



A reliability challenge for the Human Mortality Database

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A look at the Human Mortality Database

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Correcting population exposures with fertility data

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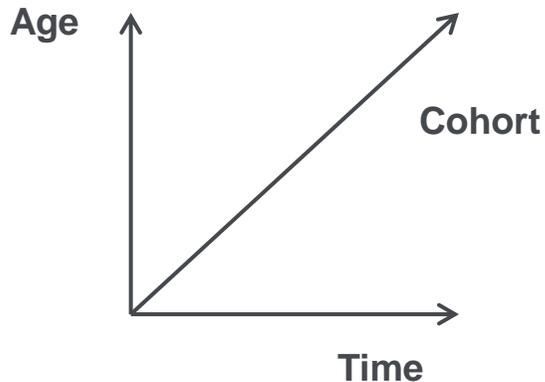
Conclusion and next steps

Context

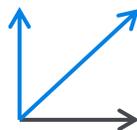
National mortality tables

- How to estimate the **mortality rate** based on national population data?
 - The statistical inference of a death rate with two crossing dimensions (age and time) is an **old (Lexis, 1875) and still challenging estimation problem**
- In practice, individuals are grouped into **age and time blocks**, and the death rate is assumed to be constant on each block
 - This leads to the so-called **Lexis diagram**

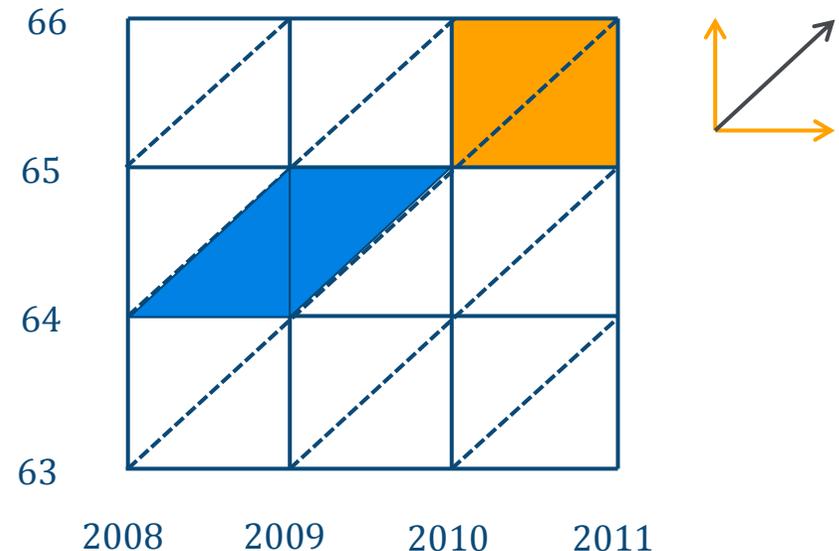
Three directions of analysis



Cohort tables
=
Death rate assumed constant over parallelograms



Period tables
=
Death rate assumed constant over squares



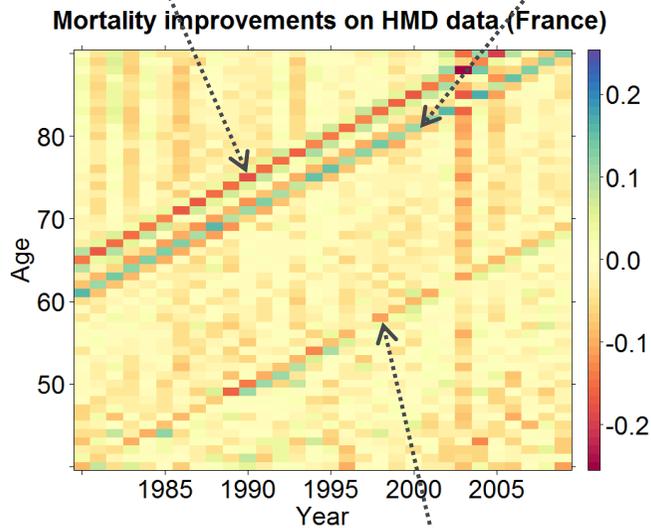
Context

Mortality improvement rates and “cohort effects” (ex: France)

- **Period tables** are useful to study the dynamics of mortality over time
 - Period mortality rate for age x and year t denoted $\mu(x, t)$
 - Improvement rates $r(x, t) = \frac{\mu(x, t+1) - \mu(x, t)}{\mu(x, t)}$ are used to observe particular patterns
 - Clear « **cohort effects** » can be observed for specific generations (born around 1915, 1920 and 1940)

Generation ~ 1915

Generation ~ 1920



Generation ~ 1940



Literature on mortality data reliability

Step 1: Richards (2008) conjectured that the 1919 cohort effect for England and Wales is an **anomaly** in the mortality table due to **erratic birth patterns**

Step 2: Cairns, Blake, Dowd & Kessler (2016) analyzed the ONS methodology and confirmed the conjecture by Richards; they used England and Wales **monthly fertility data** to detect anomalies in the computation of death rates

This talk is based on Boumezoued (2016) and focuses on the **Human Mortality Database**, showing that **these anomalies are universal** and that the **Human Fertility Database** can be processed to correct such errors

Context

A reference: the Human Mortality Database*

- Since its launch in 2002, the Human Mortality Database has become the **reference provider** of mortality estimates (both period and cohort tables) given in an homogenous format for several countries

HMD Main Menu

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The Human Mortality Database

Vladimir Shkolnikov, *Director* Max Planck Institute for Demographic Research

Magali Barbieri, *Associate Director* University of California, Berkeley and INED, Paris

John Wilmoth, *Founding Director* United Nations and formerly University of California, Berkeley

The Human Mortality Database (HMD) was created to provide detailed mortality and population data to researchers, students, journalists, policy analysts, and others interested in the history of human longevity. The project began as an outgrowth of earlier projects in the [Department of Demography at the University of California, Berkeley, USA](#), and at the [Max Planck Institute for Demographic Research in Rostock, Germany](#) (see [history](#)). It is the work of two teams of researchers in the USA and Germany (see [research teams](#)), with the help of financial backers and scientific collaborators from around the world (see [acknowledgements](#)). The French Institute for Demographic Studies ([INED](#)) has also supported the further development of the database in recent years.

We seek to provide open, international access to these data. At present the database contains detailed population and mortality data for the following 38 countries or areas:

Australia	Finland	Latvia	Slovenia
Austria	France	Lithuania	Spain
Belarus	Germany	Luxembourg	Sweden
Belgium	Greece	Netherlands	Switzerland
Bulgaria	Hungary	New Zealand	Taiwan
Canada	Iceland	Norway	U.K.
Chile	Ireland	Poland	U.S.A.
Czech Republic	Israel	Portugal	Ukraine
Denmark	Italy	Russia	
Estonia	Japan	Slovakia	

For more information, please begin by reading an [overview](#) of the database. If you have comments or questions, or trouble gaining access to the data, please write to us (hmd@mortality.org).

- Possible anomalies in **period mortality tables** are already suggested in the HMD technical note (*Wilmoth et al. 2007*):

“ The assumption [of uniform distribution of births] is violated most severely in situations where there are rapid changes in the size of successive cohorts, owing to **fluctuations in the birth series many years before**. The worst situation is when a sharp discontinuity in births occurs in the middle of one calendar year, creating a cohort that is “heavy” at one end and “light” at the other. **We have not attempted to correct our mortality estimates for the error introduced by such occurrences, which may result in artificially elevated or depressed levels of mortality along a diagonal of the Lexis diagram that follows the cohort(s) in question. The user should be aware of this possibility and not misinterpret the data.**”

*Human Mortality Database. University of California, Berkeley (USA), and Max Planck Institute for Demographic Research (Germany). Available at www.mortality.org or www.humanmortality.de (data downloaded on October 2015).

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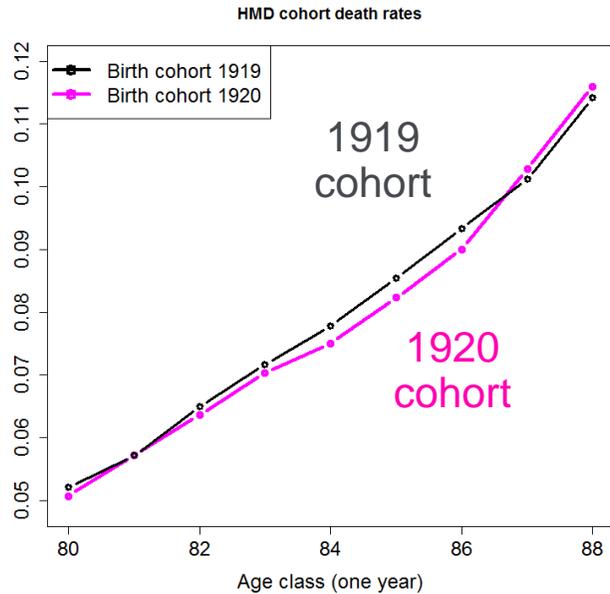
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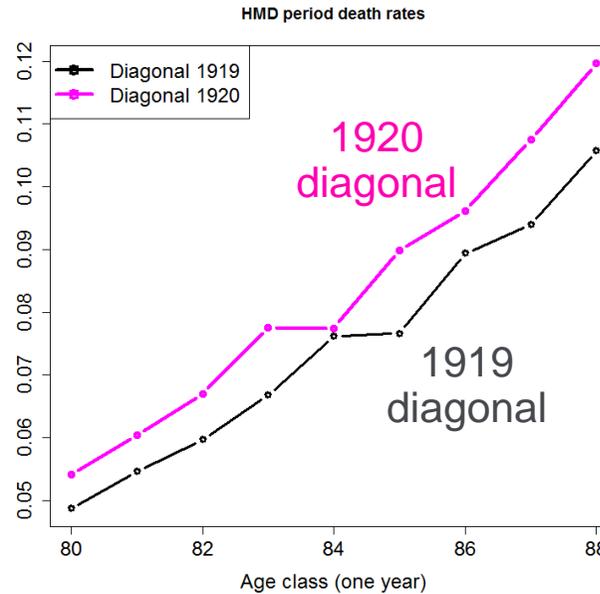
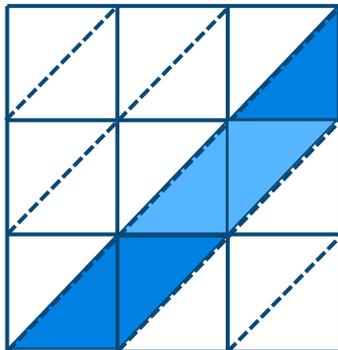
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A look at the Human Mortality Database

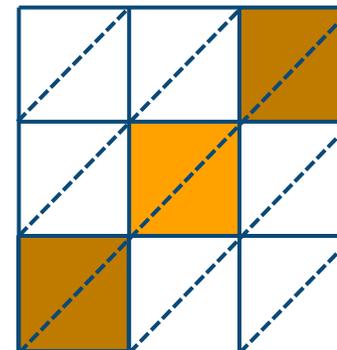
Inversion of cohort and period tables: example for France (1/2)



Cohort table

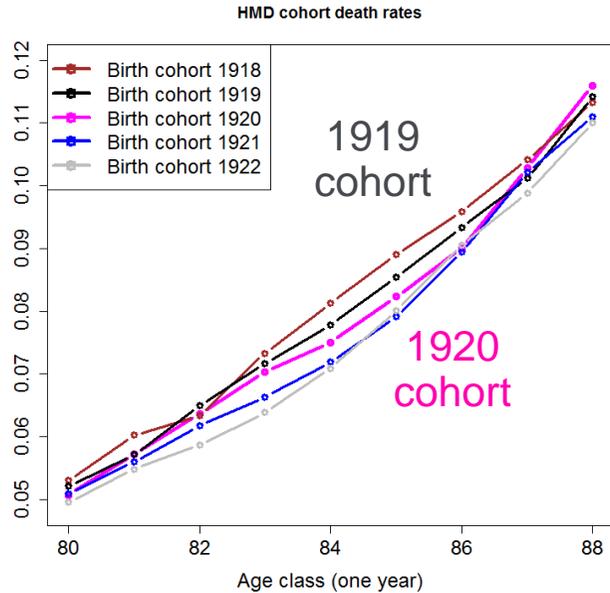


Period table

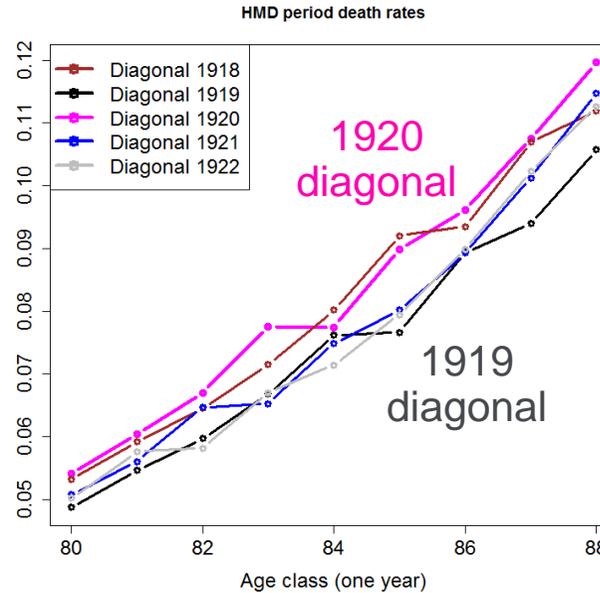
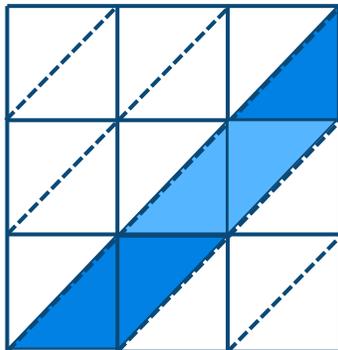


A look at the Human Mortality Database

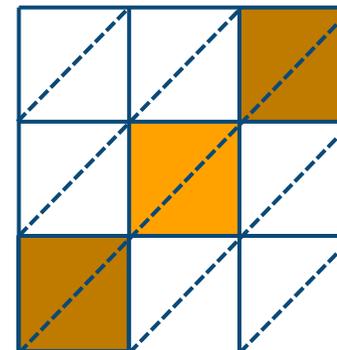
Inversion of cohort and period tables: example for France (2/2)



Cohort table



Period table



A look at the Human Mortality Database

How to properly estimate the period death rate?

- Quantity of individuals with **exact age a at exact time s** : $g(a, s)$
- The **death rate $\mu(a, s)$** drives the evolution of each cohort over time
 - Let $g(0, s)$ be given (the number of newborns at time s)
 - The number of survivors at age a in the cohort born at time s is given as:

$$g(a, s + a) = g(0, s) \exp \left\{ - \int_0^a \mu(u, s + u) du \right\}$$

- Differentiation by age and time leads to the **aging term** of the McKendrick-Von Foerster equation (1926)

$$(\partial_a + \partial_s)g(a, s) = -\mu(a, s)g(a, s)$$

= $d(a, s)$ = Number of deaths at (exact) age a and time s

- Statistical estimation:** the period death rate is assumed to be constant on squares
 - That is $\mu(a, s) = \mu(x, t)$ for each $a \in [x, x + 1)$ and $s \in [t, t + 1)$
 - Under this assumption, one recovers the classical formula of the estimated death rate, as the number of deaths divided by the so-called exposure-to-risk**

$$D(x, t) = \int_t^{t+1} \int_x^{x+1} d(a, s) da ds = \mu(x, t) \int_t^{t+1} \int_x^{x+1} g(a, s) da ds$$

$$= \mu(x, t) \int_t^{t+1} \underbrace{P(x, s)}_{\text{Population at time } s \text{ aged } x \text{ last birthday}} ds$$

Exposure-to-risk = total time lived in year t by individuals aged x last birthday

A look at the Human Mortality Database

How is the exposure-to-risk estimated in the HMD?

Number of deaths \rightarrow Exposure-to-risk

Death rate estimation : $\hat{\mu}(x, t) = D(x, t) / E(x, t)$

COHORT TABLE

PERIOD TABLE

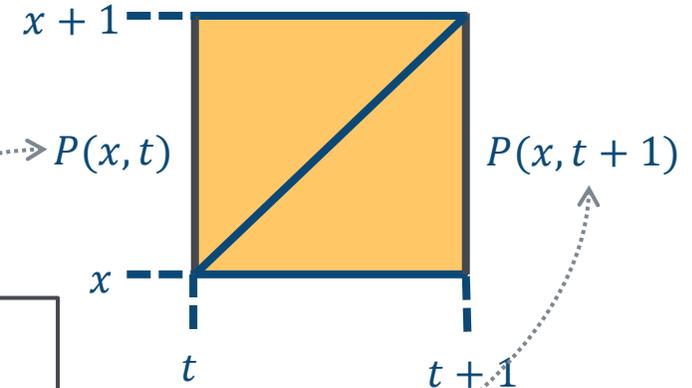
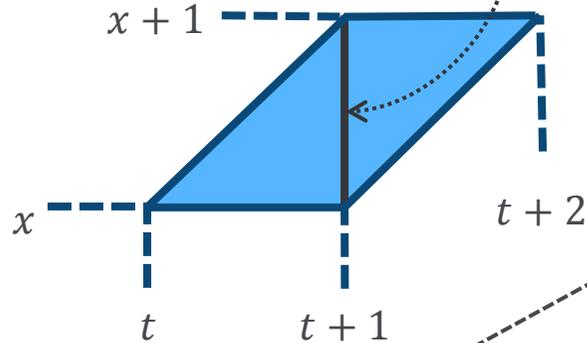
HMD Cohort Exposure-to-risk

=

Population estimate at a given time

+

Small correction based on number of deaths in each triangle



HMD Period Exposure-to-risk



Approximation under the assumption of uniform distribution of births on consecutive years

$$\frac{1}{2} [P(x, t) + P(x, t + 1)]$$

Small correction based on number of deaths in each triangle

\gg

$$\int_t^{t+1} P(x, s) ds$$

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Correcting population exposures with fertility data

Processing the HFD to correct the HMD (1/3)

- **Aim:** use **monthly fertility records** from the Human Fertility Database* (HFD) to refine exposure-to-risk computation
- A **quality indicator** for each cohort is constructed in three steps:
 1. **Extract monthly fertility estimates** $P(0, s)$ from the HFD: this is the number of individuals born in month s
 2. **Refine (annual) exposure-to-risk computation** by using monthly estimates instead of annual:
$$E(0, t) = \int_t^{t+1} P(0, s) ds \approx \sum_{i=0}^{12} w_i P\left(0, t + \frac{i}{12}\right)$$
 3. **Compare it to the annual approximation** as performed in the HMD:

An indicator $I(t)$ far from 1 shows that period mortality rates for the cohort born in year t is **not reliable**



$$I(t) = \frac{E(0, t)}{\frac{1}{2} [P(0, t) + P(0, t + 1)]}$$

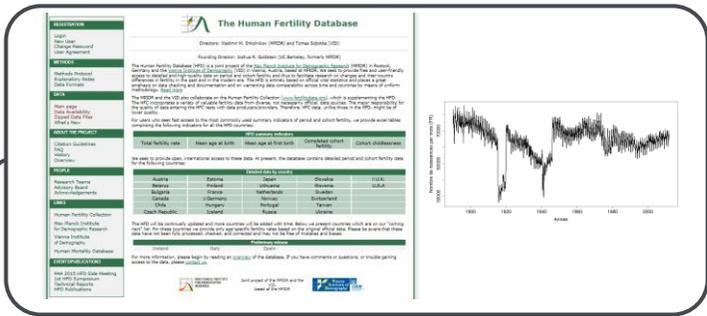
The methodology focuses on age zero, then adjusts the mortality table along the diagonal (cohort) – see the analogy in Cairns, Blake, Dowd & Kessler (2016) for the detection of anomalies

*Human Fertility Database. Max Planck Institute for Demographic Research (Germany) and Vienna Institute of Demography (Austria). Available at www.humanfertility.org (data downloaded on October 2015).

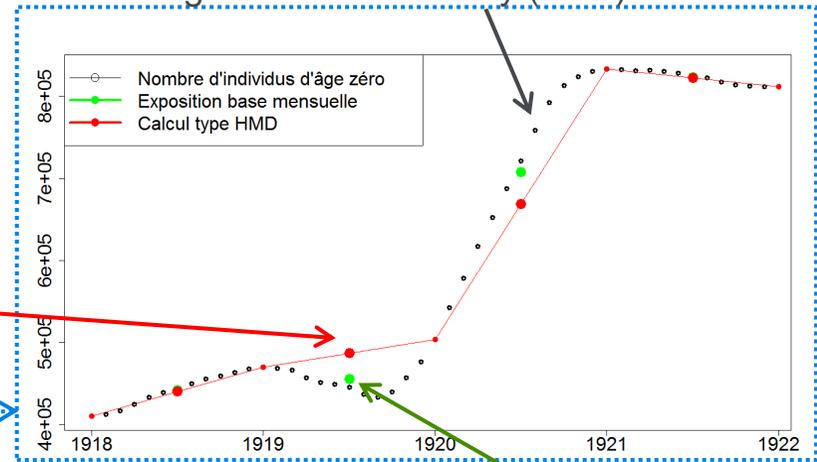
Correcting population exposures with fertility data

Processing the HFD to correct the HMD (2/3) Monthly population size with age zero last birthday (HFD)

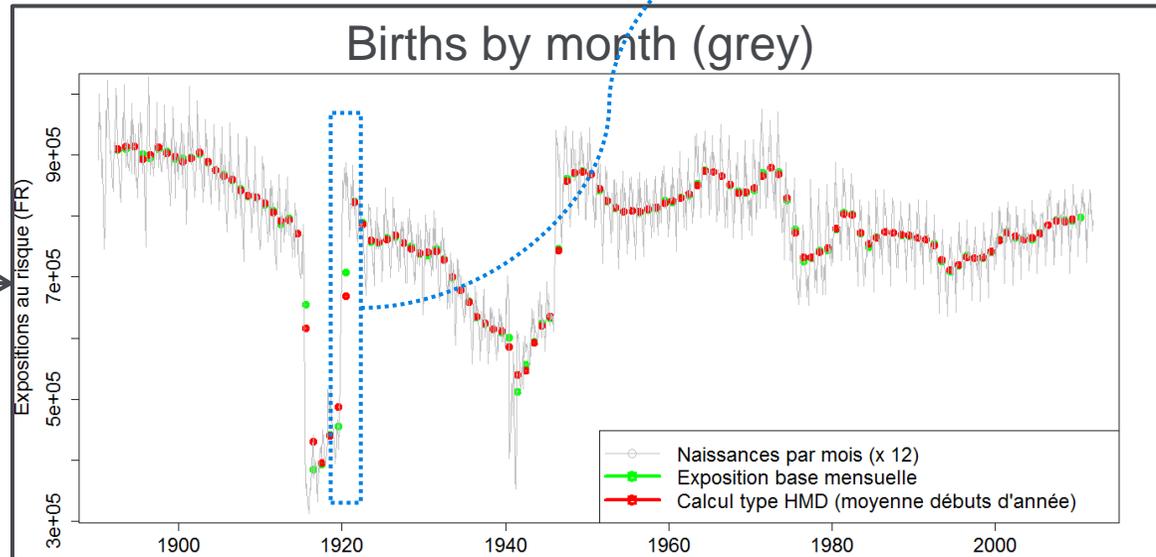
Extract monthly fertility records from the Human Fertility Database



HMD-type exposure-to-risk = linear interpolation



Refined exposure-to-risk (based on HFD)



Explanation: shocks in birth patterns create **convexity** in population numbers => HMD linear approximation is no longer valid

Correcting population exposures with fertility data

Processing the HFD to correct the HMD (3/3)

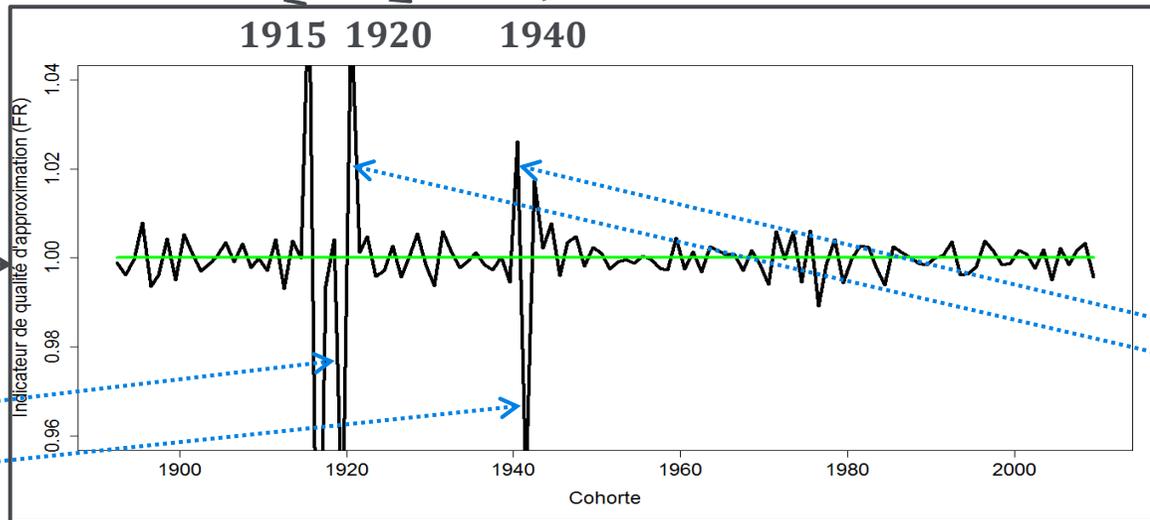
Extract monthly fertility records from the **Human Fertility Database**

Correction of period mortality tables in the **Human Mortality Database**

The Human Fertility Database website interface. It includes a navigation menu on the left with options like 'Home', 'About the Database', 'Data Access', and 'Contact Us'. The main content area features a line graph showing fertility rates over time, with a box highlighting 'Cohorts with major anomalies (born around)'. The graph shows a significant dip in fertility rates around 1915 and 1940.

The Human Mortality Database website interface. It features a 3D surface plot showing death rates over time and across different age groups. Below the plot is a table listing countries and their corresponding data sources. The table includes columns for Country, Source, and Date. Countries listed include Austria, Belgium, Canada, Czech Republic, Denmark, Estonia, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Japan, Lithuania, Luxembourg, Netherlands, New Zealand, Norway, Poland, Portugal, Slovakia, Slovenia, Spain, Sweden, Switzerland, Taiwan, U.K., and Ukraine.

Cohorts with major anomalies (born around)



Quality indicator for each year of birth

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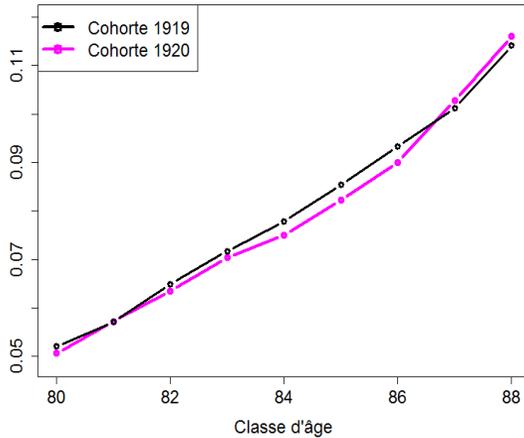
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What can be learned from corrected tables?

Corrected period mortality tables – focus on 1919-1920 cohorts

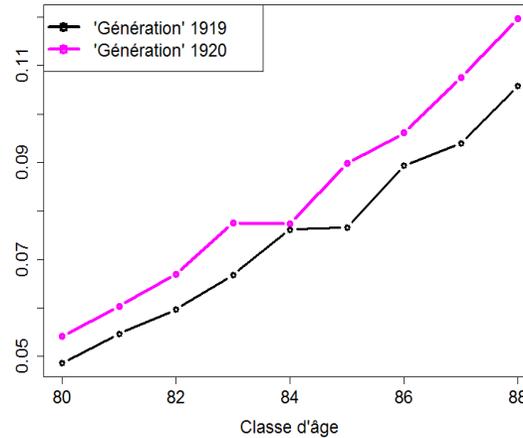
HMD cohort table

Taux de mortalité bruts France (vision cohorte)



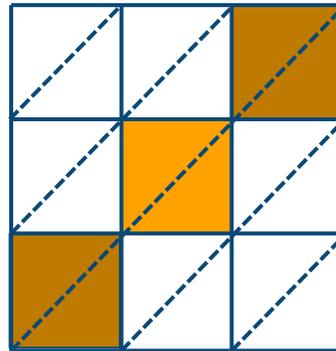
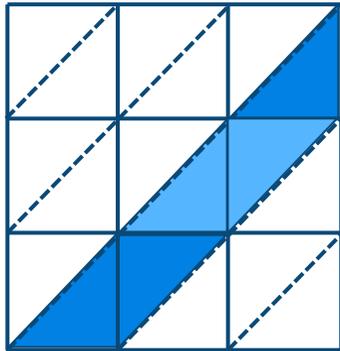
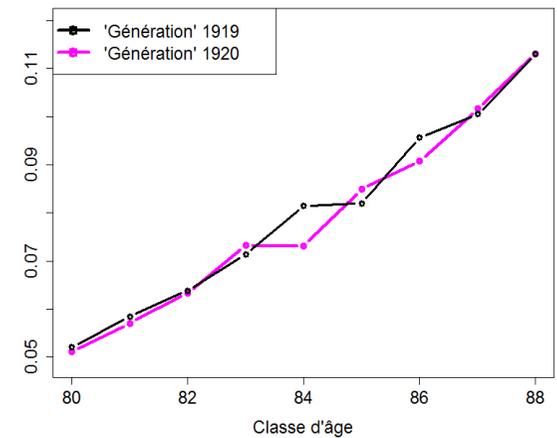
HMD period table

Taux de mortalité bruts France (vision période)

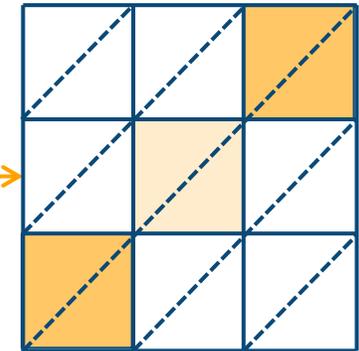


Corrected period table

Taux de mortalité ajustés France (vision période)



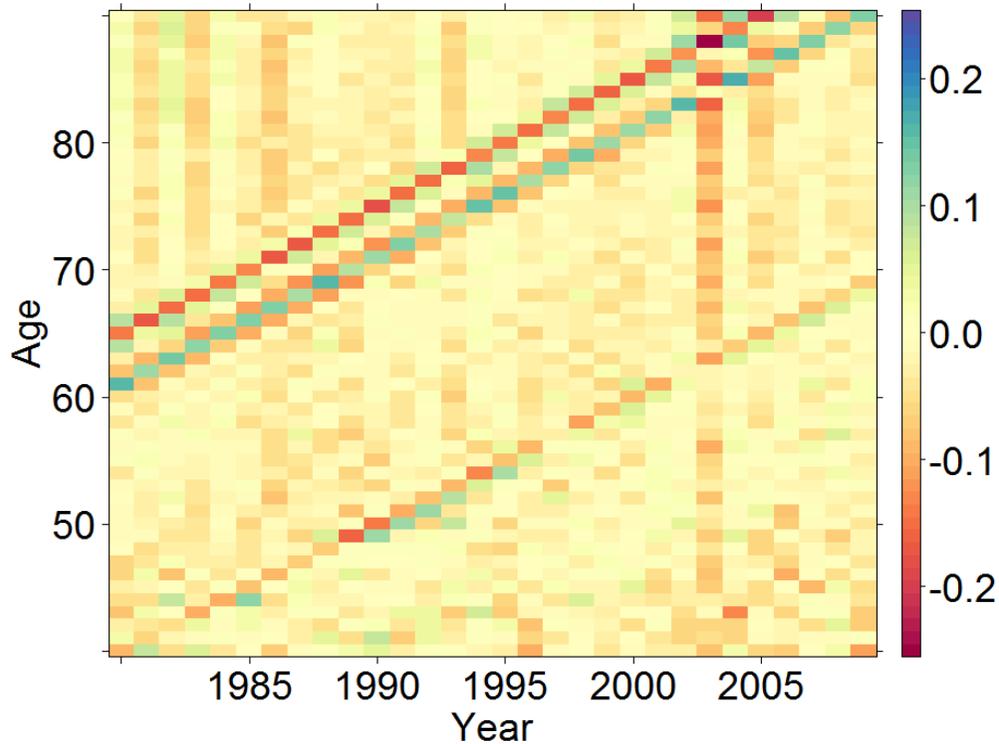
Correction based on the quality indicator $I(t)$



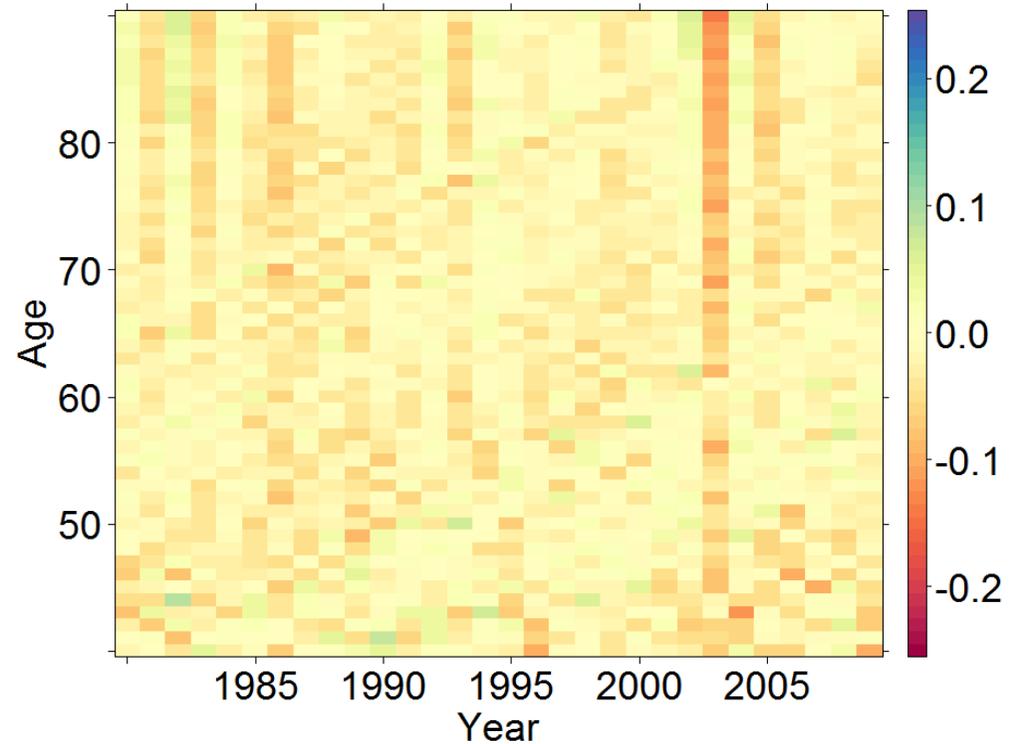
What can be learned from corrected tables?

Isolated cohort effects as data anomalies

Mortality improvements on HMD data (France)



Mortality improvements on corrected data (France)



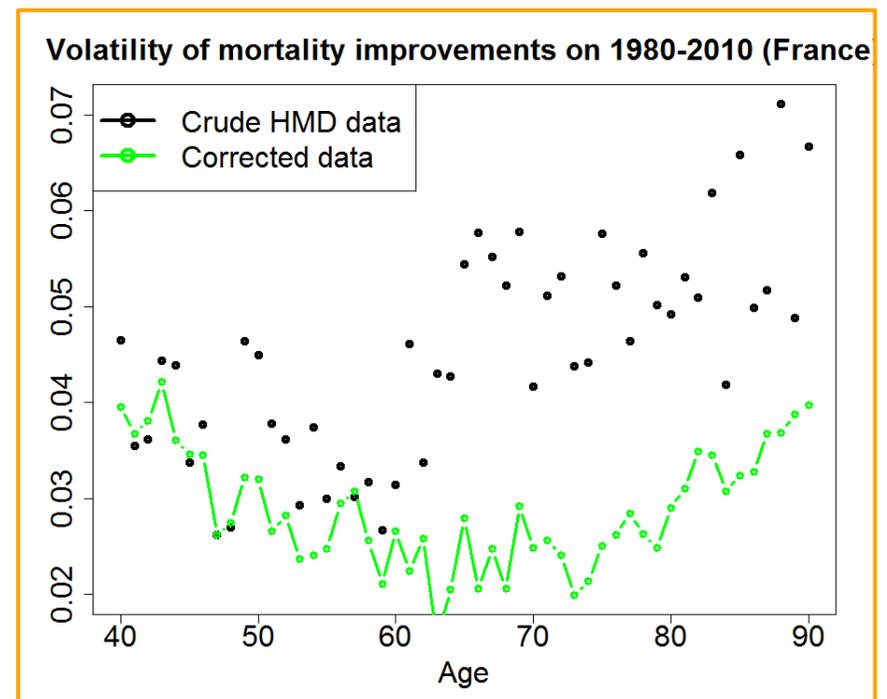
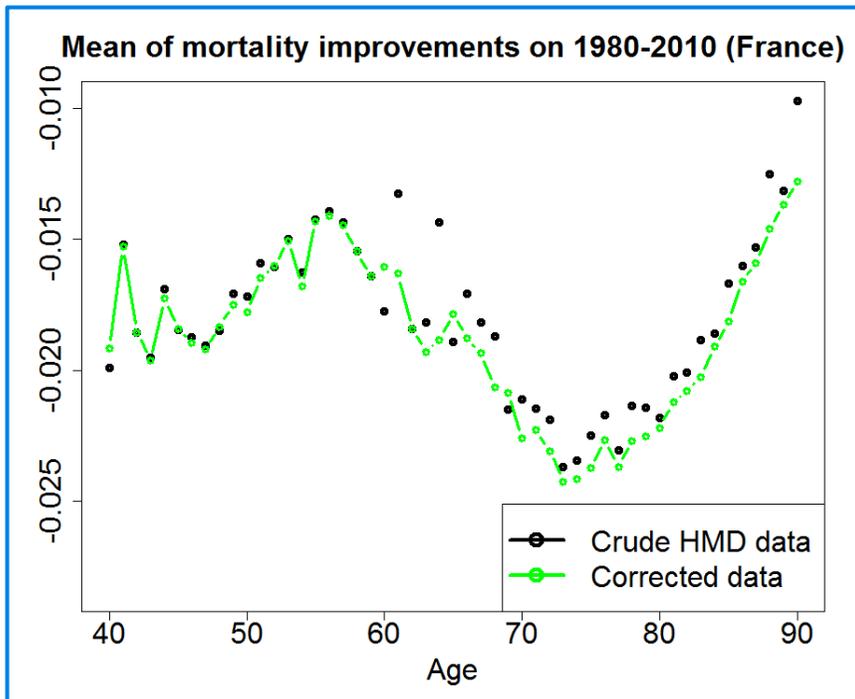
$$r(x, t) = \frac{\mu(x, t+1) - \mu(x, t)}{\mu(x, t)}$$

What can be learned from corrected tables?

Improvement rates properties after data correction

Average mortality improvements by age are **smoothed** after data correction

Volatility of mortality improvement is **reduced** at high ages after correction



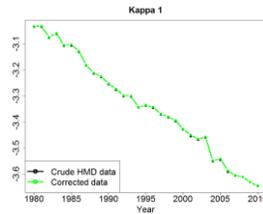
What can be learned from corrected tables?

Choice and fitting of classical mortality models*

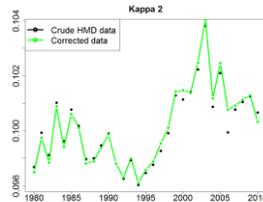
Conclusion 1

The estimated parameters are close

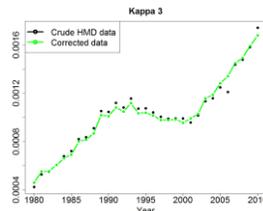
$\kappa_1(t)$



$\kappa_2(t)$



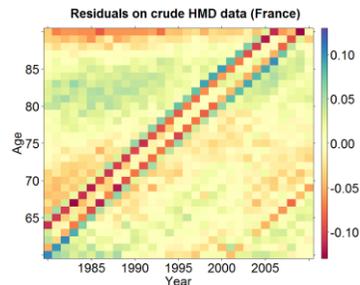
$\kappa_3(t)$



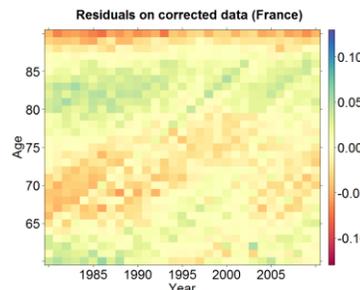
Conclusion 2

The residuals do not embed clear cohort trends anymore

– Residuals on crude data:



– Residuals on corrected data:

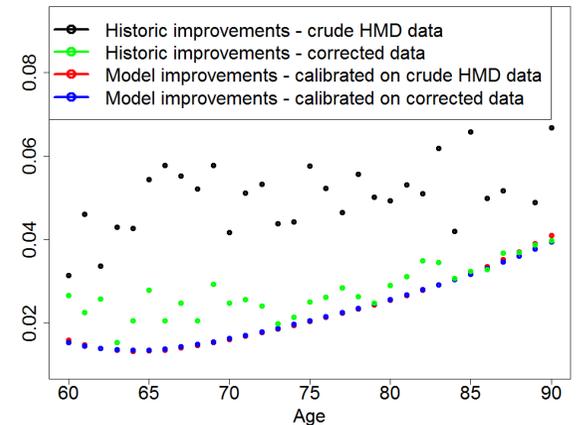


Conclusion 3

The **historical volatility is better reproduced**

– The historical mortality volatility is **better reproduced** by the classical model:

Volatility of mortality improvements



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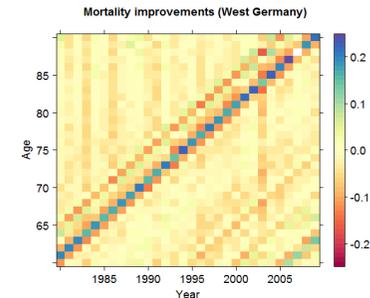
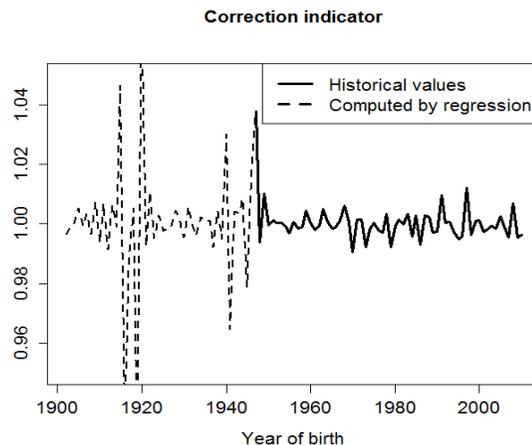
Conclusion and next steps

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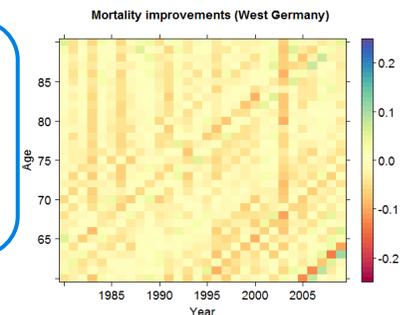
Extending the scope of countries

- The present methodology allows to correct a given cohort if the associated date of birth is included in the monthly fertility history from the **Human Fertility Database**
 - A **reasonable scope of countries** for which the 1919-1920 anomaly can be corrected includes: Austria, Finland, France, Italy, Sweden, Switzerland,...
- **Issue:** for many countries, the fertility historical depth is **not sufficient** to correct crucial anomalies as those for generations 1919-1920
- **Idea:** develop a method to **reconstruct the quality indicator** for those countries
 - Illustration below: first insights for the example of Germany

Step 1: Key countries are used to reconstruct the adjustment ratio history



Step 2: The original method then allows to correct the abnormal 1919-1920 effect



References

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Thank you

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