;

1. Introduction

The aim of this paper is to construct common mortality trends from a pool of countries with similar mortality experiences, and accordingly to model and forecast mortality rates for each individual country in a coherent manner, allowing for age-period effects. Many authors have discussed the benefits of common mortality modeling and coherent forecasts. Li and Lee (2005) report that mortality patterns and trajectories in closely related populations are likely to be similar in some respects, and differences are unlikely to increase in the long run, and it should therefore be possible to improve the mortality forecasts for individual countries by taking into account the patterns in a larger group. It is apparent that the populations of the world are becoming more closely linked by communication, transportation, trade, technology, and disease. They state that it would be improper to prepare mortality forecasts for individual national populations in isolation from one another and still more so for the regions within a country. They further argue that it seems likely that forecasts for individual countries could be improved by exploiting the additional information contained in the experience of similar countries. Non-divergent forecasts for sub-populations within a larger population have been labeled "coherent". Lee (2003) reports that national mortality trends should be viewed in a larger international context rather than being analyzed and projected individually, and the approach of forecasting mortality for individual countries with reference to the international context is very appealing, and should be the natural route for future developments to take. Also, he believes that whether this approach is applied to life expectancy itself, or to a Lee- Carter type k factor, or in some other way, will have to be settled by further research. Wilson (2001) has documented a global convergence in mortality levels, and states that, if we consider demographic transition in the light of a broader modernization theory, it is clear that social and demographic change has progressed far more rapidly than economic development, and that a large majority of the world's population is (or soon will be) demographically "modern" by any definition. White (2002) has reported convergence in life expectancy among 21 industrialized countries during the postwar period, and he mentions that the wealthy world is merely becoming more similar in its lifestyles, and globalization may be occurring among rich countries in practices affecting mortality, and this could lead to converging mortality patterns. Further, many authors discuss the processes of catch-up and convergence. Oeppen and Vaupel (2002) have noted that some countries converge toward the leader (e.g. Japan), some have moved away from it (e.g. the US in recent decades), and some move more or less parallel to it. White (2002) has found that nations experience more rapid life expectancy gains when they are farther below the international average, and conversely, and therefore tend to converge towards the average.

The remainder of the paper is organised as follows. In section 2, utilizing mortality data from the "Human Mortality Database, we group 35 countries using fuzzy c-means cluster analysis. In this way, we form the West-cluster and East-cluster countries, for both sexes, and we construct the common age-time mortality dynamics, using 19 males West-cluster countries. Next, we employ Sparse Principal Component Analysis (SPCA) to these common mortality rates, in order to derive the *common age-period model* structure, for both sexes. In section 3, we construct the sex difference mortality dynamics, and compare the mortality experience of males and females. In section 4, we analyze the residual particularities for each country, based on the *common age-period model* for males, and the *common age-period* and *sex difference model* structure for females. In section 5, we utilize dynamic linear regression (DLR) model structures, to implement coherent forecasts. Finally, in section 6, we discuss the results and offer some concluding comments.

2. Common age-period mortality dynamics

Initially, we need to choose which countries will be selected to describe the common patterns of mortality dynamics. We require the pooled countries to contain similar characteristics. Cluster analysis is a reasonable approach to separate the countries into clusters with similar mortality dynamics. Data clustering is the process of dividing data elements into classes or clusters so that items in the same class are as similar as possible, and items in different classes are as dissimilar as possible.

Following Hatzopoulos and Haberman (2009)), the log-graduated central mortality rates, in age-period effects, can be decomposed as an *age-period association model* structure (see model 2, Hatzopoulos and Haberman (2009)). According to this model structure, the main time effects component, $b(t)$ values, is an index of the level of mortality that captures the overall time trend at all ages, and summarizes the overall mortality dynamics across time. Also, the main time trends are independent of the level of mortality (a zero centred vector, constructed by linear combinations of principal component scores). Therefore, we could base our cluster analysis on these main time trends. In classic cluster analysis, the data are divided into distinct clusters, where each data element belongs to exactly one cluster. Alternatively, in fuzzy clustering, data elements can belong to more than one cluster, each associated with a membership level. This indicates the strength of the association between that data element and a particular cluster. Utilizing Fuzzy C-Means cluster analysis on the main time effects, for each country, we can distinguish the similarities or the dissimilarities among the countries. One of the most widely used fuzzy clustering algorithms is the Fuzzy C-Means (FCM) Algorithm. This technique was originally introduced by Jim Bezdek as an improvement on earlier clustering methods (Bezdek, 1981). The FCM algorithm attempts to partition a finite collection of *c* elements $X = X_1, X_2, ..., X_c$ into a collection of f fuzzy clusters. The algorithm returns a list of f *cluster* multidimensional *centres* $C = C_1, C_2, ..., C_f$, and a partition matrix of *membership grades* $U = u_{ij} \in [0, 1]$, *i=1, . . .,c, j=1, . . .,f*, where each element u_{ij} tells the degree to which element X_i belongs to cluster C_j.

We utilise the mortality data from the "Human Mortality Database" (HMD) (www.mortality.org). The bulk of countries (35 countries), from the HMD, have a common time range 1960-2006, and hence we apply the FCM algorithm to those national mortality data. Experiments with different numbers of clusters, gives a distinctive separation with *f=2* clusters. In Table 1, the k_r columns give the optimum number of GLM parameters for the *graduated (or full) model* structure, according to the Bayesian Information Criterion (BIC) (see Hatzopoulos and Haberman (2009) equation 2.1). The μ_r-values are the overall means for each country, according to the *age-period association model* structure, and equal to the average value of the logged central rates of mortality across age and time. The u_{i1}-values, give the fuzzy c-means membership levels for the first cluster (the membership value for the second cluster is complementary to the first one).

According to the u_{i1}-values, in Table 1, we form the males and females first cluster countries, which consists of 25 countries and 26 countries respectively. The common countries that belong to the first cluster, for both sexes, are the following 24 countries: Sweden, France, Denmark, E&W (England & Wales), Norway, Netherlands, Scotland, Italy, Switzerland, West Germany, Finland, Spain, Ireland, Belgium, Austria, Portugal, Luxembourg, Australia, New Zealand, Canada, USA, Japan, Czech and East Germany. The countries are sorted in decreasing

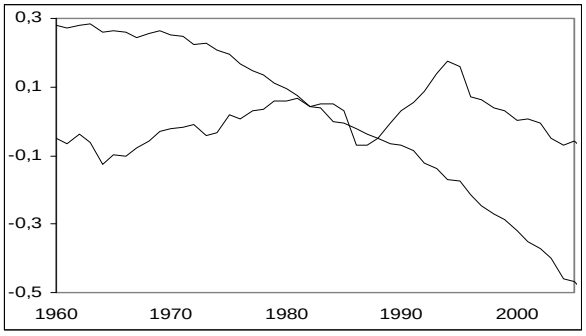
manner according to their fuzzy c-means u_{i1}-membership levels. White (2002) has observed that a group of 17 countries with a real GNP per capita of at least half that of the United States in 1970 and continuously democratic government, show strong convergence on life expectancies, for the period 1955-96. The countries involved are: Australia, Austria, Belgium, Canada, Denmark, Finland, France, West Germany, Italy, Japan, Netherlands, New Zealand, Norway, Sweden, Switzerland, United Kingdom and USA. We note that all of these 17 countries belong to the first West-cluster (Table 1, u_{i1} values). Also, Wilson (2001), using data from the *World Population Prospects* (United Nations 1999), has discussed the fundamental differences in the respective histories of the First, Second, and Third Worlds over the last 50 years which justify the trichotomy: developed, developing and former Communist states of the Soviet Union and Eastern Europe. In that assessment, "former Communist" is defined as the Soviet Union and all European countries ruled by Communist parties in the Cold War era, and the "developed" category includes the other European countries, along with the United States, Canada, Australia, New Zealand, and Japan, and "developing" is the rest of the world. In Table 1, all of the countries with large u_{i1} values belong to the "developed" countries, except for the Czech Republic and East Germany.

In addition, applying the FCM clustering algorithm to the remaining East-cluster countries (10 countries for males and 9 for females), gives another distinct pair of countries. The v_{i1}-values, in Table 1, give their fuzzy c-means membership levels for the first East sub-cluster. We observe distinct v_{i1}-values for the countries: Belarus, Ukraine and Russia, for both sexes, which form the first sub-cluster of the East-countries.

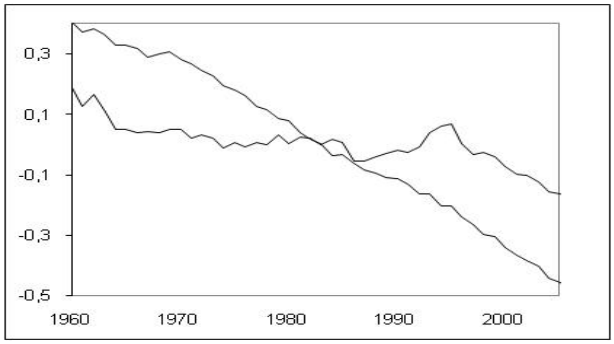
	Males	k_r	μ_r	u_{i1}	v_{i1}	***Females***	k_r	μ_r	u_{i1}	v_{i1}
1	***Sweden***	16	-5.452	99%		***Canada***	17	-5.859	99%	
2	***E&W***	23	-5.318	99%		***Sweden***	15	-5.986	98%	
3	***France***	23	-5.152	99%		***Switzerland***	15	-5.934	98%	
4	***Belgium***	16	-5.773	98%		***France***	17	-5.847	98%	
5	***Netherlands***	16	-5.397	98%		***Belgium***	16	-5.773	98%	
6	***Switzerland***	16	-5.310	98%		***Australia***	17	-5.844	96%	
7	***Canada***	17	-5.266	98%		***Austria***	16	-5.778	96%	
8	***New Zealand***	16	-5.181	98%		***E&W***	17	-5.837	95%	
9	***Portugal***	16	-4.934	98%		***W.Germany***	17	-5.787	95%	
10	***Italy***	18	-5.284	97%		***Portugal***	15	-5.584	95%	
11	***Norway***	16	-5.335	96%		***Spain***	17	-5.881	93%	
12	***Australia***	17	-5.249	96%		***Italy***	18	-5.901	92%	
13	***Spain***	17	-5.249	96%		***Finland***	15	-5.828	92%	
14	***W.Germany***	23	-5.199	96%		***New Zealand***	10	-5.714	90%	
15	***Austria***	16	-5.127	96%		***E. Germany***	16	-5.692	90%	
16	***USA***	24	-5.071	96%		***Ireland***	10	-5.764	88%	
17	***Finland***	16	-5.068	96%		***Scotland***	15	-5.677	83%	
18	***Luxembourg***	9	-5.009	96%		***Netherlands***	16	-5.921	82%	
19	***Iceland***	9	-5.287	93%		***Japan***	17	-5.930	80%	
20	***Scotland***	16	-5.126	93%		***Luxembourg***	8	-5.536	80%	
21	***Ireland***	10	-5.204	89%		***Czech***	16	-5.675	78%	
22	***E. Germany***	16	-5.101	88%		***USA***	24	-5.666	78%	
23	***Japan***	24	-5.360	87%		***Denmark***	11	-5.788	76%	
24	***Czech***	16	-5.004	87%		***Poland***	17	-5.629	73%	
25	***Denmark***	16	-5.269	81%		***Norway***	10	-5.973	70%	
26	***Poland***	22	-4.908	44%	9%	***Slovakia***	15	-5.634	60%	
27	***Slovakia***	16	-4.935	42%	10%	***Hungary***	16	-5.506	33%	13%
28	***Hungary***	16	-4.889	18%	5%	***Iceland***	6	-5.742	15%	34%
29	***Belarus***	16	-4.730	7%	95%	***Russia***	27	-5.280	12%	94%
30	***Ukraine***	19	-4.643	7%	98%	***Ukraine***	20	-5.386	9%	98%
31	***Russia***	24	-4.445	7%	95%	***Belarus***	16	-5.520	8%	95%
32	***Estonia***	10	-4.654	5%	20%	***Estonia***	10	-5.486	7%	14%
33	***Latvia***	15	-4.604	4%	35%	***Bulgaria***	16	-5.496	5%	15%
34	***Bulgaria***	16	-4.954	3%	31%	***Latvia***	10	-5.429	5%	15%
35	***Lithuania***	15	-4.717	1%	56%	***Lithuania***	14	-5.514	4%	6%

Table 1: Number of optimum GLM parameters, grand means, and fuzzy c-means membership levels, for time period 1960-2006, for both sexes, with countries in decreasing manner according to their fuzzy c-means membership levels.

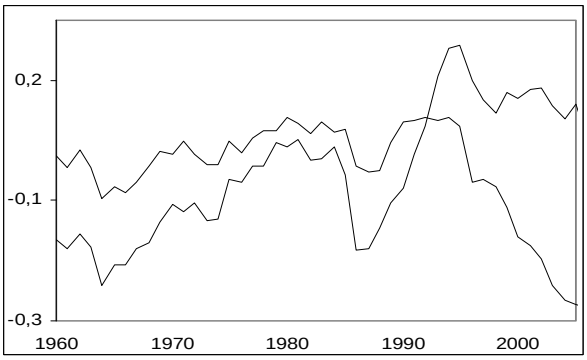
In panel 1.M.a of Figure 1, we display the fuzzy cluster centres, (C_1, C_2), in time effects for the males West-cluster countries (graph with decreasing trend) and the males East-cluster countries (graph with relative steady trend). Panel 1.F.a, similarly displays the cluster centres for the females West-cluster countries (graph with decreasing trend) and the females East-cluster countries (graph with slight decreasing trend). In panels 1.M.b & 1.F.b, respectively, we display the cluster centres, (C_1, C_2), for the two East sub-cluster countries for both sexes. We note the change in the trend of the cluster centres after 1990s, for each East sub-cluster, for both sexes. The increasing trend, particularly after the 1990s, for males refers mainly to Belarus, Lithuania, Ukraine and Russia and for females refers to Belarus, Ukraine and Russia (with larger v_{i1} values, Table 1). For the remaining East-cluster countries, namely: Poland, Slovakia, Hungary, Estonia, Latvia and Bulgaria for males, and Hungary, Iceland, Estonia, Bulgaria, Latvia and Lithuania for females (with smaller v_{i1} values, Table 1), the decreasing trend is noticeable after the 1990s, for both sexes.



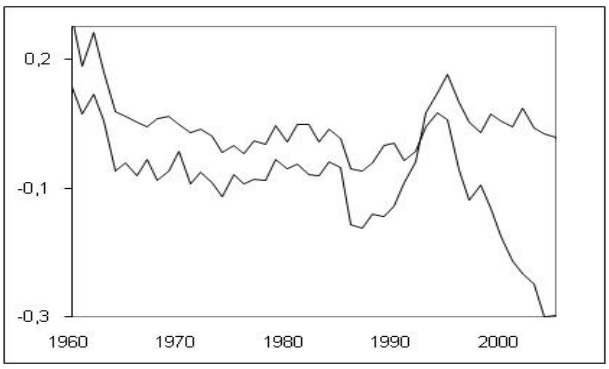
1.M.a Males West-East cluster centres



1.F.a Females West-East cluster centres



1.M.b Males East sub-cluster centres



1.F.b Females East sub-cluster centres

Figure 1: Cluster centres in fuzzy c-means clustering. *1.M.a & 1.F.a* graphs refer to all 35 countries, which form the West (graphs with decreasing trend) and East cluster countries, for males-females respectively. The *1.M.b & 1.F.b* graphs refer to the sub-clusters of the East-cluster countries (the increasing trend, after the 1990s, refers mainly to Belarus, Ukraine and Russia), for males-females respectively.

Although we could employ the West-cluster mortality experience for the time period 1960-2006 for fitting the models, we need to refer to as long a mortality history as possible, in order to produce viable long term forecasts. Many authors begin their mortality analyses after the second half of the 20th century, effectively after the end of World War II, for modelling and forecast purposes. For example, Lee (2003) comments that the mortality age schedule has changed shape between the first and second halves of the 20th century. These results indicate that any forecasts would better be based on the post-war mortality experience, when mortality patterns have changed, in comparison with earlier periods of time, on the assumption that these dynamics will continue into the future. Therefore, we utilize the post-war mortality experience to construct common mortality trends, including all of those countries which belong to the West-cluster countries, and have available mortality data from the HMD since 1947. As a result, the countries included are the following 19 countries: Sweden, France, Denmark, E&W, Norway, Netherlands, Scotland, Italy, Switzerland, Finland, Spain, Ireland, Belgium, Australia, Canada, USA, Portugal, Japan and Austria.

We next proceed to construct a model for common mortality trends, based on the above mentioned 19 West-cluster countries, for both sexes. In Hatzopoulos and Haberman (2009), the GLM parametric method for

modeling the age mortality effects is based on heteroscedastic Poisson error structures. In this context, the data for analysis, which are denoted by $(d_{x,t,r}, R_{x,t,r})$, comprise the observed number of deaths, $d_{x,t,r}$, with matching central exposures to the risk of death, $R_{x,t,r}$, defined over rectangular data grids (*x*,*t*), with *t* ranging over the individual calendar years range $[t_1, t_n]$ and *x* ranging over the age range $[x_1, x_a]$, for each country $r = r_1, r_2, ..., r_c$. We model the response variates, the observed number of deaths as independent realizations of Poisson random variables, $D_{x,t,r}$, conditional on the central exposures $R_{x,t,r}$, i.e. $D_{x,t,r} \sim Poisson(m_{x,r}(t) \cdot R_{x,t,r})$ (Brillinger, 1986), for each calendar year independently:

$$E(D_{x,t,r}) = m_{x,r}(t) \cdot R_{x,t,r} \quad \text{and} \quad Var(D_{x,t,r}) = \varphi_{t,r} \cdot E(D_{x,t,r})$$

where $m_{x,r}(t)$ denotes the central rate of mortality, for each age, calendar year and country. The over-dispersed parameter $\varphi_{t,r}$ is independent of the response variate, and is the theoretical equivalent of the empirical variance ratio *r* discussed by Forfar et al (*1988*) and can be estimated by the ratio of the quasi-deviance divided by the associated degrees of freedom.

Under this approach, we need to construct pooled common number of deaths with matching central exposures in order to construct common central rates. We note that, if we were just to add up the actual number of deaths from all the countries together, say $d_{x,t,.} = \sum_{r=r_1}^{r_c} d_{x,t,r}$, treating them as independent realizations of Poisson random variables, $D_{x,t,.}$, conditional on the central exposures $R_{x,t,.} = \sum_{r=r_1}^{r_c} R_{x,t,r}$, i.e. $D_{x,t,.} \sim Poisson(\hat{D}_{x,t,.})$, for each calendar year independently, then the countries with the biggest populations would dominate the overall mortality analysis. We need weighted deaths $d^w_{x,t,r}$, and matching weighted central exposures $R^w_{x,t,r}$, such that, each country will contribute equivalent to the pooled common mortality experience. Applying unweighted deaths, to the model structure proposed in this paper, results in reducing the coherent structure. We construct a set of weights under the assumption that, for each calendar year, the sum of the weighted deaths over all ages are equal for each country. For identification reasons, the sum of the weights, per calendar year, over all countries must sum up to the number of countries. The weights that satisfy the above two constraints for each country and calendar year are given by $w_{t,r} = \frac{c}{\left[\sum_{r=r_1}^{r_c} \frac{1}{d_{.,t,r}}\right] \cdot d_{.,t,r}}$, where $d_{.,t,r} = \sum_{x=x_1}^{x_a} d_{x,t,r}$ denote the sum of deaths over all the ages, for each country and calendar year. The constructed weighted deaths are the product of the constructed weights and the observed deaths, i.e. $d^w_{x,t,r} = w_{t,r} \cdot d_{x,t,r}$, with matching weighted central exposures $R^w_{x,t,r} = w_{t,r} \cdot R_{x,t,r}$. In the specific situation, where the sum of deaths over all the ages are equal for each country, then the weights are equal to one and the weighted deaths are equivalent to the observed deaths. We now model the weighted number of deaths, $d^w_{x,t,r}$, as independent realizations of Poisson random variables, $D^w_{x,t,r}$, conditional on the weighted central exposures $R^w_{x,t,r}$, i.e. $D^w_{x,t,r} \sim Poisson(m_{x,r}(t) \cdot R^w_{x,t,r})$, for each calendar year independently: $E(D^w_{x,t,r}) = m_{x,r}(t) \cdot R^w_{x,t,r}$ and $Var(D^w_{x,t,r}) = \varphi_{t,r} \cdot E(D^w_{x,t,r})$. Then, the sum of the independent Poisson random variables $D^w_{x,t,r}$ from the pool of countries follows a Poisson process:

$$D^w_{x,t,.} = \sum_{r=r_1}^{r_c} D^w_{x,t,r} \sim Poisson(m_x(t) \cdot R^w_{x,t,.})$$

per calendar year independently: $E(D^w_{x,t,.}) = m_x(t) \cdot R^w_{x,t,.}$ and $Var(D^w_{x,t,.}) = \varphi_t \cdot E(D^w_{x,t,.})$, where $m_x(t)$ denotes the "common" central rate of mortality, for each age and calendar year.

Similarly to the approach of Hatzopoulos and Haberman (2009), we can define the *common graduated (or full) model* structure:

$$\log(\hat{m}_x(t))=\sum_{j=1}^{k}\beta_{j-1}(t)\cdot L_{j-1}(x) \quad (1)$$

where $L_{j-1}(x)$ denotes an orthonormal (Legendre) polynomial of degree *j-1*, the random variables $\beta_{j-1}(t)$ are the GLM estimated parameters, for each calendar year independently, and k denotes the optimum number of parameters, determined by maximizing the Bayesian (or Schwarz) Information Criterion.

Following the approach of Hatzopoulos & Haberman (2011), we apply sparse principal component analysis (SPCA) to the matrix *B* of the estimated GLM parameters. As discussed by Lansangan and Barrios (2009), in the case of a non-stationary time series, the simultaneous drifting of the series may register as correlations between the columns, and a single linear combination of all the time series can explain the variability existing in the input data and hence explain the failure to achieve dimension-reduction. SPCA improves this problematic feature by giving a better clustering of significant high factor loading values. Sparseness can be attained in constructing principal components of non-stationary time series by imposing constraints on the estimation of the component loadings. The SPCA approach can be differentiated from the Lee-Carter (LC) model, since it utilizes more than one (sparse) principal component (extracted from the GLM non-stationary time series parameter estimates of lower dimension). LC is based on the method of principal components (PC), which combines together, into the same component, variables with similar loadings, thus giving equal importance to most of the variables. The basic LC method requires that the mortality improvements at all ages will follow a fixed pattern, modelling (possible different) mortality dynamics with the same factor. This approach may lead to spurious interpretations and problems with forecasting (Hatzopoulos & Haberman (2011), section 3.5). We note, in passing, that the basic LC model has been enhanced by the inclusion of higher order terms – see, for example, Booth et al (2002) and Renshaw and Haberman (2003).

In various mortality studies, substantial age-time interactions have been observed, which, under the SPCA approach, can be modelled by different SPCs. The common mortality trends, constructed for the 19 West-cluster countries and for the 2 genders combined, reveal decreasing rate of mortality improvements for the childhood-early middle ages, relative stable mortality improvements for the middle ages, and accelerating rates for the old ages, during the last few decades. Many authors have described similar features of the mortality dynamics. Thus, Lee (2003) has commented that the mortality age schedule has changed shape between the first half of the 20th century, when the mortality decline was much more rapid for the young than for the old, and the second half of the century, when there has been little difference among the rates of decline above age 20 or so. Also, Horiuchi and Wilmoth (1998) have noted that, just when the age-specific death rates of the young have become very low, the rates of decline in mortality rates at the older ages have begun to accelerate, and Glei and Horiuchi (2007) conclude that, for the industrialized countries during recent decades, the gain in life expectancy is mainly due to changes in adult mortality.

As a result, applying SPCA to the matrix *B* of the estimated GLM parameters, we extract the most important mortality dynamics in age-time effects, after keeping an optimum subset $p\ (<k)$ of the SPCs which explains the "majority" of the variance, thereby giving the *common age-period (sparse) model* structure:

$$\log(\hat{m}_x(t))=A(x)+\sum_{i=1}^{p}g_i(x)\cdot Y_i(t)+\varepsilon_x(t) \quad (2)$$

where $A(x)$ is a set of age-specific constants, describing the relative pattern of mortality by age. The $g_i(x)$ values describe the relative importance for age *x* of the responses to the variations and trends in the time variable. The $g_i(x)$ and $Y_i(t)$ terms embody the interactions between age and time. The model structure (2) can be decomposed into a *common age-period association model* structure (Hatzopoulos and Haberman (2009)):

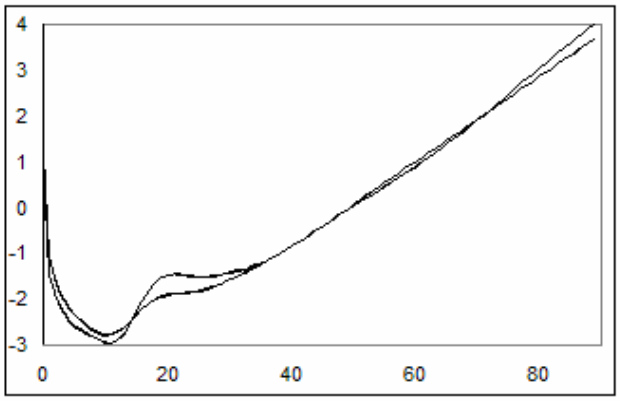
$$\log(\hat{m}_x(t))=\mu+\alpha(x)+b(t)+\sum_{i=1}^{p}f_i(x)\cdot Y_i(t)+\varepsilon_x(t) \quad (3)$$

The component μ is the overall mean, $\alpha(x)$ and $b(t)$ are the main age and time effects respectively (zero centred independent components). The main time effect is an index of the level of mortality that captures the overall time trend at all ages. The main time effect is a linear combinations of the PCs with weights from the first row of the (sparse) eigenvector matrix. The shape of the (zero centred) $f_i(x)$ profile indicates which age specific rates respond rapidly and which slowly over which period of time, in response to particular trends in $Y_i(t)$. For negative $f_i(x)$ values, increasing (decreasing) values of $Y_i(t)$ represent a faster rate of improvement (deterioration) relative to the independent model, and for positive $f_i(x)$ values, increasing (decreasing) values of $Y_i(t)$ represent a faster rate of deterioration (improvement) relative to the independent model, with the relative degree of deterioration (improvement) indicated by the first derivative of the $Y_i(t)$'s.

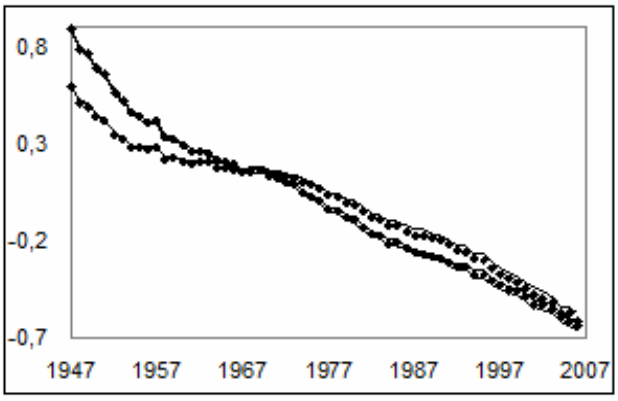
Luss and Aspremont (2006) show that, given a covariance matrix $A \in S_k$, the (dual) problem of finding the sparse factors which explain the maximum amount of variance in the data can be written as follows (using semidefinite relaxation techniques to compute the approximate solutions): Minimize $\lambda^{\max} \cdot (A + X)$ subject to $\left|X_{ij}\right| \le s$, $X \in S_k$ where *s* is a scalar which defines the sparsity (higher values of *s* gives more sparsity). In our case, the covariance matrix $A \in S_k$, is the covariance matrix of the estimated GLM parameters *B*. The (sparse) covariance matrix *X* is the solution of this problem. The sparse loadings are now calculated by the eigenvalue decomposition of the sparse covariance matrix *X*. According to the above (dual) problem, the sparse *s*-value is the maximum value we give to the sparse covariance matrix, with different *s*-values leading to different age-time dynamics. The sparse *s*-value should, if possible, reflect the observed age-time interactions of the mortality dynamics in a parsimonious and convenient way. In experiments with various national mortality experiences, we obtain interpretable results when the sparse *s*-value is equal to the variance of the first column vector $\underline{\beta}_0$ in matrix *B*, which is the biggest value of the covariance matrix *Cov(B)*. This particular choice for the sparse *s*-value, produces primarily two SPCs, which explain the majority of the total variance (usually above 97%). We find that the first age group corresponds to young-early middle ages mortality dynamics and the second age group corresponds to middle-senescent mortality (the exact definition, and hence separation, of the two age groups depend on the time period involved). The resulting first two sparse eigenvectors have a particular structure. The ratio of their first two row values, say $a = e_{1,1} / e_{1,2}$, is equal to the inverse of the remaining row ratios, i.e. $e_{i,1} / e_{i,2} = 1/a \quad \forall\ i = 1,...,k$. This feature leads to a linear relationship between the first two age profiles in model (2), or equivalently a fixed ratio between the first two age profiles in model (3): $a = f_2(x) / f_1(x)$, since $g_i(x) = e_{1,i} \cdot L_0 + f_i(x)$, where $f_i(x) = \sum_{j=2}^{k} e_{j,i} \cdot L_{j-1}(x)$ and *L* denotes the design GLM matrix (Hatzopoulos and Haberman (2009), model (2.3)). Therefore, the first two sparse interaction terms in model (2) can be rewritten as $b'(t) + f_1(x) \cdot Y(t)$, where $Y(t) = Y_1(t) - a \cdot Y_2(t)$ and $b'(t) = l \cdot \left[a \cdot Y_1(t) + Y_2(t)\right]$, for $l = L_0 \cdot e_{1,2}$. We note that the $b'(t)$ term is almost equal to the main time trend $b(t)$ in model (3), and that the difference between them is the contribution of the remaining SPCs to the main time trend. As a result, this structure defines a scaling factor, a, which, under linear combinations, transforms the dependent first two main SPCs into two different mortality dynamics: the main time trend caused by the two age groups; and the time trend representing the relative difference between young and adult mortality. This particular structure is further investigated for forecast purposes in section 5.

In ordinary PC analysis, the PCs are uncorrelated and their loadings are orthogonal. In SPCA, the loadings are forced to be orthogonal but the uncorrelated components condition is not explicitly imposed. Thus, the total variance explained by the correlated SPCs cannot be represented by $tr(Y' \cdot Y)$, where *Y* denotes the SPCs. According to Zou et al (2006), using QR decomposition, the adjusted variance can be easily computed. Thus, if $Y = Q \cdot R$, where *Q* is orthonormal and *R* is upper triangular, then the explained total variance is equal to $\sum_{j=1}^{k} R_{jj}^2$, and the percentage variance explained by the *j*-component is $R_{jj}^2 / \sum_{j=1}^{k} R_{jj}^2$.

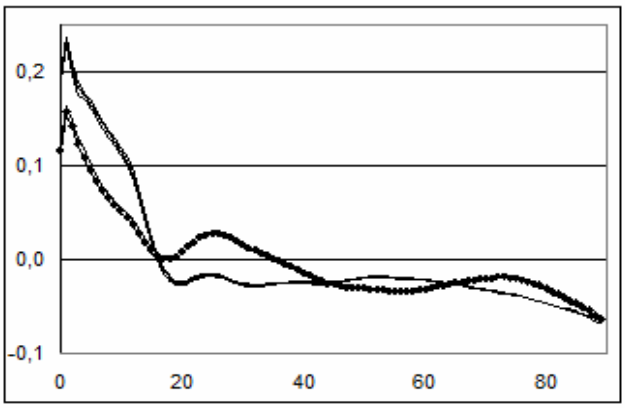
Figure 2, displays the sparse components based on the *common age-period (sparse) association model* structure (3), for both sexes, from the pooled experience of the West-cluster 19 countries and time period 1947-2006. The optimum number of GLM parameters, by maximizing the Bayesian (or Schwarz) Information Criterion, for both sexes, is *k=23*. Concerning the graduation process (model structure (1)), the standardized deviance residuals (SDR) plotted against age, time and cohort effects, shows that the overall patterns of the total SDR indicate an appropriate fit, with R-squared statistics 99,92%. The first two (sparse) interaction terms describe the different dynamics of the two age groups. For the males experience, the first two SPCs account for 97.21% of the total adjusted variance explained and for females 98.61% the total adjusted variance explained (after QR decomposition). For males, the first interaction term accounts for 96.14% of the total adjusted variance and refers mainly to young ages 0-17, and for females it accounts for 98.41% and refers mainly to ages 0-35 (positive $f_1(x)$ values, Figure 2). For males, the ages 18-35 have higher $\alpha(x)$ values than females (Figure 2, graph $\alpha(x)$), and are grouped on the second SPC. Thus, for males, we separate the young 0-17 ages which belong to the most significant mortality dynamic, as described by the $Y_1(t)$ graph (the steeper curve corresponds to females experience), and the remaining ages which are described by the $Y_2(t)$ graph (the steeper curve corresponds to males experience).



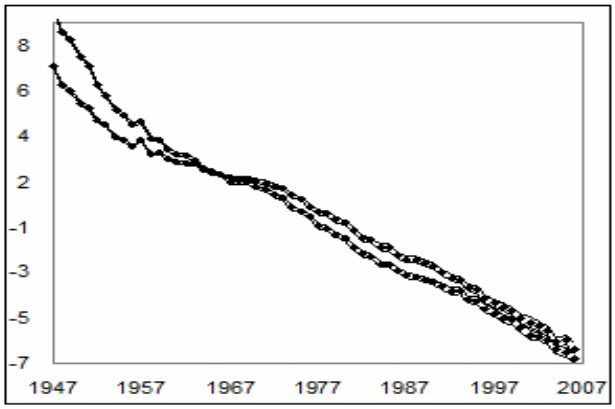
$\alpha(x)$



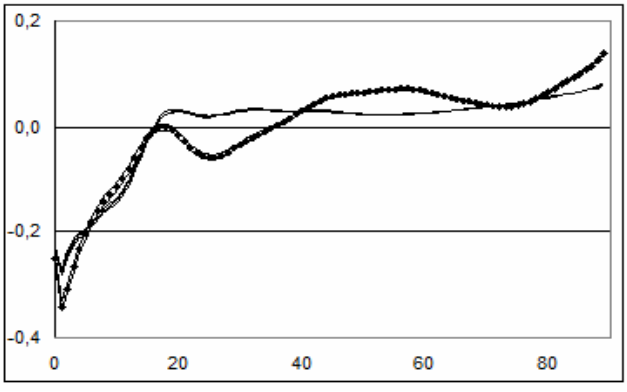
$b(t)$



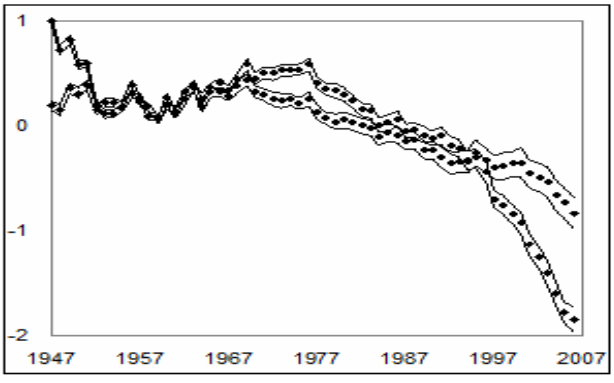
$f_1(x)$



$Y_1(t)$



$f_2(x)$

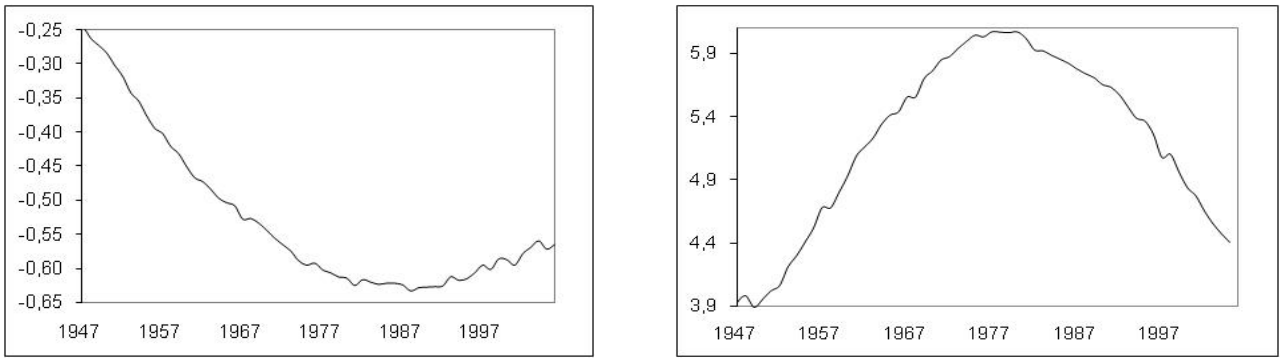


$Y_2(t)$

Figure 2: Dynamics in age-time effects based on the *common age-period (sparse) association model* structure (3), with associated CIs, for both sexes. $\alpha(x)$ & $b(t)$ graphs, display the independent main age and time effects respectively. $f_i(x)$ & $Y_i(t)$ graphs (for *i=1,2*), display the first two (sparse) interaction terms. The shape of the $f_i(x)$ age profile indicates which age specific rates respond rapidly and which slowly over which period of time, in response to particular time trends in $Y_i(t)$.

3. Common Sex Difference mortality dynamics

Figure 3, presents the time profile of the sex difference between the common main time trends plus the sex difference between their overall means, $D(\mu + b(t))$, and the sex difference between the life expectancies, $D(e_0(t))$. In both graphs, we observe increasing differences up to 1980s and thereafter a decline (in a more accelerated way for life expectancies, in comparison with the main time trend).



$D(\mu + b(t))$ $D(e_0(t))$

Figure 3: Sex differences, in main common time trends and in common life expectancies, in time effects.

Sex differentials in mortality are normally attributed to trends in behavioral and social risk factors such as cigarette smoking, heavy drinking, violence and occupational hazards (Preston 1970). Also, many authors have discussed the observed narrowing effect in life expectancies between the sexes. Mesle (2004) has stated that sex differences in life expectancies began to narrow, around the 1980s, in the industrialized countries of Northern Europe, Northern America and Oceania. Glei & Horiuchi (2007) have demonstrated that, more recently, the sex differential has begun to decline in Western Europe and appears to be leveling off among several countries in Southern Europe. Attempts to explain the recent narrowing have focused on causes of death, as well as behavioral and medical factors that would lead to reduced sex ratios in mortality rates. These factors include increased smoking among women while its prevalence has declined among men, and advances in medical treatments for cardiovascular disease that have benefited men more than women (Waldrom, 2005).

In order to model the sex differentials and identify the ages which have contributed to the changes in the mortality gap between the sexes, both during the period when it widens (1947-1980) and during the period when it began to narrow (1980-2006), we construct the *sex difference common age-period model* structure. Based on the *males common age-period graduated model* structure (1), we produce a matrix of GLM parameter estimates, of order *n* by *k*, of $\beta_{j-1}(t)$ entries, say $\mathbf{B}^M = \{\beta_{j-1}(t)\}$, for *t*=1,2,…*n* and *j=1,2,…,k*, and a matrix of graduated logged central mortality rates, of order *n* by *x*, of entries $\hat{m}_x(t)$, say $\log(\hat{\mathbf{M}}) = \mathbf{B}^M \cdot L'$, where L denotes an orthonormal zero-centered polynomial. Let $\underline{\beta}(t)$ denote the GLM estimated multivariate random variable at time *t*. From the properties of GLMs, each cross-sectional vector of the estimated parameters is a *k*-dimensional random variable, which follows asymptotically a multivariate *k*-dimensional normal distribution with associated covariance matrix, say $\mathbf{\Sigma}_t$, for each calendar year *t*. Constructing in an analogous manner the *females common age-period graduated model* structure, with the same 19 West-cluster countries, we produce another matrix of GLM parameter estimates, of order *n* by *k*, say $\mathbf{B}^F$. The difference between these two matrices, i.e. the random matrix $\mathbf{B}^D = \mathbf{B}^F - \mathbf{B}^M$, defines another cross-sectional *k*-dimensional random vector of parameters, which follows asymptotically a multivariate *k*-dimensional normal distribution, with mean

equal to the difference between the females and males mean, and covariance matrix equal to the sum of the females and males covariance matrices, for each calendar year *t*.

Applying PCA to the $\mathbf{B}^D$ matrix, we construct the *sex difference common age-period model*:

$$\log(\hat{m}_x^D(t)) = A^D(x) + \sum_{i=1}^{p} g_i^D(x) \cdot Y_i^D(t) + \varepsilon_x(t) \quad (4)$$

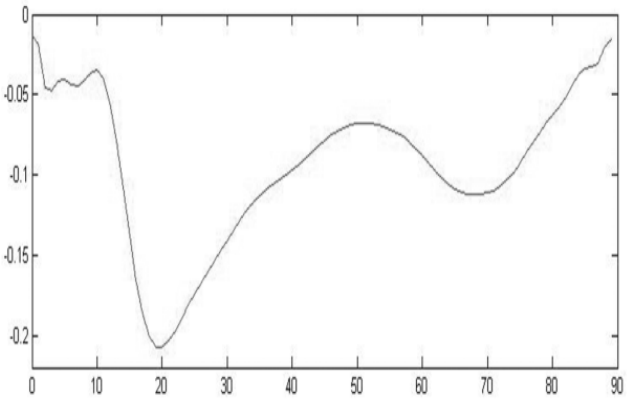
where the $\log(\hat{m}_x^D(t))$ is the sex ratio of the logged graduated common central mortality rates, i.e. $\log(\hat{m}_x^D(t)) = \log \frac{\hat{m}_x^F(t)}{\hat{m}_x^M(t)}$, where $\hat{m}_x^M(t)$ denotes the males graduated common central mortality rates, and $\hat{m}_x^F(t)$ denotes the females graduated common central mortality rates. Under model (4), we are able to identify the most important components of the sex differential in mortality, in terms of age and time effects.

In Figure 4, panels 4.1.a & 4.1.b, display the first interaction component for the time period 1947-1980, which explains 95% of the total variance. We note the widening effect in time trend ($Y_1^D(t)$ graph), which is influenced by all of the ages, and especially the age groups 15-35 and 60-75 ($g_1^D(x)$ graph). We also note the curvature, and hence the diminishing rate of divergence, in the time trend. These results are similar to those of Glei & Horiuchi (2007), who have concluded that ages 40 and over were the biggest contributors to this increase, and especially ages 60-79 (based on their analysis of the sex differential effects, for 21 countries separately between the years 1950-54 to 1975-79 and 1975-79 to 2000-04, after pooling the data into 5-year time intervals and 5-year age groups).

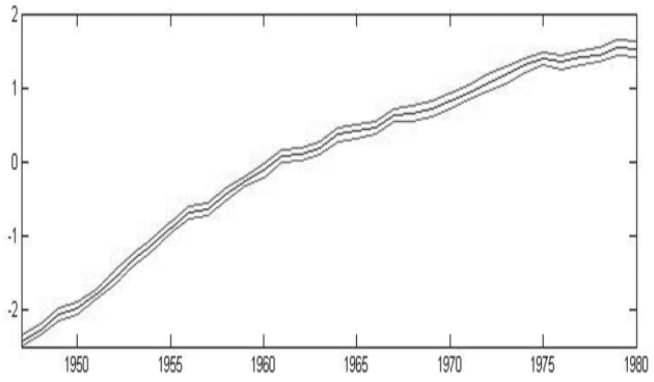
Panels 4.2.a, 4.2.b, 4.3.a and 4.3.b display the first two interaction components for the second time period 1980-2006. The first interaction term (panels 4.2.a & 4.2.b), shows the narrowing effect for the age groups 0-20 and 40-75, and the widening effect for ages 75+, and it explains 57% of the total variance. The age group 20-40 refers to the second interaction term (panels 4.3.a & 4.3.b), which shows a widening effect until the 1990s and a narrowing thereafter; it explains the 20% of the total variance. These results are in accordance with the findings of Glei & Horiuchi (2007), where the biggest contributors to reducing the mortality gap were those aged 40-79, and in contrast, the mortality of those aged 80 and older continued to have a widening effect on the gap (for all countries execpt USA).

Panels 4.4.a & 4.4.b display the first interaction component for the whole time period 1947-2006, which explains 88% of the total variance. We note the widening effect in the time trend until the 1980s, and the narrowing effect afterwards, which is influenced by all ages, and especially by the age groups 15-35 and 60-75. This is the overall effect from the two different time periods (1947-1980 & 1980-2006) which describe adequately the dynamics of the sex differential in mortality over the whole time period, since the widening effect before 1980s and the narrowing effect after 1980s refer mostly to the same age groups. Glei & Horiuchi (2007) confirm that the age groups which contributed to widening the gap in the earlier period also contributed to the narrowing in this more recent period (between the years 1950-54 to 1975-79 and 1975-79 to 2000-04 respectively).

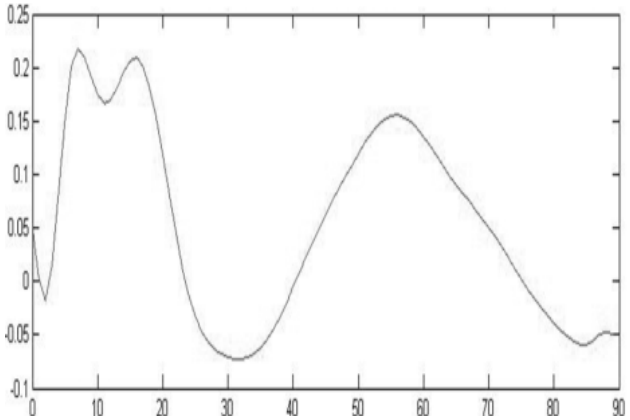
The main reasoning for applying PCA instead of SPCA to the $\mathbf{B}^D$ matrix, comes from this result where only the first interaction term can effectively describe the major mortality sex differentials over time. Also, the observed stationarity for the $Y_1^D(t)$ time series (Panel 4.4.b), enhances the use of the simpler PCA structure.



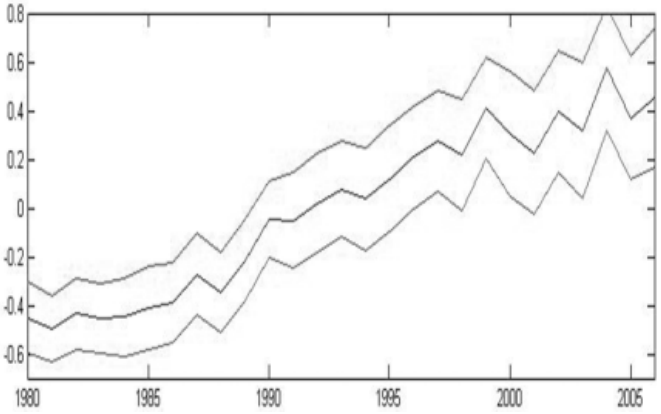
4.1.a (1947-1980) $g_1^D(x)$



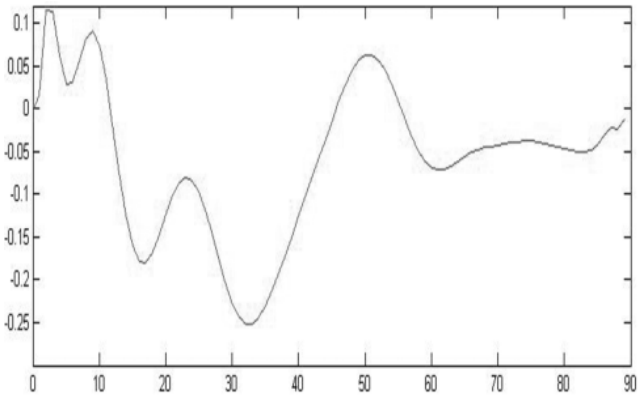
4.1.b (1947-1980) $Y_1^D(t)$



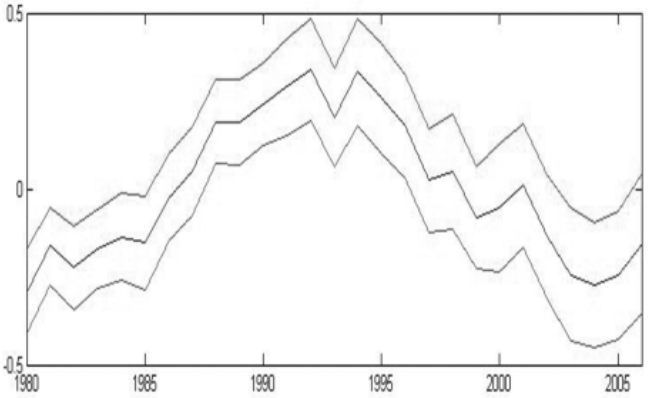
4.2.a (1980-2006) $g_1^D(x)$



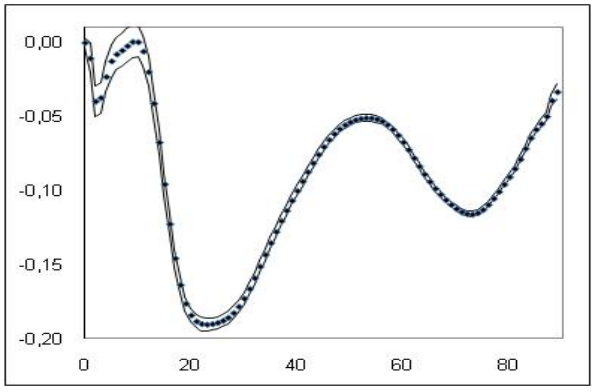
4.2.b (1980-2006) $Y_1^D(t)$



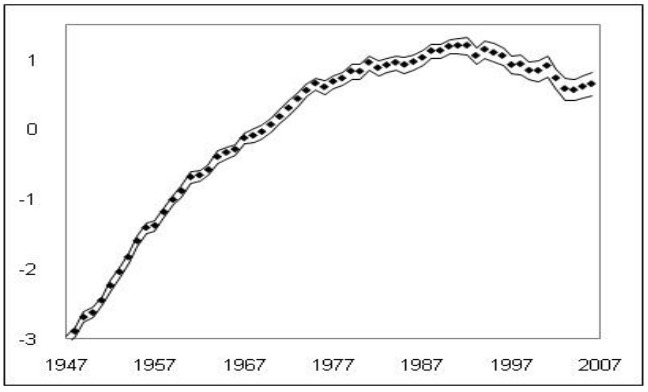
4.3.a (1980-2006) $g_2^D(x)$



4.3.b (1980-2006) $Y_2^D(t)$



4.4.a (1947-2006) $g_1^D(x)$



4.4.b (1947-2006) $Y_1^D(t)$

Figure 4: Dynamics in age-time effects based on the *sex difference common age-period model* structure (4), for different time periods. Left graphs display the age profiles $g_i^D(x)$ in response to particular time trends $Y_i^D(t)$ (with associated CIs). Graphs 4.1.a & 4.1.b display the first interaction component for the time period 1947-1980, graphs 4.2.a, 4.2.b, 4.3.a & 4.3.b display the first two interaction components for the time period 1980-2006, and graphs 4.4.a & 4.4.b display the first interaction component for the whole time period 1947-2006.

In order to measure how well the common male two-factor model (model structure (2)) and the common male two-factor model plus the common sex difference factor model describes the common female mortality experience, we adopt similar explanation ratios with Li&Lee(2005). Thus, we define the females' common explanation ratio for the common factor model, say R_C^F, and the females' common explanation ratio for the augmented common factor model, say R_{AC}^F:

$$R_C^F = 1 - \frac{\sum_{t=t_1}^{t_n}\sum_{x=x_1}^{x_a}\left(\log(m_x^F(t)) - A^F(x) - \sum_{i=1}^{2} g_i(x)\cdot Y_i(t)\right)^2}{\sum_{t=t_1}^{t_n}\sum_{x=x_1}^{x_a}\left(\log(m_x^F(t)) - A^F(x)\right)^2} = 86.8\%$$

and

$$R_{AC}^F = 1 - \frac{\sum_{t=t_1}^{t_n}\sum_{x=x_1}^{x_a}\left(\log(m_x^F(t)) - A^F(x) - \sum_{i=1}^{2} g_i(x)\cdot Y_i(t) - g_1^D(x)\cdot Y_1^D(t)\right)^2}{\sum_{t=t_1}^{t_n}\sum_{x=x_1}^{x_a}\left(\log(m_x^F(t)) - A^F(x)\right)^2} = 96.76\%$$

where $m_x^F(t)$ denote the females' common crude central rates, and $A^F(x)$ denotes the females' main age profile as constructed by the females' common model structure.

4. Residual analysis for each country

In this section, we turn to the particularities of the mortality dynamics for each country and consider the residuals after subtracting the two common interaction terms from the pooled mortality model structure (2). This approach follows the suggestions of Lee (2003) and Cairns et al (2008, 2009). Preliminary experiments with the common mortality experience for females (as well as with the common mortality experience for the 2 sexes combined), to model and forecast coherently the country specific experience has shown that the males mortality experience gives more distinct and better results in terms of goodness of fit and forecast performance. Consequently, we base the residual analysis, for both sexes, on the common mortality dynamics for males. Under this approach, we also need the common sex difference mortality dynamics (4) to model the female residuals.

Thus, for the males experience, we consider the residuals for each country, conditional on the main individual age profile, say $A_r(x)$ and conditional on the two common interaction terms for males:

$$\log(E(D_{x,t,r})) = \log(R_{x,t,r}\cdot m_{x,r}(t)) = \log(R_{x,t,r}) + A_r(x) + \sum_{i=1}^{2} g_i(x)\cdot Y_i(t) + \sum_{j=1}^{k_r^{res}} \beta_{j-1,r}^{res}(t)\cdot L_{j-1}(x)$$

This defines the *males residual age-period graduated model* structure, for each country, where the $\log(R_{x,t,r}) + A_r(x) + \sum_{i=1}^{2} g_i(x)\cdot Y_i(t)$ term is treated as an offset. The main age profiles, $A_r(x)$, are estimated separately for each country, since they do not cause mortality divergence. Then, we apply ordinary

PC analysis to the associated matrix of these conditional GLM estimates, $\beta^{res}_{j-1,r}(t)$, leading to the *males residual age-period model* structure:

$$\log(\hat{m}_{x,r}(t))=A_r(x)+\sum_{i=1}^{2} g_i(x)\cdot Y_i(t)+\sum_{i=1}^{p_r^{res}} g^{res}_{i,r}(x)\cdot Y^{res}_{i,r}(t)+\varepsilon_{x,r}(t) \quad (5)$$

Similarly, for the females experience, we consider the residuals conditional on the individual main age profile, $A_r(x)$, and conditional on the two common interaction terms for males, and conditional on the common sex difference interaction term under model structure (4):

$$\log(E(D_{x,t,r}))=\log(R_{x,t,r})+A_r(x)+\sum_{i=1}^{2} g_i(x)\cdot Y_i(t)+g_1^D(x)\cdot Y_1^D(t)+\sum_{j=1}^{k_r^{res}}\beta^{res}_{j-1,r}(t)\cdot L_{j-1}(x)$$

This defines the *females residual age-period graduated model* structure, in which the $\log(R_{x,t,r})+A_r(x)+\sum_{i=1}^{2} g_i(x)\cdot Y_i(t)+g_1^D(x)\cdot Y_1^D(t)$ term is treated as an offset, for each country. Then , we apply the eigenvalue decomposition to the associated covariance matrix of these conditional GLM estimates, leading to the f*emales residual age-period model* structure, for each country:

$$\log(\hat{m}_{x,r}(t))=A_r(x)+\sum_{i=1}^{2} g_i(x)\cdot Y_i(t)+g_1^D(x)\cdot Y_1^D(t)+\sum_{i=1}^{p_r^{res}} g^{res}_{i,r}(x)\cdot Y^{res}_{i,r}(t)+\varepsilon_{x,r}(t) \quad (6)$$

The percentage of the variance explained by each interaction term involved in the *residual age-period model* structures (5) & (6) (2+ p_r^{res} interaction terms for males and 3+ p_r^{res} interaction terms for females) can be evaluated by QR decomposition on the matrix of all the (S)PCs (2+ p_r^{res} PCs for males and 3+ p_r^{res} PCs for females).

The criterion, which will define which residual interaction term will be included in the *residual age-period model* structures (5) & (6), is based on the following three conditions: a) if the residual variance explained is more than 0,5%, or b) if the confidence level (CL) value is more than 99% (see Hatzopoulos and Haberman (2011), section 2.1) or c) if the residual variance explained is more than 0,1% and the confidence level (CL) value is more than 95%.

In Tables 2 &3, we give the results obtained according to the *residual age-period model* structures (5) & (6), for males and females respectively. For each of the 35 countries, we give the first calendar year with available mortality data (after 1947) as provided by the HMD, the number of optimum residual parameters (k_r^{res} values), and the optimum number of residual interaction terms (p_r^{res} values). Also, we present the common adjusted variances (CV) as explained by the two common interaction terms for males, the common sex difference variance (CDV) for females as explained by the common sex difference interaction term, and the total common variances (TCV) for both sexes. For the female case, the TCV explained is equal to the sum of the adjusted common variance explained plus the adjusted common sex difference variance. The Tables are sorted according to the TCV. Finally, we give the first three adjusted residual variances explained (RV), and the total variance (TV) explained as defined by the sum of the adjusted TCV plus the RVs explained.

We note that the second common variances explained (2nd CV), which refer to adult ages, show relative values which are remarkably steady, for almost all the countries. This result is in accordance with Glei and Horiuchi (2007), who state that, for industrialized countries during recent decades, the rate of mortality decline does not vary markedly across adult ages and thus adult mortality changes can be approximated well by parallel vertical shifts.

Males	*First year*	k_r^{res}	*1st CV*	*2nd CV*	*TCV*	p_r^{res}	*1st RV*	*2nd RV*	*3rd RV*	*TV*
Luxembourg	1960	1	97.1%	1.2%	98.3%	1	1.7%	0.0%	0.0%	100.0%
Sweden	1947	4	97.1%	1.1%	98.2%	3	0.8%	0.7%	0.3%	99.9%
Denmark	1947	4	97.1%	1.1%	98.2%	1	0.8%	0.4%	0.5%	99.0%
USA	1947	16	96.7%	1.1%	97.8%	4	0.5%	1.0%	0.2%	99.8%
Norway	1947	4	96.4%	1.1%	97.5%	3	1.0%	1.2%	0.2%	99.8%
N. Zealand	1948	4	96.3%	1.2%	97.5%	2	1.0%	1.1%	0.3%	99.6%
Netherlands	1947	7	96.1%	1.1%	97.2%	3	1.2%	0.6%	0.8%	99.8%
W. Germany	1956	12	96.1%	1.3%	97.5%	1	1.4%	0.3%	0.3%	98.9%
Switzerland	1947	5	96.0%	1.1%	97.1%	3	1.9%	0.6%	0.3%	99.9%
Iceland	1947	1	96.0%	1.1%	97.0%	1	3.0%	0.0%	0.0%	100.0%
E&W	1947	11	95.8%	1.1%	96.9%	3	2.0%	0.3%	0.2%	99.4%
Canada	1947	7	95.6%	1.1%	96.6%	2	2.5%	0.4%	0.3%	99.5%
Belgium	1947	7	95.5%	1.1%	96.5%	3	0.5%	2.1%	0.7%	99.8%
France	1947	15	95.3%	1.1%	96.4%	4	0.9%	1.9%	0.2%	99.5%
Austria	1947	9	95.3%	1.1%	96.3%	3	1.2%	1.1%	0.6%	99.2%
Czech	1950	7	95.2%	1.3%	96.4%	3	1.8%	0.8%	0.4%	99.4%
Australia	1947	9	94.7%	1.1%	95.8%	3	2.5%	0.7%	0.6%	99.4%
Poland	1958	8	94.1%	1.3%	95.4%	2	3.3%	0.4%	0.3%	99.2%
Scotland	1947	5	94.0%	1.1%	95.0%	3	4.3%	0.2%	0.2%	99.8%
Italy	1947	17	93.1%	1.0%	94.1%	4	3.9%	0.5%	0.3%	99.1%
Slovakia	1950	7	92.9%	1.3%	94.2%	2	3.5%	1.2%	0.4%	98.9%
E. Germany	1956	12	92.3%	1.3%	93.6%	5	3.3%	0.3%	1.0%	99.4%
Japan	1947	21	92.0%	1.0%	93.0%	3	4.2%	1.3%	0.7%	99.2%
Ukraine	1959	13	91.2%	1.2%	92.4%	2	5.4%	1.0%	0.5%	98.8%
Ireland	1947	4	90.8%	1.0%	91.8%	3	6.3%	1.3%	0.3%	99.8%
Portugal	1947	14	90.2%	1.0%	91.2%	3	5.4%	1.5%	0.7%	98.8%
Finland	1947	7	90.0%	1.0%	91.0%	2	6.8%	1.2%	0.5%	99.1%
Lithuania	1959	7	89.2%	1.2%	90.3%	4	5.5%	2.1%	1.1%	99.6%
Belarus	1959	10	88.9%	1.2%	90.1%	3	5.2%	3.2%	0.6%	99.0%
Estonia	1959	5	88.2%	1.2%	89.4%	3	8.0%	0.9%	1.2%	99.6%
Latvia	1959	7	87.2%	1.2%	88.4%	3	6.9%	3.2%	0.6%	99.1%
Hungary	1950	9	86.9%	1.2%	88.0%	3	9.1%	1.1%	0.4%	98.7%
Russia	1959	23	86.1%	1.2%	87.2%	3	9.7%	1.7%	0.5%	99.2%
Bulgaria	1947	12	83.8%	0.9%	84.8%	3	13.0%	0.6%	0.8%	99.1%
Spain	1947	15	83.6%	0.9%	84.5%	3	13.1%	0.5%	1.1%	99.2%

Table 2: Males starting calendar year, number of optimum GLM residual parameters, common and total common variance explained, optimum number of residual interaction terms, residual variance explained for each residual interaction term and total variance explained, for each country.

Females	k_r^{res}	*1st CV*	*2nd CV*	*CDV*	*TCV*	p_r^{res}	*1st RV*	*2nd RV*	*3rd RV*	*TV*
Canada	6	97.0%	1.1%	0.8%	98.9%	2	0.7%	0.2%	0.1%	99.8%
Australia	5	96.9%	1.1%	0.8%	98.8%	2	0.5%	0.4%	0.2%	99.7%
Netherlands	5	96.7%	1.1%	0.8%	98.6%	4	0.7%	0.4%	0.1%	100.0%
USA	18	96.7%	1.1%	0.8%	98.6%	3	0.5%	0.3%	0.3%	99.7%
N. Zealand	2	96.6%	1.2%	0.8%	98.5%	2	1.2%	0.3%	0.0%	100.0%
Sweden	5	96.5%	1.1%	0.8%	98.3%	3	0.9%	0.3%	0.3%	99.8%
E&W	10	96.4%	1.1%	0.8%	98.3%	2	0.4%	0.7%	0.2%	99.4%
Belgium	5	96.3%	1.1%	0.8%	98.2%	2	1.4%	0.2%	0.1%	99.8%
W. Germany	12	96.5%	1.3%	0.3%	98.1%	2	0.8%	0.2%	0.3%	99.1%
Austria	5	96.2%	1.1%	0.8%	98.0%	2	1.3%	0.4%	0.2%	99.7%
France	9	96.0%	1.1%	0.8%	97.9%	5	1.3%	0.2%	0.3%	99.9%
Luxembourg	1	96.3%	1.2%	0.3%	97.8%	1	2.3%	0.0%	0.0%	100.0%
Iceland	1	95.7%	1.1%	0.8%	97.5%	1	2.5%	0.0%	0.0%	100.0%
Norway	4	95.6%	1.1%	0.8%	97.5%	3	1.6%	0.7%	0.2%	99.9%
Switzerland	5	95.5%	1.1%	0.8%	97.4%	3	1.8%	0.1%	0.2%	99.5%
Czech	4	95.3%	1.3%	0.6%	97.2%	1	2.2%	0.5%	0.2%	99.4%
Japan	19	95.3%	1.1%	0.8%	97.1%	3	0.9%	0.9%	0.6%	99.5%
Italy	16	94.8%	1.1%	0.8%	96.6%	4	1.7%	0.7%	0.4%	99.5%
Denmark	6	94.6%	1.1%	0.8%	96.4%	3	1.2%	1.2%	0.9%	99.6%
Scotland	6	94.1%	1.1%	0.8%	95.9%	4	2.9%	0.3%	0.6%	99.8%
Finland	5	94.0%	1.1%	0.8%	95.8%	2	2.6%	1.2%	0.1%	99.6%
Poland	9	94.2%	1.3%	0.2%	95.8%	3	3.1%	0.3%	0.6%	99.6%
Spain	13	93.8%	1.1%	0.8%	95.7%	3	2.1%	1.0%	0.6%	99.3%

E. Germany	6	94.0%	1.3%	0.3%	95.6%	2	3.2%	0.7%	0.2%	99.5%
Portugal	13	93.7%	1.1%	0.8%	95.5%	3	1.4%	1.7%	0.4%	99.0%
Slovakia	4	93.5%	1.3%	0.6%	95.3%	3	3.7%	0.6%	0.3%	99.9%
Ireland	4	93.4%	1.0%	0.8%	95.2%	4	3.6%	0.5%	0.6%	100.0%
Ukraine	14	93.3%	1.3%	0.2%	94.8%	2	3.1%	0.5%	0.8%	98.3%
Belarus	5	93.2%	1.2%	0.2%	94.7%	2	3.7%	1.0%	0.4%	99.4%
Hungary	8	92.3%	1.2%	0.6%	94.2%	3	4.2%	0.5%	0.6%	99.5%
Lithuania	5	91.0%	1.2%	0.2%	92.5%	3	5.5%	1.0%	0.7%	99.6%
Bulgaria	10	90.2%	1.0%	0.7%	92.0%	3	5.8%	0.6%	0.9%	99.2%
Russia	25	90.5%	1.2%	0.2%	92.0%	3	5.3%	1.2%	0.7%	99.1%
Latvia	5	90.3%	1.2%	0.2%	91.8%	3	6.1%	1.2%	0.6%	99.6%
Estonia	2	88.8%	1.2%	0.2%	90.2%	2	9.4%	0.4%	0.0%	100.0%

Table 3: Females starting calendar year, number of optimum GLM residual parameters, common and total common variance explained, optimum number of residual interaction terms, residual variance explained for each residual interaction term and total variance explained, for each country.

5. Coherent Forecasts

As described in section 4, for the construction of the *residual age-period model* structures (5) & (6), we treat the term $\sum_{i=1}^{2} g_i(x) \cdot Y_i(t)$ as an offset in the GLM structure. According to the discussion in section 2, the offset term can be rewritten: $b'(t) + f_1(x) \cdot Y(t)$, where $Y(t) = Y_1(t) - a \cdot Y_2(t)$ and $b'(t) = l \cdot \left[a \cdot Y_1(t) + Y_2(t) \right]$, for $l = L_0 \cdot e_{1,2}$. As a result, the offset term consists of two different mortality dynamics: the main time trend, which encapsulates the overall mortality dynamics for both age ranges (the first age range refers to young ages 0-17, and the second age range refers to adult ages 18+), and a second time trend, which describes the relative divergent trend from the main time trend between the two age groups.

Figure 5 displays the offset component according to the *males common age-period (sparse) association model* structure (3), from the common experience of the West-cluster 19 countries, for time period 1947-2006. The main time trend (Figure 5, panel 5.1.b) exhibits a linear trend since the 1970s. The $Y(t)$ term (Figure 5, panel 5.2.b) describes the relative divergent trend from the main time trend between mortality rates for the young and for adults. With reference to the $f_1(x)$ age profile (positive values for the young ages and negative values for the adult ages, Figure 2), the $Y(t)$ trend indicates a faster mortality improvement for the young (and slower mortality improvement for the adults) than the main time trend. Meanwhile, the concave shape of the $Y(t)$ trend reveals that the faster mortality improvement for the young (than the main time trend) decreases with time and at the same time the relative slower mortality improvement for the adults increases with time.

Similarly to the approach of Hatzopoulos and Haberman (2009, 2011), we utilize dynamic linear regression (DLR) model structures. The DLR time series models are simply regression models in which the explanatory variables are functions of time and the parameters are time-varying. State space models employ the Kalman filter technique through which smoothed estimates of the stochastic parameters and predicted future values (Harvey, 1991) can be derived. The computations have been implemented in Matlab using the Captain Toolbox (Taylor, 2007).

We model the common main time trend with a specific class of DLR models: $b'(t) = \alpha_1 + b_{1,t} \cdot t + e_{1,t}$, for each calendar year *t*, with the slope being a stochastic time variable parameter that follows a smoothed random walk process: $\Delta b_{1,t} = \varphi_1 \cdot \Delta b_{1,t-1} + \zeta_{1,t-1}$ and $0 < \varphi_1 < 1$, where $\Delta b_{1,t} = b_{1,t} - b_{1,t-1}$ denotes the difference operation (similar DLR models are defined in Captain Toolbox, by Pedregal, D., Taylor C., and Young P., 2007). Smoothed $\hat{b}_{1,t}$ rates are given in panel 5.1.a of Figure 5, with an associated estimated value $\hat{\varphi}_1$=0.91 (0.057)). The innovations $e_{1,t}$ and $\zeta_{1,t}$ are assumed to be white noises random variables, with associated standard deviations 0.0209 and 0.00016 respectively. The coefficient of determination is 99.8%. Under this model structure, the main time trend is being modelled finally as a linear stochastic time variable (panel 5.1.b), giving it a slightly tilted S-shape to the short-medium forecasts and also a smooth progression to the mortality

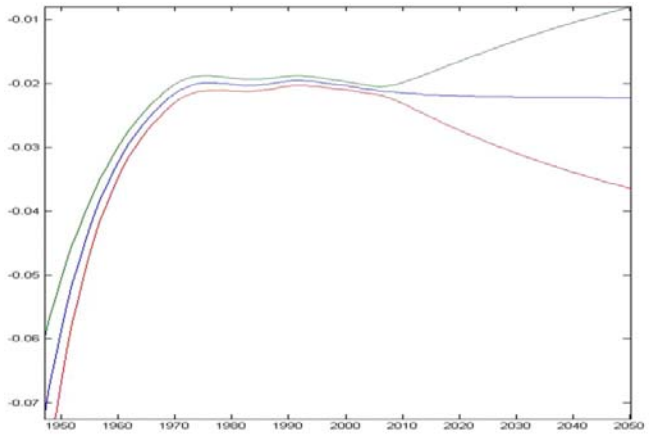
dynamics. The $b_{1,t}$ represents the overall rate of mortality improvements, which has a (smoothed) rate of mortality improvements of 0.0212 at calendar year 2006 and an extrapolated rate of mortality improvements of 0.0222 at calendar year 2050. Experiments with the males common central mortality trends, as described in section 2, show decreasing rate of mortality improvements for the young ages and accelerating rates for the old ages. The observed main time trend, which summarizes the mortality movements from all the ages, displays an almost linear trend since the 1970s, and an extrapolation of this feature seems to be a plausible choice. Panels 5.1.a & 5.1.b describe the dynamics and the forecasts of the main time trend. The ACF and the PACF indicate an acceptable residual structure and the Lillilifors test has a 3.9% *p*-value.

Next, we model the $Y(t)$ time trend, which describes the relative deviations from the main time trend. We use a DLR structure: $Y(t) = \alpha_2 + b_{2,t} \cdot t + e_{2,t}$, with the slope being a stochastic time variable parameter that follows a first order autoregressive (AR(1)) process: $b_{2,t} = \varphi_2 \cdot b_{2,t-1} + \zeta_{2,t-1}$ (smoothed $\hat{b}_{2,t}$ rates are shown at graph 5.2.a, with associated estimated value $\hat{\varphi}_2$ =0.99 (0.06)). The innovations $e_{2,t}$ and $\zeta_{2,t}$ are assumed to be white noises random variables, with associated standard deviations 0.16 and 0.0035 respectively. The coefficient of determination is 99.7%. Under this structure, the $Y(t)$ tends to a constant level, which causes ultimately identical rate of mortality improvements, for each age group. The ACF and the PACF indicate an acceptable residual structure, the Lillilifors test has a 50% *p*-value, and the Jarque-Bera test has a 93% *p*-value.

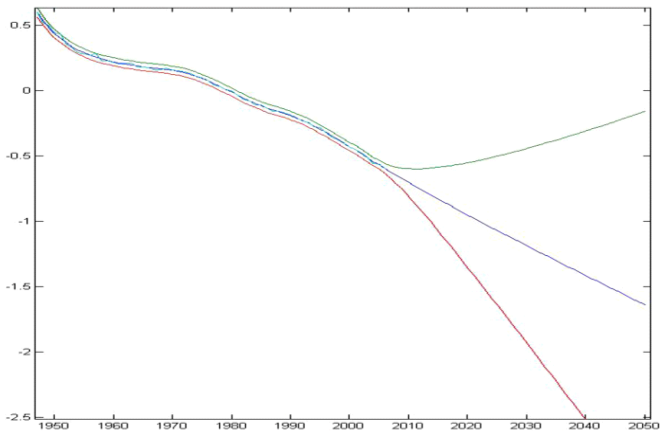
The above DLR model structures cause particular trends to the associated SPCs ($Y_1(t)$ & $Y_2(t)$), as displayed in panel 5.3.a. For the 1st SPC, which describes mostly the mortality experience of the young, we forecast (slightly) decreasing rates of mortality decline, with the rate of improvement equal to 0.22 at calendar year 2006 and a forecast rate of improvement of 0.16 at calendar year 2050. Lee (2005) and Wilmoth (1998), Oeppen and Vaupel (2002) and White (2002), discuss the processes of catch-up and convergence. They argue that some countries converge toward the leader (e.g. Japan), and in preparing mortality forecasts for a given country, the extrapolated trend for the leader country should form the basis for a long-run scenario. As defined by Wilmoth (1998), the leader country at any given point in history is the country whose overall level of mortality equals the minimum achieved at that time by any national population. If we represent the overall level of mortality with the overall means (Table 1, μ_r -values), then the most important leader countries, for the time period 1960-2006, are Sweden, Netherlands, Japan and Norway, for both sexes. The (sex combined) common mortality trends, constructed from these 4 leader countries, show a decreasing rate of mortality improvements for the very young ages (we obtain the same results from the construction of the common mortality trends, utilizing 19 West-cluster countries). Therefore, if we base the future mortality dynamics on the decreasing rate of mortality progress from the leader countries, then we are in accordance with the forecast 1st SPC trend. For the 2nd SPC, the above modelling produces almost steady rates of mortality improvements, with the rate of mortality improvement equal to 0.135 at calendar year 2006 and a forecast rate of mortality improvement of 0.137 at calendar year 2050. This leads to a forecast that adult mortality rates follow an almost linear trend, which follows the dynamics since 1990s (panel 5.3.a). White (2002) has noted that the predominant types of mortality reduction has shifted from curing infectious diseases, that heavily affect the young, to degenerative diseases that largely affect the elderly, and noted that this transition was neither instantaneous nor absolute. He has concluded that the major targets for mortality decline in the near future will probably be the same as over the past four decades. Experiments with the sex combined, common mortality trends, constructed from the 4 leader countries, show a steady rate of mortality improvement for the adult ages and an increasing rate of mortality improvements for the old ages. This remark is in accordance with the forecast 2nd SPC (panel 5.3.a), which describes the dynamics of adult mortality.

The (bootstrap) forecast males common life expectancy shows that life expectancy rises at a decreasing rate (panel 5.3.b.). As noted by White (2002), based on the analysis of mortality rates over time for 21 countries, if the age-specific death rates decline at constant exponential rates, then life expectancy will rise at a declining rate, and, if life expectancy changes linearly, then the rate of decline of the underlying death rates must be nonlinear, and in particular must be accelerating for at least some ages. Thus, the near linearity in the extrapolated mortality rates for adults and the extrapolated declining rates of improvement for mortality among the very young is associated with the declining rate of improvement extrapolated for life expectancy, which are key features of the males common mortality experience.

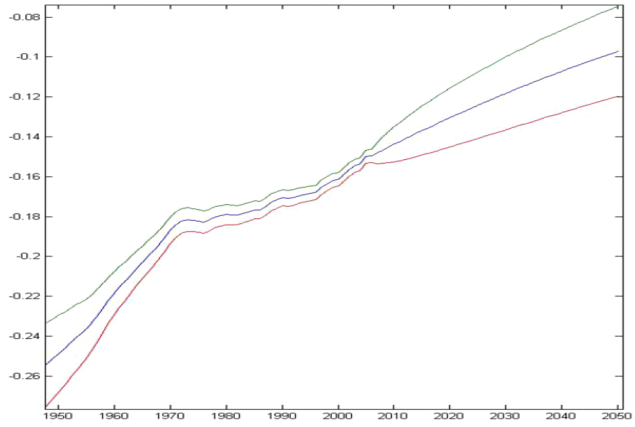
For the females experience, according to the *females residual age-period model* structure (5), we model the *common sex difference* PC, with a DLR model: $Y_1^D(t) = \alpha^D + b_t^D \cdot t + e_t$, with the slope being a stochastic time variable parameter that follows a first order autoregressive process. In panel 5.4.a, we show the smoothed $\hat{b}_t^D$ estimated values, from the common sex difference PC, which follow a first order autoregressive process with $\hat{\varphi} = 0.9819$ (0.029). Under this DLR model structure, we achieve coherent forecasts for both sexes, since the $\hat{Y}_1^D(t)$ trend reaches a constant value (panel 5.4.b). The ACF and the PACF indicate an acceptable residual structure: Lillilifors test has a 50% *p*-value, and the Jarque-Bera test has a 93% *p*-value.



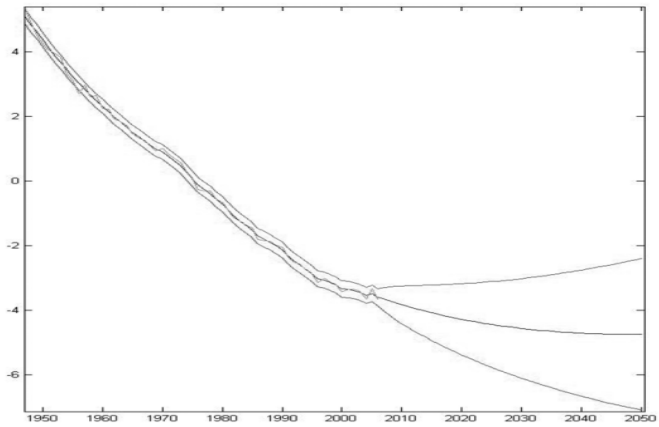
5.1.a DLR forecast rates, $\hat{b}_{1,t}$, for $b'(t)$



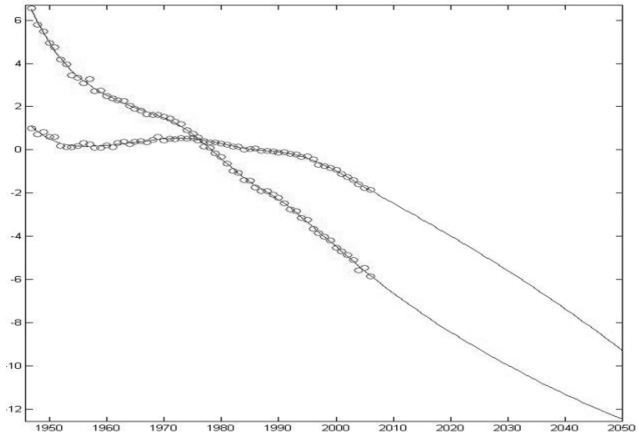
5.1.b forecast common main time, $\hat{b}'(t)$



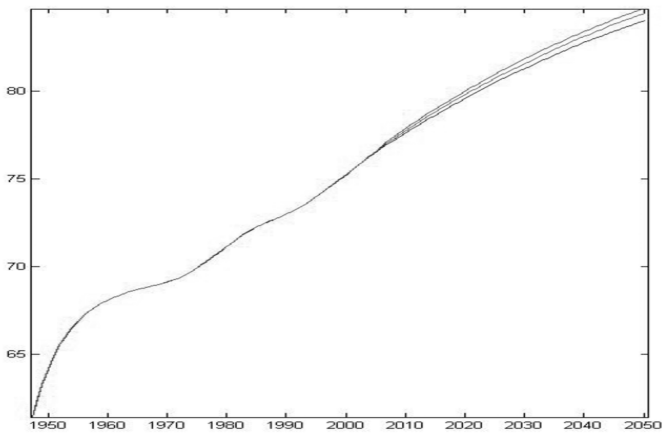
5.2.a DLR forecast rates, $\hat{b}_{2,t}$, for $Y(t)$



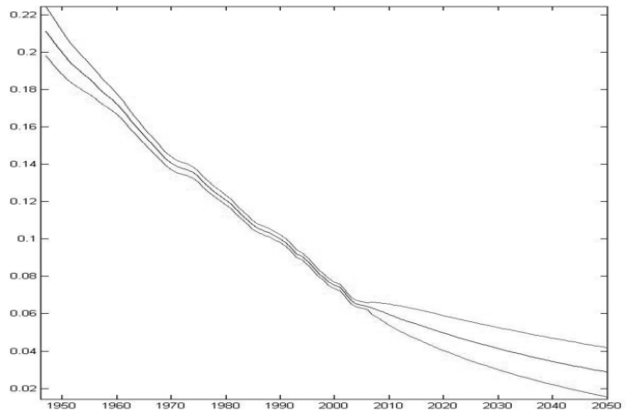
5.2.b forecast relative deviations, $\hat{Y}(t)$



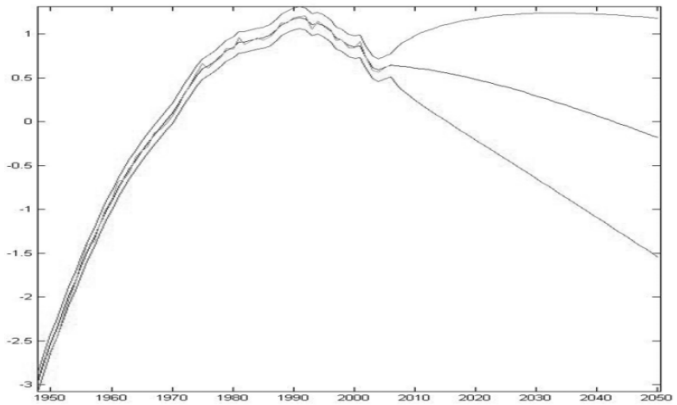
5.3.a forecast SPCs, $\hat{Y}_1(t)$ & $\hat{Y}_2(t)$



5.3.b (bootstrap) males common life expectancy



5.4.a DLR forecast rates, $\hat{b}_t^D$, for $Y_1^D(t)$



8.4.b forecast *common sex difference* PC, $\hat{Y}_1^D(t)$

Figure 5: Dynamics and forecasts, in time effects, for the males common time trend ($\hat{b}'(t)$ and $\hat{Y}(t)$ forecast values and resulting $\hat{Y}_1(t)$, $\hat{Y}_2(t)$ and bootstrap males common life expectancy forecast values) based on the *common age-period (sparse) association model* structure (3), and the common sex difference time trend ($\hat{Y}_1^D(t)$ forecast values) based on the *sex difference common age-period model* structure (4), with associated CIs.

According to the *residual age-period model* structures (5) & (6), the residual PCs for both sexes are modeled by *dynamic linear regression* (DLR) models: $Y_{i,r}^{res}(t) = \alpha_{i,r} + b_{i,r,t} \cdot t + e_{i,r,t}$, for each calendar year *t* and country *r*, with the slope being a stochastic time variable parameter that follows either a first order autoregressive process for stationary residual PCs, or a random walk process for non-stationary residual PCs: $b_{i,r,t} = \varphi_{i,r} \cdot b_{i,r,t-1} + \zeta_{i,r,t-1}$, where $0 < \varphi_{i,r} \leq 1$, for *i=1,2,...,* p_r^{res} and *r=1,2,...,c*. The innovations $e_{i,r,t}$ and $\zeta_{i,r,t-1}$ are assumed to be white noise random variables. If the estimated parameters $\hat{\varphi}_{i,r} < 1$ then the residual PC is stationary and the experience for *r*-country can be forecasted coherently by the common time trends, and if $\hat{\varphi}_{i,r} = 1$ then the residual PC is non-stationary and the *r*-country experience diverges from the common time trends. Under this forecast structure, in the case of stationarity, the forecasts allow divergent patterns to continue for a while until they become negligible (see Appendix A, for selective countries). Therefore, in projecting individual country trends in the short or medium term, individual country mortality differences in mortality trends may be conserved, but ultimately age-specific central mortality rates are constrained to maintain a constant ratio to one another. This is similar with the approach of Lee (2003), where the trends relative to the common factor are projected to continue for a while in the future, although eventually their position relative to the common factor stabilizes.

Table 4 gives the estimated DLR $\hat{\varphi}_{i,r}$-values, according to the DLR *residual age-period model* structures (5) & (6), for both sexes. From the estimated DLR $\hat{\varphi}_{i,r}$ variance, we can define the probability of $\varphi_{i,r} = 1$, i.e. the probability of non-coherence. If we assume that the $\varphi_{i,r}$ random variables follow the Normal distribution if $0 < \varphi_{i,r} < 1$, and has a mass probability if $\varphi_{i,r} = 1$, then $\Pr(\varphi_{i,r} = 1) = 1 + F(0) - F(1)$, where *F* denotes the Normal cumulative distribution with mean equal to the estimated $\hat{\varphi}_{i,r}$ value and variance equal to the DLR estimated variance. Table 4 is sorted according to the inner product of the adjusted residual variances (RV) explained (Table 3) by the associated DLR estimated probabilities of non-coherence, multiplied by the membership level of not belong to the West-cluster countries (Table 1). The resulting values define the dissimilarity between a particular country and the common mortality experience (independently from the level of mortality), in terms of clustering, modelling and coherence. Small membership values imply a strong correlation with the (fuzzy) main time trend (Figure 1) and similarity in the mortality dynamics. Small values for the residual variances indicate sufficient modeling and a minor non-coherent effect in the case of divergence (i.e. if $\varphi_{i,r} = 1$) and small coherent probability values gives more confidence to forecasting coherently the country's experience . Thus, the overall effect of these products can quantify the significant level of coherence, for each country.

From Table 4, we note that, for both sexes, all of the West-cluster countries can be modelled in a coherent way, except for E&W females, according to the estimated DLR $\hat{\varphi}_{i,r}$-value. For the case of E&W females, the significant level of coherence is well above that of the other West-cluster countries, and therefore we can produce forecast values with minor divergence. The countries which exhibit strong divergent trends (i.e. where $\hat{\varphi}_{i,r}=1$) are Lithuania, Latvia, Slovakia, Belarus, Russia and Ukraine for males, and Latvia, Belarus, Russia and Ukraine for females. For males: Poland, Bulgaria, Hungary and Estonia, and for females: Iceland, Bulgaria, Hungary, Lithuania and Estonia, have estimated DLR $\hat{\varphi}_{i,r}$-values less than 1, and they do not belong to the West-cluster (Table 1). Based on the DLR model structure, the above countries could be modelled and forecasted coherently in accordance with the common structure. As discussed by Lee (2003), sometimes a population may not have been regarded as belonging to a certain group in the past, but its mortality may be expected to follow and may catch up to and join the group trend in the future, and he argues that the mortality experience of the group's is a better guide to their future than the individual population histories would be.

	$\hat{\varphi}_{i,r}$			$\Pr(\varphi_{i,r}=1)$				$\hat{\varphi}_{i,r}$				$\Pr(\varphi_{i,r}=1)$		
Males	***i=1***	***i=2***	***i=3***	***i=1***	***i=2***	***i=3***	**Females**	***i=1***	***i=2***	***i=3***	***i=1***	***i=2***	***i=3***
E&W	0.93	0.99	0.92	1%	57%	0%	***Belgium***	0.91	0.97		0%	17%	
France	0.89	0.95	0.92	0%	17%	0%	***Switzerland***	0.90	0.87	0.97	0%	0%	35%
Scotland	0.93	0.96	0.91	0%	10%	2%	***France***	0.91	0.98	0.94	0%	49%	6%
Luxembourg	0.91			7%			***Canada***	0.98	0.94		56%	0%	
Belgium	0.98	0.93	0.86	29%	0%	11%	***Austria***	0.93	0.95		11%	0%	
Sweden	0.97	0.94	0.94	31%	13%	29%	***Australia***	0.98	0.95		33%	4%	
Austria	0.86	0.93	0.96	2%	10%	14%	***Sweden***	0.99	0.92	0.95	58%	1%	3%
Switzerland	0.89	0.96	0.95	2%	47%	11%	***Finland***	0.95	0.92		3%	7%	
Netherlands	0.97	0.98	0.92	17%	47%	0%	***E&W***	1.00	0.94		100%	0%	
USA	0.98	0.95	0.95	42%	3%	39%	***W. Germany***	0.97	0.98		44%	45%	
Canada	0.95	0.92		23%	1%		***Slovakia***	0.93	0.94	0.83	0%	2%	13%
N. Zealand	0.97	0.96		42%	13%		***Norway***	0.90	0.96	0.79	2%	3%	9%
Italy	0.94	0.93	0.97	8%	5%	43%	***Czech***	0.92			5%		
Portugal	0.93	0.98	0.95	0%	39%	39%	***Scotland***	0.94	0.96	0.92	0%	12%	26%
Australia	0.94	0.94	0.95	10%	8%	15%	***Italy***	0.96	0.94	0.91	26%	0%	1%
Norway	0.98	0.94	0.92	44%	12%	3%	***Spain***	0.97	0.94	0.87	27%	0%	1%
W. Germany	0.97			47%			***Portugal***	0.99	0.95	0.92	48%	0%	24%
Finland	0.95	0.95		4%	35%		***N. Zealand***	0.97	0.95		36%	4%	
Spain	0.96	0.88	0.94	10%	0%	10%	***Luxembourg***	0.90			11%		
Iceland	0.97			32%			***Japan***	0.98	0.95	0.92	32%	0%	0%
Denmark	0.99			49%			***USA***	0.99	0.94	0.92	45%	8%	0%
Ireland	0.91	0.96	0.96	14%	11%	37%	***Poland***	0.90	0.96	0.92	3%	33%	9%
Japan	0.98	0.95	0.91	24%	0%	0%	***Ireland***	0.94	0.97	0.95	7%	38%	37%
Czech	0.99	0.91	0.91	78%	15%	0%	***Netherlands***	0.99	0.90	0.95	64%	0%	2%
E. Germany	0.98	0.98	0.97	48%	77%	45%	***E. Germany***	0.97	0.91	0.00	45%	12%	0%
Poland	0.99	0.94		62%	15%		***Denmark***	0.99	0.91	0.87	51%	0%	5%
Slovakia	1.00	0.92		100%	0%		***Lithuania***	0.88	0.91	0.94	4%	13%	13%
Bulgaria	0.95	0.97	0.92	29%	7%	1%	***Iceland***	0.97			40%		
Estonia	0.98	0.90	0.73	50%	12%	0%	***Bulgaria***	0.96	0.97	0.92	19%	17%	2%
Hungary	0.99	0.95	0.93	50%	16%	22%	***Hungary***	0.97	0.95	0.95	46%	11%	14%
Belarus	1.00	0.93	0.87	93%	22%	5%	***Ukraine***	1.00	0.94		100%	14%	
Ukraine	1.00	0.92		100%	33%		***Belarus***	1.00	0.93		100%	4%	
Lithuania	1.00	0.96	0.88	97%	41%	16%	***Estonia***	0.97	0.95		47%	34%	
Latvia	1.00	0.92	0.84	100%	30%	2%	***Russia***	1.00	0.90	0.95	100%	30%	18%
Russia	1.00	0.93	0.92	100%	26%	27%	***Latvia***	1.00	0.83	0.37	100%	17%	1%

Table 4: Estimated DLR $\hat{\varphi}_{i,r}$-values and associated probability of non-coherence, sorted according to the significant level of coherence, for each country, and both sexes.

According to Li & Lee (2005), the residuals are modeled by a simpler model structure. In order to achieve a trend that moves toward a constant value, they assume a first order autoregressive model with a coefficient that yields a bounded short term trend: $Y_{i,r}^{res}(t)=\alpha_{i,r}+b_{i,r}\cdot Y_{i,r}^{res}(t-1)+\sigma_{i,r}\cdot e_{i,r,t}$, where $\alpha_{i,r}$ and $b_{i,r}$ are coefficients and $\sigma_{i,r}$ is the standard deviation of the AR(1) model. The innovations $e_{i,r,t}$ are assumed to be

white noise random variables. If the estimated coefficient $\hat{b}_{i,r} < 1$, then the *r*-country can be forecasted coherently by the common time trends, otherwise the *r*-country experience diverges from the common time trends. Utilizing the Li & Lee(2005) approach, the countries which exhibit strong divergent trends (i.e. where $\hat{b}_{i,r} \geq 1$) are E&W, Scotland, Australia, Bulgaria, Hungary, Lithuania, Slovakia, Belarus, Russia and Ukraine for males, and USA, Netherlands, Lithuania, Belarus, Russia, Ukraine for females. The DLR approach seems to be more consistent, in terms of coherence, with the countries' West-East classification, than the Li & Lee(2005) approach.

6. Discussion

In section 2, we classify 35 countries by fuzzy c-means cluster analysis, for the time period 1960-2006. We construct the males West-cluster which consists of 25 countries and the females West-cluster of 26 countries. Further, another distinct pair of clusters is detected from the remaining East-cluster countries, which gives a sub-cluster consisting mainly of Russia, Ukraine and Belarus. For these countries, the mortality dynamics are distinguishable from the rest of the East-cluster countries (Estonia, Hungary, Lithuania, Latvia, Bulgaria), and their life expectancies decrease after 1990's.

The clustering method is based on the main time trends. The main time trends are a linear combination of the normally distributed GLM parameter estimates. In comparison with the life expectancy index, Lee (2003) comments that the age specific force of mortality or death rate are the fundamental measures of mortality which we should model and interpret. He concludes that period life expectancy is just a very particular and highly nonlinear summary measure, with little or no causal significance, and that risks of death are fundamental and the age at death is derivative. Our modeling and forecasts are based on (S)PCs, which are linear combinations of the (asymptotic) normally distributed GLM parameter estimates and characterize the logged central mortality dynamics. The (S)PCs sum to zero across time, with a rate of improvement that does not depend on the level of mortality, in contrast with the life expectancy. A weighted combination of the (S)PCs is used to construct the main time trend, which summarizes the logged central mortality dynamics in time effects, for all of the ages combined.

For the post-war time period (1947-2006), 19 male countries, namely Sweden, France, Denmark, E&W, Norway, Netherlands, Scotland, Italy, Switzerland, Finland, Spain, Ireland, Belgium, Australia, Canada, USA, Portugal, Japan and Austria, are pooled to construct the *common age-period model* structure (2), giving equal weight to each country's mortality dynamics. To avoid the problems arise, if we were just to add up the actual number of deaths from all the countries together, where in this case the biggest populations would dominate the overall mortality analysis, we introduce weighted deaths and matching weighted central exposures. This particular structure for the weights treats equally the countries mortality trends and enhances coherence. Experiments with unweighted deaths, produced more non-coherent countries.

Similar to Hatzopoulos and Haberman (2011), we employ SPCA to the estimated common GLM parameter estimates, and for a particular choice for the sparse *s*-value, we derive two interaction terms which summarize the basic common mortality dynamics in age-time effects. These two common interaction terms split the age range in two age groups, young and adults. By exploiting the correlated structure of these two age profiles, based on a linear combinations of the two SPCs, we construct two different mortality dynamics, the main time trend and the young-adults relative differential time trends, in a smoothed way. These trends appear to be very informative for the description of the mortality dynamics, giving an improved confidence to forecast those mortality dynamics, in a compacted way. The two common SPCs are forecasted according to these time trends.

The method described for the comparison of two mortality experiences in section 3, is based on (graduated) logged central mortality ratios. The method is applied to investigate the sex differentials and to extract the main sex difference mortality dynamics in age-time effects. The sex difference model structure shows divergence until the 1980s and convergence thereafter, referring to similar age groups, and hence the dynamics in these mortality trends are modeled by a single structure. The most significant, first sex difference PC, over the whole time period (1947-2006), is modeled by a stationary process, providing a coherent structure between the sexes.

For males, the analysis of the residual particularities for each country is based on the residuals after subtracting (by offsetting GLM techniques) the two males common interaction terms, and for females the analysis is based on the residuals after subtracting the two males common interaction terms plus the common sex-difference interaction term. The results are very satisfactory, in terms of the common variance explained for the majority of the countries. Further, the common *sex difference age-period model* structure (4) describes effectively the females differential experience, in age-time effects. Experiments with various countries, show that the mortality dynamics are better described after embedding the two common interaction terms rather than modeling them independently. Under the common structure, the residual interaction terms, based on model structures (5) & (6), for each country are more easy to interpret and distinguish in a more comprehensible manner the remaining age-time interactions. When using more than one interaction term, country independently analysis often gives ambiguous age-time interaction trends, especially in cases where the related time period is restricted or when the reliability of the corresponded national crude mortality data is poor.

In the dynamic linear regression (DLR) model structure, the results are very supportive. For males, all of the males West-cluster 25 countries can be modelled in a coherent way, and also for females where all of the females West-cluster 26 countries can also be modelled in a coherent way. Finally, countries which do not belong to the West-cluster can also be modelled and forecasted coherently under the common structure.

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Appendix A

Figure A displays the first residual interaction terms ($g^{res}_{1,r}(x)$ left graphs, and $Y^{res}_{1,r}(t)$ right graphs), and the forecast residual PCs ($\hat{Y}^{res}_{1,r}(t)$ estimates), for calendar years 2007-2050, with associated confidence intervals, according to the *residual age-period model* structures (5) & (6), for both sexes, and for selected countries.

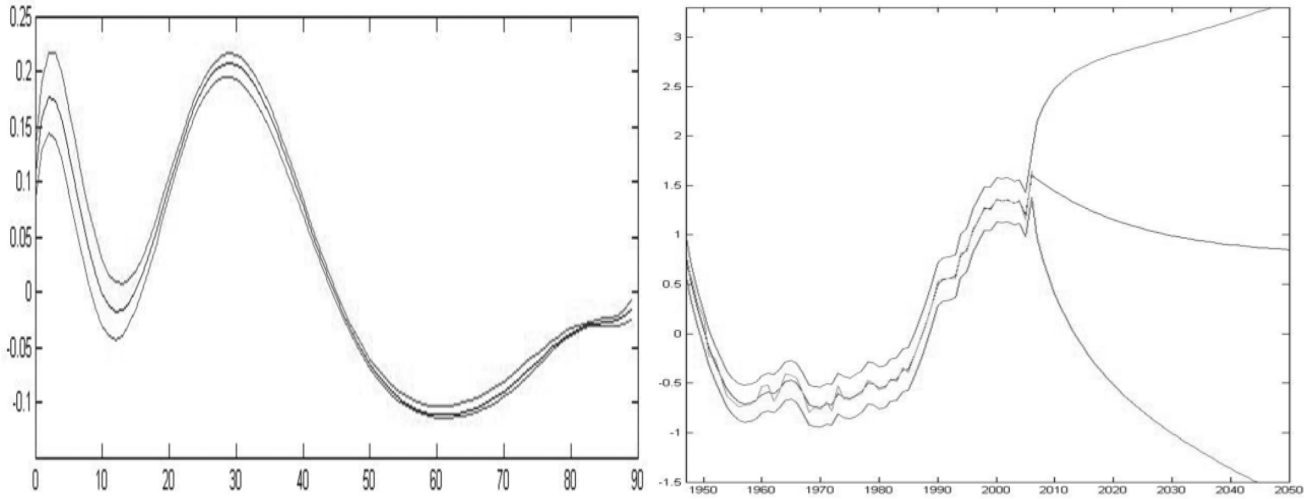
For E&W males, the first residual interaction term refers mainly to age group 25-35 with positive values and to the age group 50-70 with negative values, indicating a relative deterioration for the first age group and a relative improvement for the second age group after the 1980s; and after the 2000s these trends become steady. For E&W females, the first residual interaction term refers mainly to the age groups 0-15 and 60-70 with positive values, indicating a relative deterioration for these age groups, with diverging forecast values.

For USA, for both sexes, the first residual interaction term refers mainly to the ages 20-40, indicating a relative deterioration, with relative improvement forecast values for males and with forecast values reaching a constant level for females.

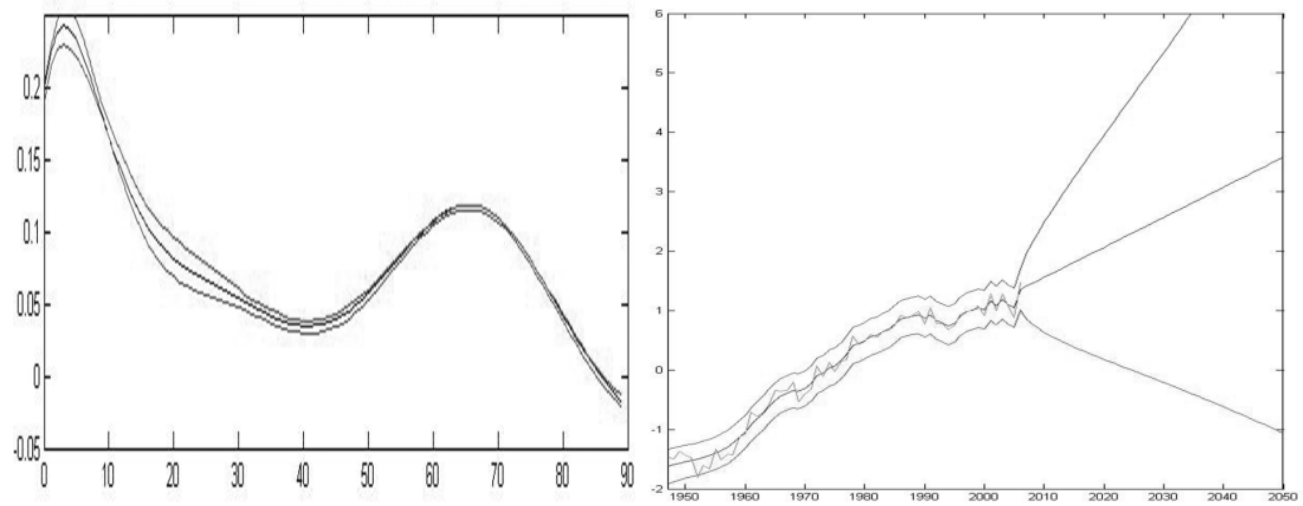
For Japan, for both sexes, the first residual interaction term refers especially to the age group 20-40, indicating a relative improvement until the 1980s, and thereafter a deterioration with forecast values supporting this last trend.

For Hungary, for both sexes, the first residual interaction term refers especially to the age group 40-70, indicating a relative deterioration until the 1990s which thereafter becomes almost stable, with forecast values supporting this steadiness after the 1990s for males, and forecast values with a relative improvement for females.

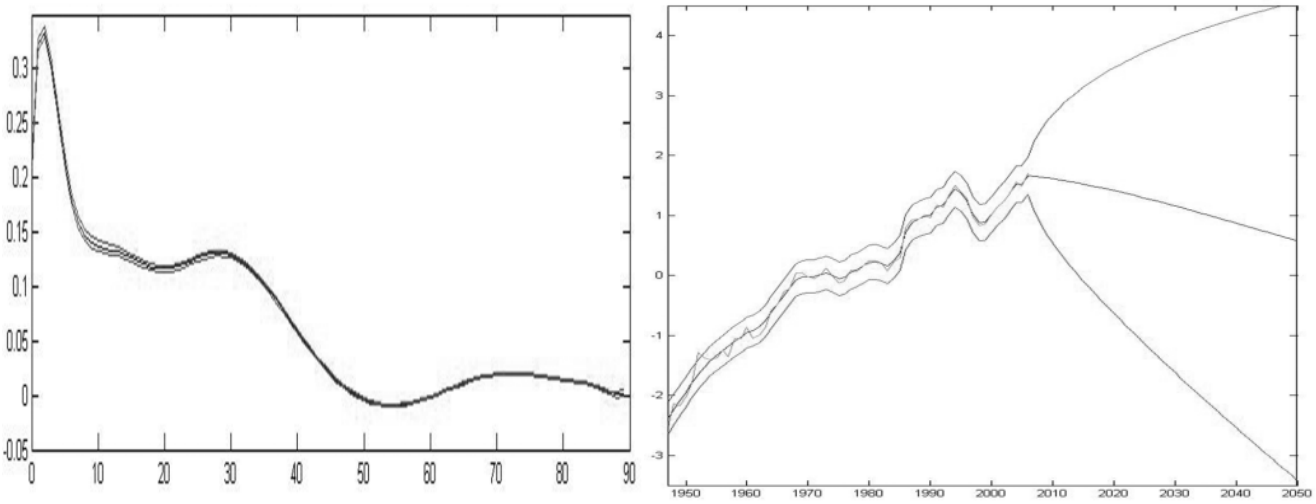
For Russia, for both sexes, the first residual interaction term, refers especially to the age group 30-60, indicating a relative deterioration for all the time range, with diverging forecast values.



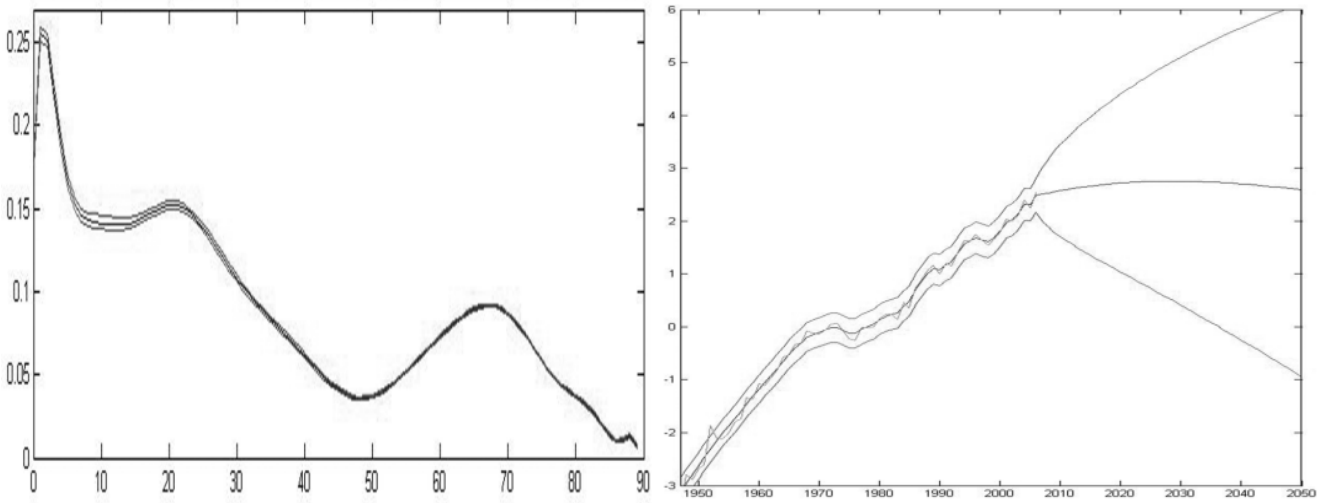
E&W-males



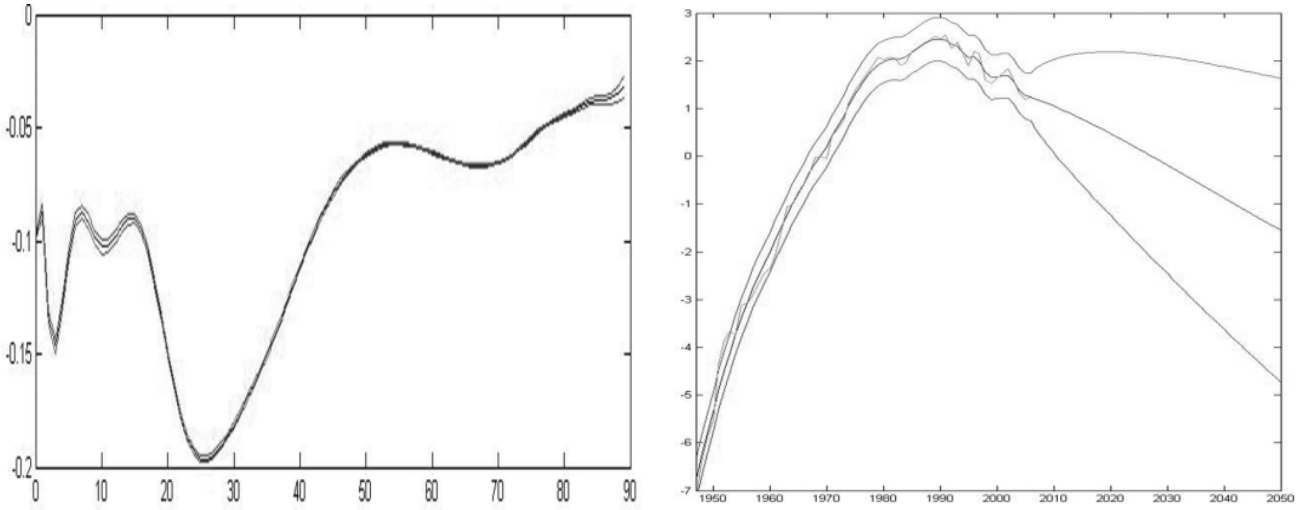
E&W-females



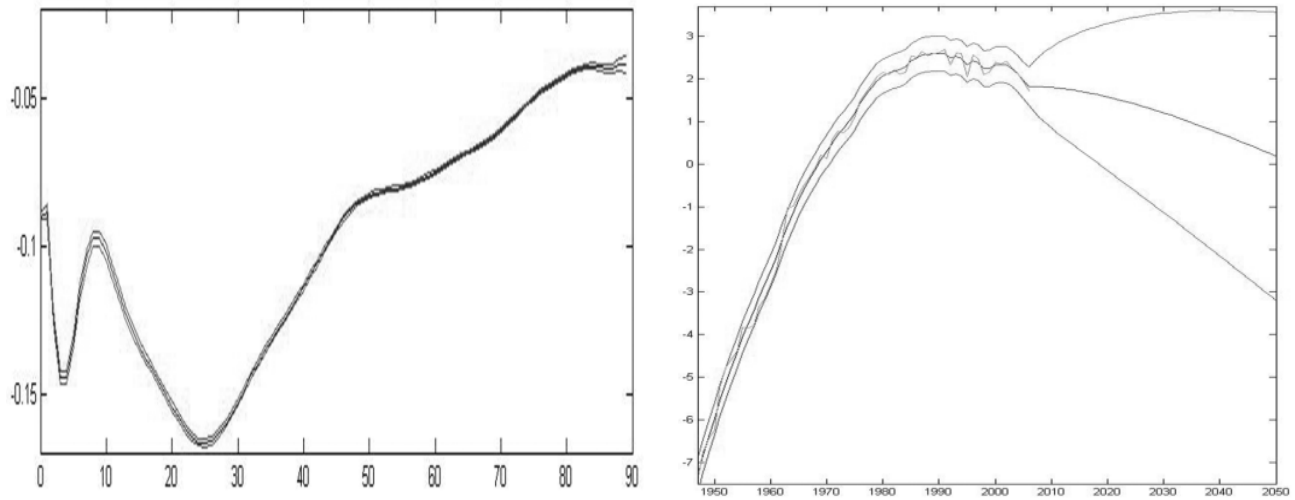
USA-males



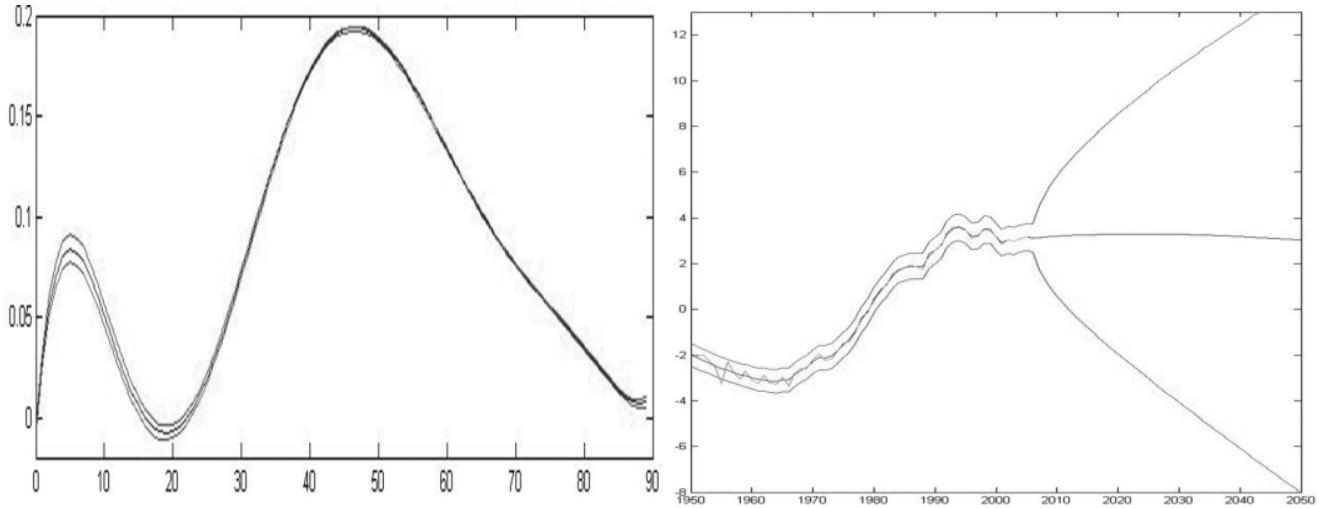
USA-females



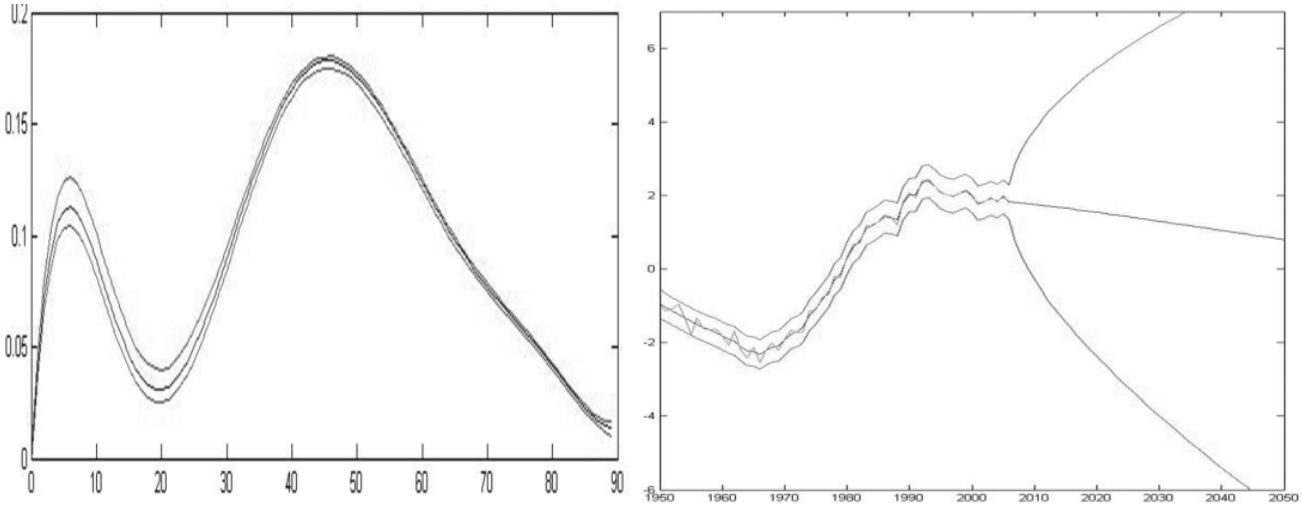
Japan-males



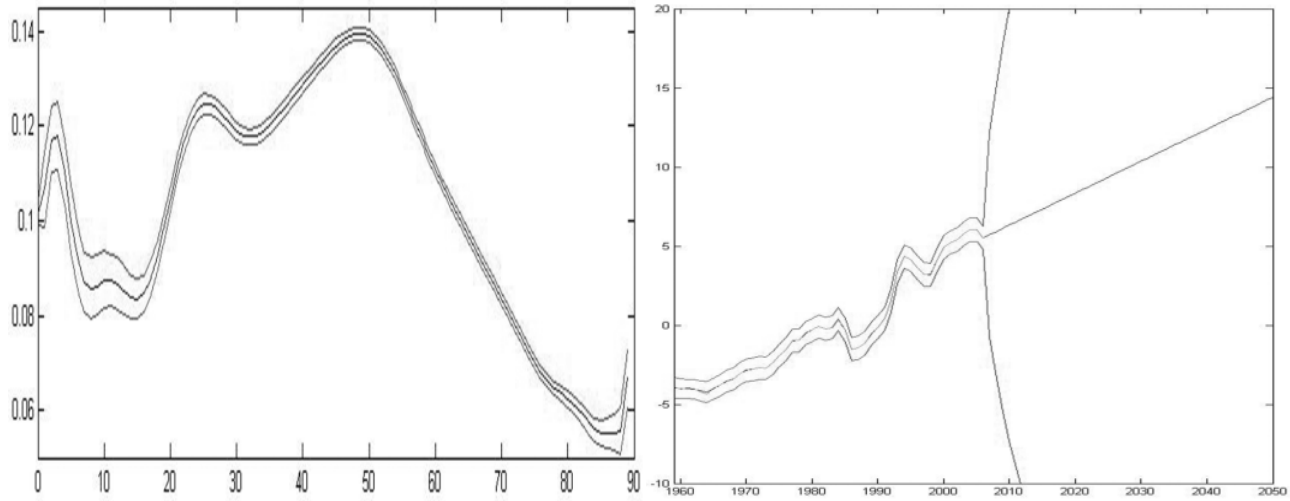
Japan-females



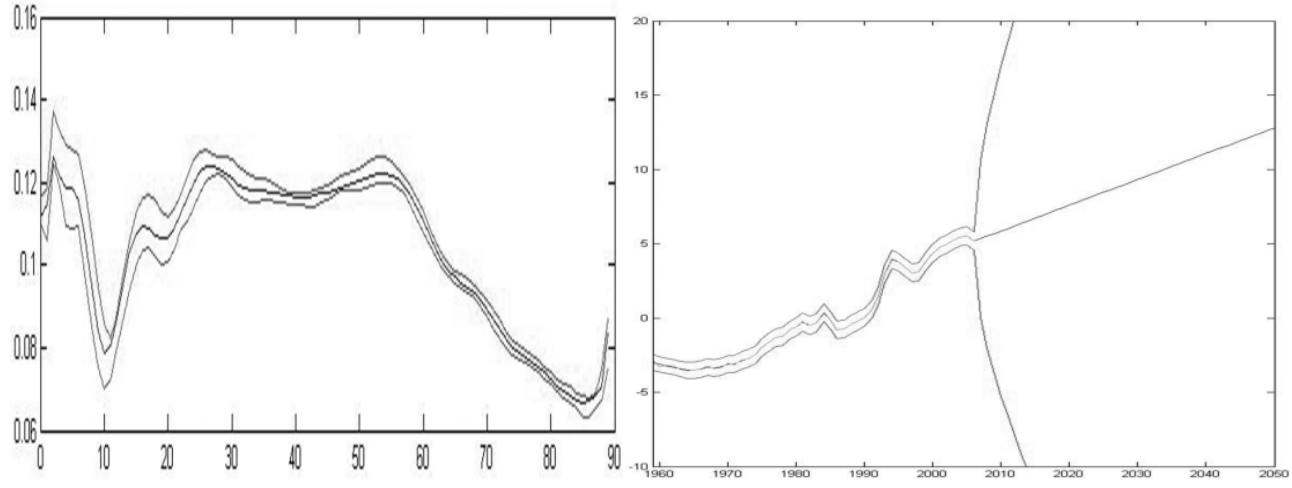
Hungary-males



Hungary-females



Russia-males



Russia-females

Figure A: First residual interaction terms, $g_{1,r}^{res}(x)$ and $Y_{1,r}^{res}(t)$ values, according to the *residual age-period model* structures (5) & (6), for both sexes and selective countries.