Modelling and Forecasting Mortality in Related Populations: A Comparison

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Intro

- forecasting mortality

 - Social cost of longevity → see IMF [12] report
 - > valuation of life insurance and pension liabilities
 - > socio-demographic studies
 - wide literature on forecasting mortality in the last 20 years, since the pioneering paper by Lee and Carter

Looking at More than One Population

- Related populations
 - > share common features
- issues/advantages in joint mortality forecasting
 - > consistency
 - exploit common patterns

 - > convergence?
- examples
 - > regions of a country
 - > males/females

 - > annuity/pension fund book vs general population

 - ▷ affluence measures → pension amount, salary
 - ...

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 - > lower sampling error in small populations
 - convergence?
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 - Socio economic covariates → IMD in UK
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Transfering Longevity Risk

- pension funds are exposed to longevity risk; typical de-risking solutions include
 - reinsurance
 - pension scheme buy-in and buy-out
 - derivative based transactions
- the last 10 years have seen, in UK and North-America, many bespoke derivative transactions (see Blake et al.
 - → perfect hedging
 - > not transparent
 - > costly
 - unattractive for other parties
- an index based (q forward, longevity swaps) transaction requires modelling the basis to understand the risk reduction → multi (2?) population modelling to understand risk reduction (see Li and Hardy [11], Cairns et

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Different Approaches

- when modelling and forecasting mortality, several approaches are possible
 - b target central death rates, normal errors (Lee-Carter [92]), log link function
 - bright price target number of deaths as Poisson (Brouhns et al. [02]), log link function
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 - > target improvement rates, identity link function
- looking then at the (sub)populations, at least two routes can be followed

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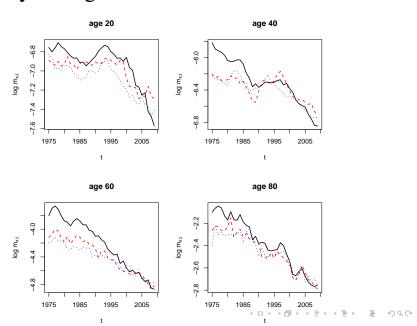
What we do

- extend (Poisson) Lee-Carter to several populations ⇒ focus on 5 specific examples
- model improvement rates for several populations and the 5 equivalent models
- focus on simple, straightforward extension of the basic Lee-Carter
- estimate and compare the 10 models on a data set of mortality data for 18 regions of Italy

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Mortality - 3 regions



Data

- I populations i = 1, ..., I
- *T* calendar years $t = t_0, t_0 + 1, \dots, t_0 + T 1$
- *X* age groups $x = x_0, x_0 + 1, \dots, x_0 + X 1$
- for population i, year t, age group x, we have

$$d_{x,t}^i = \text{ number of deaths in } [t, t+1) \text{ aged } x \text{ last birthday,}$$

$$ETR_{x,t}^{i} = central exposed to risk$$

$$\Rightarrow$$
 central death rate $m_{x,t}^i = \frac{d_{x,t}^i}{\text{ETR}_{x,t}^i}$



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Poisson Model

- number of deaths $d_{x,t}^i$ realizations of $D_{x,t}^i$ (Brouhns et al [02])
- Cox (doubly-stochastic model): conditionally on $(m_{x,t}^i)_{x,t,i}$, the number of deaths
 - > are independent
 - have distribution

$$D_{x,t}^i \sim \text{Poisson}(\text{ETR}_{x,t}^i \, m_{x,t}^i)$$

• we model $m_{x,t}^i$ as follows (Hyndman and Ullah [06]) assuming there are L time indices

$$\log m_{x,t}^i = \alpha_x^i + \sum_{j=1}^L \beta_{x,j}^i k_{t,j}$$

- idea:
 - \triangleright number of factors L related to I
 - \triangleright choose k_t ; appropriately
 - Description and identifiability constraints as appropriato → ()

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• $\mathcal{P}1$ — (Booth et al. [02], Haberman and Renshaw [03])

$$\log m_{x,t}^{i} = \alpha_{x}^{i} + \beta_{x,1}^{i} k_{t,1}^{i} + \beta_{x,2}^{i} k_{t,2}^{i}$$

• $\mathcal{P}2$ — (Augmented Common Factor, Li and Lee [05], Li and Hardy [11], Hyndman et al. [13]): $k_{t,1}$ common factor, $k_{t,2}^i$ i^{th} population specific factor

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• P3 — (Lee and Carter [1992], Li and Hardy [11])

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each group has its own factor $k_t^i \Rightarrow$ correlation arises from the modelling of $(k_t^i)_i$

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- $\mathcal{P}4 J_1, J_2, \dots, J_g$ partition of $\{1, \dots, I\}$ (I > 2)
 - > some populations are 'more related' than others
 - \triangleright g time indices, one for each of subgroup \Rightarrow reduce number of parameters
 - \triangleright if $i \in J_h$ then the time index is k_t^h

for
$$i \in J_h$$

$$\log m_{x,t}^i = \alpha_x^i + \beta_x^i k_t^h$$

• in our case, choose (see next slide) $J_1 = \{1, 2, 3, 4, 5, 6\}$, $J_2 = \{7, 8, 9\}$, $J_3 = \{10, 11, 12\}$, $J_4 = \{13, 18\}$, $J_5 = \{14, 15, 16, 17\}$ clustering obtained by similarity with respect to period life expectancy at birth



Figure: Italy divided in the considered 18 areas.

P5 — (Joint K Model, Carter and Lee [92], Li and Hardy [11], Wilmoth and Valkonen [01], Delwarde et al. [06]) a single time index driving all the rates ⇒ perfect correlation

$$\log m_{x,t}^i = \alpha_x^i + \beta_x^i k_t$$

• models are nested: $P5 \subset P4 \subset P3 \subset P2 \subset P1$

- use mortality improvement rates rather than rates ⇒ slope vs level
- used recently by
 - → Willets [04]
 - ▷ Richards et al. [05]
 - ▶ Baxter [07]
 - ▶ Haberman and Renshaw [12,13]
 - ▶ Mitchell et al [13]
- idea

 - provides an alternative route: given *m*'s, transform, model, estimate and forecast the improvement rates, transform back



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 - provides an alternative route: given m's, transform, model, estimate and forecast the improvement rates, transform back

• suppress the population index i here; define for $t = t_0 + 1, \dots, t_0 + T - 1$ (T - 1 calendar years) the relative improvement rates (Haberman and Renshaw [12])

$$z_{x,t} = \frac{m_{x,t-1} - m_{x,t}}{\frac{1}{2}(m_{x,t-1} + m_{x,t})} = 2\frac{1 - \frac{m_{x,t}}{m_{x,t-1}}}{1 + \frac{m_{x,t}}{m_{x,t-1}}}$$

- note that
 - \triangleright given z, recover m

$$m_{x,t} = m_{x,t-1} \frac{2 - z_{x,t}}{2 + z_{x,t}}$$

 \triangleright z is the (discrete version of the) time derivative of m

$$z_{x,t} \approx \frac{1}{m_{x,t}} \frac{\partial m_{x,t}}{\partial t}$$

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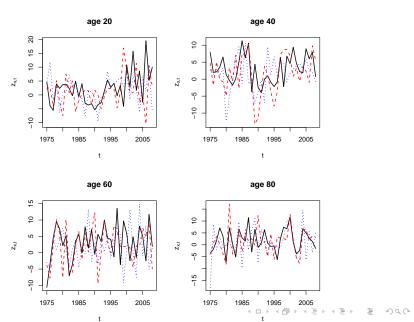
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... Improvement Rates

• Assume $z_{x,t}^i$ are realizations of iid rv $Z_{x,t}^i$ with

$$Z_{x,t}^i \sim N(\eta_{x,t}^i, \sigma_i)$$

• similarly to death rates

$$\eta_{x,t}^i = \sum_{i=1}^L \beta_{x,j}^i k_{t,j}$$

• note that there is no 'time-average' α_x^i term



... Improvement Rates

I1

$$\eta_{x,t}^i = \beta_{x,1}^i \, k_{t,1}^i + \beta_{x,2}^i \, k_{t,2}^i$$

I2

$$\eta_{x,t}^i = \beta_{x,1}^i \, k_{t,1} + \beta_{x,2}^i \, k_{t,2}^i$$

I3

$$\eta_{x,t}^i = \beta_x^i \, k_t^i$$

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I5

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• models are nested: $\mathcal{I}5 \subset \mathcal{I}4 \subset \mathcal{I}3 \subset \mathcal{I}2 \subset \mathcal{I}1$



Application

- use mortality data from I = 18 Italian regions
- ages 20 89 (X = 70)
- years 1974-2008, use 1974-1999 (T = 26) for estimation, 2000-2008 (9 yr) for forecasting
- maximize likelihood
 - $\triangleright \mathcal{P}$ models:

$$l = K + \sum_{x,t,i} \left(d_{x,t}^i \log m_{x,t}^i - \text{ETR}_{x,t}^i \, m_{x,t}^i \right)$$

 $\triangleright \mathcal{I}$ models:

$$l = -\frac{1}{2} \sum_{x,t,i} \left(\log(2\pi\sigma_i^2) + \frac{(z_{x,t}^i - \eta_{x,t}^i)^2}{\sigma_i^2} \right)$$



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Comparison - Goodness of Fit

• $AIC = 2(np - l^*)$, $AIC^c = AIC + \frac{2np(np+1)}{nd-np-1}$, $BIC = np \log(nd) - 2l^*$ ($l^* = \text{maximized likelihood}$, np = number of estimable parameters, nd = number of data)

	AIC		1	AIC^c		BIC	
1st	$\mathcal{P}2$	$\mathcal{I}1$	$\mathcal{P}2$	$\mathcal{I}1$	$\mathcal{P}5$	$\mathcal{I}2$	
2nd	$\mathcal{P}1$	$\mathcal{I}2$	$\mathcal{P}4$	$\mathcal{I}2$	$\mathcal{P}4$	$\mathcal{I}3$	
3rd	$\mathcal{P}4$	$\mathcal{I}5$	$\mathcal{P}3$	$\mathcal{I}3$	$\mathcal{P}2$	$\mathcal{I}5$	
4th	$\mathcal{P}3$	$\mathcal{I}3$	$\mathcal{P}1$	$\mathcal{I}4$	$\mathcal{P}3$	$\mathcal{I}4$	
5th	$\mathcal{P}5$	$\mathcal{I}4$	$\mathcal{P}5$	$\mathcal{I}5$	$\mathcal{P}1$	$\mathcal{I}1$	

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Forecast

- if $(k_{t,j}^i)$ in \mathcal{P} is modelled using a VARIMA process, then the corresponding $(k_{t,j}^i)$ in \mathcal{I} should be modelled using a VARMA process
- in the application, we use
 - \triangleright a multivariate random walk with drift for \mathcal{P} , where appropriate
 - \triangleright a VAR(1) for \mathcal{I} , where appropriate



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Comparison - Forecast

• Compare truncated expected cohort residual lifetimes (MAPE in % across all regions)

	$\mathcal{P}1$	$\mathcal{P}2$	$\mathcal{P}3$	$\mathcal{P}4$	$\mathcal{P}5$
$e_{60:\overline{9}}^{\mathrm{cohort}}$	0.06	0.11	0.12	0.18	0.50
$e_{70.\overline{\Omega}}^{\text{cohort}}$	0.11	0.20	0.20	0.21	0.88
$e_{80:\overline{9}}^{\text{cohort}}$	0.29	0.43	0.38	0.45	1.46
	$\mathcal{I}1$	$\mathcal{I}2$	$\mathcal{I}3$	$\mathcal{I}4$	$\mathcal{I}5$
$e_{60.\overline{9}}^{\text{cohort}}$	<i>I</i> 1 0.21	<i>I</i> 2 0.24	<i>I</i> 3		75 0.19
$e^{\text{cohort}}_{60:\overline{9}}$ $e^{\text{cohort}}_{70:\overline{9}}$			0.21		

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$e_{60:\overline{9}}^{\text{cohort}}$	0.06	0.11	0.12	0.18	0.50
$e_{70.\overline{0}}^{\text{cohort}}$	0.11	0.20	0.20	0.21	0.88
$e_{80:\overline{9}}^{\text{cohort}}$	0.29	0.43	0.38	0.45	1.46
	$\mathcal{I}1$	$\mathcal{I}2$	$\mathcal{I}3$	$\mathcal{I}4$	$\mathcal{I}5$
$e_{60.\overline{9}}^{\text{cohort}}$	<i>I</i> 1 0.21	72 0.24	<i>T</i> 3	74 0.16	75 0.19
$e_{60:\overline{9} \atop e^{\text{cohort}}_{70:\overline{9} }$					

Conclusion

- in terms of goodness of fit,
 - when modelling death rates, more elaborate models seems to be preferable
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Conclusion

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Thanks for Your attention!