A measure for comparing the mortality history of cohorts in Latin-American countries: TCAL

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Abstract

The commonly used period life expectancy comparisons between populations correspond to juxtapositions of current mortality levels. In order to construct actual life expectancies as experienced by cohorts one needs complete historical series of mortality, which are only found in a subset of developed countries. The Truncated Cross-sectional Average Length of life (*TCAL*) is a novel measure that captures historical information of all the cohorts present at a given moment and is not limited to countries with complete cohort mortality data. The value of *TCAL* depends on the rates used to complete the cohort series. However, differences between *TCAL*s of two populations remain very similar irrespective of the data used to complete the cohort series. We illustrate this by comparing the mortality of Chile and Costa Rica with an aggregate of high-longevity countries using *TCAL*. Specific cohorts that account for most of the disparity in mortality between the populations are identified.

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Introduction

Life expectancy in developed and several middle-income countries has been increasing steadily during the past century (Oeppen and Vaupel 2002; White 2002; Canudas-Romo 2010), simultaneously a widening gap between longevity in high- and middle-income countries has evolved (Ho and Preston 2010; Murray and Frenk 2010; Glei et al. 2011; National Research Council 2011; Canudas-Romo and Engelman 2012). Life expectancy rankings are exclusively based on the current mortality profile of populations through period life tables. Historical information indicates that an increasing gap exists between period life expectancy and actual life expectancy experienced by cohorts (Goldstein and Wachter 2006). As such, mortality rankings based uniquely on period information display a limited one-dimensional image of the health of populations, namely current mortality levels. Furthermore, more subtle aspects of how cohorts in a population progressed to these current mortality levels are omitted in such rankings.

The use of period life tables, and in particular life expectancy, as a measure describing population health, dates back to Dublin and Lotka in the 1920s and 1930s (Robine 2006). Yet, it remains a core production of statistical offices today. New technology and data availability have facilitated the use of historical data for constructing long series of cohort mortality. In this project, we study the mortality experience of each cohort present at a given time in a population. Using the available information of all cohorts and a summarizing measure, analogous to life expectancy, we assess and compare the cohort mortality levels between populations.

The focus of the present analysis is on the way cohorts survive over time, how cohort survival compares across countries, and how cohort survival contributes to the overall survival level of a population. These objectives are different from cohort analysis, also known as age-period-cohort (APC) models which aim at separating and distinguishing between the age, period

and cohort effects that are constraint by their linear dependency, Age = Period – Cohort (Fu et al. 2011). Our goal is to compare mortality between populations, similar to the period life expectancy ranking, but based on the available information of cohort survival.

A birth cohort is defined as persons who are born during the same time period and are destined to pass through life together, i.e. reach specific ages at the same time (Preston et al. 2001). From now on we refer to birth cohorts simply as cohorts. The study of specific cohorts' survival has a long tradition and examples of these vary from good to bad outcomes (Willets 2004; Richards et al. 2006). The cohort in utero during the Spanish flu in 1918 displayed reduced educational attainment, higher physical disability, lower income and socioeconomic status, compared with other cohorts (Almond, 2006), although its cohort survival disadvantage is not evident (Cohen et al. 2010). Another example of a further granulation of cohorts is the study of adult mortality depending on the season when persons were born and their early-life conditions (Doblhammer and Vaupel 2001). In the present study our effort is to compare available survival of cohorts across countries.

The best practice life expectancy (Oeppen and Vaupel 2002) – or the world's highest life expectancy in a given year – summarizes the collective experience of mortality reductions in countries. As shown in the study by Shkolnikov et al. (2011), the best practice life expectancy based on cohorts has increased at a faster rate than on periods. This notorious gap between the two best-practice life expectancies is a consequence of persistent mortality decline over time captured in different ways by the period and cohort perspectives (Canudas-Romo and Schoen 2005; Goldstein and Wachter 2006). The gap is also likely to persist in the near future (Shkolnikov et al. 2011), which underpins the need to study the survivorship of cohorts. However, in many situations mortality comparisons over cohorts are limited to those populations

that have complete mortality information starting at birth. The aim of our study is to use the mortality information of all cohorts present at a given time, irrespective if they have complete or truncated series of mortality history. We achieve our aim by concentrating on cohort survival comparisons between countries.

There are five sections in this study with this introduction as the first one. Sections on data and methods follow, where we present the cohort measure the Truncated Cross-sectional Average Length of life, or *TCAL* for short. The methodology to calculate this measure and to decompose its difference between populations over cohorts and age-contribution is included in this section. Illustrations of the use of *TCAL* to compare cohort mortality between the United States and Denmark, Japan and other high-longevity countries (HLCs) are presented. This example serves to illustrate the use of *TCAL* for populations that have incomplete mortality history of cohorts; furthermore, it contributes to the current debate of the widening gap in mortality between high-longevity countries (Ho and Preston 2010; Murray and Frenk 2010; Glei et al. 2011; National Research Council 2011; Canudas-Romo and Engelman 2012).

Data

The data source used in this study is the Human Mortality Database (HMD: www.mortality.org). The HMD database compiles census and vital statistics information for entire country populations. The HMD has high quality historical mortality data for industrialized countries; the same methodology to build the mortality series is used for all countries and times, making the HMD a unique comparative tool. This analysis is based on HMD data from 1949 to 2009 for 23 relatively high-longevity countries (HLCs) listed below, and with Costa Rica and Chile highlighted to exemplify cases of Latin-American mortality profiles as opposed to the HLCs

group. In order to compare mortality levels of various high-longevity countries, all included mortality series are truncated in the year 1970 for the comparisons with Costa Rica and 1992 for Chile. This starting year of 1970 is the first year with Costa Rican data available. Thus, we included the year of 1970 as our initial year for all the series. High-longevity countries included in this analysis for the period (1970-2008) are: Austria, Belgium, Czech Republic (starting at 1950), Denmark, Finland, France, Iceland, Italy, the Netherlands, Norway, Portugal, Spain, Sweden, Switzerland, United Kingdom, Canada, Japan, Australia, New Zealand, Luxembourg, and East and West Germany are included from 1970 to 2008. This selection of countries is similar to the group of countries used in recent studies (Ho and Preston 2010; Glei et al. 2011; Canudas-Romo and Engelman 2012), and it is also referred to as high-income countries, and corresponds to countries with high quality of mortality information for an extended period of time.

The life tables of high-longevity countries (HLCs) were constructed using standard methods (Preston et al. 2001) based on age-specific death rates calculated by adding death counts and exposures for all HLCs excluding the US. This is equivalent to having average age-specific death rates weighted by population size and allows comparisons between persons in the HLCs region and the US.

Methods

Countries are compared at three different levels: differences between mortality rates, between survival functions, and between an aggregated measure of cohort survival. A series of age-specific death rates enables the calculation of the life table survival functions. Thus, differences observed between countries at the age-specific death rate level is perceived also at the aggregated

level of survival functions. Now one further aggregation of all the survival functions over age is life expectancy. However, since our interest is in trajectories of mortality for all the cohorts present at a given time, we will instead use the Truncated Cross-sectional Average Length of life defined below.

The Cross-sectional Average Length of Life, CAL.

The Cross-sectional Average Length of life, *CAL*, was introduced by Brouard (1986), further elaborated by Guillot (2003) and used in the debate on tempo effects (Bongaarts and Feeney 2006; Guillot 2006). As mentioned by (Guillot 2003: 42) "*CAL(t)* is an index that accounts for the real mortality conditions experienced by the various birth cohorts whose survivors are present in a population at a particular time *t*". Formally, in order to calculate *CAL(t)* for year *t* the survival functions for all the cohorts present in that year are calculated. These cohorts arrive to year *t* at ages *x*, ranging from zero to the highest age attained by a person in the population $0 \leq x \leq \omega$, as

$$\ell_c(x,t) = \exp\left[-\int_0^x \mu(a, t-x+a)da\right], \qquad (1)$$

where $\mu(a, t-x+a)$ is the force of mortality at age *a* and time *t-x+a* and $\ell_c(x,t)$ is the cohort survival function reaching age *x* at time *t*, or the cohort born in year *t-x*. The aggregate measure including the survival information of all the cohorts present in year *t* from ages zero to the last age attained in the population ω, is calculated as $CAL(t) = \int_0^{\omega} \ell_c(x,t)dx$.

For Latin-American countries, only partial mortality information is available during the first part of the 20th century and thus limiting the use of *CAL* (Guillot 2003; Guillot and Kim 2011). For these countries, *CAL* can be approximated in several ways, for instance by back extrapolating their historical mortality information drawing on available information for some other country or using model life tables. As our interest is to compare across countries, we opt to construct a truncated *CAL*, denoted as *TCAL* and defined in the next section.

The Truncated Cross-Sectional Average Length of Life, TCAL.

Let Y_1 be the earliest year for the mortality information for the population with the shortest mortality series, and let us assume that there is no missing mortality information from that year onwards, e.g. here we use $Y_1 = 1970$. As mentioned before, this is the year when the population of Costa Rica starts its mortality series. Truncated cross-sectional average length of life, *TCAL*, thus depends on both years t and Y_1, and we denoted as $TCAL(t, Y_1)$. The truncated *TCAL* is constructed similarly to *CAL* by aggregating the survival information of all the cohorts present at time *t*. Cohorts born after Y_1 will have complete mortality information and equation (1) will apply to them,

$$\ell^*(x,t) = \exp\left[-\int_0^x \mu(a, t-x+a)da\right], \quad if \ \ t \geq Y_1, \tag{2a}$$

where $\mu(a, t-x+a)$ is, as in eq. (1), the force of mortality at age *a* and time *t-x+a*. However, for cohorts born before year Y_1, without complete cohort mortality data, we use the period mortality experienced in the earliest year Y_1. For our illustrations we use the information of all the high-

longevity countries (HLCs) combined, described in the data section. The survival function at age *x* and year *t* for cohorts born before year Y_1 is calculated as:

$$\ell^*(x,t) = \exp\left[-\int_0^z \mu^*(a,Y_1)da - \int_z^x \mu(a,t-x+a)da \right], \quad \text{if } t < Y_1, \qquad (2b)$$

where *x* is the age achieved by the cohort at time *t*, $z = x-(t-Y_1)$ is the threshold age when the complete cohort mortality information becomes available, $\mu(a,t-x+a)$ is, as in eq. (1), the force of mortality at age *a* and time *t-x+a*, with ages ranging from $z \le a \le x$, and $\mu^*(a,Y_1)$ is the period force of mortality in year Y_1 for age *a*, with $0 \le a < z$. Finally, *TCAL* in year *t* is defined as the aggregation of all the survival functions in equations (2a) and (2b), as $TCAL(t,Y_1) = \int_0^\omega \ell^*(x,t)dx.$

TCAL condenses the entire available mortality history of cohorts present at a given time into one measure. For our application, the set of weighted average death rates for all HLCs combined is assigned to all countries for the year 1970. The selection of death rates for 1970 is an arbitrary selection, and the values of *TCAL* will vary depending on the series of mortality selected for year Y_1. However, our interest is on differences between populations, and our results of comparisons between countries hold as long as there is consistency, and the same death rates in year Y_1 are used for all examined countries.

Cohort-Decomposition of the Difference between Two TCALs

General methods of decomposition are widely known (Vaupel and Canudas-Romo 2002; Horiuchi et al. 2008). Also, specialized methods exist for investigating differences between life expectancies (Arriaga, 1984; Pressat 1985; Pollard 1988; Vaupel and Canudas-Romo 2003; Beltran-Sanchez et al. 2008; Shkolnikov et al 2011). For our purposes, the interest is in examining the difference between *TCAL*s of two populations and to partition it by cohorts. Let the truncated cross-sectional average length of life for population *i* be denoted as $TCAL_i(t)$. The difference in *TCALs* between two populations is:

$$TCAL_1(t,Y_1) - TCAL_2(t,Y_1) = \int_0^{\omega} \left[\ell^*_1(x,t) - \ell^*_2(x,t) \right] dx , \qquad (3a)$$

where the integral corresponds to cohorts aged 0 to ω, present at time *t*. The cohort survival differences seen on the right side of equation (3a) allow us to identify the mortality contribution for all the cohorts present at a given year/period. Analytically it can be shown that the difference in *TCAL*s corresponds exclusively to differences in the known cohort mortality rates, weighted by the common set of mortality information for both populations imputed in year Y_1. From equation (3a) and the definition of the truncated cohort survival in equation (2) it is deducted:

$$TCAL_1(t,Y_1) - TCAL_2(t,Y_1) = \int_0^{\omega} e^{-\int_0^z \mu^*(a,Y_1)da} \left[e^{-\int_z^x \mu_1(a,t-x+a)da} - e^{-\int_z^x \mu_2(a,t-x+a)da} \right] dx , \qquad (3b)$$

where $\mu_i(a,t-x+a)$ is the force of mortality at age *a* and time *t-x+a* for population *i* and $\mu^*(a,Y_1)$ is the period force of mortality in year Y_1 for age *a*, as in equation (2b). Equations (3a) and (3b) are different from period or cohort life expectancy decompositions, which can only

reveal current mortality conditions or conditions of one specific cohort, respectively. Mortality of cohorts differs from year to year and from age to age, *TCAL* condenses all the available history in one measure, and their differences allow us to identify the cohort specific contributions in *TCAL* gaps. The selection of the "standard" mortality for the first year Y_1 is arbitrary, but it has little weight in comparisons. Particularly interesting is the selection of death rates for year Y_1 of all equal to zero, which simplifies the difference in equation (3b) to include only comparisons of the available cohort information as

$$TCAL_1(t,Y_1) - TCAL_2(t,Y_1) = \int_0^{\omega} \left[e^{-\int_z^x \mu_1(a,t-x+a)da} - e^{-\int_z^x \mu_2(a,t-x+a)da} \right] dx . \qquad (4)$$

Furthermore, it is possible to decompose each of the cohorts present in equations (3a), (3b) and (4) by their age-contribution. These age-contributions allow comparison of cohorts in different populations and assess their mortality transitions over the life course. Details of the derivation and estimation of this decomposition can be found in the appendix.

Illustration

Figure 0 presents the time trend in life expectancy in Costa Rica and Chile from 1970-2008 and 1992-2008, respectively. Both countries show similar time trends after 1990s, but before this time Costa Rica had periods of stagnation.

[Figure 0 about here]

Although, period life expectancy trend is informative, as shown in Figure 0, the way cohorts experienced these summarized mortality is hiding in a period measure. Figure 1A and 1B shows

the details of all the mortality information by age and time and even when short it is possible to see transitions in mortality. For example at young ages in Costa Rica it is possible to see that mortality has declined in the Figure 1A depicted in the change in color.

The Lexis surface of the difference in age-specific death rates between the populations of Costa Rica and Chile versus other high-longevity countries (HLCs) is shown in Figure 2A and 2B, respectively. Similar patterns were found when looking at these differences for females and males separately. In these contour charts, each data point represents the difference in age-specific death rates (scale on the right) for a specific year (horizontal axis) and age (vertical axis). Negative values correspond to higher Costa Rican/Chilean mortality, while positive values are associated with higher mortality in the other countries.

[Figure 1 & 2 about here]

Figure 2A of the difference of all HLCs combined versus Costa Rica shows higher mortality in Costa Rica until advanced ages. In the last decade of the twentieth century and first years of the new century the Costa Rican disadvantage can be seen until age 80, and then for ages above 80 in some years Costa Rican mortality is higher and in others lower. In recent years, also higher mortality levels are found in Chile at all ages except the old ones when compared to the HLCs. If we only focused on the current mortality (seen in the period life expectancy measure) as opposed to all the available mortality series of the second half of the twenty and first years of the twenty first century, we would only have had a partial information on how cohorts arrived to those levels.

To further analyze the existent disparities between Costa Rica/Chile and high longevity countries, we look at the difference in *TCAL*s between these countries and HLCs for the year of

2008. For the Costa Rica, *TCAL* had a level of 74.45 years in 2008, while the HLCs 77.93 years based on the 1970-2008 data. Chile with a shorter mortality series has a *TCAL* of 76.9 and for the same years of 1992-2008 the HLCs has 79.2 years. Both Costa Rica and Chile are behind in longevity, as captured by TCAL, than the high-longevity countries by more than 2 years. As presented in eq. (3), the difference in *TCAL*s is the result of adding all the differences between cohort survivals. The age-pattern of these disparities is found in Figure 3.

[Figure 3 about here]

Discussion

How useful a measure of mortality is depends on its ability to inform us on the health situation of a population in comparison to others. Period and cohort life expectancies have long been used as measures that represent the mortality of populations even when they correspond to a synthetic or a specific cohort. For countries with partial mortality information of the cohorts present at a given time, it is useful to try to use as much of their actual cohort mortality as possible. This is the aim of the Truncated Cross-sectional Average Length of life, *TCAL*s, and its comparison between populations.

The difference between *TCAL*s is comparable to life expectancy differences by showing on the number of years one population is lagging behind another. Analogous to asking which age-groups help explain the gap between life expectancies, for *TCAL* differences we inquire on the cohort survival contribution. To our knowledge this is a novel approach in studies interested in comparing mortality of populations.

TCAL takes advantage of all the cohort mortality information existent for persons present at a given time. The optimal situation for comparison is when full cohort information is available and

CAL instead of *TCAL* can be used. However, a substantial number of developed countries lack complete cohort mortality information. Furthermore, our TCAL measure could be of particular use in middle-income countries in which it would require waiting more than half a century to have complete cohort series of mortality.

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Figure 0. Period life expectancy for Costa Rica and Chile.

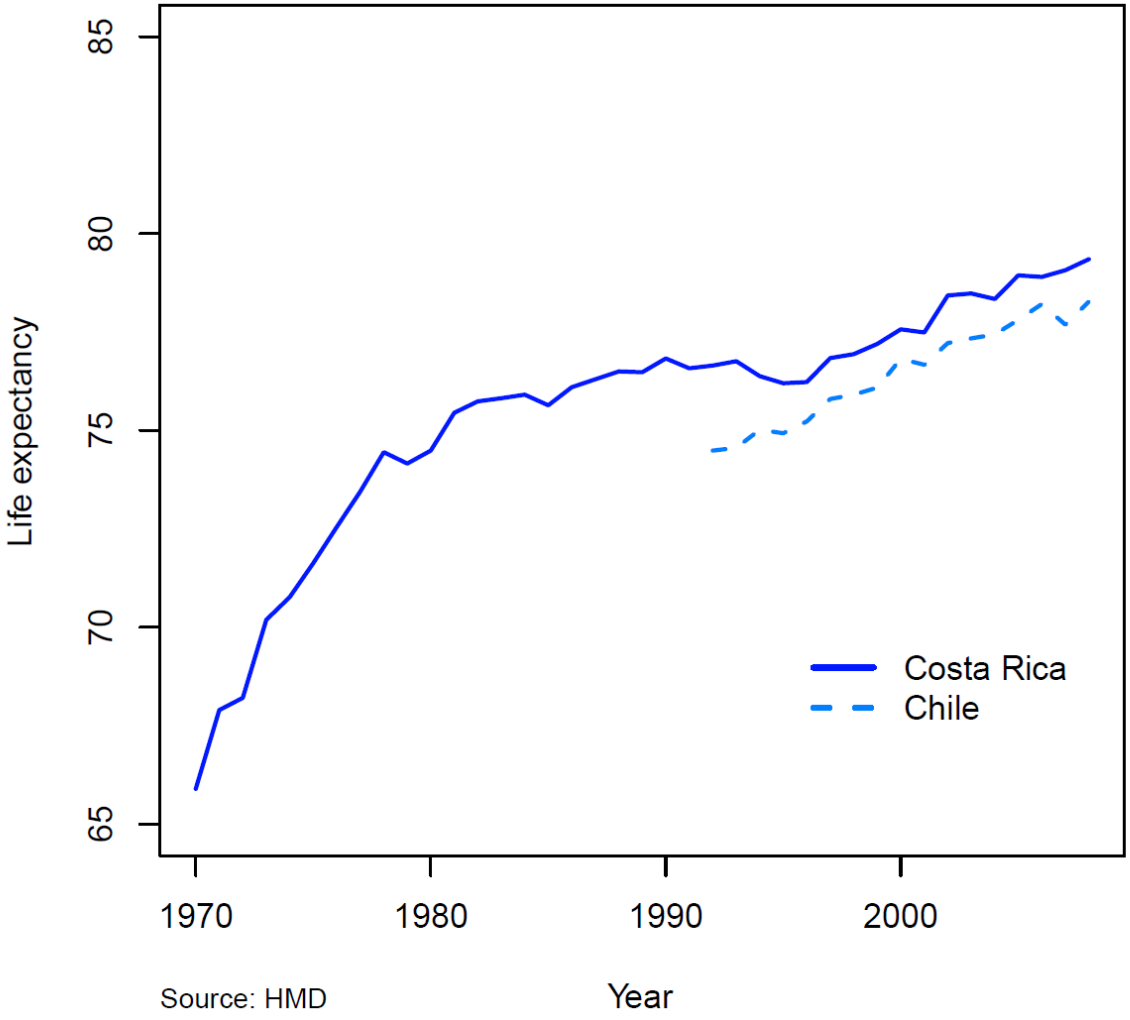
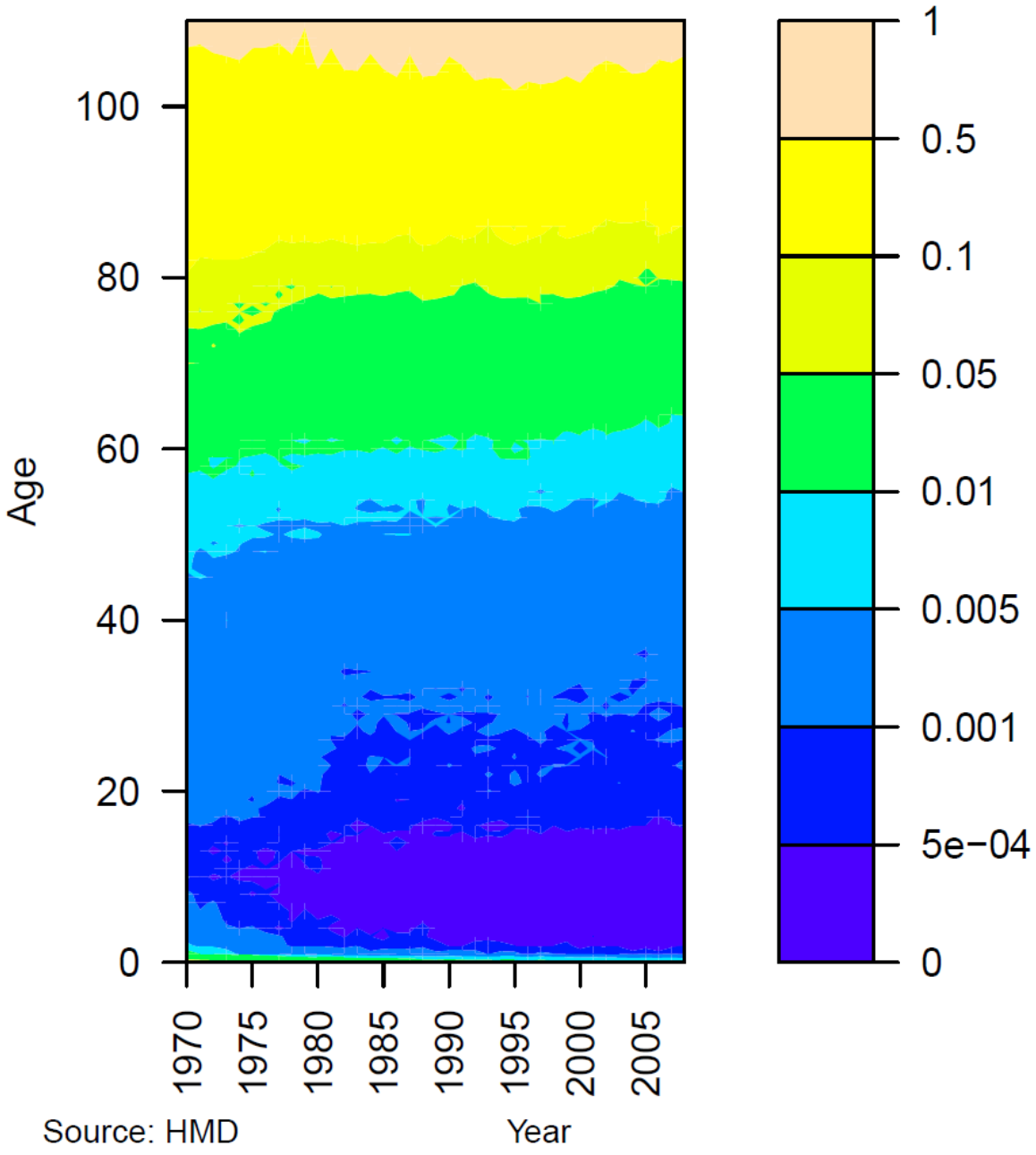
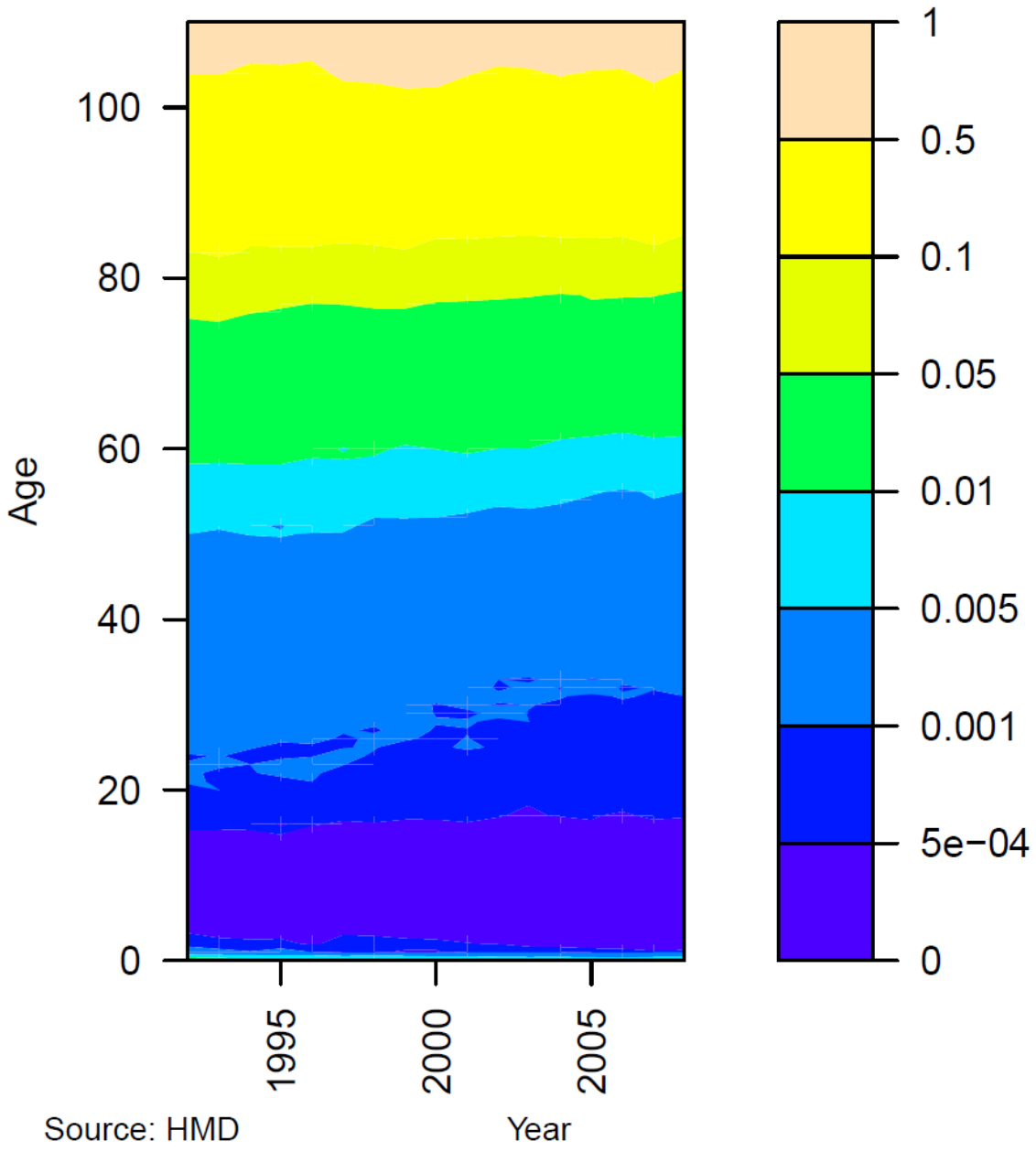


Fig. 1A. Lexis surface of death rates in Costa Rica from 1970−2008



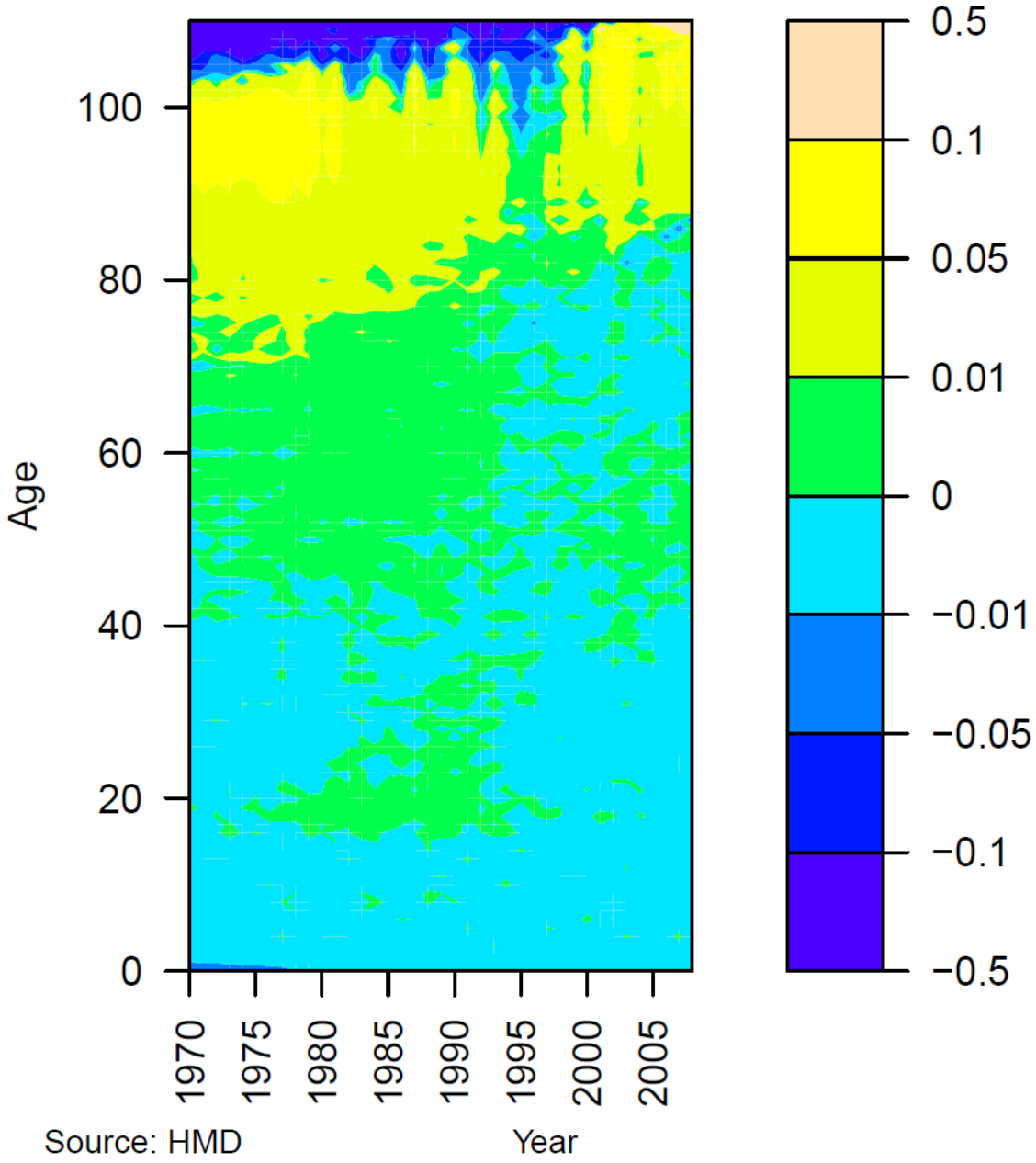
Source: HMD

Fig. 1B. Lexis surface of death rates in Chile from 1992−2008



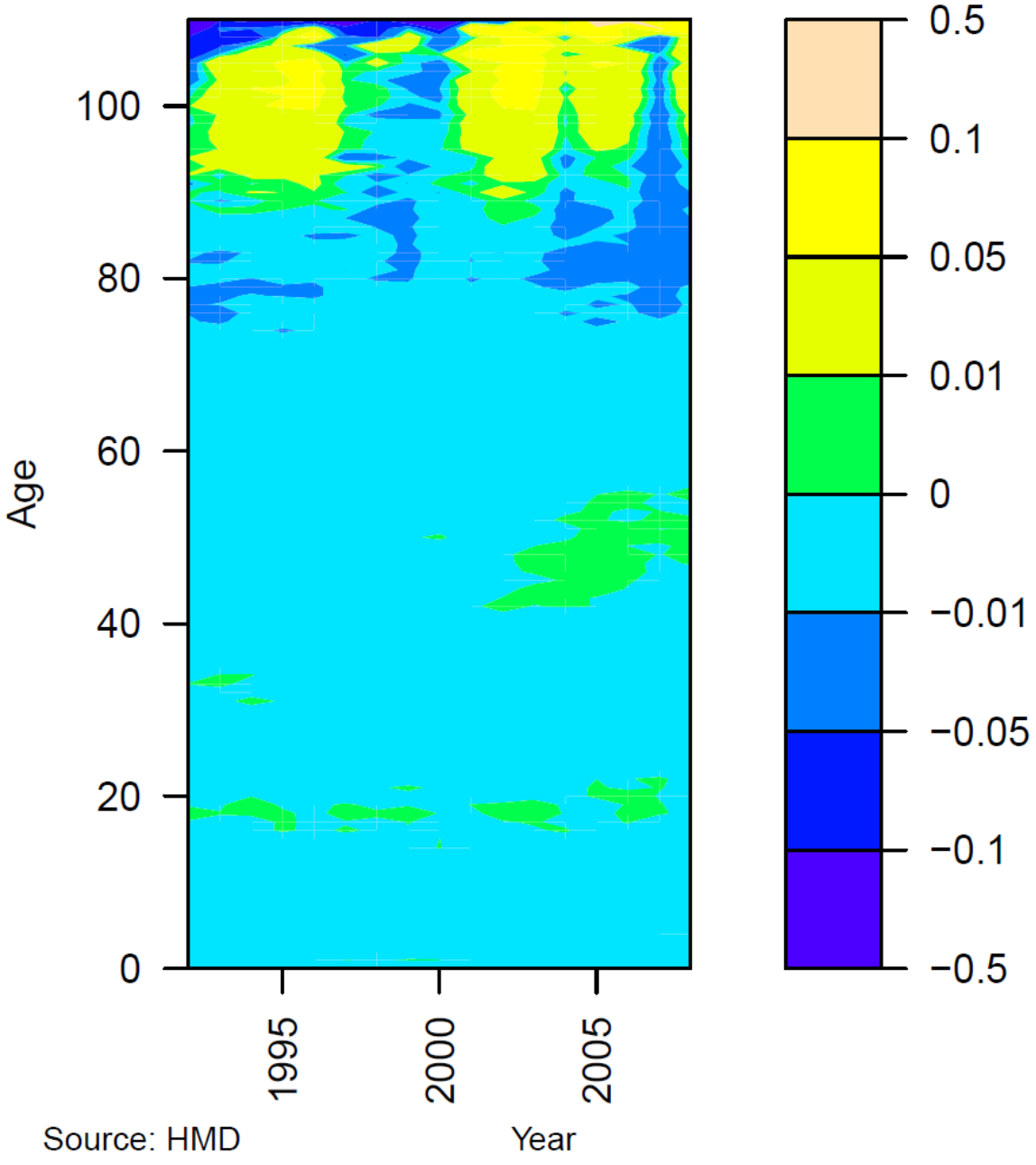
Source: HMD

Fig. 2A. Lexis surface for differences in death rates between h−longevity countries and Costa Rica, 1971−2008. Each point represents the difference, Mx(HLC)−Mx(CRI). Negative values correspond to higher mortality in Costa Rica .



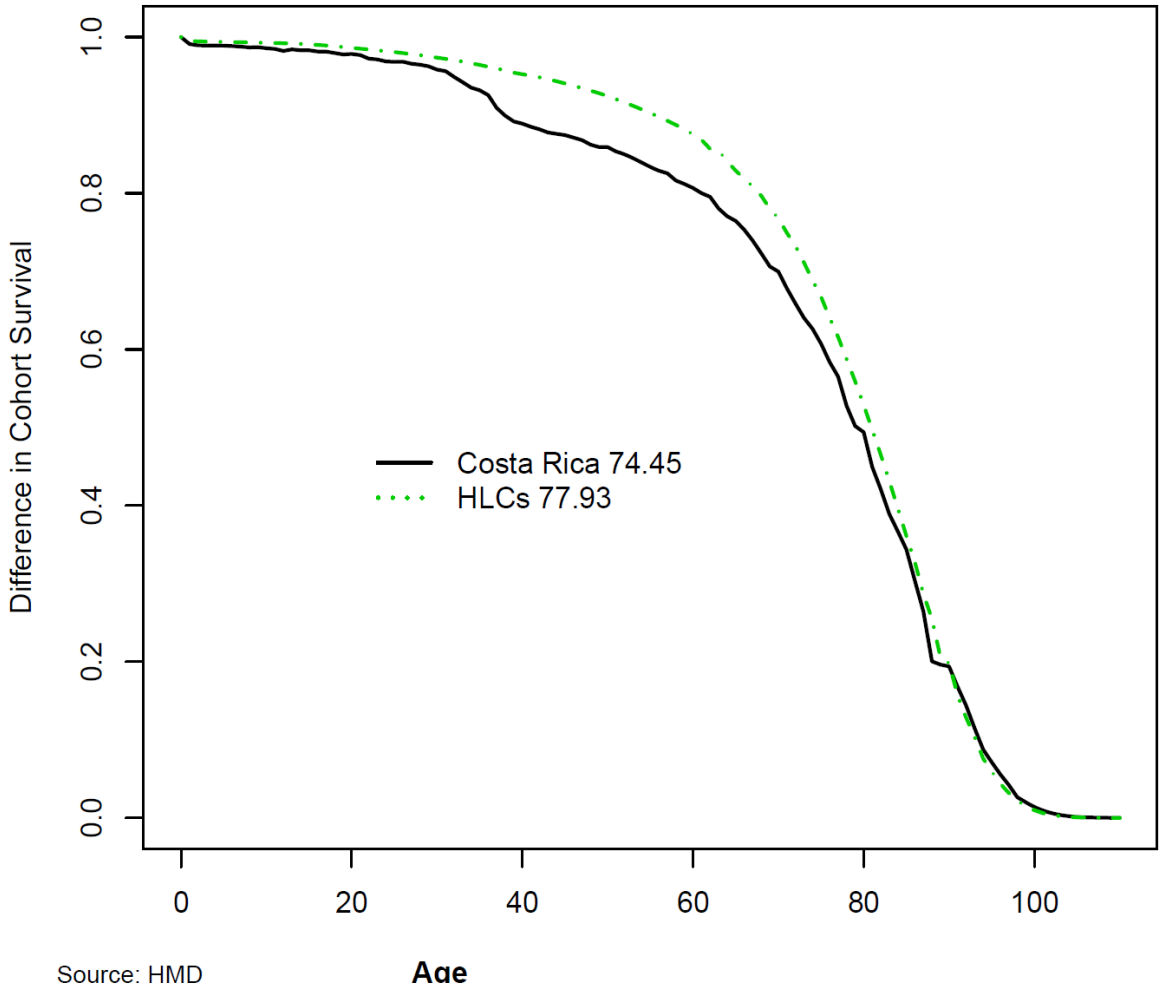
Source: HMD

Fig. 2B. Lexis surface for differences in death rates between high−longevity countries and Chile, 1993−2008. Each point represents the difference, Mx(HLC)−Mx(CHL). Negative values correspond to higher mortality in Chile .



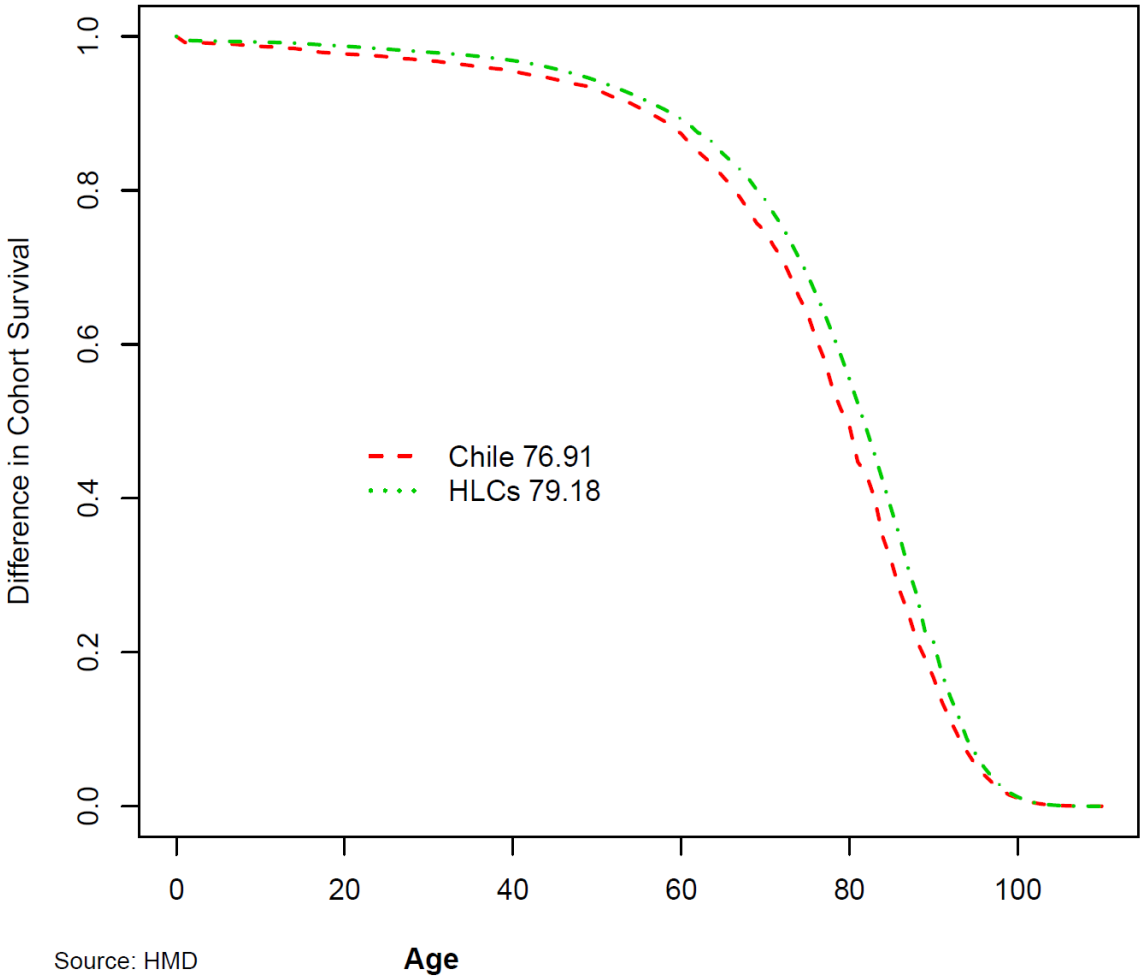
Source: HMD

Fig. 3A. Cohort survival functions for the truncated CALs for Chile and high−longevity countries (HLC) in 2008 with initial common mortality data for HLCs.



Source: HMD

Fig. 3B. Cohort survival functions for the truncated CALs for Chile and high−longevity countries (HLC) in 2008 with initial common mortality data for HLCs.



Source: HMD