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The impact of nursing homes on small-area life expectancies

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ABSTRACT

The geographical distribution of nursing homes can significantly distort small-area life expectancy estimations. Consequently, uncorrected life expectancies should not be used for small-area life expectancy comparisons. Instead, several nursing home corrections have been proposed. The practical use of these corrections, however, is severely limited by data availability. This paper introduces a new, model-based nursing home correction that requires considerably less detailed nursing home data. A formal comparison shows that the proposed model-based approach is the recommended correction for all small-area life expectancy estimations where detailed previous residential address information of the nursing home population is not available. This makes the approach highly relevant for a wide range of empirical applications.

1. Introduction

There are several measures that summarize the mortality experience of a population, such as standardized mortality ratios, comparative mortality figures, life expectancies, and directly or indirectly age standardized rates. All of these measures aim to express mortality in a single number that can be compared across populations and over time. Accordingly, these measures facilitate the exploration of geographical variations in health and the monitoring of populations' health and health inequalities over time.

Based on their simpler interpretation and direct age-standardization, life expectancies are usually preferred over alternative summary measures (e.g. Silcocks et al., 2001). Life expectancies, however, are thus far only occasionally used in small-area analyses. An important reason is that traditional life table methodology cannot be used to calculate reliable life expectancy estimates for populations smaller than approximately 5000 person years at risk. Below this threshold, the bias in the estimates as well as the size of the standard errors becomes too large for meaningful interpretation (Eayres and Williams, 2004; Scherbov and Ediev, 2011). Using a Bayesian random effects approach, however, it is possible to calculate accurate life expectancies and accompanying confidence intervals for life table populations as small as 2000 person years at risk (Congdon, 2009; Jonker et al., 2012). This is achieved using a modelling approach that recognizes correlations (i.e. borrows strength) between different age groups, geographic areas, and genders.

A major advantage of the Bayesian random effects approach, next to its ability to estimate accurate life expectancies for much smaller populations, is that it is easily extendible to incorporate corrections for area-specific confounders, such as, for example, the location of nursing homes. The latter affects life expectancy through the age-specific mortality rates of nursing home residents that are substantially higher than those of non-nursing home residents (Nimmo et al., 2006; Gandarillas et al., 2011). In fact, the asymmetric geographical distribution of nursing homes has been shown to have a large influence on small-area life expectancies: areas without nursing homes appear relatively healthy whereas areas with nursing homes appear relatively unhealthy, which can seriously distort small-area life expectancy comparisons (Williams et al., 2004).

Hence several strategies have been proposed to correct for the impact of nursing home deaths. Ideally, the life table data that constitute the life expectancy calculations are corrected by making use of previous residential address information. Under this approach, all nursing home residents and nursing home deaths are re-assigned to their previous residential address prior to the creation of the life table data. This approach is used by Veugelers and Hornibrook (2002) but its application is difficult because the required individual data are often unavailable or of insufficient quality.

When previous address information is unavailable it might still be possible to exclude the entire nursing home population

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from the life table data. This approach has been suggested by Williams et al. (2004) and only requires aggregated data about the size of the nursing home population and number of nursing home deaths. It has the disadvantage, however, that it results in small area life expectancies that only represent the health status of the healthier subset of people that does not reside in nursing homes. Consequently, this correction results in small-area life expectancies that are incomparable to those calculated at the regional or national level, where nursing home residents are not excluded from the life table data.

Accordingly, when previous address information is not available it might be preferable to correct the small area life expectancy estimates in a different way. A theoretically attractive approach is to take into account that nursing home deaths only affect the age-specific mortality rates of older age groups and hence to model the impact of nursing home deaths directly in the life table calculations for age groups of 65 years and older. Such a correction is easily incorporated in a Bayesian random effects approach, which has the additional advantage that all uncertainty regarding the correction is also accurately reflected in the estimated standard errors and 95% confidence intervals. Most importantly, however, is that this correction only requires information about the total percentage of nursing home deaths in each area. This is considerably less detailed and consequently easier to obtain than the data for the other two corrections.

The primary aim of this paper is hence to describe the impact of nursing homes on small-area life expectancies and to present evidence on the relative performance of nursing home corrections. Based on this evidence it becomes possible to provide guidance on which methodology to use and in which situation (e.g. based on the available data). The secondary aim of this paper is to provide a coherent framework for estimating reliable life expectancies at the small-area level that can be used in a wide range of small-area applications.

2. Methods

2.1. Study setting and small-area level

Our study setting is the census metropolitan agglomeration (CMA) of Amsterdam, the capital city of the Netherlands. The CMA of Amsterdam has a population of approximately 3.1 million people, is located in the western part of the country (see Fig. 1) and has stable geographical borders for the period under investigation (i.e. 2007–2009). The small-area definition used is the official neighborhood-level as established by Statistics Netherlands. Dutch neighborhoods adhere to physical obstacles that break up urban landscapes (important traffic arteries, bodies of water, green spaces, etc.) and are relatively homogeneous in terms of type of housing and inhabitants. Neighborhoods are also the smallest geographical unit in the Netherlands for which routinely gathered data are available. Note that a number of neighborhoods has been excluded from the analysis: either because they have populations that are too small for reliable life expectancy estimations (i.e. smaller than 2000 person years at risk, cf. Jonker et al., 2012) or because they comprise a public hospital, city park, zoo, train station, or one of the various industrial and harbor areas and consequently have no population at all.

2.2. Population and mortality data

The population and mortality data cover the 2007–2009 period and are obtained from the Dutch population (GBA) and deaths (DO) registrations. Both databases are maintained by Statistics Netherlands and provide complete and continuous coverage of all

Fig. 1. Geographic location of the census metropolitan agglomeration of Amsterdam.

Dutch inhabitants. The GBA includes current as well as previous address information (dating back until 1995), which implies that more than 98% of the nursing home residents can be re-assigned to their previous residential address. In contrast, Veugelers and Hornibrook (2002) could retrieve previous address information for approximately 80% of the nursing home population. It should also be noted that the GBA only records address-changes when the intention is to stay at the new address for at least several months. Accordingly, people who are admitted to a nursing home in the last few weeks before their imminent death are not registered as being part of the nursing home population.

For the life table population data, midyear population counts were extracted from the GBA at the first of July of 2007, 2008, and 2009 and the sum of these counts was taken as the population at risk for the 2007–2009 period. For the life table mortality data, all deaths in the same 3-year period were aggregated. The population and mortality data were differentiated by sex, neighborhood, and age and converted into standard 5-year abridged life tables with 95+ as the final age group. In total, three different life table datasets have been constructed: one standard (uncorrected), one in which all nursing home residents and nursing home deaths are fully excluded from the data, and, finally, one in which all nursing home residents and nursing home deaths are re-assigned to their previous residential addresses. The descriptive statistics of these life table data are provided in Table 1.

2.3. Nursing home data

To be able to exclude all nursing home residents and deaths from the life table data, assign all nursing home residents and deaths to their previous residential address, and calculate the percentage of individuals who were registered at a nursing home address in the GBA at the time of their death, a list of institutional addresses has been obtained from Statistics Netherlands. This list contains old age and nursing home locations -only available as a single category- at two different points in time: January 1st of 2008 and January 1st of 2009.

Unlike the GBA and DO registrations, the list of institutional addresses is solely based on information supplied by the Dutch municipalities without being audited or verified by Statistics Netherlands. Due to privacy regulations, only address-numbers (instead of verifiable addresses) were available to researchers. This makes it impossible to verify the list of institutional