

# SCOR Papers

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## Microscopic longevity modeling and its practical applications

### *Abstract*

*The current ageing of the population prompts analysis of the mortality and longevity of individuals. The study of individual longevity necessitates multi-disciplinary modeling, since it is at the crossroads of numerous fields such as demographics, economics and medicine, to name but a few. Increased life expectancy is a critical challenge, which moreover has major consequences in western countries. In particular, the financial flows linked to population ageing are colossal, including for example the financing of retirement and long-term care. Governments, pension funds and insurance policies are consequently highly exposed to the evolution of longevity in the future. It seems necessary to better understand this risk, to model it and to find ways in which to manage and transfer it.*

*This article proposes a mathematical modeling of longevity and an analysis of longevity risk in the field of demographics and life insurance. It is constructed as follows:*

*The first section models mortality, taking into account features other than age.*

*The second section approaches longevity modeling with the help of a microscopic population dynamic model, which enables us to describe the evolution of a population on an individual scale.*

*The third section deals with some practical applications for this modeling to the fields of demographics and life insurance.*

*These results are taken from a doctoral thesis entitled "Rate and longevity risks: dynamic modeling and application to derivative products and life insurance" backed by the Ecole Polytechnique and available at <http://www.cmap.polytechnique.fr/~bensusan>*

# 1. Mortality modeling

The evolution of mortality rates is random and is generally studied using probabilistic models. The most traditional models are the models of Lee Carter [11, 12] and the CDB models introduced by Cairns, Dowd and Black [4, 5, 6], which are age-specific mortality projection models on a logarithmic scale. We are seeking to extend this type of model to an age and feature-specific mortality model. After describing the standard two-factor CDB model and identifying the features that influence mortality, we propose an individual mortality model that enables us to integrate these explicative variables.

## 1.1 Age-specific CBD model

Let us note as  $q_0(a, t)$  the mortality rate of a person at age  $a$  and at time  $t$ . The standard 2-factor Cairns model is written on the dynamic of  $\text{logit}[q_0(t, a)]$  using a vector of factors  $A(t) = [A_1(t), A_2(t)]^T$ .

$$\begin{aligned}\text{logit}[q_0(t, a)] &= \log\left(\frac{q_0(y, x, a, t)}{1 - q_0(y, x, a, t)}\right) = A_1(t) + aA_2(t), \\ A(t+1) &= A(t) + \mu + CZ_{t+1}.\end{aligned}$$

where  $\mu = (\mu_1, \mu_2)^T$  is the trend represented by a  $2 \times 1$  constant vector and  $C$  is an inferior triangular  $2 \times 2$  Cholesky matrix, corresponding to the variance covariance matrix of factors  $A_1$  and  $A_2$ . The components of the Gaussian  $Z_T$  vectors are independent, centred and reduced Gaussian variables. Thus, this modeling consists of a trend projection of the mortality rate  $\text{logit}$ , with noise around the trend. The estimation of the parameters,  $\mu$  and  $C$ , parameters is made through linear regression along the historical national age-specific mortality curves.

## 1.2 Influence of features

It is known that the sex of an individual has an influence on his or her mortality level. There are, moreover, mortality tables for men and women on a national scale. Nevertheless, there are other features that are not taken into account in national mortality tables.

Recent studies [10] list certain socio-economic features that impact mortality level, such as marital status, socio-professional category, level of education, and level of income. Of course, features relating to an individual's health are deciding factors, but these are fairly difficult to quantify and obtain. In this study we will be looking at socio-economic features, using the example of marital status, which is a determining factor and is also fairly complex because it can evolve throughout an individual's life, with marriage, divorce or the death of a spouse.

## 1.3 Age and feature-specific mortality model

We propose an extension to the traditional Cairns model, into which we incorporate the impact of certain features on mortality. The idea is to conduct a logistical regression of the mortality rate with regard to age and a set of given features. In the absence of age and feature-specific mortality national tables, we have to find new data that provides this information. This new data will be less rich than the data used to constitute national tables, and consequently we have to limit modeling to age brackets in order to accurately estimate death probabilities by age and by feature. Thus, it is possible to estimate the probability of death of an individual at age  $a$  within a given age bracket and with feature  $x$ . The age brackets must be fairly small so that the impact of features on mortality is the same for a given age bracket.

### 1.3.1 Description of the model

Noting the number of age brackets as  $N$ , we define the division of age brackets as  $A = \{A_1, 1 \leq 1 \leq N\}$ . We note the number of individual features as  $M_x$  and the number of environmental variables as  $M_y$ . We define  $q_1(x, y, a, t)$  as the probability of death at date  $t$  of an individual possessing features  $x = (x_i)_{1 \leq i \leq M_x}$  at age  $a \in A$ , living in an environment (or region) with features  $y = (y_i)_{1 \leq i \leq M_y}$ . The logistic regression for each age

$$\text{logit}[q_1(x, a, t)] = \alpha_1(t) + a\alpha_2(t) + \sum_{i=1}^{M_x} \beta_i^l(t)^\top x_i + \sum_{j=1}^{M_y} \gamma_j^l(t)^\top y_j.$$

bracket may be written as follows:  $\forall l \in \{1, \dots, N\}, \forall a \in A_l$ ,

This intuitive model takes account of the influence of all features, using the stochastic factors  $\alpha_i(t)$ ,  $\beta_i^l(t)$  and  $\gamma_j^l(t)$ . The dynamic of these factors is analogous with those of the Cairns model. In fact, when consi-

$$\begin{aligned} \beta^l(t) &= \beta^l(t-1) + \mu^{l,\beta} + C^{l,\beta} Z_{t+1}^\beta, \\ \gamma^l(t) &= \gamma^l(t-1) + \mu^{l,\gamma} + C^{l,\gamma} Z_{t+1}^\gamma, \end{aligned}$$

dering the vectors  $\beta^l = (\beta_1^l, \dots, \beta_{M_x}^l)^\top$  and  $\gamma^l = (\gamma_1^l, \dots, \gamma_{M_y}^l)^\top$ , we get  $\forall l \in \{1, \dots, N\}$ :

where  $\mu^{l,\beta}$  (resp  $\mu^{l,\gamma}$ ) is a vector of size  $M_x$  (resp  $M_y$ ) and  $C^{l,\beta}$  (resp  $C^{l,\gamma}$ ) is a matrix of correlations between the various different features of size  $M_x \times M_x$  (resp  $M_y \times M_y$ ).

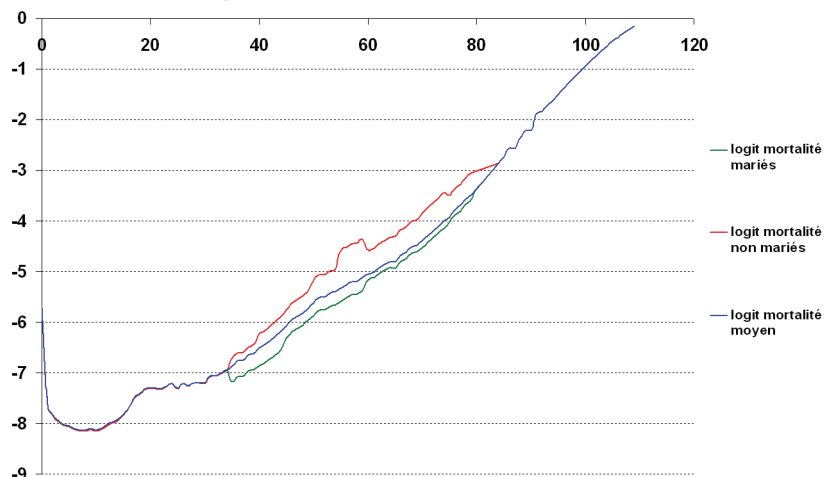
### 1.3.2 Calibration of the model

The factor parameters must be calibrated on a fairly rich historical basis. We have calibrated this model on both national mortality data (for the factors  $\alpha_i(t)$ ) and on real data that INSEE agreed to give us<sup>1</sup>. This data constitutes a sample of the French population called the permanent demographic sample (échantillon démographique permanent or EDP), covering 992,711 people (dead and alive). These people were potentially part of a census on different dates: 1968, 1975, 1982, 1990 and 1999. At each census date, numerous variables were noted such as sex, socio-professional category, matrimonial status and level of education. The censuses enable us to conduct a longitudinal study of the influence of features on mortality, taking into account changes in features over the lifetime of an individual. The determining influence of these features on mortality has been analysed [10] and this model enables us to project mortality tables, which comply with the point of view of the demographers.

## 1.4 The example of marital status

The mortality model estimates the influence of features on mortality and the evolution of this influence over time. For example, we consider the influence of marital status on the mortality of men as well as the evolution of this influence over time. By gathering EDP data from between 2002 and 2007, it is possible to calculate the probabilities of death according to age, depending on marital status. On the following graph we show the mortality of married men compared to that of non-married men in 2007:

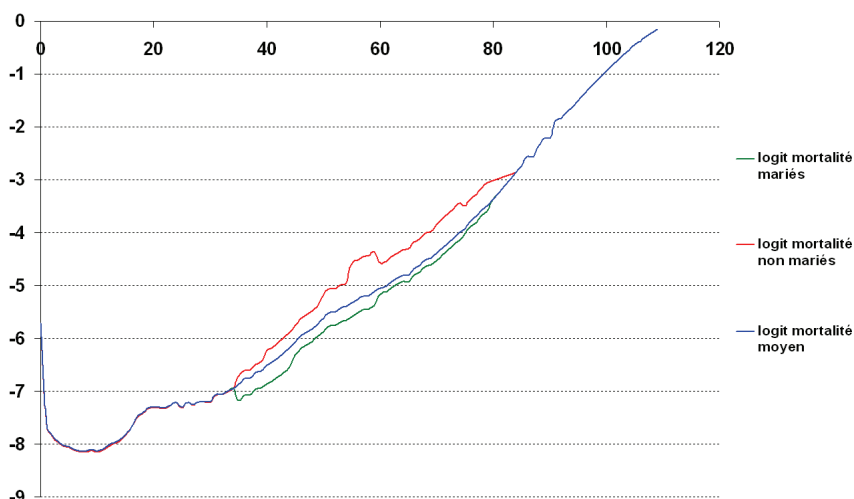
FIGURE 1: Mortality logit of men by age for different marital statuses, calculated with data from 2000 to 2007



(1) Thanks to Antoine Frachot, Alain Trognon and Xavier Niel for their help in obtaining this data.

Subsequently, we calibrate the mortality model by age and by marital status using national data and EDP data, in order to calculate the parameters of the model factors. Using the mortality model, it is possible to obtain a mortality projection by age and by marital status in 2017 (see next page): It appears that marriage is a protective factor compared to other marital statuses and the model suggests that it will maintain its protective status in the future. This example shows that the projections resulting from this model are informative in terms of the evolution over time of the influence of features on mortality level.

FIGURE 2: Mortality logit curves for men in 2017 by age for different marital statuses



## 2. Longevity modeling

The following step in this analysis of longevity is the modeling of population evolution on an individual scale. What we propose here is a specific modeling of the population in which each individual is represented by a Dirac measure  $\delta_{x,a}$ , which is described by features, called traits in ecology, noted as  $x$ , belonging to the space  $\mathcal{X}$ , and by the individual's age  $a$ , which takes its value in  $\mathbb{R}_+$ . Based on recent methods used in ecology and in population dynamics by S. Méléard and others [7, 8, 15], it is possible to develop an "aggregate evolution" model tailored to human beings where the state space is a set of occasional measurements of individuals. The model consists of an occasional Poisson process describing the evolution of a population structured by age and by traits based on evolution rates.

### 2.1 Evolution intensities

In this modeling, evolution rates such as birth, death, trait change and immigration rates may depend on time and on individual features. Moreover, these rates may be stochastic, which notably enables us to use a stochastic mortality model for mortality rate dynamics.

In insurance, mortality modeling generally involves evolution rates corresponding to the probability of the associated event occurring. In population dynamics, modeling tends to use evolution intensities. There is a mathematical link between rates and intensity: considering a mortality rate  $q(a, t)$ , we can attribute to it a mortality intensity of  $d(a, t)$  expressed as:

$$d(a, t) \sim \ln \left( \frac{1}{1 - q(a, t)} \right)$$

The proposed modeling naturally uses evolution intensities rather than evolution rates. These evolution intensities must be fairly general in order to obtain the most refined modeling possible.

### 2.1.1 Birth rate intensity

An individual with trait  $x \in \chi$  and at age  $a \in \mathbb{R}_+$  may give birth to a new individual with an intensity of  $b(x, a)$ , where  $b$  is a function of  $\chi \times \mathbb{R}_+$  in  $\mathbb{R}_+$  and majorated by  $\bar{b}$ . New-borns will be characterised by an age equal to 0 and by the trait  $x' \in \chi$ . The trait  $x' \in \chi$  is the execution of a random variable of law  $k^b(x, a, dx')$  which represents the distribution of descendent traits.

### 2.1.2 Mortality intensity

An individual at age  $a \in \mathbb{R}_+$  and with trait  $x \in \chi$  may die with an intensity of  $d(x, a)$ , which is majorated by  $\bar{d}$ . The form of the intensity  $d$  enables us to take account of natural phenomena such as an increase in the probability of death when an individual gets older. Moreover, certain features will determine the mortality level of an individual throughout his or her life.

### 2.1.3 Intensity of trait evolution

In this modeling, the traits of an individual may evolve over time. An individual at age  $a$  and with trait  $x$  may change traits with an evolution intensity of  $e(x, a)$ , majorated by  $\bar{e}$ , and may acquire a new trait  $x'$ . The trait  $x'$  is selected according to a trait distribution  $k^e(x, a, x')$  which depends on the initial features of the individual. The form of intensity  $e$  describes the rate of transition from one trait to another and will also depend on the age of the individual.

### 2.1.4 Introduction of stochastic factors

We observed in the previous section that the intensity of mortality is likely to vary over time period  $e$  in a random way, as is the birth rate intensity and the intensity of trait change. Thus, we introduce the random factors  $Y^b_t, Y^d_t$  and  $Y^e_t$  associated with the various evolution intensities that enable us to describe this stochastic evolution. The evolution intensities will now be noted as  $b(x, a, Y^b_t), d(x, a, Y^d_t)$  and  $e(x, a, Y^e_t)$ .

As data is available every year, we propose the following discrete dynamic:

$$\begin{aligned} Y_k^b &= Y_{k-1}^b + \mu^b(k-1, Y_{k-1}^b) + \sigma^b(k-1, Y_{k-1}^b)\epsilon^b, \\ Y_k^d &= Y_{k-1}^d + \mu^d(k-1, Y_{k-1}^d) + \sigma^d(k-1, Y_{k-1}^d)\epsilon^d, \\ Y_k^e &= Y_{k-1}^e + \mu^e(k-1, Y_{k-1}^e) + \sigma^e(k-1, Y_{k-1}^e)\epsilon^e, \end{aligned}$$

where  $\epsilon^b, \epsilon^d$  and  $\epsilon^e$  are random centred reduced Gaussian variables,  $\mu = (\mu^b, \mu^d, \mu^e)$  represents the evolution trend vector and  $\sigma = (\sigma^b, \sigma^d, \sigma^e)$  describes the variations in intensity of their trends.

## 2.2 Description of the microscopic model

Let us define as  $Z$  a process describing population evolution over time. We note as  $M_P(\chi \times \mathbb{R}_+)$  the space of random measurements on  $\chi \times \mathbb{R}_+$ , which is the space associated with age and traits. At all times  $t$ , the population may be described by the measure  $M_P(\chi \times \mathbb{R}_+)$  written as:

$$Z_t = \sum_{i=1}^{N_t} \delta_{(x_i(t), a_i(t))}$$

where  $N_t = \langle Z_t, 1 \rangle = \int_{\chi \times \mathbb{R}_+} Z_t(dx, da)$  is the number of individuals at time  $t$ .

In this modeling, the population is ageing continually and is modified from time to time at certain event dates with a birth, a death or a trait change. Thus, the process is modelled by a continuous process on the right and limited on the left (càd-làg) with values in the occasional measure space  $M_P(\chi \times \mathbb{R}_+)$ .

For a given population  $Z$ , we note as  $X_i(Z)$  (resp.  $A_i(Z)$ ) the trait (resp. age) of the individual  $i$  within the population  $Z$ . Considering an initial population  $Z_0$ , and an occasional Poisson measure  $Q(ds, di, d\theta, dx')$  on the space  $\mathbb{R}_+ \times \Xi = \mathbb{N}^* \times \mathbb{R}_+ \times \chi$ , the process  $Z$  is described as follows:

$$\begin{aligned}
Z_t &= \sum_{i=0}^{N_0} \delta_{(X_i(Z_0), A_i(Z_0)+t)} + \int_0^t \int_{\Xi} \mathbf{1}_{i \leq N_{s-}} \left[ \delta_{(x', t-s)} \mathbf{1}_{0 \leq \theta < m_1(s, Z_{s-}, i, x')} \right. \\
&- \delta_{(X_i(Z_{s-}), A_i(Z_{s-})+t-s)} \mathbf{1}_{m_1(s, Z_{s-}, i, x') \leq \theta < m_2(s, Z_{s-}, i, x')} \\
&+ \left. (\delta_{(x', A_i(Z_{s-})+t-s)} - \delta_{(X_i(Z_{s-}), A_i(Z_{s-})+t-s)}) \mathbf{1}_{m_2(s, Z_{s-}, i, x') \leq \theta < m_3(s, Z_{s-}, i, x')} \right] Q(ds, di, d\theta, dx')
\end{aligned}$$

where

$$\begin{aligned}
m_1(s, Z_{s-}, i, x') &= b(X_i(Z_{s-}), A_i(Z_{s-}), Y_s^b) k^b(X_i(Z_{s-}), A_i(Z_{s-}), x') \\
m_2(s, Z_{s-}, i, x') &= m_1(s, Z_{s-}, i, x') + d(X_i(Z_{s-}), A_i(Z_{s-}), Y_s^d) k^d(X_i(Z_{s-}), A_i(Z_{s-}), x') \\
m_3(s, Z_{s-}, i, x') &= m_2(s, Z_{s-}, i, x') + e(X_i(Z_{s-}), A_i(Z_{s-}), Y_s^e) k^e(X_i(Z_{s-}), A_i(Z_{s-}), x')
\end{aligned}$$

Concerning the Poisson Q measure, ds represents the selection of time, di represents selection of individual, dθ represents the selection of an event and dx' represents the selection of the new trait of the selected individual. The various m<sub>i</sub> are occurrence thresholds of events (birth, death and trait change), which are linked to the probability of an event occurring at each evolution date.

The evolution process is described as a measure, but we can also determine the evolution process naturally by  $\langle Z_t, f_t \rangle$  on the set of bounded functions:  $f: (x, a, s) \mapsto f_s(x, a) \in \mathbb{B}_b(\mathcal{X} \times \mathcal{R} \times \mathcal{R}_+)$ :

$$\begin{aligned}
\langle Z_u, f_u \rangle &= \langle Z_0, f_0 \rangle + \int_0^u \int_{\Xi} \left( f_s(x', 0) \mathbf{1}_{0 \leq \theta < m_1(s, Z_{s-}, i, x')} \right. \\
&- f_s(X_i(Z_{s-}), A_i(Z_{s-})) \mathbf{1}_{m_1(s, Z_{s-}, i, x') \leq \theta < m_2(s, Z_{s-}, i, x')} \\
&+ \left. [f_s(x', A_i(Z_{s-})) - f_s(X_i(Z_{s-}), A_i(Z_{s-}))] \mathbf{1}_{m_2(s, Z_{s-}, i, x') \leq \theta < m_3(s, Z_{s-}, i, x')} \right) \\
&Q(ds, di, d\theta, dx').
\end{aligned}$$

This form no longer involves the Dirac masses representing particles; instead interpretation takes place in the form of counting, which is the standard form for births and deaths.

The population size at time t is noted as N<sub>t</sub> and is equal to  $\langle Z_t, 1 \rangle$  (test function f equals 1). Thus, the population size is written as

$$N_t = N_0 + \int_0^t \int_{\Xi} \left( \mathbf{1}_{0 \leq \theta < m_1(s, Z_{s-}, i, x')} - \mathbf{1}_{m_1(s, Z_{s-}, i, x') \leq \theta < m_2(s, Z_{s-}, i, x')} \right) Q(ds, di, d\theta, dx')$$

bringing into the equation the births and deaths that have taken place within the population. It is clearly possible to study the structure of the population rather than its size by using suitable test functions.

### 2.3 Simulation of the evolution process

In order to describe this process more simply, we analyse the manner in which the population is actually evolving. We place ourselves at a date T<sub>n</sub> and note as N<sub>T<sub>n</sub></sub> the size of the population at this date. We draw the next occurrence date of an event T<sub>n+1</sub> by taking a random exponential variable with parameter (b + d + e)N<sub>T<sub>n</sub></sub>. Next, we select an individual from the population. The age and features of the individual determine the value of the evolution rates corresponding to probabilities of birth, death and trait change. We draw a random variable θ, which determines the event that takes place, and we modify the population accordingly. Following the example of the trait evolution rate, it is possible to introduce an immigration rate in order to manage migratory flows.

We notice that the simulation procedure is adapted to the size of the population, because the space of time between two events gets shorter as the population gets larger. On average, this simulation process consists of selecting each individual once each year and determining the evolution of those individuals depending on their features. The simulation techniques are highly efficient and enable us to easily simulate a range of scenarii. They also constitute a medium through which to demonstrate the existence and strong uniqueness of the evolution process, which has an infinitesimal generator and moment properties.

## 2.4 Micro-Macro link

This evolution process has a number of interesting properties. We have proven, for a population of initial size  $N$ , the existence of a density  $g^N(a,x,t)$  for population distribution by age and by trait, guaranteeing the regularity of the process.

A key property is the behaviour of this microscopic process in the case of large populations (when  $N$  tends towards infinity). In fact, numerous macroscopic-scale models exist that describe the evolution of a population. A standard equation in demographics is the McKendrick and Von Foerster partial differential equation [16], which describes the evolution of population density by age  $g(a, t)$  depending on the intensity of mortality  $d$  and the intensity of birth rate  $b$ .

We have proven that population density by age and by trait  $g^N(a,x,t)$  converges towards a function  $g(a,x,t)$ , which is almost certainly the sole solution to the following stochastic partial differential equation (SPDE):

$$\left(\frac{\partial g}{\partial t} + \frac{\partial g}{\partial a}\right)(a, t) = -d(a)g(a, t), \quad g(0, t) = \int_0^\infty b(a)g(a, t)da$$

This equation spreads the McKendrick and Von Foerster equation in several directions: adapting to the specific traits of each individual, adding a trait evolution rate and introducing random factors for the use of stochastic evolution rates. For both small and large populations, we prefer to use efficient simu-

$$\begin{aligned} \left(\frac{\partial g}{\partial t} + \frac{\partial g}{\partial a}\right)(\omega, x, a, t) &= -\left[d(x, a, Y_t^d(\omega)) + e(x, a, Y_t^e(\omega))\right]g(\omega, x, a, t) \\ &\quad + \int_{\mathcal{X}} e(x', a, Y_t^e(\omega))k^e(x', a, x)g(\omega, x', a, t)P(dx') \\ g(\omega, x, 0, t) &= \int_{\mathcal{X} \times \mathbb{R}_+} b(x', a, Y_t^b(\omega))k^b(x', a, x)g(\omega, x', a, t)P(dx')da \\ g(\omega, x, a, 0) &= g_0(\omega, x, a), \end{aligned}$$

lation techniques rather than this approximation, given the complexity of this stochastic partial differential equation. Nevertheless, this micro-macro link ensures the consistency of the model on both a microscopic and macroscopic scale.

## 3. Applications to demographics and life insurance

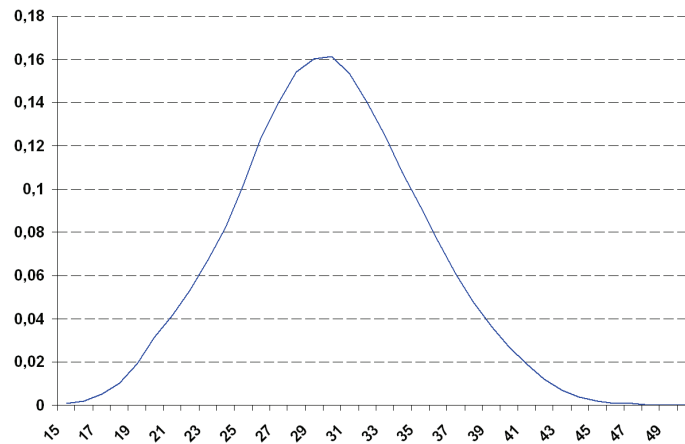
The last section of this paper looks at the applications for this modeling to demographics and life insurance. By calibrating individual demographic rate models **FIGURE 3: Fertility rate of women by age 2007** (mortality by age and by traits) and injecting population dynamics into the model, it is possible to analyse population evolution in the future.

### 3.1 Evolution of the French population

Demographic models are generally macroscopic and generate an average evolution scenario, possibly along with a scenario under static hypotheses [13]. Models also exist that use microsimulation techniques, but do not take account of all the available information [9]. We propose using a microscopic population dynamics model in order to describe the evolution of the French population in the future.

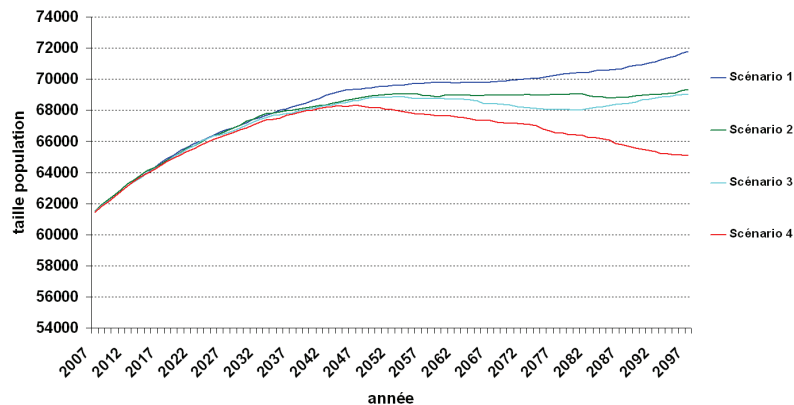
Initially, we consider the French population in 2007, with each individual characterised purely by age. In order to simulate evolution scenarii, we use the population dynamics model described in the previous section. The mortality rate is given by the mortality model from section 1, calibrated on national data by age and by sex, and the fertility rate is presumed to be constant and equal to that of 2007. The fertility rate by age corresponds to the number of births per woman at a given age, which enables us to calculate the probability that a woman of a given age has a child (see figure 3 above).

Taux de fécondité par âge des femmes 2007



Using these evolution rates, we represent several evolution scenarii up until 2097.

FIGURE 4: Evolution scenarii for population size until 2097 with a mortality scenario



The diversity of the scenarii is due to both the uncertain nature of evolution rates and the unexpectedness intrinsic to the evolution process. This double stochasticity generates rich scenarii and we observe that the stochasticity resulting from the rate of evolution (in this case the mortality rate) is predominant with regard to the evolution process. A range of scenarii provides not just an average evolution scenario, but also quantiles that enable us to define extreme scenarii. We introduce here a constant age-specific immigration rate equal to that of 2007 and describe the demographic projections of the French population in 2050.

TABLE 1: Projection statistics until 2050 with static birth and immigration rates (2007)

Statistics until 2050	Lower limit 10%	Central 50%	Upper limit 90%
Standardised Fertility Index	2.04	2.04	2.04
Population size (millions)	71.56	73.12	74.94
Over 60s (%)	36	37.8	39.2
Number of active people / inactive people	1.54	1.63	1.75
Number of deaths (millions)	22.01	23.25	24.6
Number of births (millions)	30.82	32.25	34.22
Number of immigrants (millions)	2.8	2.951	3.133



The average scenario appears to be fairly consistent with certain demographic projections [9, 13, 14]. We observe that the number of people over 60 is very high and that the ratio of active people to inactive people has reduced sharply, which translates into significant population ageing in the future. It is also possible to approach the complex problem of retirement, from a purely demographic point of view, by testing for example the impact of immigration policies and retirement age.

### 3.2 Longevity risk study in life insurance

There are a certain number of problems linked to modeling and longevity risk management in life insurance. The introduction of longevity models incorporating individual features along with their evolution over time is a challenge in view of the issues linked to this problem, notably financial and societal issues [2]. Microscopic models enable us to refine insurers' modeling, which is often too macroscopic.

#### 3.2.1 Study of systemic risk

We are seeking to quantify the systemic longevity risk associated with an annuity portfolio. This risk is calculated using an age-specific mortality model and presupposes that the mortality rate of each insured is the national mortality rate. We consider the example of a life annuity portfolio comprised of 10,000 60-year-old French women, for which we simulate evolution scenarii that also represent the annuity flow series (see figure 5 on the right). The mortality model associated with the microscopic model enables us to simulate a range of survival scenarii for those insured by the annuity portfolio. The average scenario is used in order to assess the value of the annuity portfolio, while extreme scenarii enable us to quantify extreme risks using quantiles.

FIGURE 6: Average flows of an annuity portfolio for 10,000 women and 10,000 men

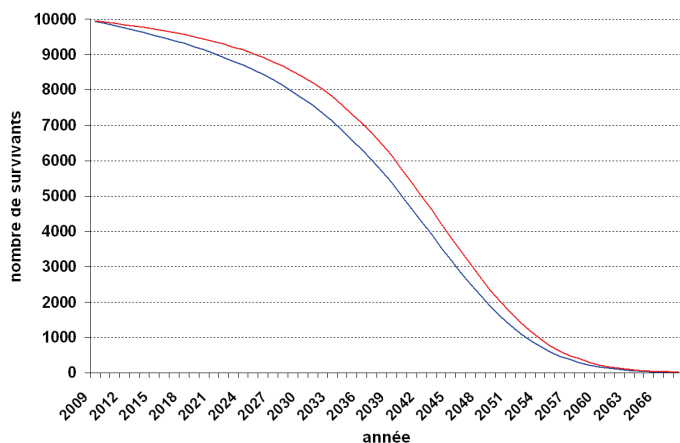
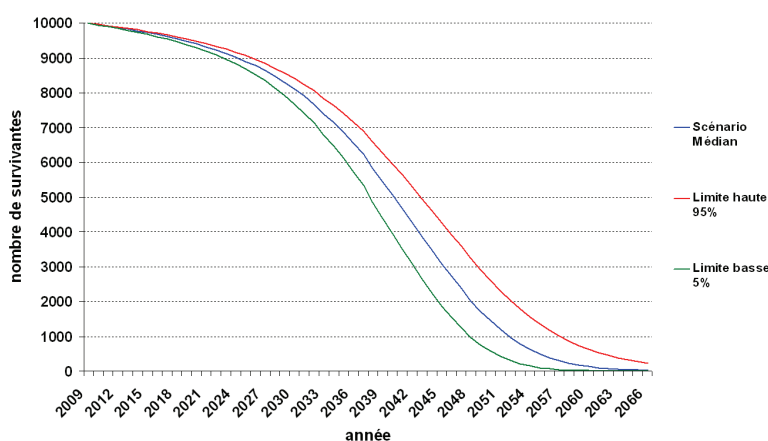


FIGURE 5: Extreme evolution scenarii of a life annuity portfolio of 10,000 60-year-old French women



It is standard practice to take account of the difference between men and women in national mortality tables. Thus, differences in evolution between a portfolio comprised of men and a portfolio comprised of women are presented in Figure 6.

Because female mortality is lower than male mortality, the value of the female annuity portfolio is higher than that of the male portfolio. This example highlights the impact of sex on mortality. Nevertheless, there are many other features that have a determining impact on the mortality level and that must be taken into account.

In fact, in general we observe that insureds have a lower mortality level than the national level, and we will try to quantify this gap taking the various different features into account.

### 3.2.2 Study of the basis risk

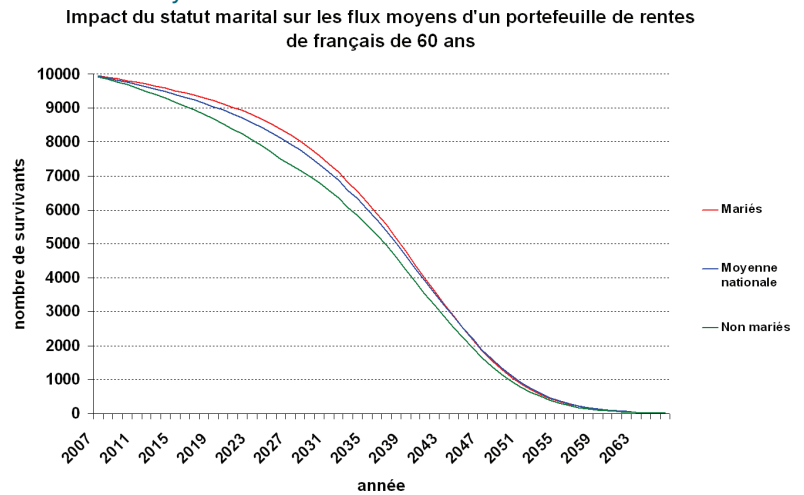
The estimation of the insureds' longevity depends heavily on the reference database. The models are calibrated on the reference data and are used to describe the evolution of the insureds' longevity. Given the difference between the behaviour of the insureds and that of the reference population, the estimates of the insureds' longevity are biased. This bias, linked to the specificity of the insureds on the portfolio, is called "basis risk".

The longevity model is used to quantify the basis risk inherent to life insurance products, taking into account the heterogeneity of actual annuity portfolios. In fact, it is possible to estimate the annuity risk on a real portfolio by considering the specific features of each insured (marital status, socio-professional category, etc.) and making a comparison with the estimate made for the reference population. We describe the influence of marital status on a portfolio of 10,000 French men (see figure 7 above).

We observe that the marital status of insureds has an impact on the value of the annuity portfolio, which is higher for married men. Moreover, the evolution model also takes into account the evolution of individuals' features in the future, which is very useful when studying the impact of the marital status of insureds. The trait evolution rate of the model enables us to take account of the evolution of marital status. Here we have used the example of marital status, but the model may be used with a whole set of determining features if the database is rich enough [3]. Moreover, it is possible to model open portfolios, incorporating new insureds into the simulation process.

The marital status of an individual is likely to evolve over time, with marriage, divorce or the death of a spouse. The trait evolution rate of the model enables us to take account of the evolution of marital status. Here we have used the example of marital status, but the model may be used with a whole set of determining features if the database is rich enough [3]. Moreover, it is possible to model open portfolios, incorporating new insureds into the simulation process.

FIGURE 7: Central flow scenario of a life annuity portfolio for 10,000 60-year-old men with different marital statuses



## 4. Conclusion

We are at the beginning of a major reflection on the issues associated with longevity. We have tried to propose new solutions to practical and complex questions. Mortality and longevity modeling on a microscopic scale seems to be numerically efficient and provides consistent results on a microscopic and macroscopic scale.

In the field of demographics, the model generates a range of projection scenarios rather than an average scenario. This enables us to provide a more precise description of possible future evolutions. It would be interesting to improve a number of aspects, such as the modeling of birth and immigration rates. Moreover, this model could be used to study the influence of demographics on the issue of retirement.

In the field of life insurance, this microscopic modeling is useful for estimating longevity risk. Based on a mortality scenario, it is possible to obtain an evolution scenario for a group of individuals. Moreover, it is possible to quantify the basis risk inherent to the portfolio by taking the impact of insureds' features into account. This work also leads to other research subjects concerning longevity, such as the taking into account of health factors in this type of modeling.

All of the results obtained are highly promising, but their potential is limited by the fact that data is not always provided for all of the points necessary. All of these advances depend on the quality of the information available.

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