Exploring the Diversification of Some Countries’ Longevity Risk

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Outline

1. Background
2. Mortality Data and Models for Examining the Goodness-of-fit
3. The Case of Japan
4. The Cases of England and Wales, the United States, France, and Canada
5. Exploring the Diversifiable Part of Longevity Risk by Examining the Mortality Indices
6. Discussion
7. Conclusions and Remarks
Increase of life expectancy

Life expectancies are increasing in many countries of the world, with influences on pensions and social security systems. This increases longevity risk and raises longevity problems.

Source: Human Mortality Database
How to cope with longevity?

There are two approaches to cope with longevity.

- **Financial diversification of Longevity Risk:**
  - Buy out
  - Buy in
  - Longevity swap
  - Longevity bond

- **Social security planning adapted to the elderly:**
  - employment of older workers through raising of the commencement age to receive pensions
  - utilizing private pensions
  - planning social security systems effectively
Role of mortality models

Mortality models are necessary for longevity risk management and in making demographic projections for social security planning.

- The Lee-Carter (LC) Model is widely used for future projection, because it considers age and period effects and makes it easy to project future mortality level by mortality index $\kappa_t$.

- Effects other than age and period effects can be included in the LC model, such as cohort effects in the Renshaw Haberman (RH) model or effects in the LC-VAR (vector autoregressive) model.
In longevity risk transfers, mortality index based hedges can be effective in mitigating systematic risk.

- However, there may remain basis risk that could be rejected by longevity risk sellers (Basel Committee, 2013).

- In addition, the steadily declining trend of the mortality index, especially for developed countries, may restrict the possible diversification of longevity risk.
Exploring the diversifiable part of longevity risk and discussion

In this study, by applying the mortality data of five countries—England and Wales, the United States, France, Canada, and Japan—to the LC and extended LC models:

- I specify basis risk factors and the diversifiable longevity risk among some of these countries.

- I examine the coherence of the declining trend of the mortality indices and show the limits of the possible diversification of longevity risk.

- I discuss the key points for diversifying longevity risks and developing social security systems in an aging society.
Data and models

I use the death data from the Human Mortality Database (HMD) and the following models:

- The LC model
- The RH model
- The LC-VAR model
- The extended LC-VAR model

- The LC-VAR model was proposed by Igawa (2013) in analyzing the residual structure of the LC model applied to the Japanese death data.

- I examine the goodness-of-fit of each model adapted to the death data of the five countries.
The LC model

The LC model is one of the relational models and is defined as follows:

\[
\ln m_{x,t} = \alpha_x + \beta_x \kappa_t + \varepsilon_{x,t}
\]

- \(\ln m_{x,t}\) : The logarithm of the Central Death Rate
- \(\alpha_x\) : The general shape across age \(x\) of \(\ln m_{x,t}\)
- \(\kappa_t\) : The general level of mortality for year \(t\)

Identification conditions are necessary for parameter estimation such as \(\sum_x \beta_x = 1\) and \(\sum_t \kappa_t = 0\).

\(\kappa_t\) series are applied in time series models, such as ARIMA. A random walk with drift model such as the following is often used.

\[
\kappa_t = \lambda + \kappa_{t-1} + \omega_t
\]
The RH model

The RH model is one of the extended LC models incorporating parameters related to cohort effects. It is defined as follows:

\[ \ln m_{x,t} = \alpha_x + \beta_x^{(1)} \kappa_t + \beta_x^{(2)} \iota_c + \varepsilon_{x,t} \]

- \( \kappa_t \): The general level of mortality for year \( t \)
- \( \iota_c \): The cohort-specific variable that represents cohort effects

\( c \) represents the year of birth.

Identification conditions are necessary for parameter estimation such as \( \sum_x \beta_x^{(1)} = 1 \), \( \sum_x \beta_x^{(2)} = 1 \), \( \sum_t \kappa_t = 0 \) and \( \sum_c \iota_c = 0 \) (Cairns et al., 2009).
The LC-VAR model

The LC-VAR model incorporates a VAR component considering the following two effects in addition to the effects considered in the LC model.

- Effect 1: Birth cohort effect
- Effect 2: Supplemental age-period effect

The LC-VAR model is defined as follows:

\[ M_t = A_x + B_x \kappa_t + Z_t \]

\[ M_t = \begin{bmatrix} \ln m_{0t} \\ \ln m_{1t} \\ \vdots \\ \ln m_{\omega t} \end{bmatrix}, \quad A_x = \begin{bmatrix} \alpha_0 \\ \alpha_1 \\ \vdots \\ \alpha_\omega \end{bmatrix}, \quad B_x = \begin{bmatrix} \beta_0 \\ \beta_1 \\ \vdots \\ \beta_\omega \end{bmatrix} \]

\[ Z_t = \sum_{L=1}^{q} C_L Z_{t-L} + W_t \quad (\text{VAR component}) \]
The two effects considered in the VAR component

Due to the observed correlation of residuals of the LC model, the VAR component is described as follows:

\[ Z_t = \sum_{L=1}^{q} C_L Z_{t-L} + W_t \]  

(for simplicity, I consider the first order model \( q=1 \) here)

\[ C_L = \begin{bmatrix} C_{(0,0)}^L & \cdots & C_{(0,\omega)}^L \\ \vdots & \ddots & \vdots \\ C_{(\omega,0)}^L & \cdots & C_{(\omega,\omega)}^L \end{bmatrix} \]

\[ C_{(i,j)^1} = C_{j^1} \quad j = i - 1 \quad 16 \leq j \leq 90 \quad \text{(for Effect 1)} \]

\[ C_{(i,j)^1} = C_{j^2} \quad j = i \quad 16 \leq j \leq x_{\max,2}^1 \quad \text{(for Effect 2)} \]

\[ C_{(i,j)^1} = 0 \quad \text{otherwise} \]
Parameter estimation

Assuming a Poisson distribution for \( D_{x,t} \), which denotes the number of deaths, with a mean \( E_{x,t} \) multiplied by \( \mu_{x,t} \) as follows:

\[
D_{x,t} \sim \text{Poisson} \ E_{x,t}\mu_{x,t}
\]

\( E_{x,t} \) denotes an exposure-to-risk.

In the case of the LC model, \( \mu_{x,t} = \exp(\alpha_x + \beta_x \kappa_t) \)

The log likelihood is as follows and parameters can be estimated using the maximum likelihood method.

\[
l(\Phi|D_{x,t}, E_{x,t}) = \sum_{x,t} [D_{x,t} \ln(E_{x,t}\mu_{x,t}) - E_{x,t}\mu_{x,t} - \ln(D_{x,t}!)]
\]
Results of goodness-of-fit of each model (Japan)

The LC-VAR(1) model has the best fit to the Japanese death data for male and female for ages 14-90 and for calendar years 1971-2009.

<table>
<thead>
<tr>
<th>Results of the BIC (Japan)</th>
<th>Effective Number of Parameters</th>
<th>BIC (Male)</th>
<th>BIC (Female)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1971–2009</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LC</td>
<td>191</td>
<td>56,697</td>
<td>50,212</td>
</tr>
<tr>
<td>RH</td>
<td>381</td>
<td>39,523</td>
<td>40,794</td>
</tr>
<tr>
<td>LC-VAR(1)</td>
<td>303</td>
<td>39,051</td>
<td>36,448</td>
</tr>
<tr>
<td>1951–2009</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LC</td>
<td>211</td>
<td>126,098</td>
<td>187,125</td>
</tr>
<tr>
<td>RH</td>
<td>421</td>
<td>65,673</td>
<td>57,127</td>
</tr>
<tr>
<td>LC-VAR(1)</td>
<td>323</td>
<td>64,085</td>
<td>61,750</td>
</tr>
</tbody>
</table>

BIC: The Bayesian information criterion
Residuals of each model (Japan, male)

The slanting pattern observed in the case of the LC model almost disappears in the LC-VAR(1) for male, 1971-2009.
Residuals of each model (Japan, female)

The slanting pattern observed in the case of the LC model almost disappears in the LC-VAR(1) for female, 1971-2009, as well.
The extended LC-VAR model

There may remain differences in individuals that are not captured by the parameters of the LC-VAR. Using a method similar to that of Li et al. (2009), the following extended LC-VAR model can be built.

\[ D_{x,t} | z_x(i) \sim \text{Poisson} \left( z_x(i) \frac{\lambda_{x,t}}{N_x} \right) \]

\( z_x(i) \) follows a gamma distribution with \( E[z_x(i)] = 1 \) and \( \text{Var}[z_x(i)] = \iota_x \).

\[ \lambda_{x,t} = E_{x,t} \mu_{x,t} = E_{x,t} \exp(\alpha_x + \beta_x \kappa_t + C_{j1} \epsilon_{x-1,t-1} + C_{j2} \epsilon_{x,t-1}) \]

\( D_{x,t} \) follows the negative binomial distribution as below:

\[ \Pr[D_{x,t} = y] = \frac{\Gamma(y + \theta_x^{-1})}{y! \Gamma(\theta_x^{-1})} \left( \frac{\lambda_{x,t}}{\lambda_{x,t} + \theta_x^{-1}} \right)^y \left( \frac{\theta_x^{-1}}{\lambda_{x,t} + \theta_x^{-1}} \right)^{\theta_x^{-1}} \]

where \( \theta_x = \iota_x / N_x \).
Results of goodness-of-fit of the extended LC-VAR model (Japan, male)

The goodness-of-fit of the extended LC-VAR is better than that of the LC and the LC-VAR. There may be factors of mortality variation other than those considered in the LC-VAR.

### Results of the BIC of the extended LC-VAR(1) (Japanese, Male)

<table>
<thead>
<tr>
<th></th>
<th>Effective Number of Parameters</th>
<th>BIC</th>
</tr>
</thead>
<tbody>
<tr>
<td>1971–2009</td>
<td></td>
<td></td>
</tr>
<tr>
<td>LC</td>
<td>191</td>
<td>56,697</td>
</tr>
<tr>
<td>LC-VAR(1)</td>
<td>303</td>
<td>39,051</td>
</tr>
<tr>
<td>LC-VAR(1)</td>
<td>380</td>
<td>38,294</td>
</tr>
</tbody>
</table>

BIC: The Bayesian information criterion
Results of parameter estimates of the extended LC-VAR model (Japan, male)

The estimates of the parameters $\alpha_x, \beta_x, \kappa_t, C_{j1}^1, C_{j2}^1$ are similar to those of the LC-VAR(1) and the estimates of $\theta_x$ indicate the differences in individuals by age.
The RH model has the best fit to the England and Wales death data for both male and female.

<table>
<thead>
<tr>
<th></th>
<th>Effective Number of Parameters</th>
<th>AIC</th>
<th>BIC</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Male</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LC</td>
<td>211</td>
<td>71,306</td>
<td>72,661</td>
</tr>
<tr>
<td>RH</td>
<td>421</td>
<td>51,615</td>
<td>54,319</td>
</tr>
<tr>
<td>LC-VAR(1)</td>
<td>323</td>
<td>54,686</td>
<td>56,760</td>
</tr>
<tr>
<td><strong>Female</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LC</td>
<td>211</td>
<td>63,929</td>
<td>65,284</td>
</tr>
<tr>
<td>RH</td>
<td>421</td>
<td>48,296</td>
<td>51,000</td>
</tr>
<tr>
<td>LC-VAR(1)</td>
<td>323</td>
<td>50,951</td>
<td>53,026</td>
</tr>
</tbody>
</table>

AIC: The Akaike information criterion
BIC: The Bayesian information criterion
Residuals of each model (England and Wales, male)

The slanting pattern in the case of the LC model is relatively unclear in the RH for male data.
Residuals of each model (England and Wales, female)

The slanting pattern in the case of the LC model is relatively unclear in the RH for female data as well.
Results of goodness-of-fit of each model (the United States)

The LC-VAR model has the best fit to the United States death data for both male and female.

<table>
<thead>
<tr>
<th></th>
<th>Gender</th>
<th>Effective Number of Parameters</th>
<th>AIC</th>
<th>BIC</th>
</tr>
</thead>
<tbody>
<tr>
<td>LC</td>
<td>Male</td>
<td>211</td>
<td>156,885</td>
<td>158,240</td>
</tr>
<tr>
<td>RH</td>
<td>Male</td>
<td>421</td>
<td>90,819</td>
<td>92,892</td>
</tr>
<tr>
<td>LC-VAR(1)</td>
<td>Male</td>
<td>323</td>
<td>78,603</td>
<td>80,677</td>
</tr>
<tr>
<td>LC</td>
<td>Female</td>
<td>211</td>
<td>104,224</td>
<td>105,579</td>
</tr>
<tr>
<td>RH</td>
<td>Female</td>
<td>421</td>
<td>71,884</td>
<td>74,588</td>
</tr>
<tr>
<td>LC-VAR(1)</td>
<td>Female</td>
<td>323</td>
<td>66,154</td>
<td>68,228</td>
</tr>
</tbody>
</table>

AIC: The Akaike information criterion
BIC: The Bayesian information criterion
Residuals of each model (the United States, male)

The LC-VAR model residuals are smoothed in comparison with the LC and RH model residuals for male data.
Residuals of each model (the United States, female)

The LC-VAR model residuals are smoothed in comparison with the LC and RH model residuals for female data as well.
The best fits to the French death data are the LC-VAR model for male and the RH model for female.

<table>
<thead>
<tr>
<th>Results of the AIC and BIC (France, years 1951–2009)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Effective Number of Parameters</td>
</tr>
<tr>
<td>--------------------------------</td>
</tr>
<tr>
<td><strong>Male</strong></td>
</tr>
<tr>
<td>LC</td>
</tr>
<tr>
<td>RH</td>
</tr>
<tr>
<td>LC-VAR(1)</td>
</tr>
<tr>
<td><strong>Female</strong></td>
</tr>
<tr>
<td>LC</td>
</tr>
<tr>
<td>RH</td>
</tr>
<tr>
<td>LC-VAR(1)</td>
</tr>
</tbody>
</table>

AIC: The Akaike information criterion
BIC: The Bayesian information criterion
Residuals of each model (France, male)

The slanting pattern and the relatively big residuals observed in age 20s and 30s in the case of the LC model almost disappear in the LC-VAR for male data.

<table>
<thead>
<tr>
<th>LC</th>
<th>RH</th>
<th>LC-VAR(1)</th>
</tr>
</thead>
</table>

![Graphs showing residuals for different models](image-url)
Residuals of each model (France, female)

The relatively large residuals observed in age 20s and 30s in the case of the LC model remain to an extent in the LC-VAR for female data.
According to the BIC, the RH model has the best fit to the Canadian male death data and the LC-VAR to the female data, but the differences are small.

<table>
<thead>
<tr>
<th></th>
<th>Effective Number of Parameters</th>
<th>AIC</th>
<th>BIC</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Male</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LC</td>
<td>209</td>
<td>49,377</td>
<td>50,711</td>
</tr>
<tr>
<td>RH</td>
<td>417</td>
<td>44,249</td>
<td>46,912</td>
</tr>
<tr>
<td>LC-VAR(1)</td>
<td>321</td>
<td>45,206</td>
<td>47,256</td>
</tr>
<tr>
<td><strong>Female</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LC</td>
<td>209</td>
<td>42,316</td>
<td>43,651</td>
</tr>
<tr>
<td>RH</td>
<td>417</td>
<td>40,975</td>
<td>43,638</td>
</tr>
<tr>
<td>LC-VAR(1)</td>
<td>321</td>
<td>41,196</td>
<td>43,247</td>
</tr>
</tbody>
</table>

AIC: The Akaike information criterion  
BIC: The Bayesian information criterion
Residuals of each model (Canada, male)

Even in the case of the LC model, the slanting pattern is not clear for male data.
Residuals of each model (Canada, female)

Even in the case of the LC model, the slanting pattern is not clear for female data either.
Definition of longevity risk

Based on the previous analysis, to specify the diversifiable part of longevity risk, I define the longevity risk component for population $i$ as follows:

$$LRC_{x,t,i} = \ln m_{x,t,i} - E(\ln m_{x,t,i})$$

Regarding the LC model, $LRC_{x,t,i}$ consists of the variation related to $\kappa_t$ and $\epsilon_{x,t}$. $LRC_{x,t,i}$ at $t=1$ can be described as follows:

$$LRC_{x,t,i} = \beta_{x,i}(\kappa_{t,i} - \kappa_{t-1,i} - \lambda_i) + \epsilon_{x,t,i}$$
Basis risk assuming two populations

Li and Hardy (2011) show that the following augmented common factor model proposed by Li and Lee (2005) is preferable in terms of both goodness-of-fit and ex-post forecasting.

\[
\ln m_{x,t,i} = \alpha_{x,i} + B_x K_t + \beta_{x,i} \kappa_{t,i} + \varepsilon_{x,t,i}
\]

When common parameter \( K_t \) is considered as the mortality index for swaps, the LC-VAR formulation for two populations is described as follows:

\[
M_{t,i} = A_{x,i} + B_{x,i} K_t + Z_{t,i}
\]
Coherence of mortality indices

I examine the mortality indices for male data from the United States, France, and Japan. Over the period 1971–2009, the mortality indices are cointegrated (Johansen procedure).

\( \kappa_t \) (male, 1951-2009) \hspace{2cm} \kappa_t \) (male, 1971-2009)
Although some of the mortality indices might show recent coherence, one can still diversify longevity risk related to the VAR component in the LC-VAR model.

One can explore the diversifiable part by examining the goodness-of-fit of each model and the residual series such as the figures on the next slide.
Exploring the diversifiable part of longevity risk

For example, concerning the below birth cohorts, a part of the variation of the residual series seems to be adverse and these variation can be diversified.

Born in 1949  Born in 1959  Born in 1969  Born in 1979

The United States (male)

France (male)

Japan (male)
Discussion (Exploring the diversifiable part of longevity risk)

- Some of the mortality indices might show recent coherence. However, regardless of this, owing to the declining trend, the scope for the diversification of longevity risk related to mortality indices will inevitably become limited.

- To explore the diversifiable part of longevity risk related to basis risk, it is useful to examine and compare the goodness-of-fit of the LC family models.
Discussion (Root of basis risk)

From the analysis in this study, there are clear features related to cohort effects by country and gender. It is possible to classify these as follows:

– Case 1: Countries and gender for which death data provide a good fit to the RH model and in which cohort effects exist for a long time

– Case 2: Countries and gender for which death data provide a good fit to the LC-VAR model and in which birth cohort effects and supplemented age-period effects are observed

– Case 3: Countries and gender for which death data do not provide big differences in goodness-of-fit between the LC, the RH, and the LC-VAR models and in which cohort effects are thought to be fairly weak
Discussion (Further risk analysis)

- Basis risk factors other than age, period, and cohort could exist, and it is desirable to study such factors to develop methodologies of diversifying longevity risk.

- It will become more important to specify the heterogeneity of risk and reflect this in designing pension and social security systems.
Concluding remarks

- In this study, I explore the diversifiable part of longevity risk by applying the LC and extended LC models to five countries’ death data.

- There is room for the diversification of longevity risk concerning basis risk, although this is limited regarding mortality index variations because of the steadily decreasing mortality level.

- It is important to specify the basis risk factors and heterogeneity of risk and reflect this in planning systems.
References


References


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References


