

New Directions
in the Modelling of Longevity Risk

Andrew Cairns
Heriot-Watt University,
and The Maxwell Institute, Edinburgh

Joint work (in progress!) with:

George Mavros, Torsten Kleinow, George Streftaris

Mexico City, 2 October 2012

Plan

- Genealogy
- New directions in modelling
- Numerical illustrations

Development of New Models

- Many new stochastic mortality models since Lee-Carter
- Are they fit for purpose?
- Are they robust?

GENEALOGY: 1st GENERATION MODELS

Eilers/Marx
P-splines

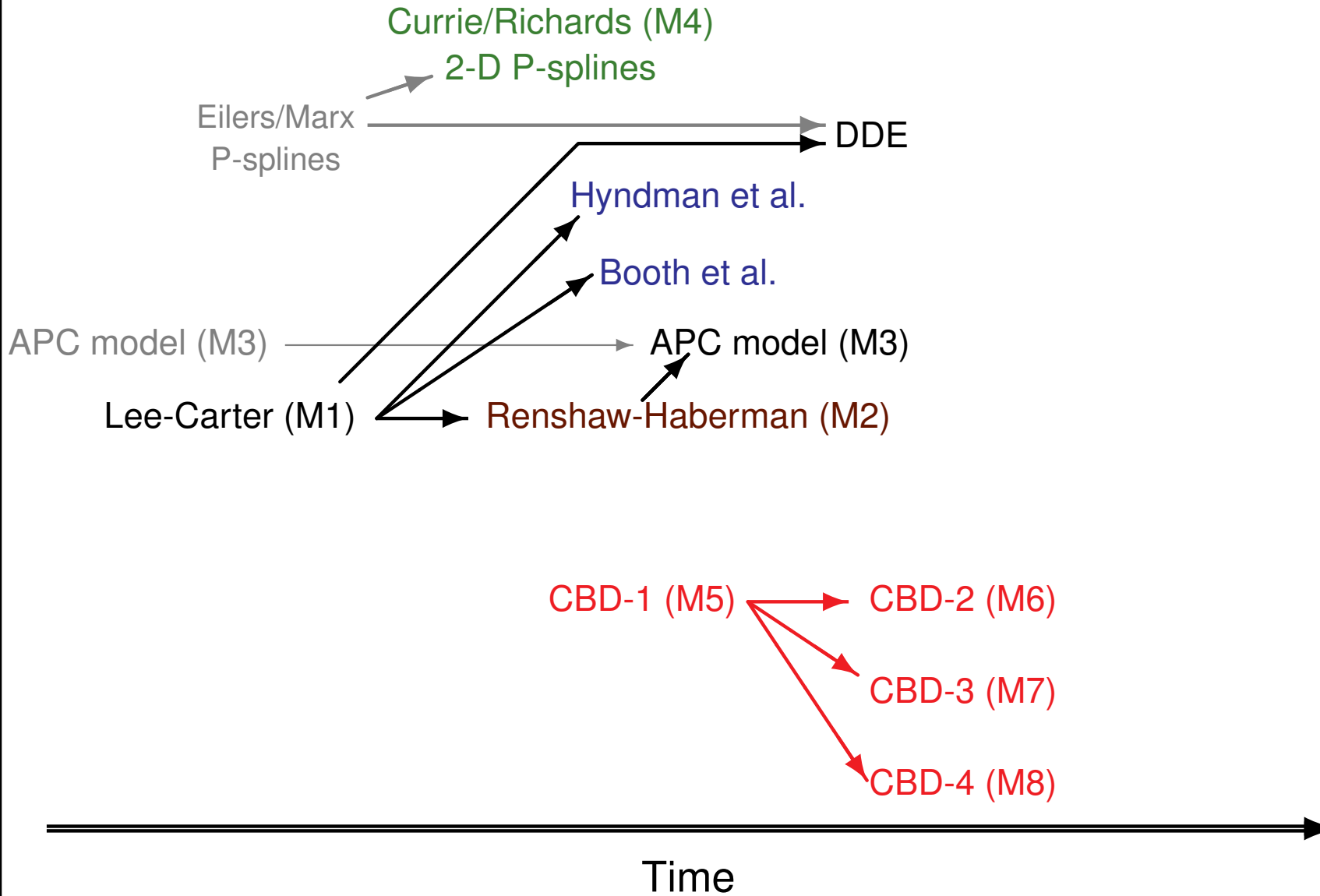
Currie/Richards (M4)
2-D P-splines
2002, ...

Lee-Carter (M1)
1992

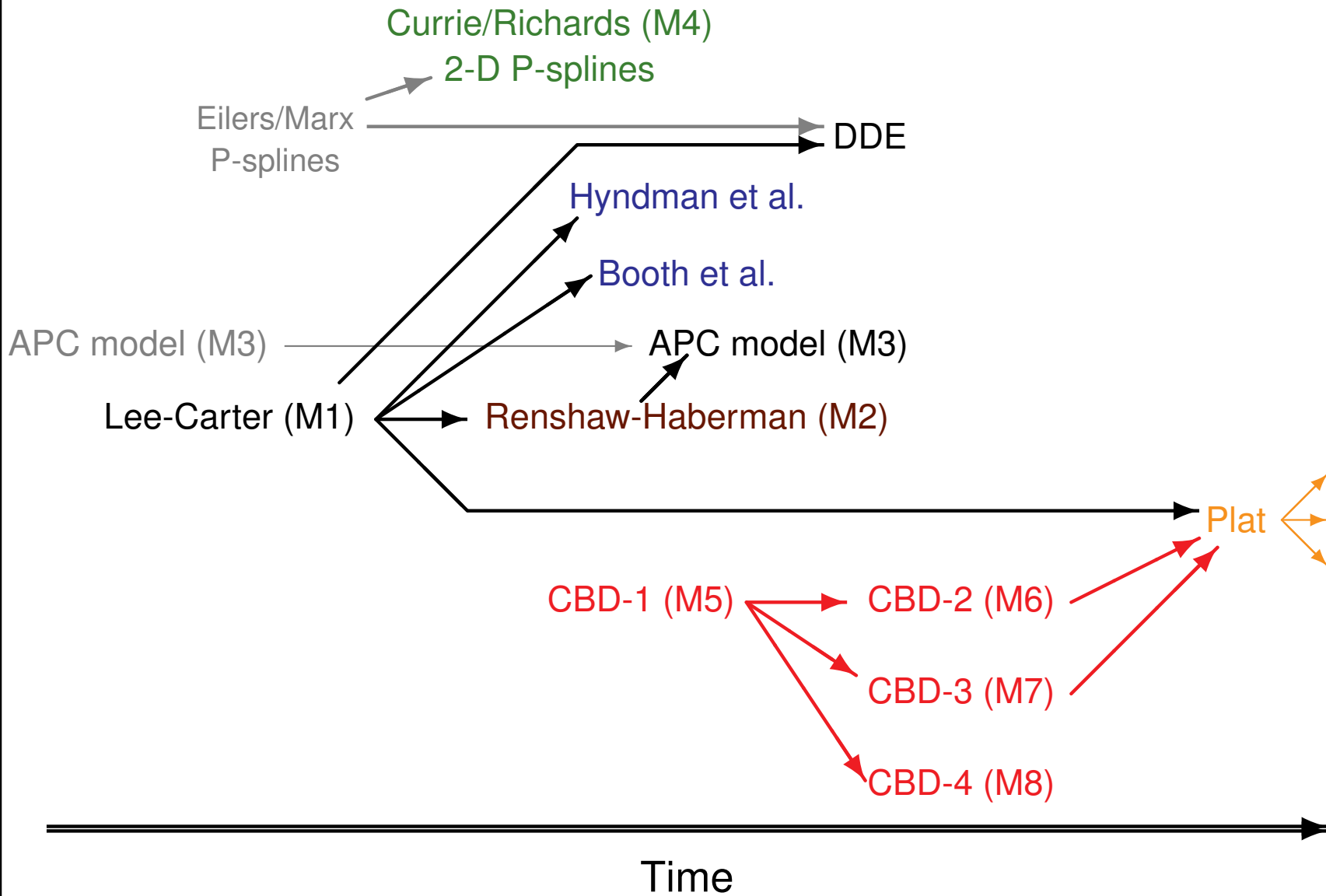
CBD-1 (M5)
2006

Time

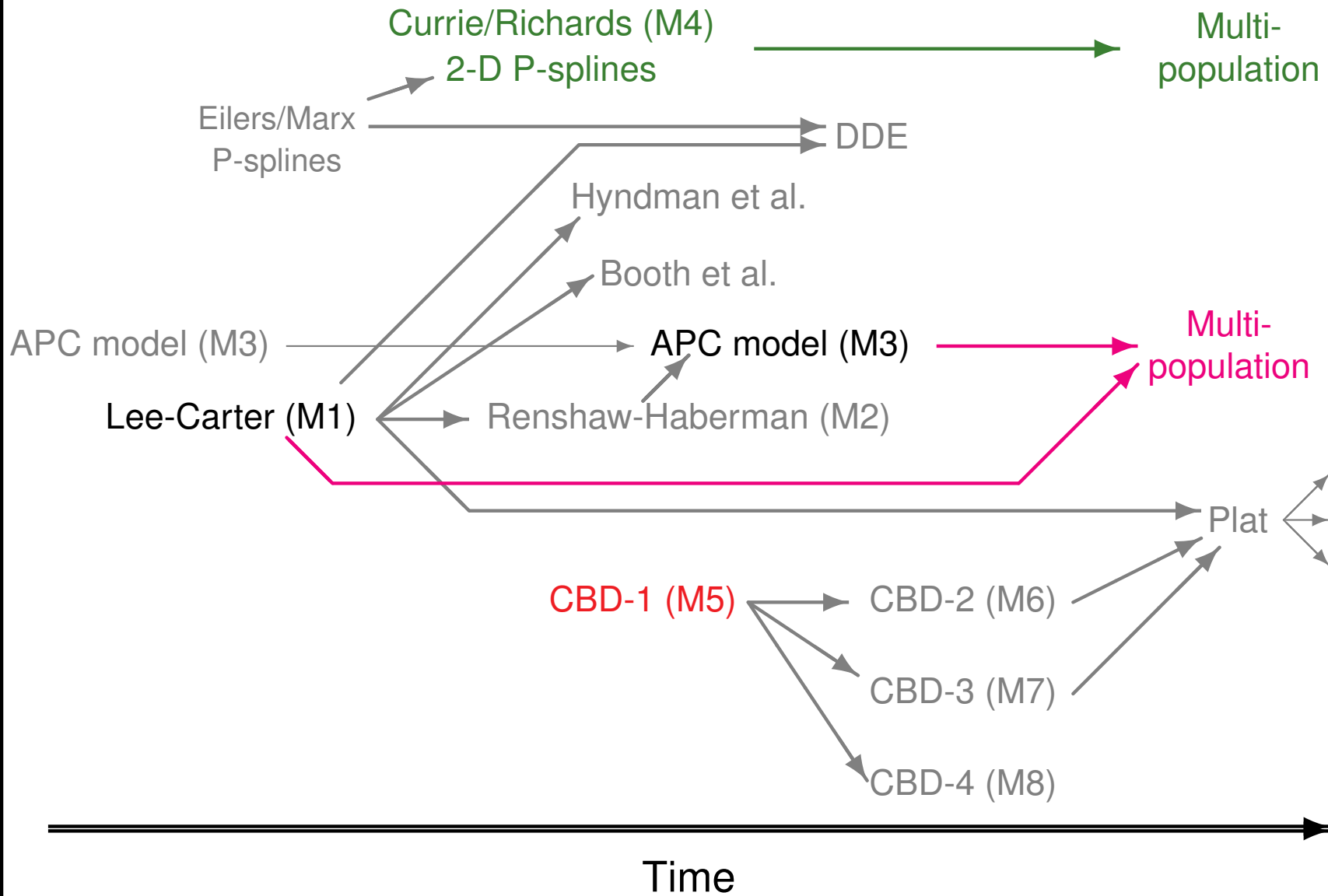
Improvements + more complexity



More improvements + even more complexity

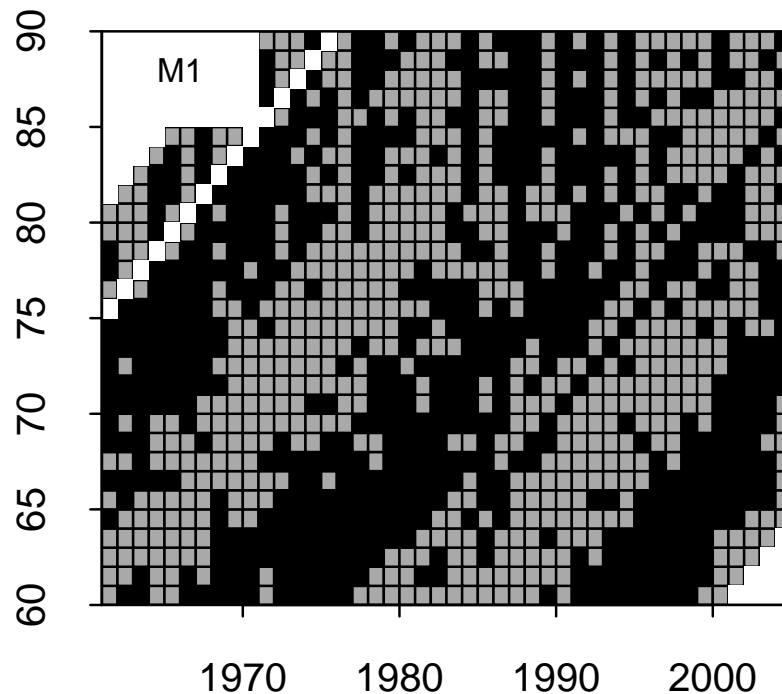


Multiple population modelling

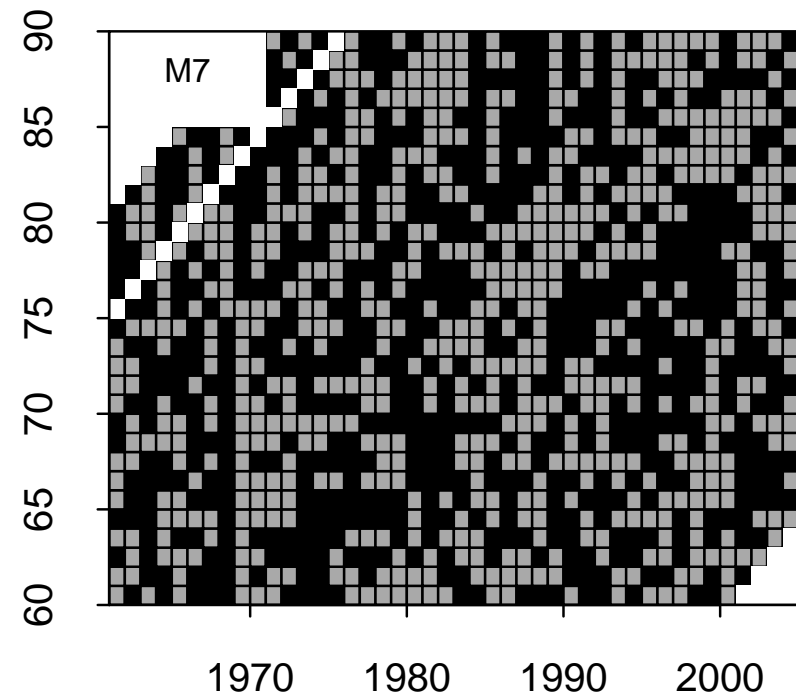


Why do we need complexity?

Lee-Carter Model



CBD Model + Cohort Effect



Black \Rightarrow model *over*-estimates $m(x, t)$ death rate

Gray \Rightarrow model *under*-estimates $m(x, t)$ death rate

LC: non-random clusters + errors are too big

Issues on complexity

- Lee-Carter, CBD-1: simple and robust
 BUT underlying assumptions are violated:
 - A: Deaths, $D(x, t)$ are cond. Poisson $\left(m(x, t)E(x, t)\right)$
 - B: Death counts in neighbouring (x, t) cells are independent
- **More complexity** e.g. CBD-1 \rightarrow CBD-3 \rightarrow Plat ...
 - Underlying assumptions now okay
 - But excessive complexity \Rightarrow **less robust forecasts???**
- Dowd et al. (2010a,b): out-of-sample backtesting
Models that fit *much better* in sample
are *not obviously better* at out-of-sample forecasting

Issues on complexity

- More complex \Rightarrow More random processes
- More random processes \Rightarrow
MUCH more difficult to model **multiple populations**

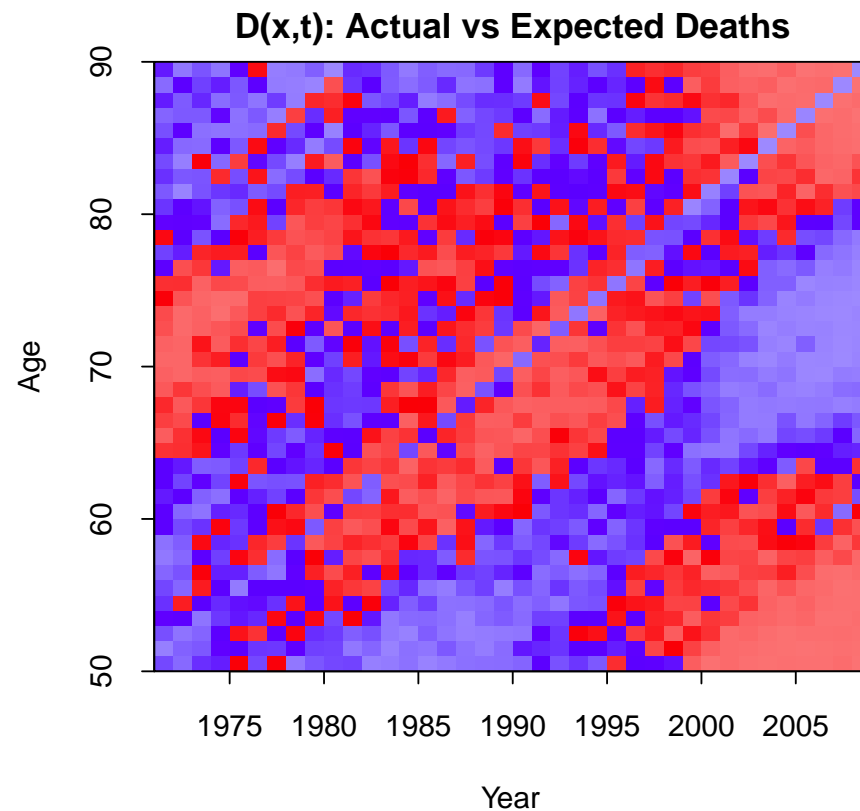
A Possible Way Forward

Single-population models

- Paradigm shift away from *independent* Poisson model
- Focus on **small number of key drivers**
 - ⇒ much easier to extend to multi-populations
- Focus on greater robustness of forecasts

Case Study: CBD/Plat Revisited

$$\log m(x, t) = \beta(x) + \kappa_1(t) + \kappa_2(t)(x - \bar{x})$$



Red \Rightarrow actual deaths $>$ expected deaths

CBD/Plat Revisited: Key Idea: Possible responses

$$\log m(x, t) = \beta(x) + \kappa_1(t) + \kappa_2(t)(x - \bar{x})$$

Add:

- Cohort effect, $\gamma(t - x)$
- Extra age-period effects
- Do something new

Key Idea: CBD/Plat Revisited

Underlying $\log m(x, t) =$

- $\beta(x) + \kappa_1(t) + \kappa_2(t)(x - \bar{x})$: **two key drivers**

PLUS

$R(x, t)$ *Residuals*

- Assume: vector $R(t) \rightarrow R(t + 1)$ mean reverting process

\Rightarrow long term risk depends on **two key drivers**

Specific Model

$$\log m(x, t) = \beta(x) + \kappa_1(t) + \kappa_2(t)(x - \bar{x}) + R(t, x)$$

- $(\kappa_1(t), \kappa_2(t))$: bivariate random walk
- $R(t) = (n_x \times 1 \text{ vector})$ VAR(2), reverting to 0

$$R(t) = AR(t - 1) + BR(t - 2) + Z(t)$$

- $Z(x, t)$ i.i.d. $\sim N(0, \sigma_Z^2)$
- $A = A_1 + A_2$ and $B = -A_2A_1$

VAR matrices A_1 and A_2

$$A_i = \begin{pmatrix} a_i & 0 & 0 & \dots & & & & & \\ c_i & d_i & 0 & 0 & \dots & & & & \\ d_i/2 & c_i & d_i/2 & 0 & 0 & \dots & & & \\ 0 & d_i/2 & c_i & d_i/2 & 0 & 0 & \dots & & \\ 0 & 0 & d_i/2 & c_i & d_i/2 & 0 & 0 & \dots & \\ \vdots & & \ddots & \ddots & \ddots & \ddots & \ddots & \ddots & \\ & & & & & & & & \end{pmatrix}$$

a_i = AR terms for new members;

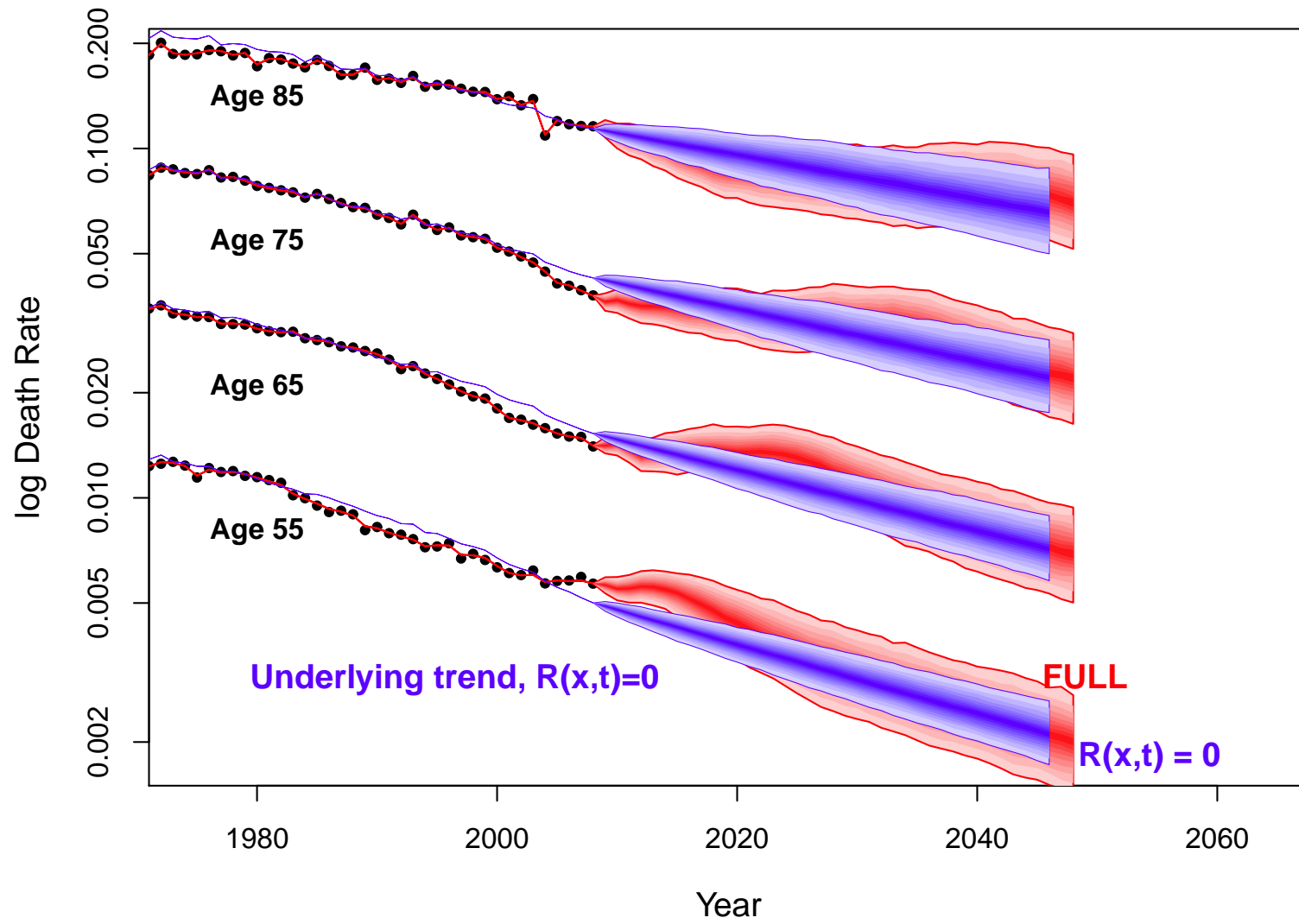
c_i = cohort persistence;

d_i = diffusion coeff.

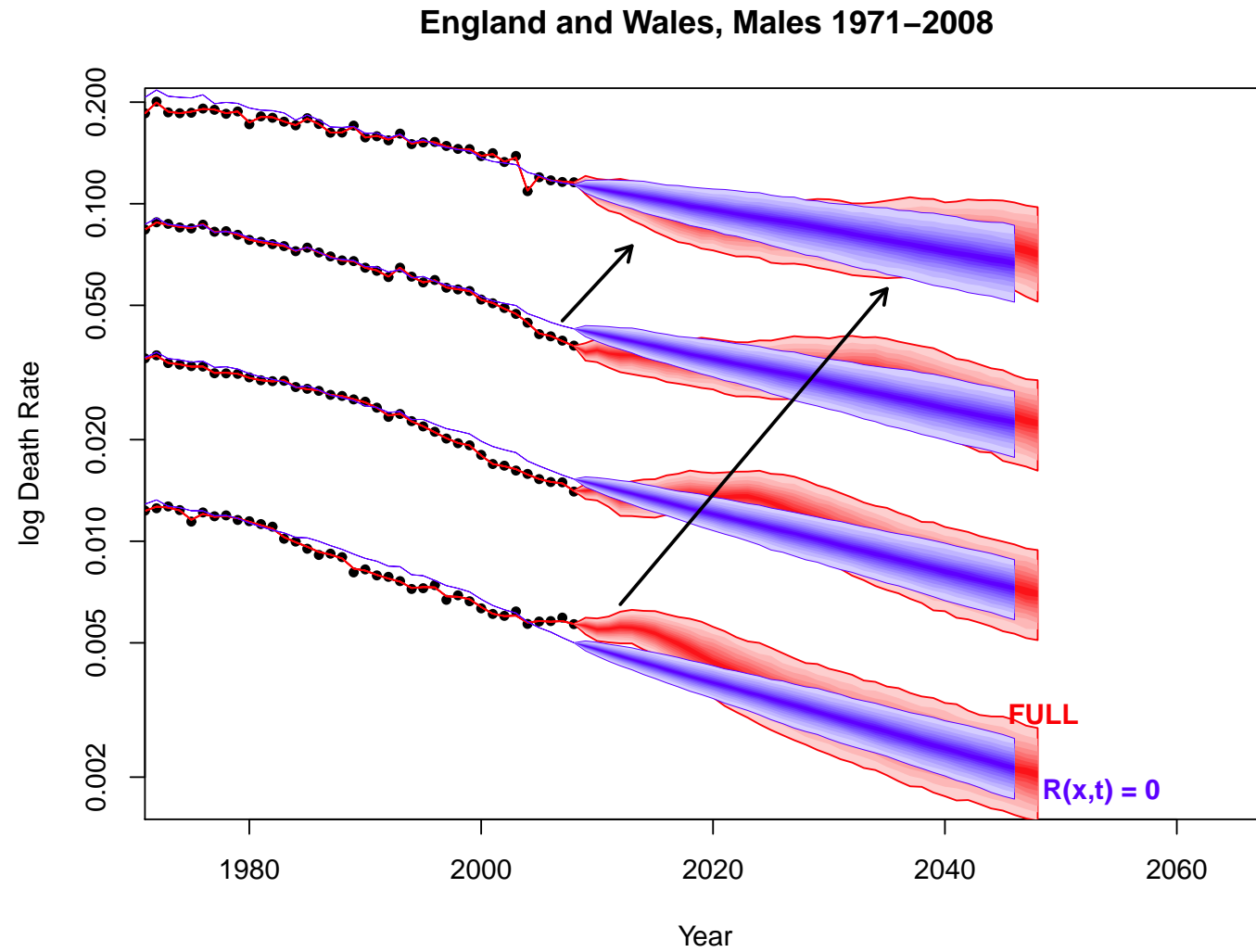
Further details

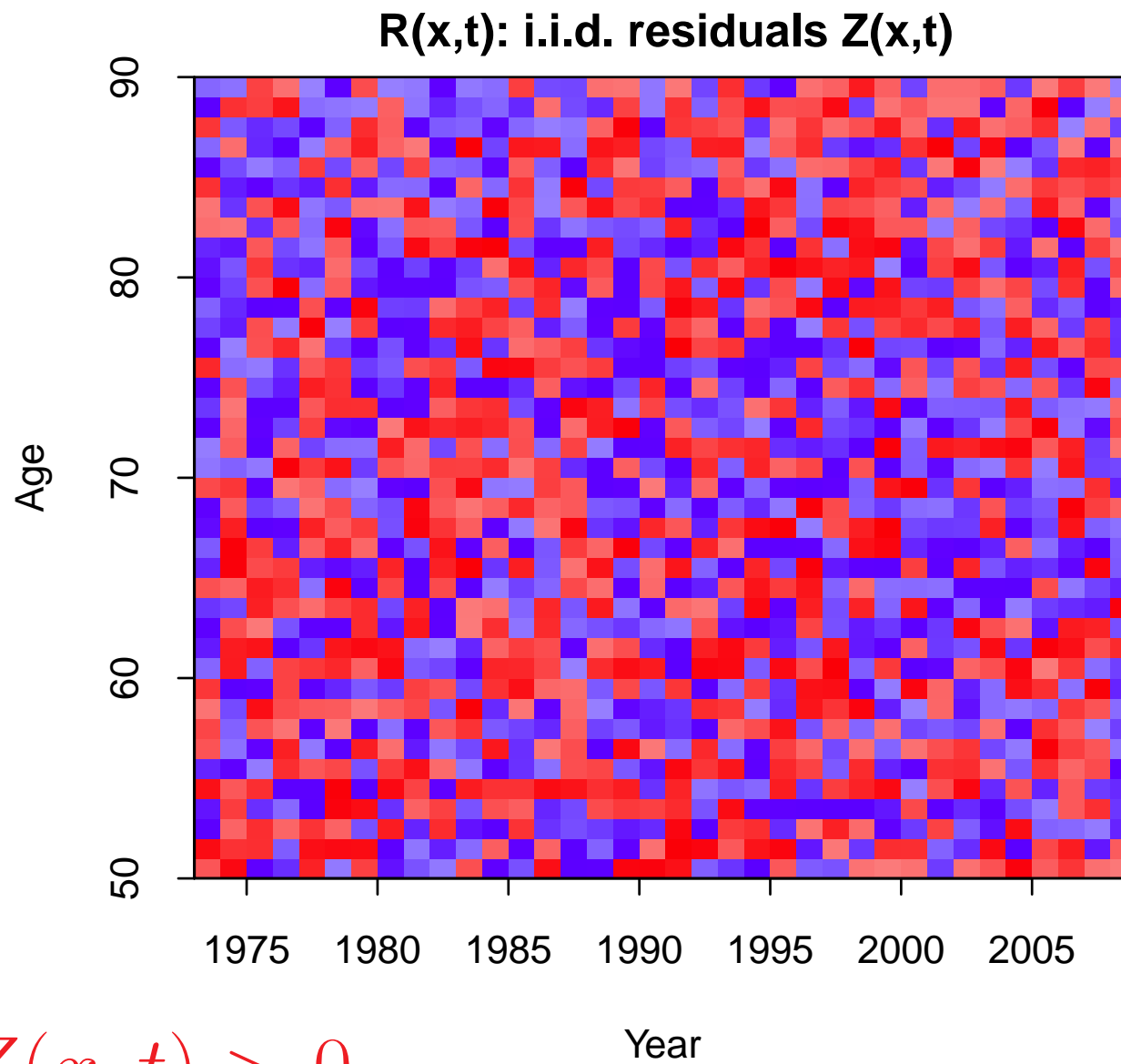
- Deaths: $D(x, t) \sim \text{Poisson}(m(x, t)E(x, t))$
- Bayesian approach:
posterior density = likelihood \times prior
- Upcoming results: mode of posterior density
- Further work: Bayesian parameter uncertainty

England and Wales, Males 1971–2008

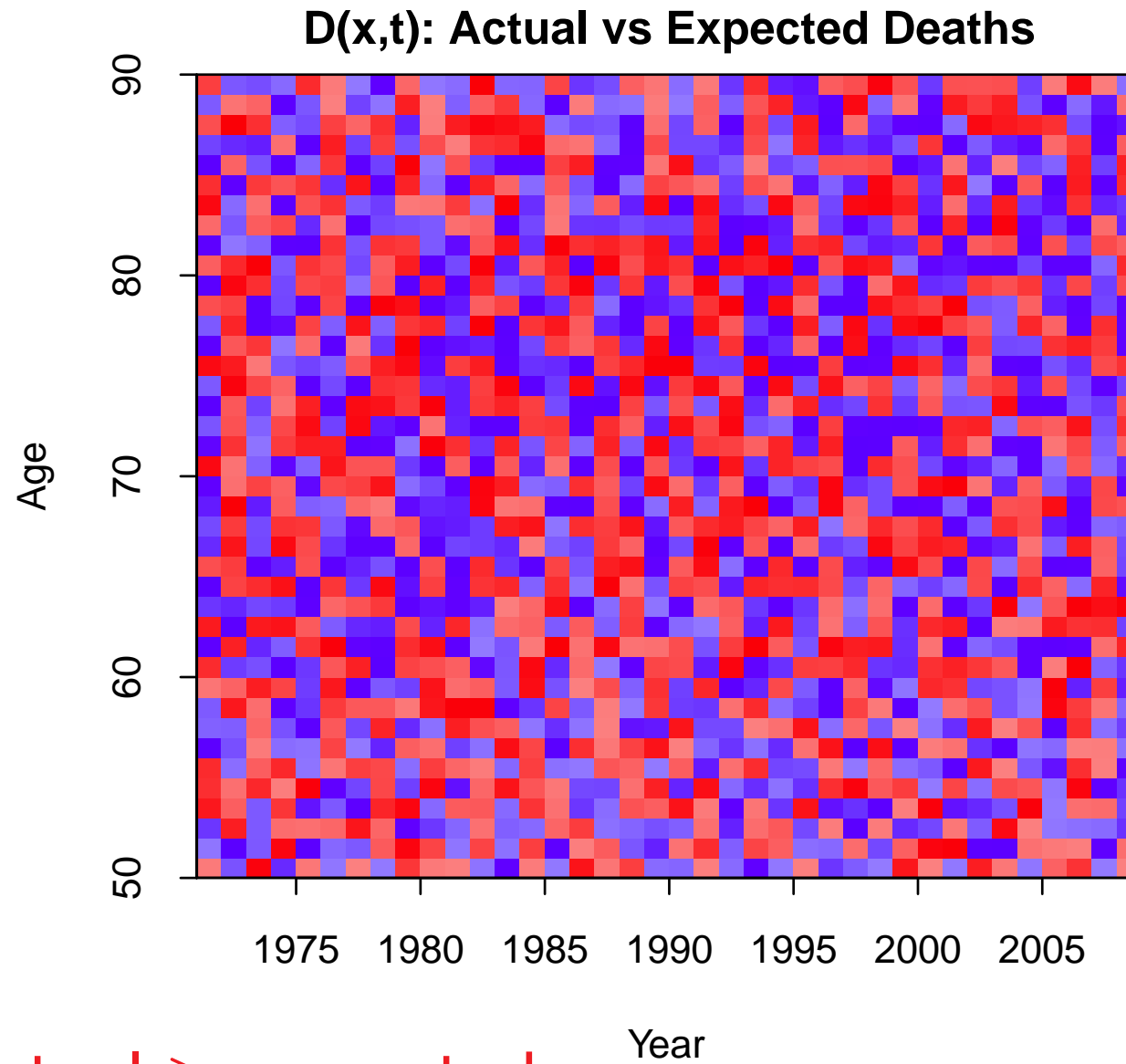


Cohort-type effects





Red $\Rightarrow Z(x, t) > 0$



Red \Rightarrow actual $>$ expected

Comparison with related models

$$\log m(x, t) = \beta(x) + \kappa_1(t) + \kappa_2(t)(x - \bar{x})$$

$$\log m(x, t) = \beta(x) + \kappa_1(t) + \kappa_2(t)((x - \bar{x}) + \gamma(t - x))$$

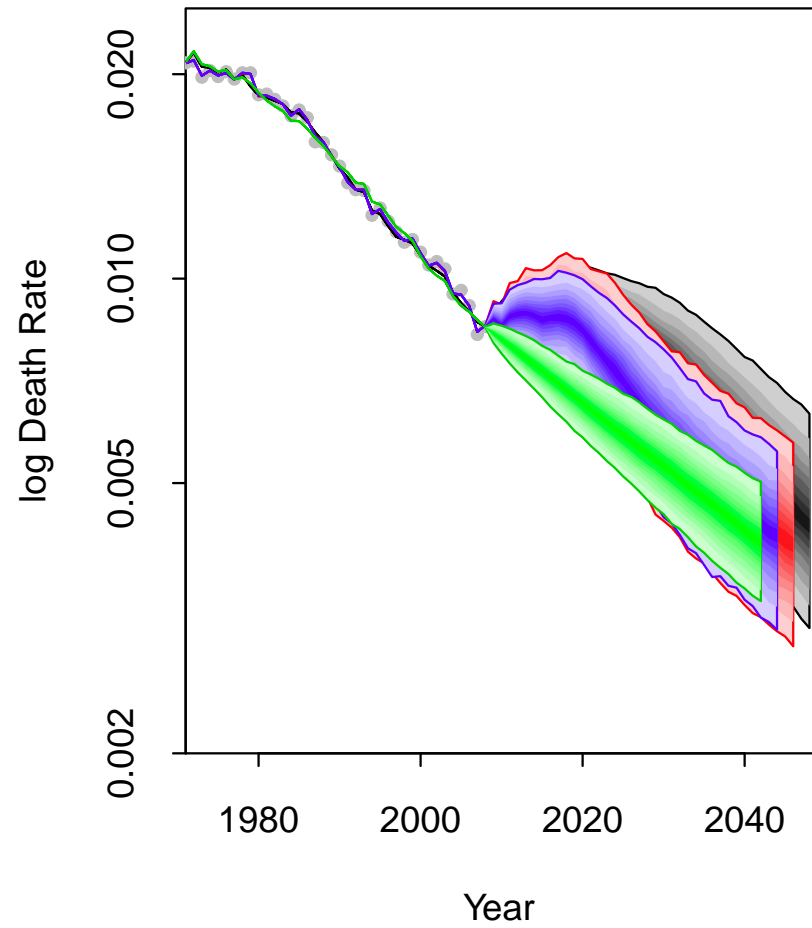
$$\log m(x, t) = \beta(x) + \kappa_1(t) + \kappa_2(t)(x - \bar{x}) + R(x, t)$$

$$R(t) = AR(t - 1) + BR(t - 2) + Z(t) \text{ (A, B as specified earlier)}$$

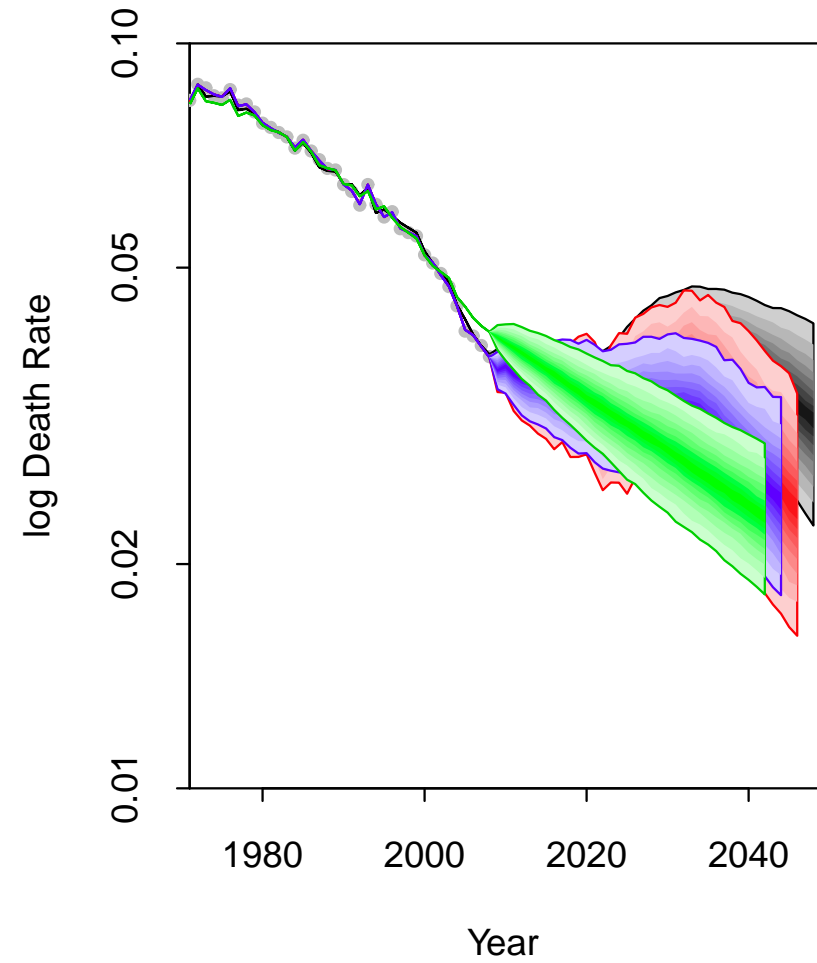
$$\log m(x, t) = \beta(x) + \kappa_1(t) + \kappa_2(t)((x - \bar{x}) + R(x, t))$$

$$R(t) = AR(t - 1) + BR(t - 2) + Z(t) \text{ (simplified A, B)}$$

Age 60



Age 75



Conclusions: Model Comparisons

- Long term underlying trends ($\kappa(t)$) are reasonably consistent
- Model risk more evident in the mean reverting $R(x, t)$

Further work

- Bayesian parameter uncertainty
- Multiple populations: focus on underlying $\kappa(t)$
⇒ less complexity

Multipopulations

Borrow from multifactor asset models: e.g.

- Asset i return: $R_i = \alpha_i + \beta_{i1}F_1 + \beta_{i2}F_2 + \epsilon_i$
- F_1, F_2 are systematic risk factors
- $\epsilon_i =$ idiosyncratic risks

Multipopulations

Mortality – version 1:

- Population, P , specific $\kappa_i^{(P)}(t)$ correlated
- $R^{(P)}(x, t)$: assume independent

Mortality – version 2:

- All populations have the same $\kappa_i(t)$
- $R^{(P)}(x, t)$: assume independent
- Greater role for $R(x, t)$ as country specific effect

Questions

W: <http://www.ma.hw.ac.uk/~andrewc>

E: A.J.G.Cairns@hw.ac.uk

Other models for $R(x, t)$

1. $R(x, t) = \phi R(x - 1, t - 1) + Z_R(x, t)$

2. $R(x, t) = \phi R(x - 1, t - 1) + \text{diffusion} + Z_R(x, t)$

3. **Smooth** underlying period effects, $\kappa_1(t), \kappa_2(t)$

plus annual shocks

e.g. $R(1), R(2), \dots$ are i.i.d. vectors, correlated

across ages