

LIVING
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SOCIETY OF ACTUARIES
INTERNATIONAL SYMPOSIUM

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Jan. 13–15
Lake Buena Vista, FL

5A – Multi Population Mortality Modeling

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2020 Living to 100 Symposium

LEONID A. GAVRILOV

Session 5A, Multi Population Mortality Modeling

Date: January 14, 2020



**SOCIETY OF
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5A: Multi Population Mortality Modeling - Discussion

Calibrating Mortality Processes with Trend Changes to Multi-Population Data

**Matthias Börger; Justin Schoenfeld; Johannes Schupp
Ulm University**

Major Challenge:

Very high uncertainty of life expectancy projections

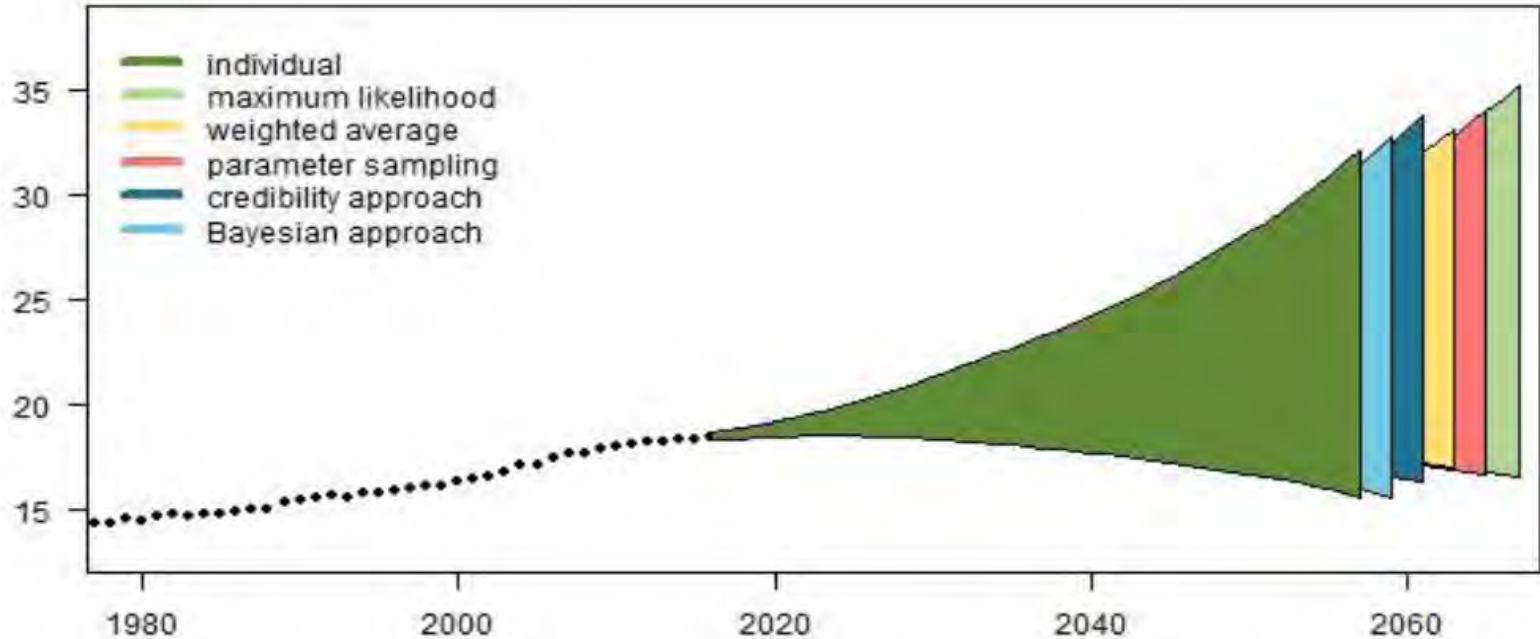


Figure 6: 90% prediction intervals for remaining period life expectancies of 65-year old US males based on different trend process calibrations

Possible Solution to Improve Accuracy of Projections (1)

**To take into account that rates of
mortality change over time are different
for different ages**

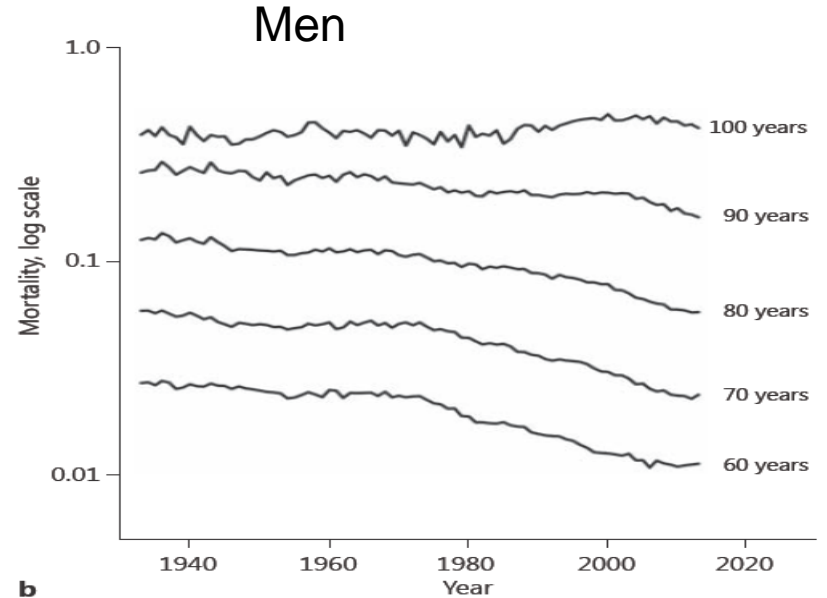
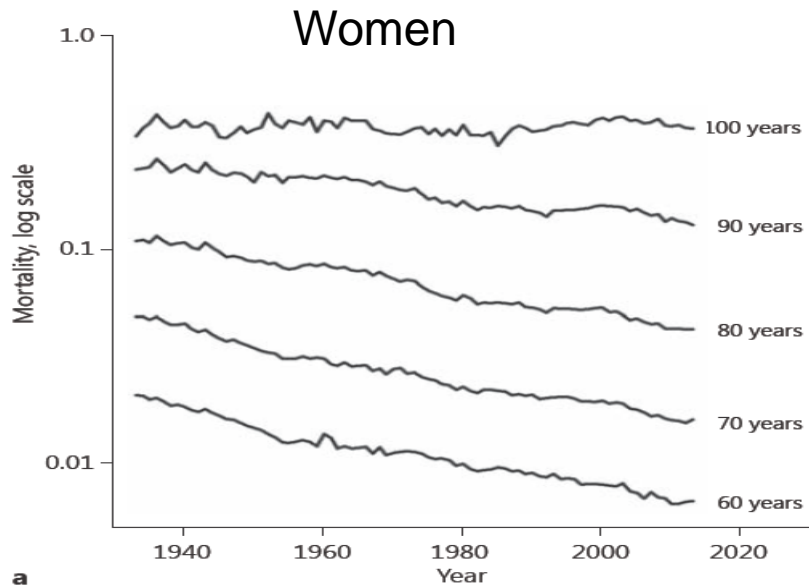
The Future of Human Longevity

Leonid A. Gavrilov^{a, b} Vyacheslav N. Krut'ko^{b, c} Natalia S. Gavrilova^{a, b}

For example, recent scientific publications suggest that human longevity records stopped increasing.

Our finding that the mortality of U.S. centenarians has not decreased noticeably in recent decades is consistent with this suggestion.

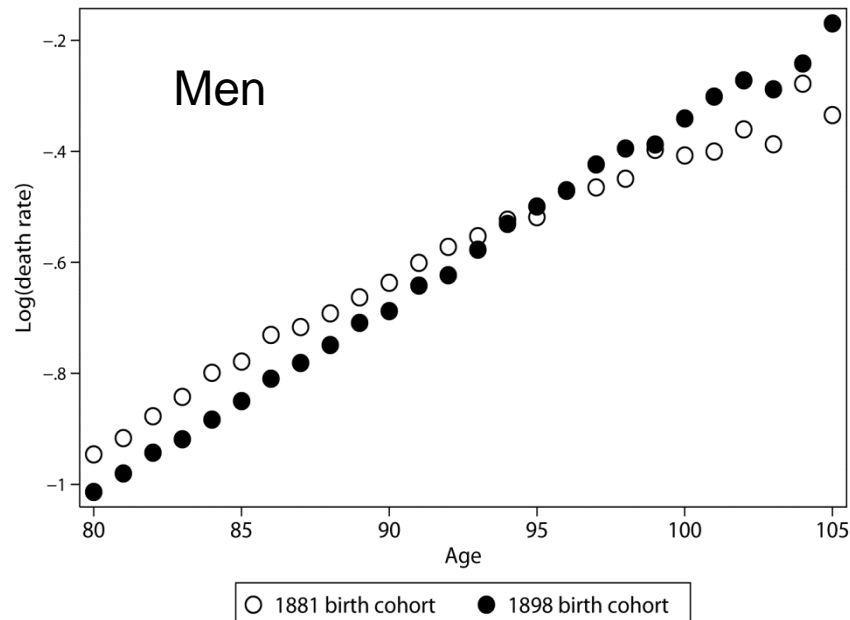
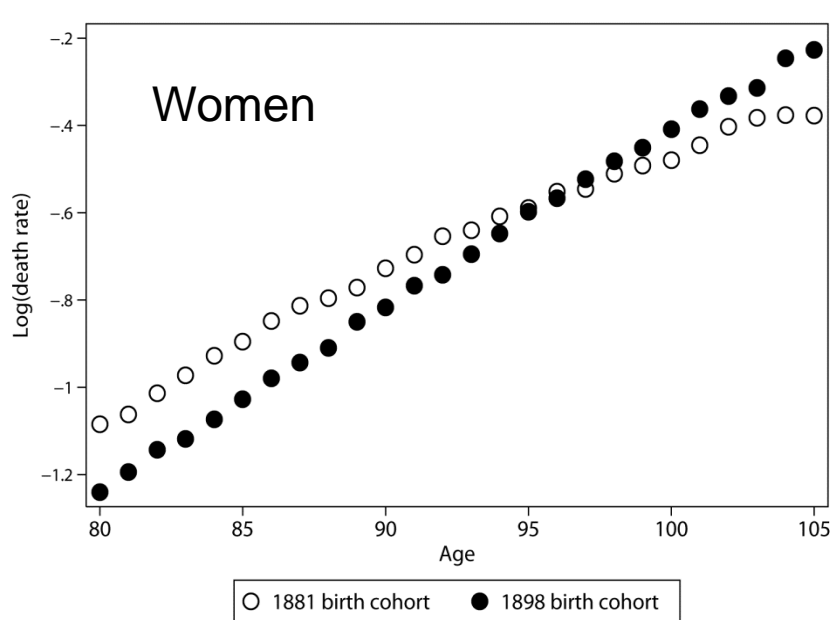
Mortality of U.S. centenarians does not decline over time



Source: Gavrilov et al., *Gerontology*, 2017

Mortality of U.S. men and women in earlier (1881) and later (1898) birth cohorts

Mortality deceleration is observed in early birth cohort only

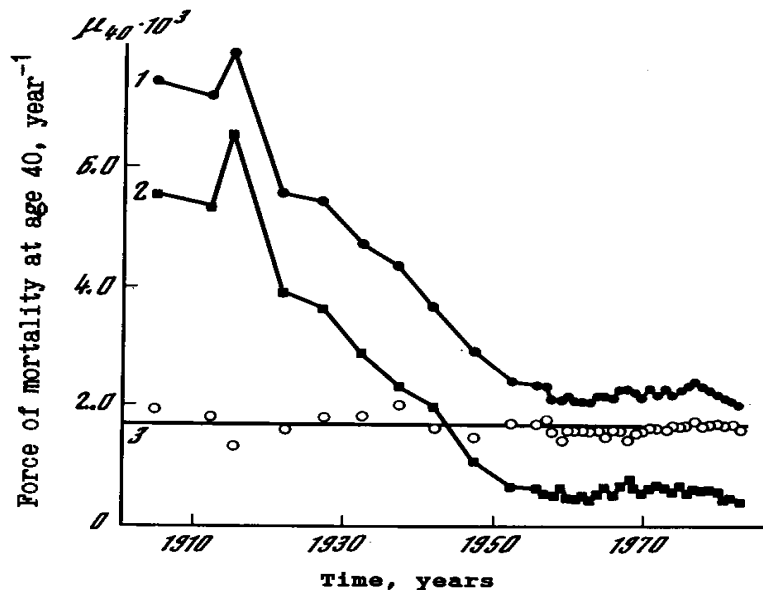


Source: Gavrilov, Gavrilova, *Gerontology*, 2019. Source of data: Human Mortality Database

Possible Solution to Improve Accuracy of Projections (2)

To eliminate from analyses old data for periods preceding the 1950s when mortality decline followed additive rather than multiplicative model

Historical changes of background (Makeham term) and senescent (Gompertzian) mortality of Swedish males



1 – total (observed) mortality at age 40

2 – background mortality (Makeham parameter)

3 – senescent mortality at age 40 calculated on the basis of Gompertz-Makeham formula

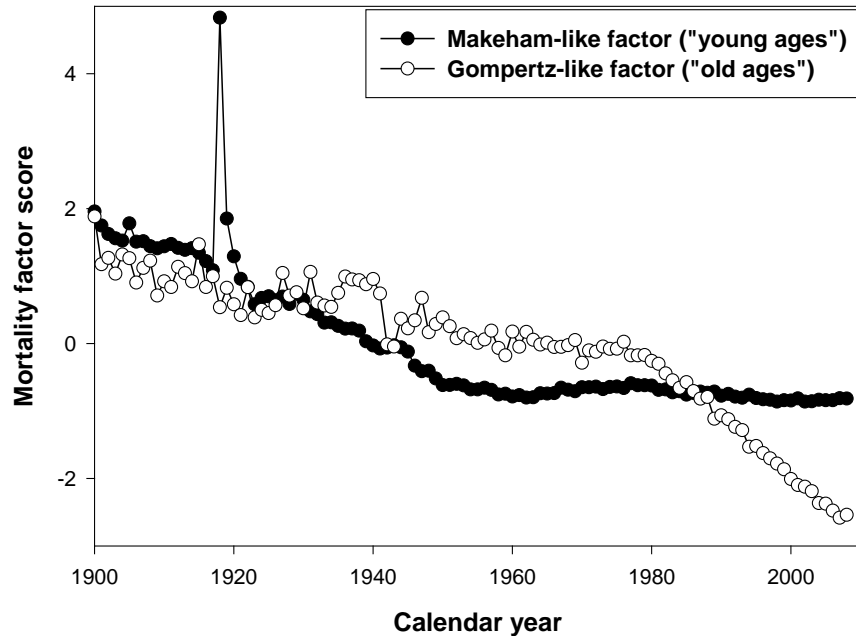
Senescent mortality is shown at age 40

Source: Gavrilov, Gavrilova, Nosov, Gerontology, 1983

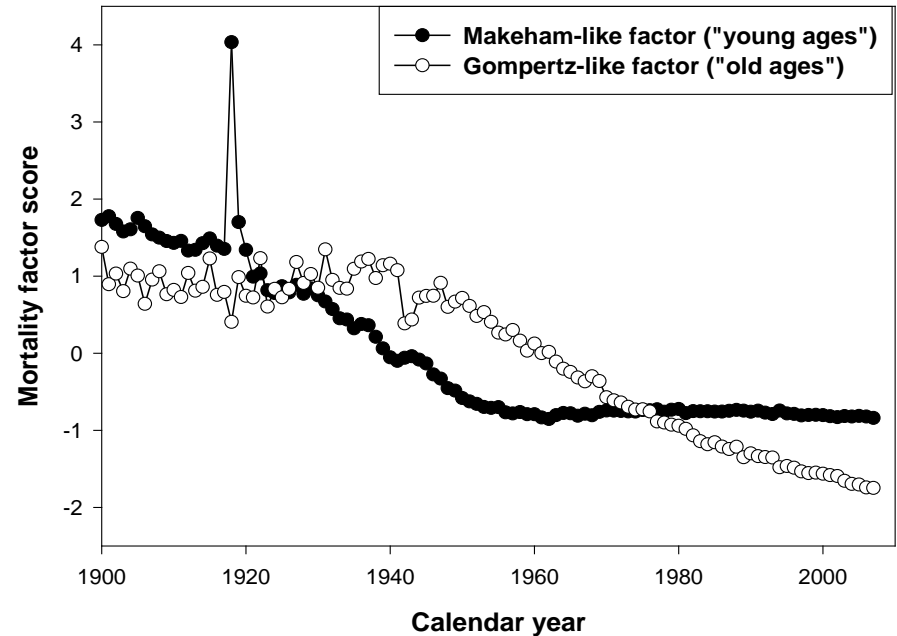
Factor Analysis of Mortality

Data for Swedish men and women

Men



Women



Source: Gavrilov, Gavrilova, Presented at the Living to 100 - 2017 Symposium

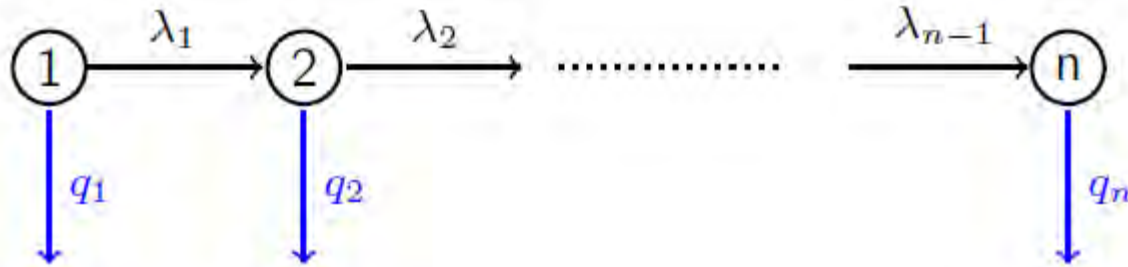
5A: Multi Population Mortality Modeling - Discussion

The Mathematical Mechanism of Biological Aging

**Boquan Cheng, Bruce Jones, FSA, FCIA, Ph.D.,
Xiaoming Liu and Jiandong Ren
University of Western Ontario**

This model uses two major assumptions

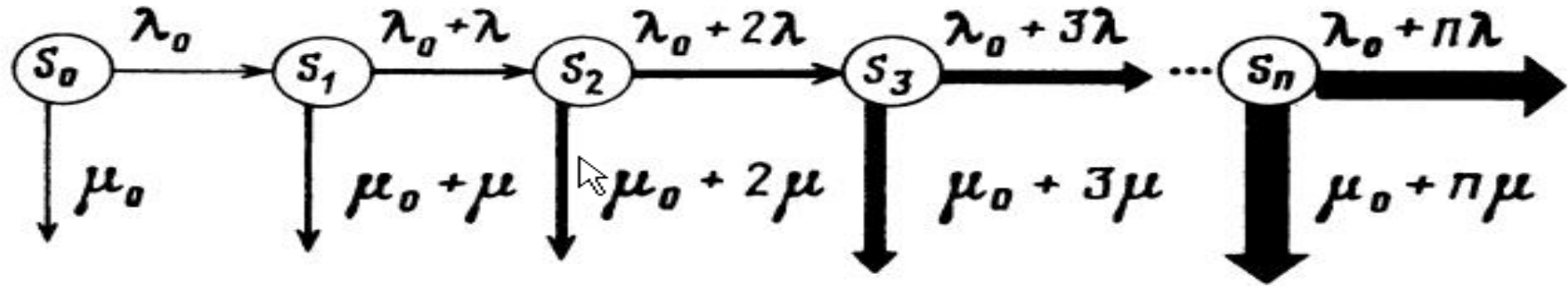
1. Transition rates (λ) are equal for all states of organism's aging.



What is the rationale for this assumption?

Alternative avalanche-like model uses rates of transition, which are increasing with each stage of aging.

Avalanche-like Mechanism of Organism's Destruction with Age

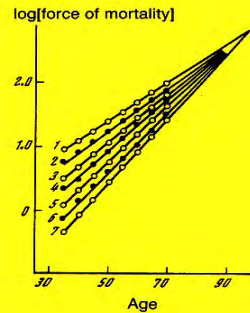


- In the initial state (S_0) organism has no defects. Then, as a result of random damage, it enters states S_1, S_2, \dots, S_n where n corresponds to the number of defects. Rate of new defects has avalanche-like growth with the number of already accumulated defects (horizontal arrows). Hazard rate (vertical arrows directed down) also has avalanche-like growth with number of defects.
- Source: Gavrilov, Gavrilova, *"The Biology of Life Span"* 1991

The Biology of Life Span: A Quantitative Approach

L. A. Gavrilov and N. S. Gavrilova

Edited by
V. P. Skulachev



harwood academic publishers
chur • london • paris • new york • melbourne

Avalanche-like model for
human aging was
published in 1991

Second assumption:

There are approximately 100 or 200-250 stages of organism's aging.

What is the rationale to use this relatively small number of stages for aging?

Alternative avalanche-like model uses unlimited number of stages that allows us to obtain analytical solution for mortality in closed form.

100-250 stages of aging appears to be very small number taking into account huge number of cells in human organism.

Overall, these are two very good papers!

The Mathematical Mechanism of Biological Aging

Xiaoming Liu

Department of Statistical & Actuarial Sciences

Western University in Ontario, Canada

Jan. 14, 2020 at SOA Living to 100 Symposium

A selfie project "Every Day" by Karl Baden

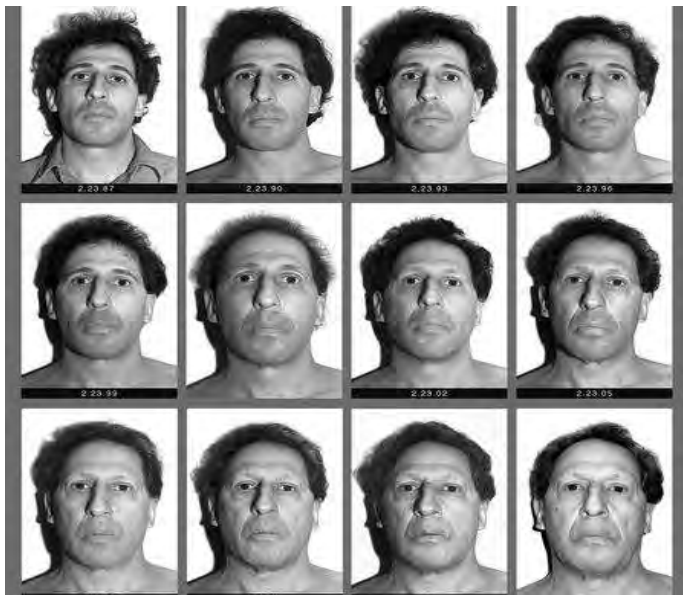


Figure: Karl Baden's selfies since his age 34 starting from Feb. 23, 1987  2/35

Karl Baden's real life photo on Feb 22nd 2017



Motivation and reflection about Baden's selfie project

What I'm interested in is making a picture that's as similar to the day before and all those before that. The idea is to make everything that I can control as similar as possible so that the only variable in the project is what I can't control which is
the aging process.

Motivation and reflection about Baden's selfie project

What I'm interested in is making a picture that's as similar to the day before and all those before that. The idea is to make everything that I can control as similar as possible so that the only variable in the project is what I can't control which is
the aging process.

Here is a comment by Howard Yezerski (a Boston gallery owner)

It's both personal and universal at the same time. He's recording a life, or at least one aspect of it that we can all relate to because we're all in same boat. We're all going to die.

My comments:

- ▶ Karl Baden provides an incomplete sample of his daily facial photos for aging (effect) demonstration.
- ▶ His underlying aging process can be observed as long as he is alive.

A Dilemma about aging

- ▶ Aging is something so real and tangible, and it has manifested itself (to us) in so many ways through every life (of human beings, particularly) who has ever existed on this planet over the past thousands of years.
- ▶ Yet, the (quantitative) study of aging is still in its infancy.

Why?

A Dilemma about aging

- ▶ Aging is something so real and tangible, and it has manifested itself (to us) in so many ways through every life (of human beings, particularly) who has ever existed on this planet over the past thousands of years.
- ▶ Yet, the (quantitative) study of aging is still in its infancy.

Why?

- ▶ How aging is defined
- ▶ How much and/or how little we know about aging
- ▶ How aging is modelled

How is aging defined?

Aging, as applied to living organisms, is **the genetically determined, progressive, and essentially irreversible diminution with the passage of time** of the ability of an organism or of one of its parts to adapt to its environment, manifested as diminution of its capacity to withstand the stresses to which it is subjected (i.e. the increase of susceptibility to certain diseases with age), and **culminating in the death of the organism**.

Jones, H.B.(1956) "A special consideration of the aging process, disease, and life expectancy" in *Advances in Biological and Medical Physics* 4:281-337.

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Two features in the above definition:

- ▶ Aging characteristics are described in a relative term.
- ▶ Aging seems better understood through aging effects, in particular, through increased mortality rates after reaching adulthood.

How much do we know about aging?

A brief summary about the latest genetic studies

- ▶ In the mid-90s, **the single gene disorder** genetic testing became available: identifying mutations in single genes that were known to be responsible for a condition.
- ▶ However, **multifactorial disorder identifying** means a **higher level of complexity**, since there are mutations in multiple genes, possibly quite large numbers of genes, each individually of small effect but in combination possibly of a considerable effect, and also interactions between genes and other genes, and between genes and the environments.

ref: The genomic underpinnings of human lifespan, British Actuarial Journal 2019 Vol.24 pp 1-15

Understanding the difficulty level

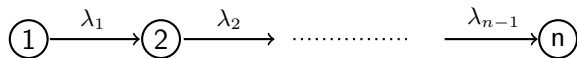
- ▶ Detecting these small effects is like looking for a very small signal among a lot of noise. It is very difficult to do in the first place.
- ▶ The real difficulty for multiple gene disorders lies in that, at this level, what has been discovered is **effects** rather than **causes**.
- ▶ In other words, what we know about the association between a genotype and a certain condition (a disorder) cannot be generalized to cellular or organismal level.
- ▶ The effect is expressed as a relative risk, and we can only quantify its likelihood. It is impossible to pinpoint the exact “cause and effect” relationship.
- ▶ This is very similar to the “**Uncertainty Principle**” in Quantum Physics.

How is aging modelled in the past?

So we are back to Jones' definition about aging, i.e. using **aging effect**.

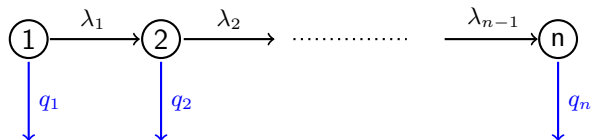
- ▶ The famous Gompertz law is remembered as a mortality law, which was a result from his enquiry on the aging process in my opinion — “if there could be any physical cause for the consistent patterns of death among people” — this part is largely forgotten today.
- ▶ Even myself, in Lin and Liu (2007), I used mortality rates to test my aging modelling idea.
- ▶ The relationship between aging and mortality is intertwined and inseparable; individuals have to be alive so that the underlying aging process can be witnessed.
- ▶ Can we do better in this situation?

Lin and Liu (2007)—The Markovian Aging Model



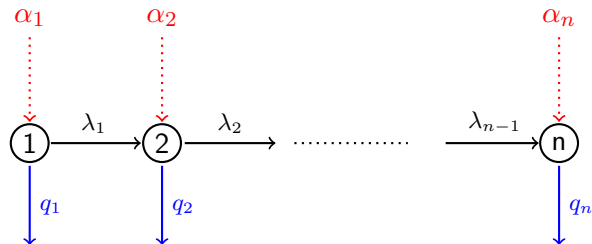
- ▶ This aging process is an internal process of deterioration of physiological capacity that undergoes all human bodies.

Lin and Liu (2007)—The Markovian Aging Model



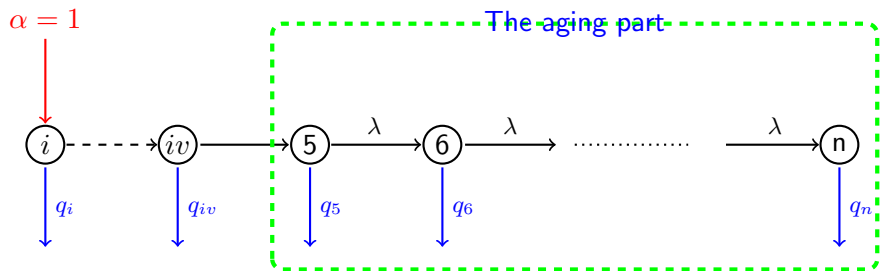
- ▶ This aging process is an internal process of deterioration of physiological capacity that undergoes all human bodies.
- ▶ This deterioration makes each life more susceptible to diseases, failures of biological systems, and death.

Lin and Liu (2007)—The Markovian Aging Model



- ▶ This aging process is an internal process of deterioration of physiological capacity that undergoes all human bodies.
- ▶ This deterioration makes each life more susceptible to diseases, failures of biological systems, and death.
- ▶ The first contribution of this approach is to differentiate the aging effect from the aging process.

The complete proposed PTAM model in Lin and Liu (2007)



$$\lambda_i = \lambda, \text{ for } i = 5, \dots, 200,$$

$$q_i = \begin{cases} b + a + i^p \cdot q & \text{for } i_1 < i \leq i_2 \\ b + i^p \cdot q & \text{otherwise} \end{cases}$$

- ▶ Part $i^p * q$ represents an increasing deterioration pattern of physiological capacities due to aging.
- ▶ Parameter b represents a general background death rate.
- ▶ Parameter a represents the extra accidental death rate.

Estimation method

- ▶ Weighted least squares is used. The function minimized is

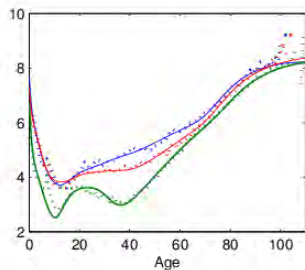
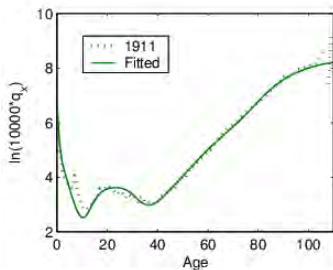
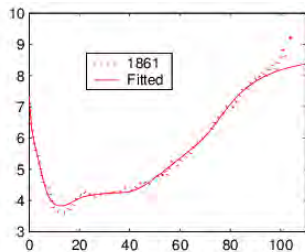
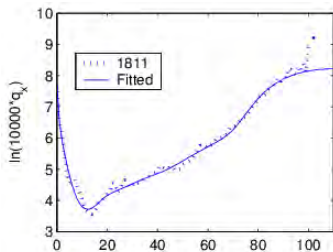
$$F = \sum_{x=0}^{\omega} (q_x - \hat{q}_x)^2 S(x)$$

Where q_x and $S(x)$ is the observed conditional death rate and survival value at age x , and \hat{q}_x is the conditional death rate calculated by:

$$\begin{aligned}\hat{S}(x) &= \alpha e^{\Lambda x} e \\ \hat{q}(x) &= 1 - \frac{\hat{S}(x+1)}{\hat{S}(x)}\end{aligned}$$

- ▶ Parameters are obtained numerically by the Nelder-Mead simplex algorithm.

Fitting to Swedish male (cohort) data

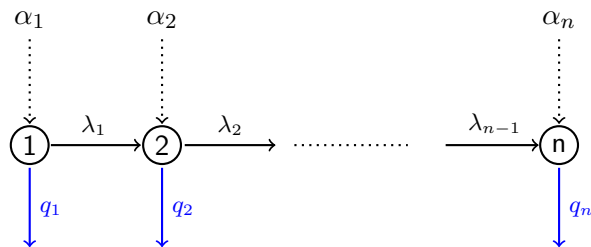


Estimated aging related parameters

Table: Estimated aging related parameters for Swedish cohorts of year 1811, 1861, and 1911

Year	Parameters					
	λ	b	a	$[i_1, i_2]$	q	p
1811	2.5657	3.1504e-03	1.9888e-03	[42, 99]	9.3157e-09	3
1861	2.4794	4.4825e-03	1.9033e-03	[42, 89]	2.6351e-13	5
1911	2.3707	9.0987e-04	2.8939e-03	[33, 70]	1.8872e-15	6

Dynamic Population Structure



- Suppose at age x , the distribution of physiological age is represented by

$$P(Y_x = i) : \boldsymbol{\alpha}_x = (\alpha_1, \alpha_2, \dots, \alpha_n).$$

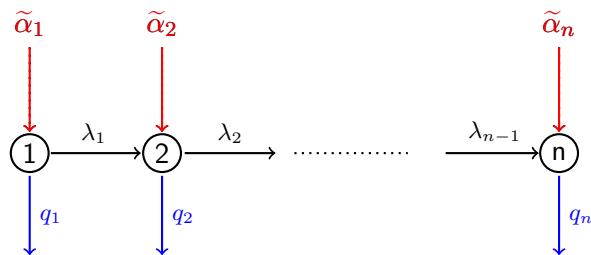
- Then in t years, the distribution of physiological age changes to

$$P(Y_{x+t} = i) : \tilde{\boldsymbol{\alpha}}_{x+t} = (\tilde{\alpha}_1, \tilde{\alpha}_2, \dots, \tilde{\alpha}_n).$$

where

$$\tilde{\alpha}_{x+t} = \frac{\alpha_x e^{\Lambda t}}{\alpha_x e^{\Lambda t} e}$$

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where

$$\tilde{\alpha}_{x+t} = \frac{\alpha_x e^{\Lambda t}}{\alpha_x e^{\Lambda t} e}$$

Summary—What were there in Lin and Liu (2007)?

- ▶ We elaborated on the relationship between mortality and physiological capacity (i.e. **physiological age or health index** in our papers), rather than a direct relationship between mortality and age.
- ▶ The model incorporated a random nature in individual's biological aging process.
- ▶ The model considered other types of causes of death (other than aging) separately and additively in the stochastic aging mechanism.
- ▶ The time-till-death r.v. T is the time-till-absorption of the process, which is easy to calculate, utilizing matrix-analytic tools.

The approach resulted in a PTAM model for **mortality**. *Again, aging and mortality are so intertwined that it is hard to separate them.*

What are in Cheng et al. (2019)

To enhance the aging model and re-define the physiological age index

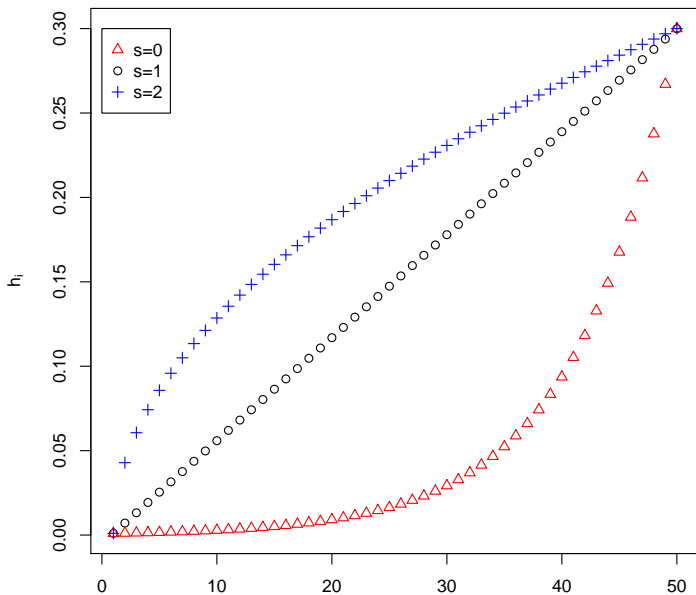
- ▶ The force of aging and the force of death are still described separately as in Lin and Liu (2007).
- ▶ Propose a functional form for the exiting rate from each state:

$$h_i = \begin{cases} \left(\frac{m-i}{m-1} h_1^s + \frac{i-1}{m-1} h_m^s \right)^{1/s} & s \neq 0, \\ h_1^{\frac{m-i}{m-1}} h_m^{\frac{i-1}{m-1}} & s = 0. \end{cases}$$

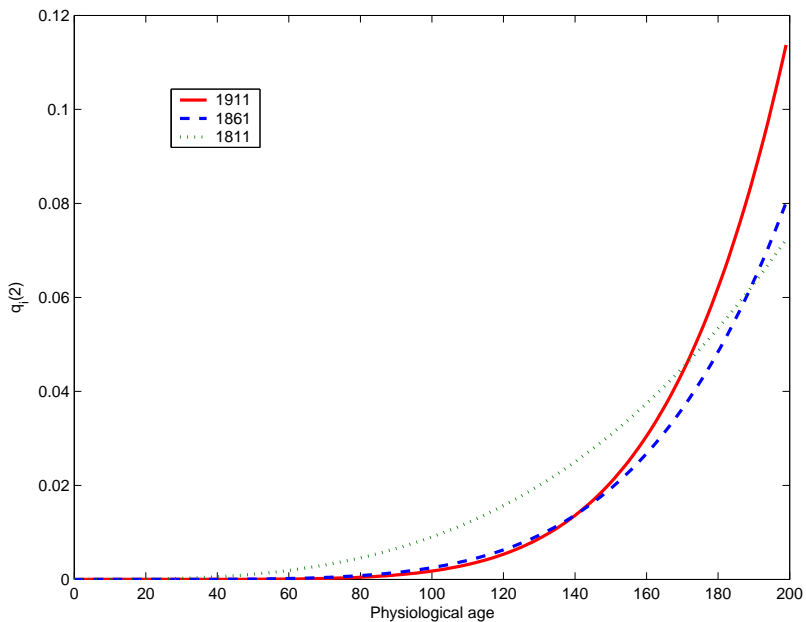
which is referred to as the Box-Cox transformation in the paper.

- ▶ Define a physiological age index in a more transparent and intuitive way.

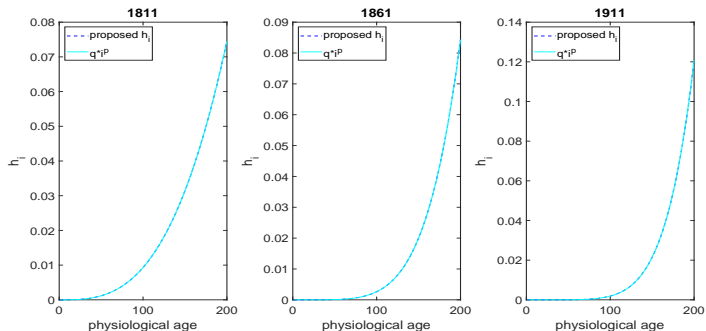
h_i using $h_1 = 0.001$, $h_m = 0.3$ and $s = 0, 1$ and 2



h_i in Lin and Liu (2007) in the form of $i^p * q$



h_i in the Box-Cox transformation



Year	q	p	h_1	h_m	s
1811	9.3157e-09	3	1.71E-08	0.074532485	0.332803361
1861	2.6351e-13	5	8.52E-13	0.084431355	0.199403613
1911	1.8872e-15	6	5.14E-14	0.120627387	0.166163239

Application using data from a retirement community

- ▶ The residents' lifetime data from Channing House, a retirement community in Palo Alto, California.
- ▶ The data set includes the entry age and age at death (or study end) for 462 people (97 males and 365 females) between January 1964 and July 1975.
- ▶ All residents were covered by a health care program, which provided easy access to care at no cost.
- ▶ We consider all females—a small group of homogeneous individuals.
- ▶ This data set was chosen carefully to ensure all other variables that are likely to affect death are as similar as possible among these individuals and the only variable that we can't control is the underlying aging process.

Survival functions of age 60+ and fitted model

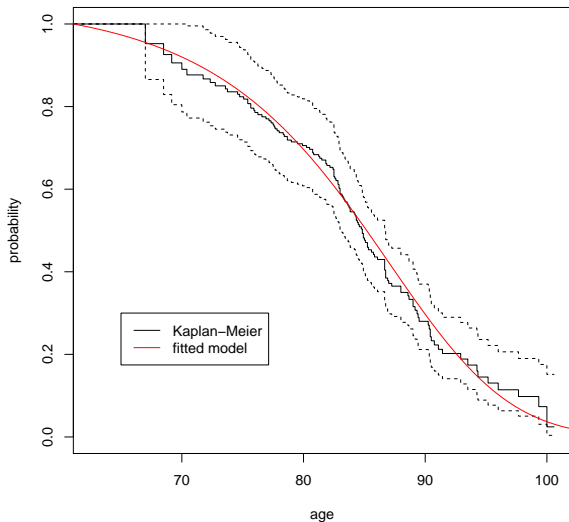
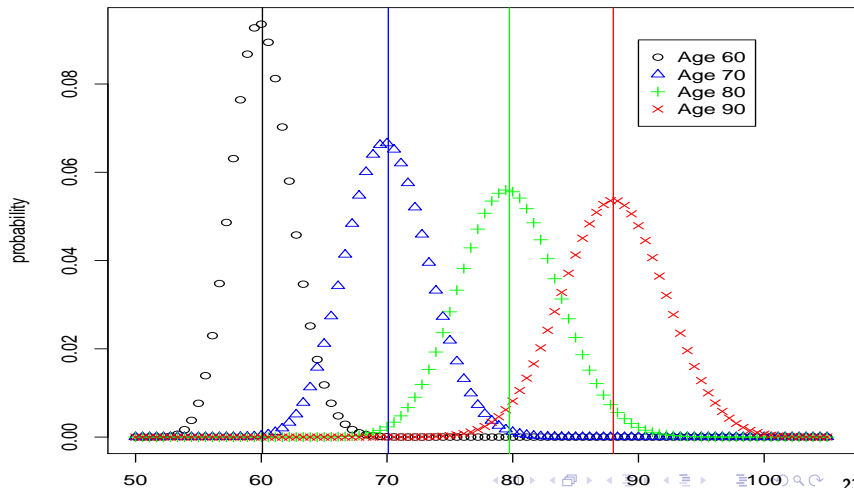


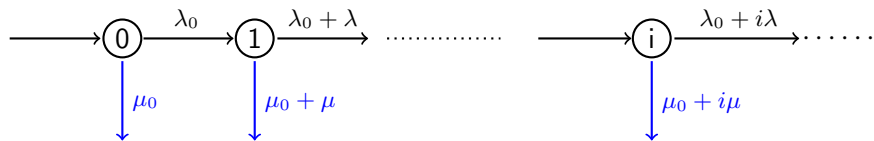
Figure: Note that $\lambda = 1.8182$, $s = -0.0734710$

The physiological age index

$$\text{Physiological age at calendar age } t = 50 + \frac{Y_t - 1}{m - 1} \psi$$



A simulation study based on the Le Bras model



$$P_i(t) = \frac{e^{-(\mu_0 + \lambda_0)t}}{i!} \left(\frac{\lambda(1 - e^{-(\lambda + \mu)t})}{\lambda + \mu} \right)^i \prod_{k=1}^i \left(\frac{\lambda_0}{\lambda} + k - 1 \right)$$

$$S(t) = \sum_{i=0}^{\infty} P_i(t) = e^{-(\lambda_0 + \mu_0)t} \left(\frac{\lambda + \mu}{\mu + \lambda e^{-(\lambda + \mu)t}} \right)^{\frac{\lambda_0}{\lambda}}$$

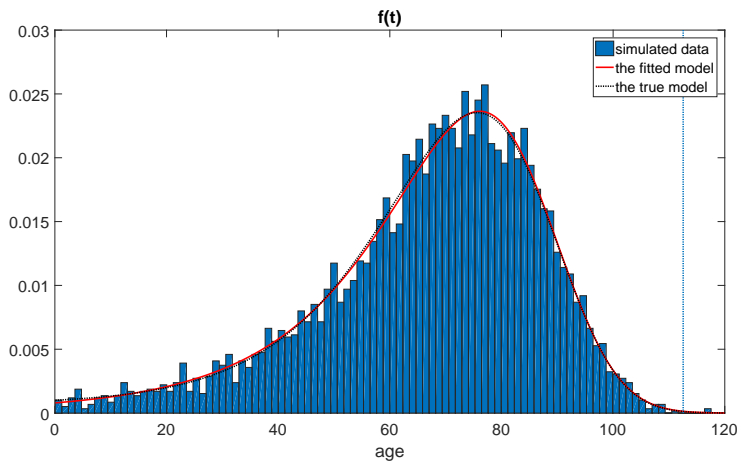
$$\mu(t) = \left(\mu_0 - \frac{\mu\lambda_0}{\lambda} \right) + \frac{\mu\lambda_0}{\lambda} e^{(\lambda + \mu)t}, \quad \text{as } \mu \ll \lambda$$

Simulation and model fitting

- ▶ We have simulated 5000 complete lifetimes based on the given Le Bras model.
- ▶ Set $\psi = \widehat{\text{TVaR}}_{0.999}(T)$ and use a MLE procedure to obtain other parameters:

	λ_0	λ	μ_0	μ
The Le Bras model	0.6	0.07	0.001	0.4×10^{-4}
Our fitted PTAM model with $m = 225$	h_1	h_m	λ	s
	0.0008	1.65349	1.99908	-0.11118

Histogram of the simulated data with the fitted model



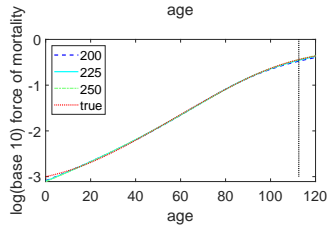
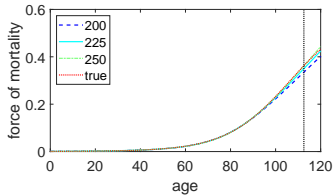
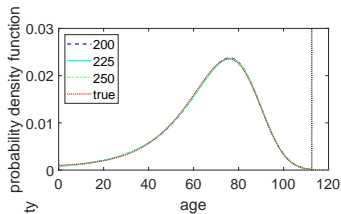
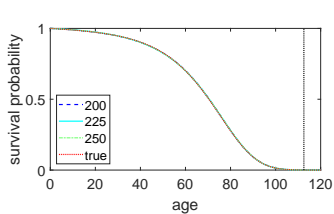
The physiological age index based on the fitted model

- ▶ Define the physiological age index as follows

$$\text{Physiological age index } X_t \text{ at calendar age } t = \frac{Y_t - 1}{m - 1} \psi.$$

- ▶ So X_t is a random variable transformed from Y_t , and its distribution can be easily derived from the distribution of Y_t .
- ▶ Note that X_t takes values from $[0, \psi]$. That is, X_t is not affected by the state number parameter m and has the same scale as the calendar age's upper limit ψ .

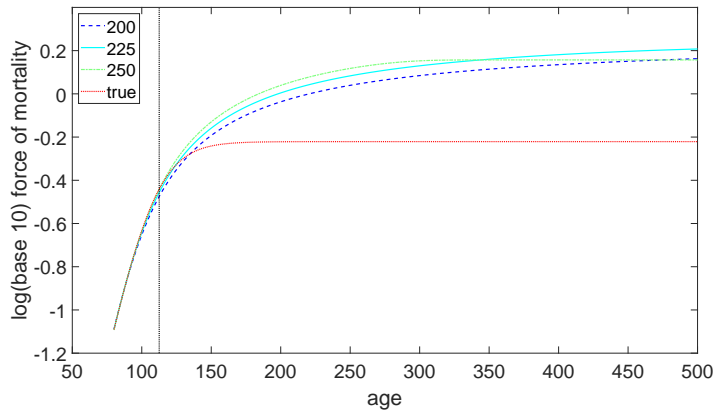
The fitted models with different m



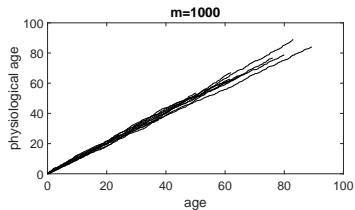
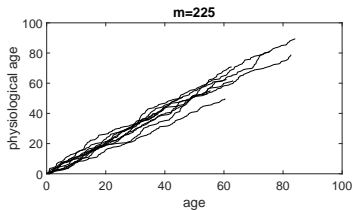
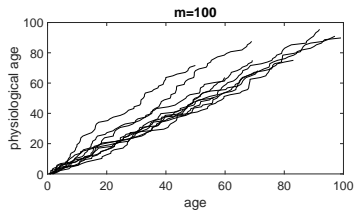
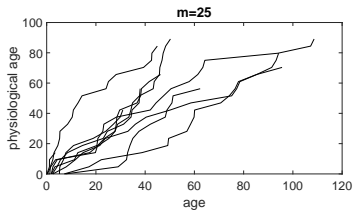
The fitted model estimates with different m

NLL	h_1	h_m	λ	s	m
21631.884	0.00081	2.00325	1.77637	-0.12373	200
21631.826	0.0008	1.83922	1.86518	-0.11829	210
21631.806	0.0008	1.70795	1.95400	-0.11336	220
21631.713	0.0008	1.65349	1.99908	-0.11118	225
21631.813	0.00079	1.60064	2.04282	-0.10886	230
21631.843	0.00078	1.51076	2.13164	-0.10469	240
21631.889	0.00078	1.43544	2.22046	-0.10089	250

The implication of different m



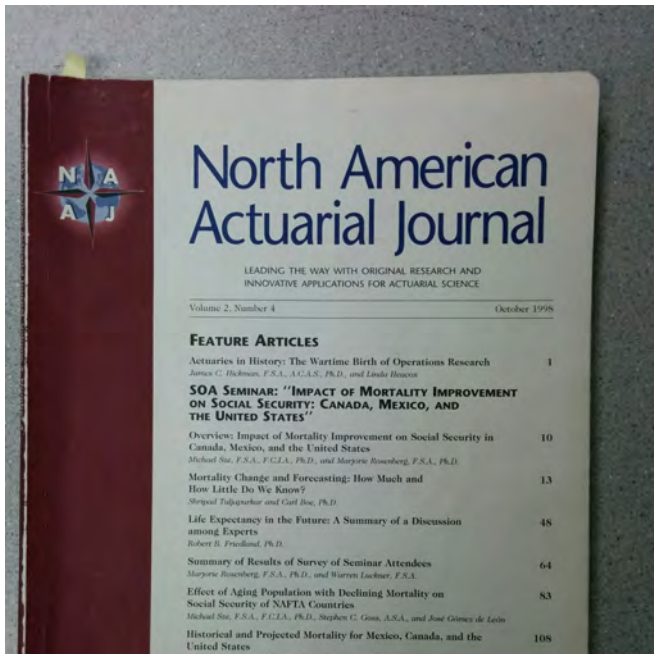
The implication of different m



Summary

- ▶ This modelling approach is to describe the deteriorating feature accompanying the aging process.
- ▶ The parameters of the model can be calibrated to the observable quantities which should be highly associated with aging; here, we choose aging-related mortality rate.
- ▶ The model is composed of a simple Markovian structure and a compact yet robust functional form.
- ▶ The model provides an index — physiological age to contrast chronological age.
- ▶ Additional references
 - ▶ Sheldon Lin and Xiaoming Liu (2007) “Markov aging process and phase-type law of mortality” NAAJ, 11(4):92-109.
 - ▶ Maria Govorun, Bruce L. Jones, Xiaoming Liu and David A. Stanford (2018), “Physiological age, health costs and their interrelation”, North American Actuarial Journal 22(3), 323-340.
 - ▶ Boquan Cheng, Bruce Jones, Xiaoming Liu and Jiandong Ren (2019), “The Mathematical Mechanism of Biological Aging”, under review.

My research interest in mortality risk started from...



Search for the law

Life Expectancy in the Future: A Summary of a Discussion among Experts

Robert B. Friedland, Ph.D.

Summary of Results of Survey of Seminar Attendees

Marjorie Rosenberg, F.S.A., Ph.D., and Warren Luckner, F.S.A.

Effect of Aging Population with Declining Mortality on Social Security of NAFTA Countries

Michael Sze, F.S.A., F.C.I.A., Ph.D., Stephen C. Goss, A.S.A., and José Gómez de León

Historical and Projected Mortality for Mexico, Canada, and the United States

Stephen C. Goss, A.S.A., Alice Wade, A.S.A., and Felicitie Bell

Forecasting Mortality Change: Questions and Assumptions

Shripad Tuljapurkar

Forecasting Changes in Mortality: A Search for a Law of Causes and Effects

Sam Gutterman, F.S.A., F.C.A., F.C.A.S., and

Irwin T. Vanderhoof, F.S.A., A.C.A.S., A.I.A., Ph.D.

Thank you!



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Calibrating Mortality Processes with Trend Changes to Multi-Population Data

- joint work with Matthias Börger and Justin Schoenfeld
- Johannes Schupp
- 2020 Living to 100 Symposium, Orlando
- January 14th



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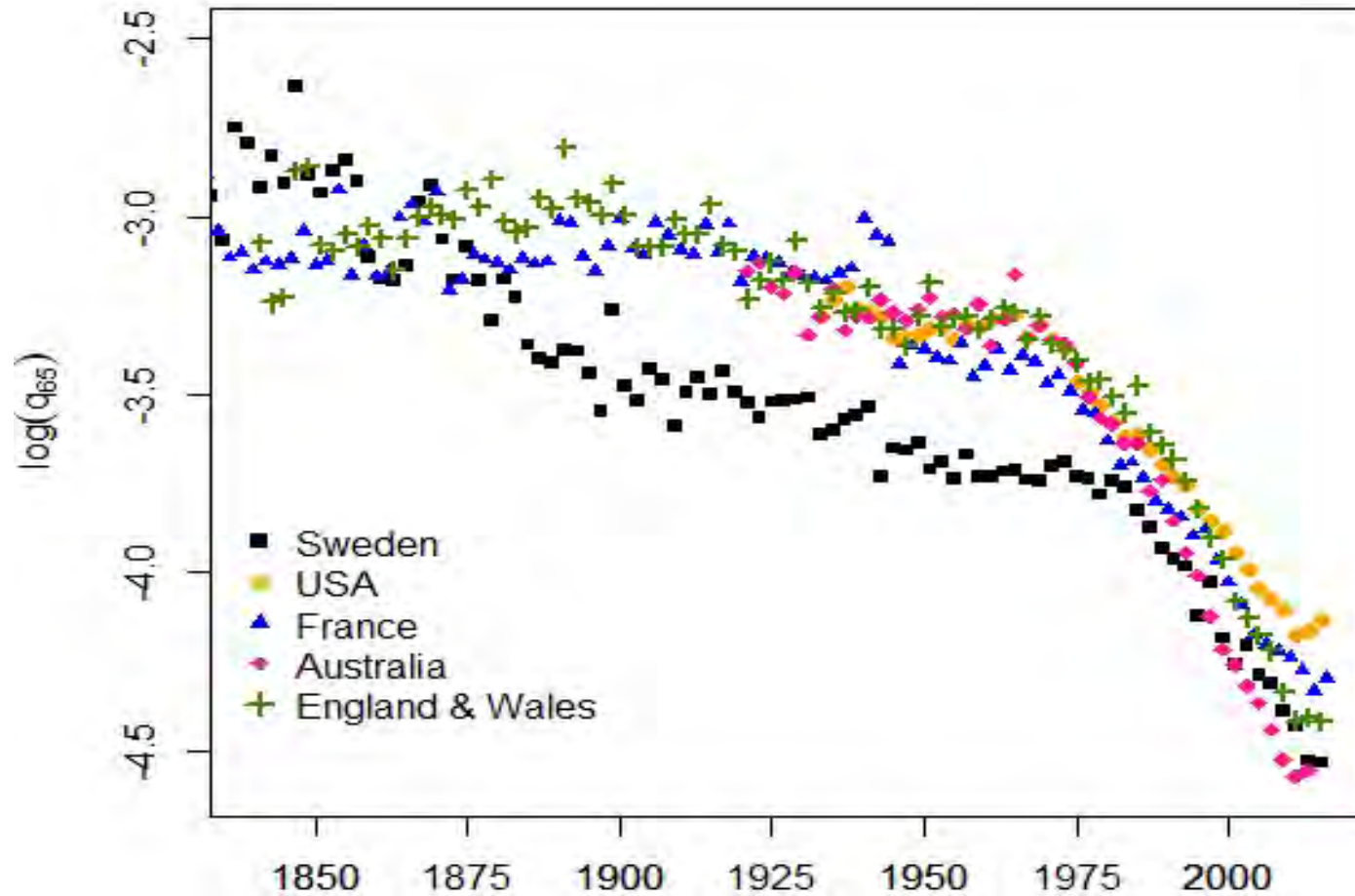
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Uncertainty about the evolution of mortality



Introduction

- Trend changes in mortality evolution have been identified by several authors for many countries:
 - Li et al. (2011), Coelho and Nunes (2011), Hainaut (2012), Sweeting (2011), Börger and Schupp (2018),...
 - Typically, only a few number of trend changes can be observed (2-6 trend changes).
 - significant amount of uncertainty → **Combine data from different countries!**
- Reliable trend changes can't be identified for countries, pension funds, with short data histories or large volatility
 - However, the underlying drivers of mortality should be similar. → **Use data from related countries!**

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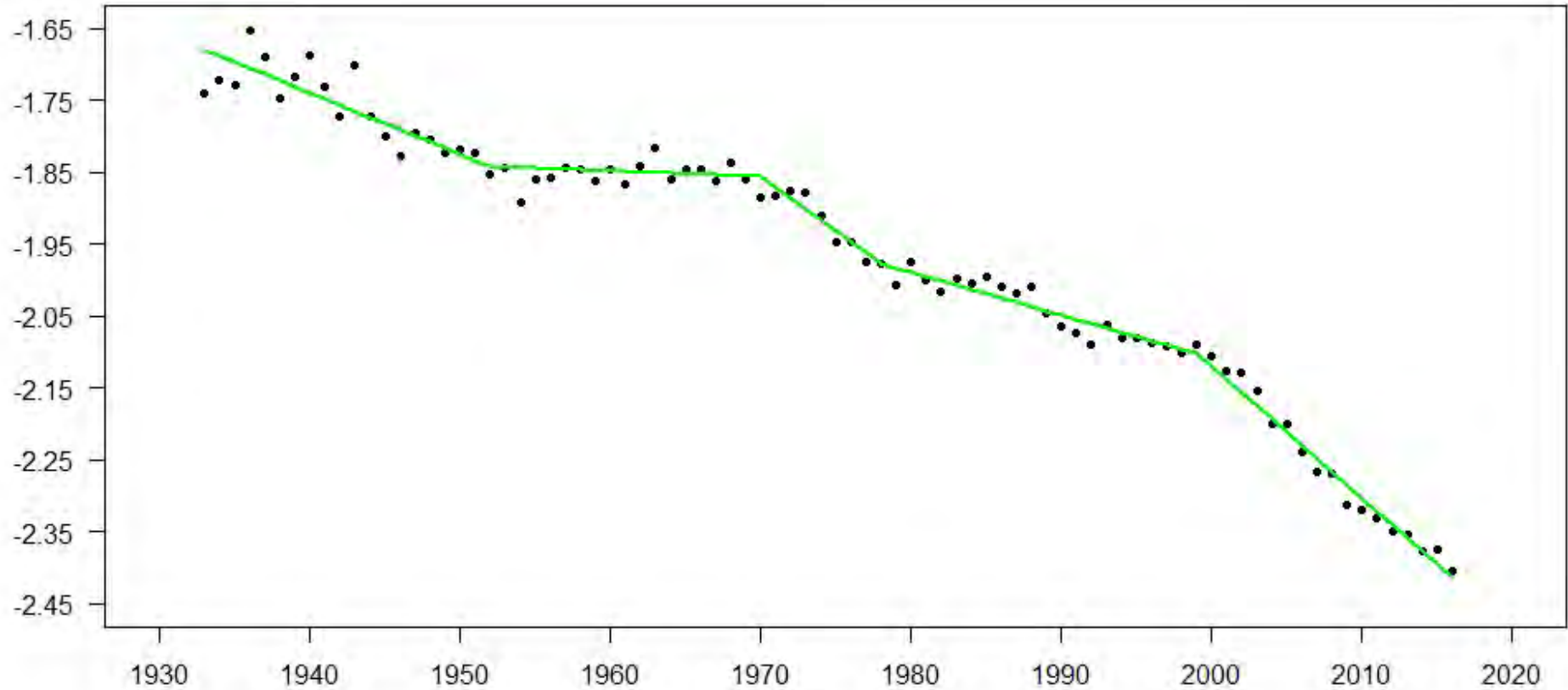
Trend change process

Underlying CBD mortality model

- Throughout, we assume that the trend process of Börger and Schupp (2018) is applied to project the period effects in the CBD mortality model of Cairns et al. (2006).
- structure of the CBD model:
 - $\text{logit}(q_{x,t}) := \log\left(\frac{q_{x,t}}{1-q_{x,t}}\right) = \kappa_t^{(1)} + \kappa_t^{(2)} \cdot (x - \bar{x})$
 - \bar{x} is some medium age
- Each period effect $\kappa_t^{(i)}, i = 1,2$ is projected by a separate instance of the trend process.

Specification of a Trend Model

Optimal historical trend realization for US males $\kappa_t^{(1)}$



Trend change process

Specification

- continuous piecewise linear trend, with random changes in the slope and random fluctuation around the trend

- Model the trend process with random noise $\rightarrow \kappa_t^{(i)} = \hat{\kappa}_t^{(i)} + \varepsilon_t^{(i)}$; $\varepsilon_t \sim \mathcal{N}(0, \Sigma)$.

- Extrapolate the most recent actual mortality trend $\rightarrow \hat{\kappa}_t^{(i)} = \hat{\kappa}_{t-1}^{(i)} + \hat{d}_t^{(i)}$.

- In every year, there is a possible change in the mortality trend with probability p .

$$\rightarrow \hat{d}_t^{(i)} = \begin{cases} \hat{d}_{t-1}^{(i)} & , \text{ without trend change in } t-1 \text{ with probability } 1-p^{(i)} \\ \hat{d}_{t-1}^{(i)} + \lambda_{t-1}^{(i)} & , \text{ with trend change } \lambda_{t-1}^{(i)} \text{ in } t-1 \text{ with probability } p^{(i)} \end{cases}$$

- in the case of a trend change $\rightarrow \lambda_t^{(i)} = S_t^{(i)} \cdot M_t^{(i)}$

- with absolute magnitude of the trend change $M_t^{(i)} \sim LN(\mu^{(i)}, \sigma^{(i)})$,

- sign of the trend change $S_t^{(i)}$ bernoulli distributed with values -1, 1 each with probability $\frac{1}{2}$

- For details on the calibration, see Börger and Schupp (2018) and Schupp (2019)



parameters to be estimated for projections starting in t_0 :

$$p^{(i)}, \mu^{(i)}, \sigma^{(i)}, \hat{\kappa}_{t_0}^{(i)}, \hat{d}_{t_0}^{(i)}, \Sigma$$

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Parameter uncertainty in case of one population

Comparison of trend process parameters

Magnitude and relevancy of uncertainty in different sets of trend process parameters

- **trend change parameters** $p^{(i)}, \mu^{(i)}, \sigma^{(i)}$
 - substantial amount of parameter uncertainty
 - typically estimated from a small number of trend changes
 - parameters have a high influence on forecasts

- **starting values** $\hat{\kappa}_{t_0}^{(i)}, \hat{d}_{t_0}^{(i)}$
 - highly case specific amount of parameter uncertainty
 - can be substantial for some period effects and almost irrelevant for other cases
 - parameters have potentially a high influence on forecasts

- **covariance matrix** Σ of the two-dimensional noise vector
 - small amount of parameter uncertainty
 - estimated from a large sample of errors
 - hardly relevant in long-time forecasts
 - moderate impact in 1-year forecasts

Parameter uncertainty in case of one population

Sources of uncertainty

Two main sources of uncertainty arise from trend process estimation

The two main sources of uncertainty are:

- The actual number of trend changes is unknown due to randomness in the data.
 - The actual number of trend changes may have a weight (based on relative likelihood) significantly different from zero, but it may be far from 1.
 - However, we can use weights to assign probabilities to different sets of parameters estimated from trend curves with varying numbers of trend changes.
- Assuming the actual number of trend changes to be known, significant uncertainty still remains due to parameter estimation from only a small number of trend changes.
 - Here, the maximum likelihood estimation provides covariance matrices of (approximate) standard errors for each value of k trend changes.

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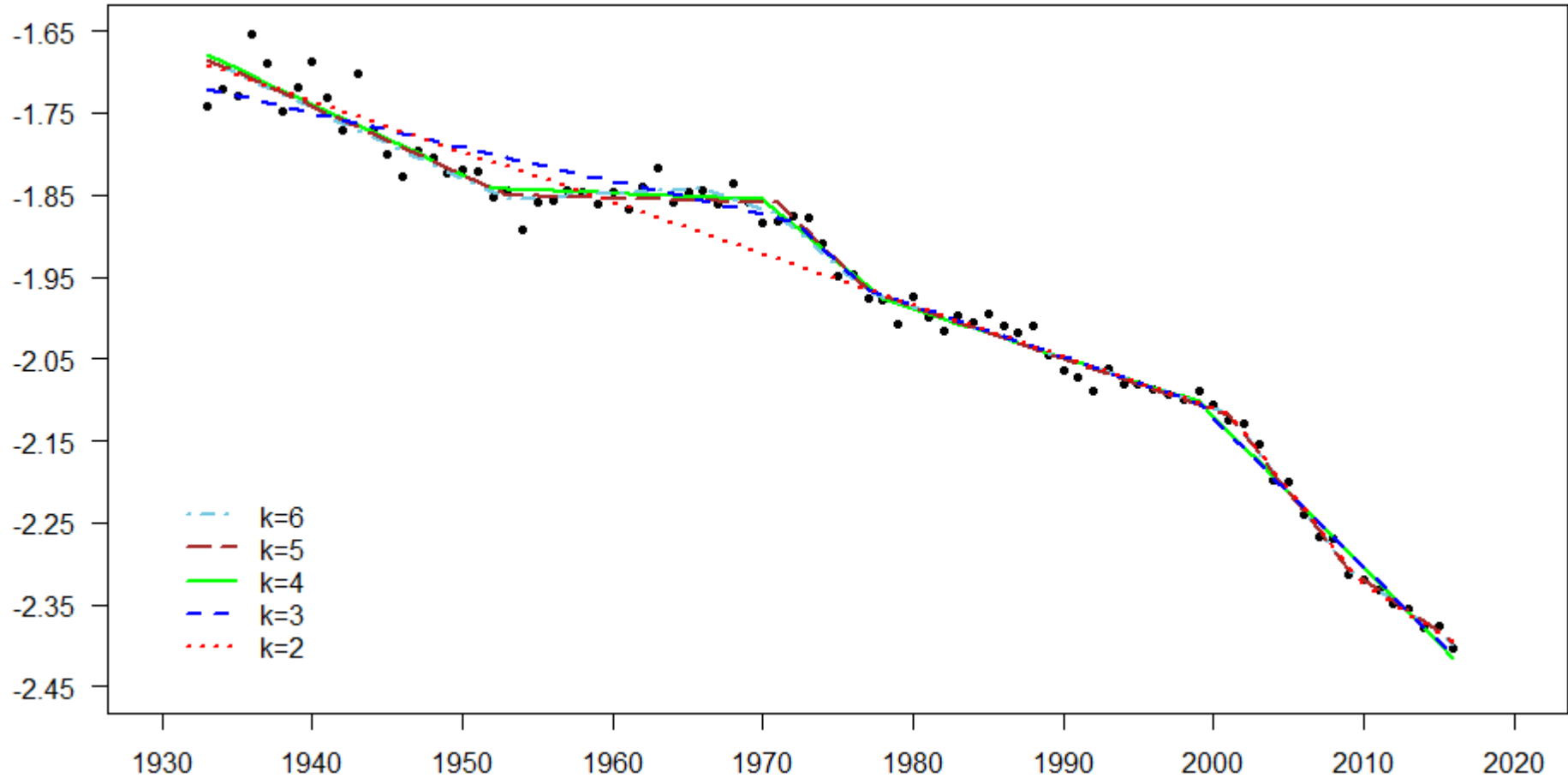
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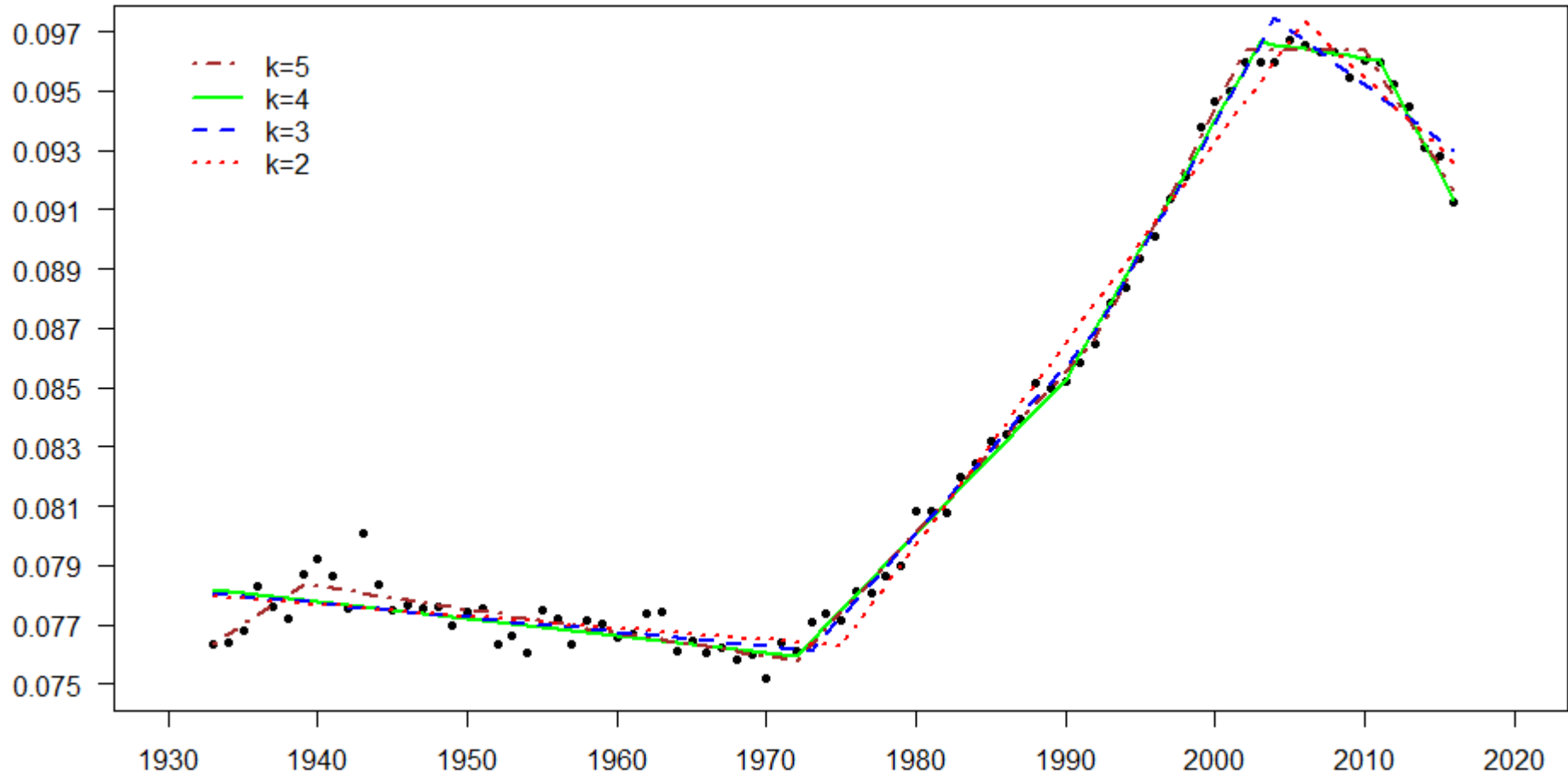
Specification of a Trend Model

Parameter estimation for US males $\kappa_t^{(1)}$



Specification of a Trend Model

Parameter estimation for US males $\kappa_t^{(2)}$



Numerical example for individual populations

Overview

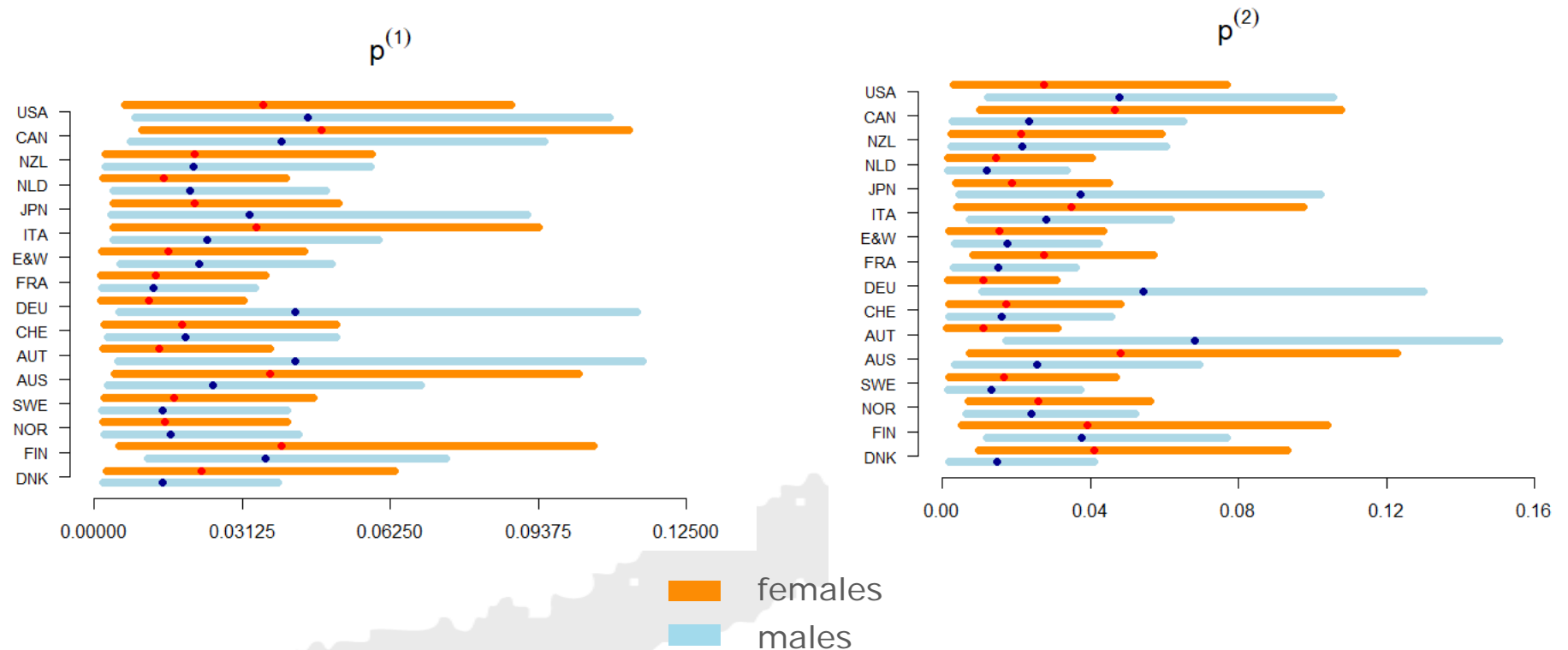
Derivation and comparison of parameter estimates for a large set of populations

- male and female populations in 16 countries
- data obtained from the Human Mortality Database (HMD)
- age range 60–109
- focus on trend change parameters
 - uncertainty in starting values is highly case specific and thus not directly comparable between populations
 - uncertainty in covariance matrix of noise vector appears negligible in general

Numerical example for individual populations

Uncertainty in trend change parameters

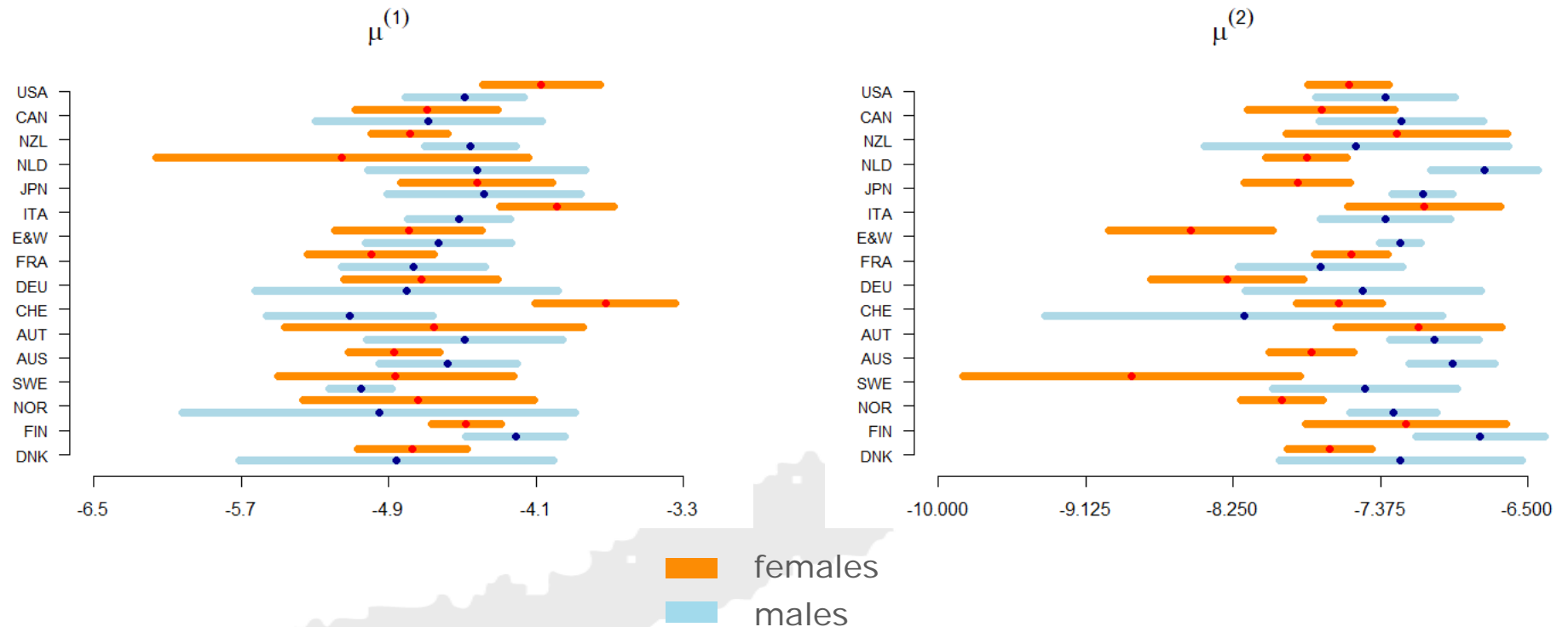
Central parameter estimates and 95% confidence intervals for the trend change probability



Numerical example for individual populations

Uncertainty in trend change parameters

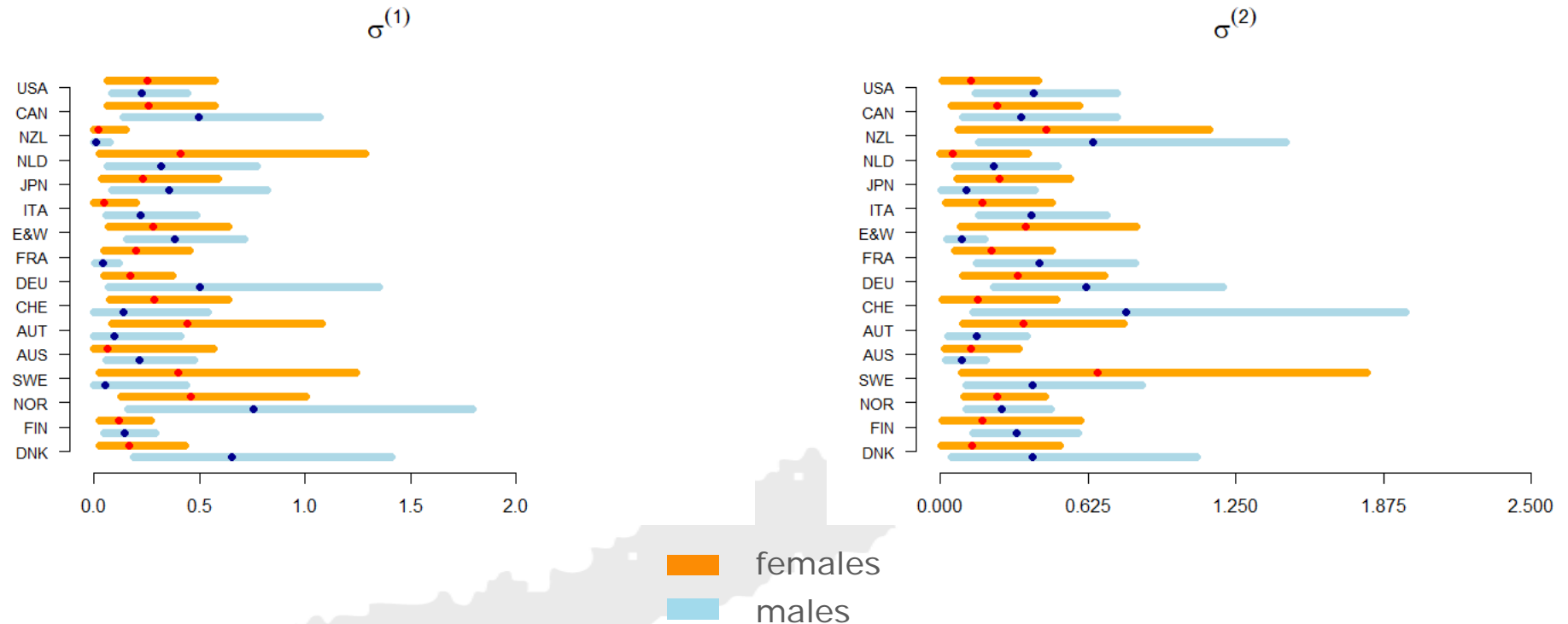
Central parameter estimates and 95% confidence intervals for the trend change magnitudes



Numerical example for individual populations

Uncertainty in trend change parameters

Central parameter estimates and 95% confidence intervals for the trend change magnitudes



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Parameter uncertainty in a multi-population setting

Overview

Combination of parameters from different populations

- trend change parameters
 - Given the similarities between parameter estimates for many populations and given the substantial parameter uncertainties, it seems reasonable to “combine” parameter calibrations from different populations.
 - different assumptions on “similarity” of parameters for different populations:
 - equal parameter values for all populations under consideration
 - population specific realizations of parameter values from one underlying distribution
 - similar parameters without any distributional assumptions
 - next slides contain details on five approaches for “common” parameter estimation

Parameter uncertainty in a multi-population setting

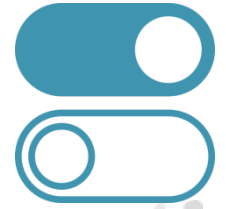
Notation

Necessary notation for explanations on the next slides

- We combine data from several populations to obtain calibrations for the trend change parameters $\theta^{(i)} = (p^{(i)}, \mu^{(i)}, \sigma^{(i)})$.
- We analyze a set P of 32 populations (see example above), and the index \cdot_p denotes specific parameter estimates etc. for population $p \in P$.
- Let N_p denote the number of data points for population p .
- Let $p^* \in P$ be the population whose future mortality evolution is to be projected in a practical application. We will consider US males to illustrate the different approaches in a numerical example below.
- Let v_p denote a weight for each population to account for population specific credibility, e.g. due to data reliability issues or longer/shorter data histories.
 - We will use $v_p = N_p / \sum_{q \in P} N_q$ in the numerical example.

Parameter uncertainty in a multi-population setting

Five approaches



1st approach: maximum likelihood

- assumption: **equal parameters** for all populations
- MLE of trend change parameters from the set of all observed trend changes.

2nd approach: weighted average

- assumption: **same but unknown distribution**.
- The common parameter estimates are

$$\theta^{(i)} = \sum_{p \in P} v_p \cdot \theta_p^{(i)}.$$

4th approach: credibility approach

- assumption: **similar parameter values** for different populations
- larger influence of population specific estimate: $v_{p^*} = 0.5$

3rd approach: parameter sampling

- assumption: parameters $\theta_p^{(i)}$ belong to the **same but unknown distribution**.
- approximation by empirical distribution $F_{\theta^{(i)}}$ derived from the population specific parameters $\theta_p^{(i)}$ and the weights v_p , i.e. $P(\theta_p^{(i)}) = v_p$ for $p \in P$ and zero otherwise.

5th approach: Bayesian approach

- assumption: **same but unknown distribution**.
- This distribution is approximated by the prior distribution $F_{\theta^{(i)}}$ (see above).
- The realized $\kappa_{p^*}^{(i)}$ processes provide additional information on likely parameter values $\theta_{p^*}^{(i)}$.

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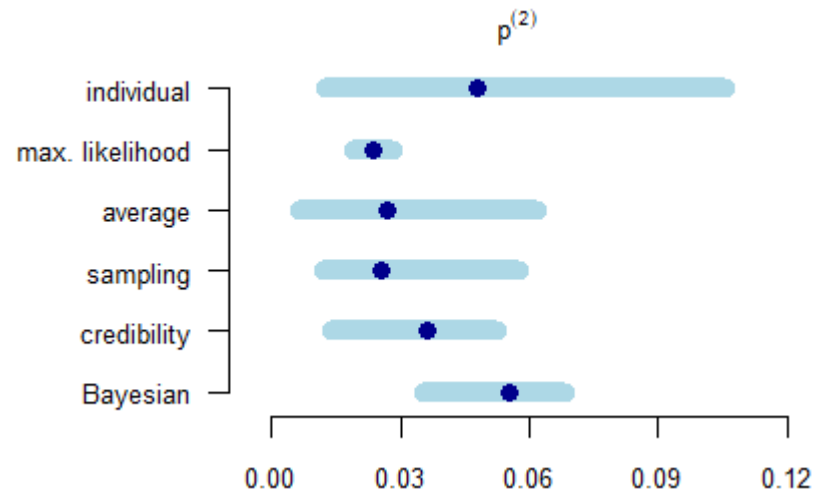
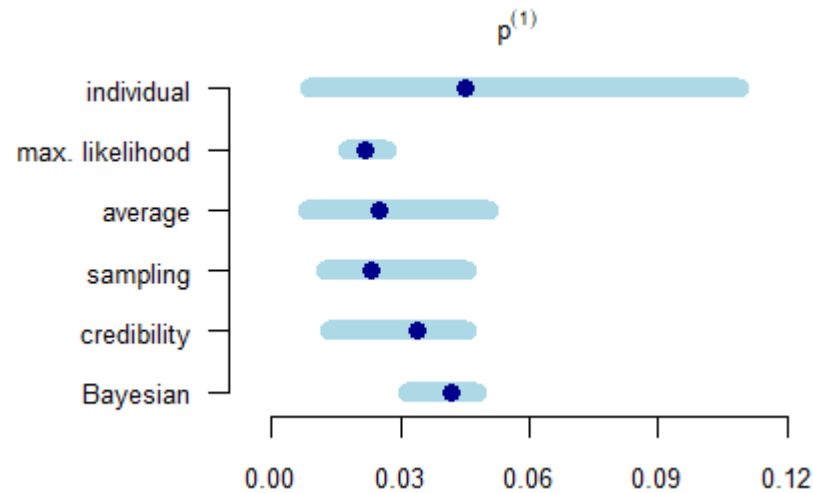
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Trend change probabilities

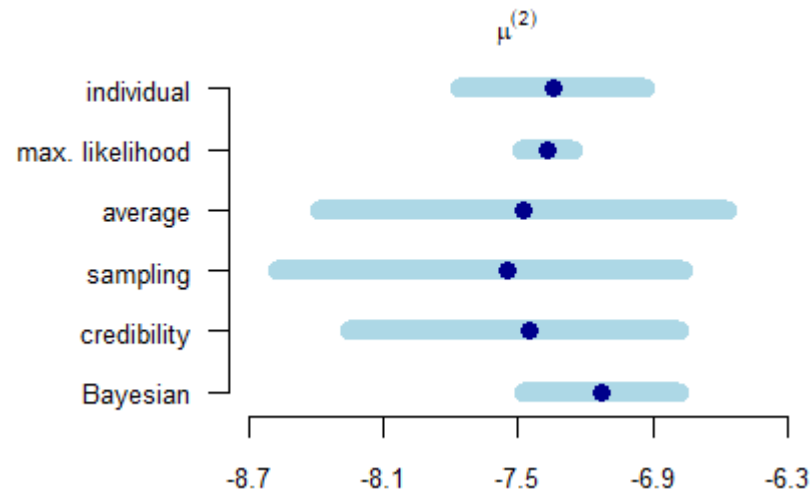
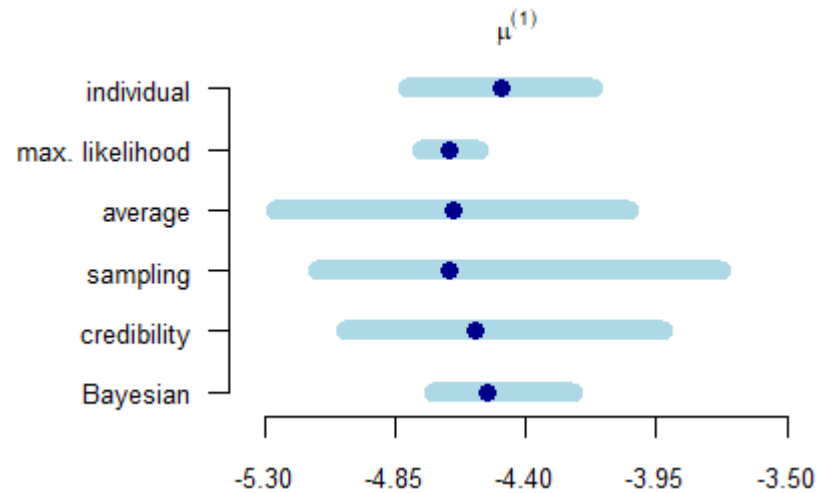


Trend change probabilities

- Central parameter estimates mostly decrease in multi-population approaches.
- compensation for comparably large number of trend changes for US males
- uncertainty in the maximum likelihood approach considerably smaller than in all other approaches, in particular the individual case.
- impact of data aggregation very obvious
- as expected, similar results for average and sampling approach
- credibility and Bayesian approaches somewhere in between the individual calibration and the averaging/sampling.
- interpretation as sampling with overweighting of individual (and in Bayesian case also similar) parameter estimates

Numerical example for multi-population calibrations

Trend change magnitudes

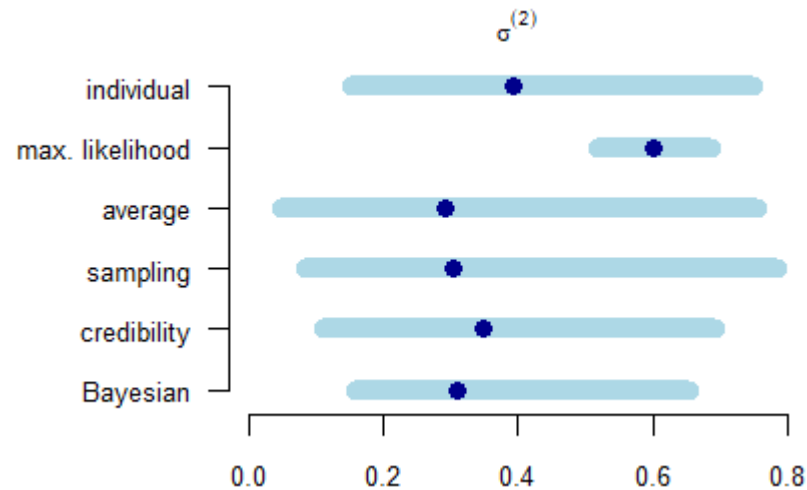
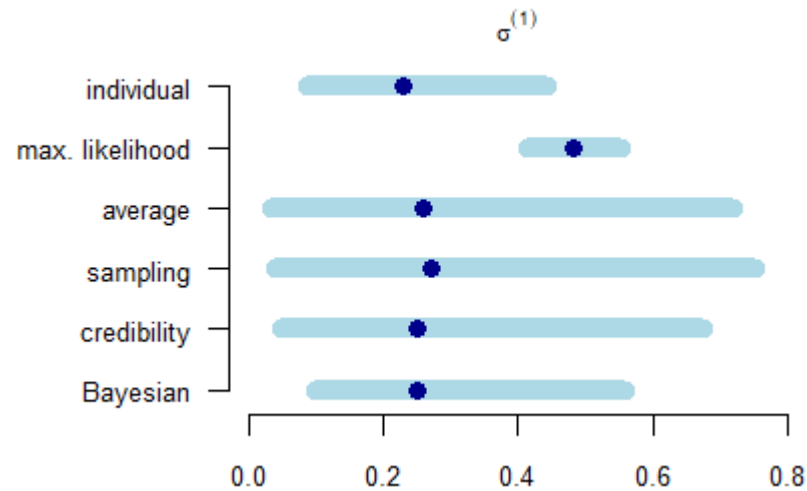


Means of trend change magnitudes

- Again, uncertainty in the maximum likelihood approach is considerably smaller than in the other cases.
- again, similar results for average and sampling approach
- Uncertainty remains or even increases compared to the individual calibration.
- This is primarily systematic uncertainty arising from the assumption of a distribution for population specific parameter values, as opposed to unsystematic uncertainty from the parameter estimation.

Numerical example for multi-population calibrations

Trend change magnitudes



Standard deviations of trend change magnitudes

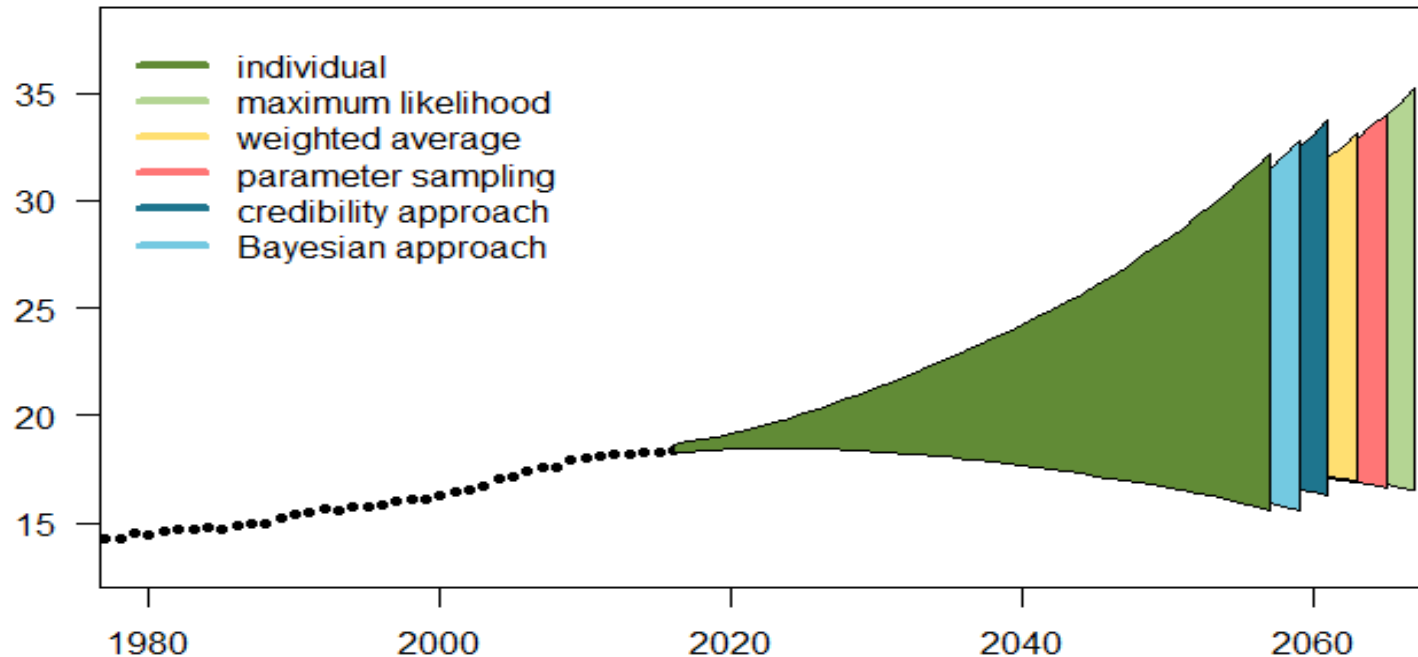
- Central estimates in maximum likelihood approach increase as variability increases due to data aggregation
- uncertainty is again considerably smaller than in the individual case.
- Uncertainty for the other approaches remains or even increases again compared to the individual calibration due to systematic uncertainty.

Numerical example for multi-population calibrations

Trend change parameters

Comparison based on remaining period life expectancies for 65-year old US males

- In each case, we use the same approach for the starting values and the covariance matrix of the errors.



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- Somehow similar trend changes in mortality for many populations worldwide
- Uncertainty in trend change parameters can be better understood when data from several countries is combined.
- Data aggregation reduces parameter uncertainty substantially in the example of US males, even though the reduction clearly depends on the aggregation approach.
- For other populations with comparably small individual parameter estimates and thus possibly underestimated uncertainty, the opposite may be observed.

Literature

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