Small-area health comparisons using health-adjusted life expectancies: A Bayesian random-effects approach

Marcel F. Jonker, Peter D. Congdon, Frank J. van Lenthe, Bas Donkers, Alex Burdorf, Johan P. Mackenbach

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A B S T R A C T
Health-adjusted life expectancy (HALE) is one of the most attractive summary measures of population health. It provides balanced attention to fatal as well as non-fatal health outcomes, is sensitive to the severity of morbidity within the population, and can be readily compared between areas with very different population age structures. HALE, however, cannot be calculated at the small-area level using traditional life table methodology. Hence we propose a Bayesian random-effects modeling approach that recognizes correlations and pools strengths between sexes, age-groups, geographical areas, and health outcomes. This approach allows for the calculation of HALE for areas as small as 2000 person years at risk and with relatively modest health state survey sample sizes. The feasibility of the Bayesian approach is illustrated in a real-life example, which also shows how differences in areas’ health performances can be adequately quantified. Such information can be invaluable for the appropriate targeting and subsequent evaluation of urban regeneration, neighborhood renewal, and community-based initiatives aimed at improving health and reducing health inequalities.

1. Introduction

Geographic inequalities in life expectancy (LE) have been well documented and provide important information on the distribution of health across countries and regions (see e.g., Bonneux et al., 2010; Vaupel et al., 2011; Leon, 2011). However, differences in life expectancy only describe differences in the mortality experience of populations and do not explicitly capture differences in morbidity for those still being alive (Murray et al., 2000). Health expectancy, a concept first introduced in the 1960s and further developed in the 1970s and 1980s, provides an attractive addition to traditional life expectancies by partitioning total life expectancy into years spent in perfect health and years spent in less than perfect health.

Similar to LE, health expectancy measures are independent of the size and composition of the population and provide an intuitive and reliable comparison between the health status of one population with that of another. Health-adjusted life expectancy (HALE), a specific type of health expectancy, measures the number of expected years of life equivalent to years lived in full health. It is one of the most attractive summary measures of population health because it takes various domains of health into account and uses pre-defined utility weights to combine these into a single measure of health-related quality of life. In contrast to other health expectancy measures, such as healthy life expectancy or disability-free life expectancy, HALE is more sensitive to changes in the severity of morbidity within the population because it uses polychotomous instead of dichotomous weights (Manuel et al., 2000; Murray et al., 2000). Consequently HALE is the only measure that can provide appropriate and balanced attention to the effects of fatal as well as non-fatal health outcomes on overall population health (Mathers et al., 2003a).

Thus far, HALE has only been calculated at the national or regional level (e.g., Manuel et al., 2000; Mathers et al., 2004; Heijink et al., 2011; Jia et al., 2011). Analyses for smaller areas are warranted because the calculation of HALE for more refined geographical areas allows for a more reliable approximation of the spatial distribution of health expectancy and for a study of its determinants on a smaller level than is currently possible (Gakidou et al., 2000). It would also constitute an important input for the targeting and evaluation of area-based initiatives aimed at reducing health inequalities (Thomson, 2008). The calculation of HALE at the small-area level, however, is not possible using traditional life table methodology. Firstly, the traditional methodology is based on analysis of each area independently, with each life table having as many parameters as there are observations. This approach works...
well for large populations, but not for small areas—with populations smaller than 5000 person years at risk—because the bias in the estimates and size of the standard errors become too large for meaningful analysis due to sparse data problems (Toson and Baker, 2003; Eayres and Williams, 2004; Scherbov and Ediev, 2011). The second barrier to the estimation of small-area HALE is a lack of adequate health surveys. Adequate health surveys first of all comprise a health state instrument such as the EQ-5D, SF-12, or HUI3 (or any other health state classification instrument with an accompanying set of utility weights) but they also need to have a sufficiently large sample size to be representative at the small-area level. Often the latter is problematic, which results in biased HALE estimates and in confidence intervals that are too large to significantly differentiate between the areas under analysis (see e.g. Manuel et al., 2000). In fact, the inability to obtain adequate sample sizes is the most common reason for the inability to calculate HALE at the small-area level (Stiefel et al., 2010).

The aim of this paper is hence to introduce a modeling approach that recognizes correlations between the mortality and morbidity information in various dimensions of the small-area data (e.g. between sexes, age groups, and adjacent geographic areas). This accommodates sparse data problems by pooling strength between the included dimensions and allows for the calculation of HALE at the small-area level using significantly smaller survey sample sizes. In contrast to existing small-area estimation techniques (see e.g. the methodological overviews of Rao, 2003 and Rahman, 2008) our proposed random-effects modeling approach is solely based on the observed small-area data and does not include or rely on covariates. It also does not rely on assumptions about the transferability of correlations from aggregate data sources (e.g. large-scale surveys) to the small-area level. In fact, the proposed random-effects methodology belongs to a class of statistical approaches that has thus far not been recognized in the small-area estimation literature. Accordingly, Fig. 1 contains an updated typology of existing small-area estimation techniques with the inclusion of our random-effects approach to small-area life table estimation.

The proposed modeling approach is illustrated in a real-life example, which shows the feasibility of the HALE estimations and demonstrates the sensitivity of HALE compared to regular LE estimates. Additionally, a selection of neighborhoods with the lowest estimated HALE, combined with estimates of the probability that each of the areas’ HALE belongs to the worst five in the entire sample, is presented. These probabilities take the full uncertainty of the life table estimates into account and are hence more reliable than traditional rankings based on point estimates. This information is, for example, relevant for the appropriate targeting and subsequent evaluation of urban regeneration, neighborhood renewal, and community-based initiatives aimed at improving health and reducing health inequalities (Thomson, 2008). Finally, a small simulation study is included that supports the reliability and validity of the proposed modeling approach.

2. Methods

2.1. The HALE model

The calculation of HALE is essentially a three-step procedure. In the first step, the age-specific mortality rates for all included

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**Fig. 1.** Abbreviations: Horvitz-Thompson (H-T), Generalized Regression (GREG), Generalized Regression and Weighting (GREGWT), Empirical Best Linear Unbiased Prediction (E-BLUP), Empirical Bayes (EB), Hierarchical Bayes (HB), Spatial Microsimulation Models (SMM) and Combinatorial Optimization (CO). (Adapted from Rahman et al. (2010)).
areas are calculated. In the second step, the age-specific health-adjustment rates are calculated. And in the third step, these two inputs are summarized into HALE via established life table calculations. The proposed HALE model reflects these three steps.

2.1.1. Mortality rate estimations

The first part of the HALE model estimates the mortality rates as required in the HALE life table calculations. Let $D_{six}$ and $P_{six}$ denote deaths and populations at risk classified by sex $(s=1,2)$, area $(i=1,...,N)$, and age group $(x=1,...,X)$. Deaths are assumed Poisson distributed

$$D_{six} \sim \text{Poisson}(P_{six}m_{six}).$$

with $m_{six}$ denoting the required mortality rates specified in the same dimensions. For larger populations, a binomial distribution could also be specified; however, given our focus on small populations with few observed deaths, the Poisson distribution is considered more appropriate. A standard log-link function is imposed, and, based on the simulation results of Jonker et al. (2012), the following specification is used:

$$\log(m_{six}) = \beta_0s + \beta_1sx + \beta_2si \times \beta_3sx.$$  

Here the $\beta$-parameters capture level differences in mortality rates for males and females, whereas the $\beta_3$-parameters represent multivariate (gender-specific) random age effects that capture the usually high correlation between the mortality rates of successive age groups and genders, and the $\beta_2$-parameters multivariate (gender-specific) random spatial effects that account for spatial clustering of mortality rates in adjacent areas while also taking the correlation between genders into account. The spatial effects are interacted with a set of $\beta_3$-parameters, which allows the spatial effects to be more pronounced for specific age-groups. The latter relaxes the assumption of an uniform (gender-specific) age-gradient for all areas while still retaining a relatively parsimonious model specification. For identification of the parameters, the $\beta_1$ and $\beta_2$ parameters are constrained to sum to zero and the $\beta_3$ parameters constrained to sum to one over dimension $s$.

2.1.2. Morbidity rate estimations

The second part of the HALE model estimates the morbidity component as required in the HALE life table calculations. Let $H_{six}$ denote average health state rates as measured on a continuous scale, ranging from 0 (death) to 1 (perfect health), classified by sex $(s=1,2)$, area $(i=1,...,N)$, and age group $(x=1,...,X)$. Given these explicit boundaries, a beta distribution is used to model the morbidity component of the HALE calculations. As explained by Paolini (2001), Ferrari and Cribari-Neto (2004), and Smithson and Verkuilen (2006), this is statistically superior to alternative modeling approaches such as assuming normality on the log-transformed average health state rates. Hence the $H_{six}$ are assumed to be beta distributed

$$H_{six} \sim \text{beta}(\alpha_{six}, \beta_{six}),$$

and based on Smithson and Verkuilen (2006) we use the following re-parametrization to translate the beta shape parameters $\alpha$ and $\beta$ into location and dispersion parameters:

$$\alpha_{six} = \text{location}_{six} \times \text{dispersion}_{six},$$

$$\beta_{six} = (1-\text{location}_{six}) \times \text{dispersion}_{six}.$$  

A logit-link function is used for the location sub-model, a log-link function for the dispersion sub-model (the dispersion has to be strictly positive), and for both sub-models the same random-effects structure as in the mortality model is used. The dispersion model additionally includes a count of the number of survey respondents that constitutes the corresponding average health state value. This reflects the standard relationship between sample size and variance.

$$\logit(\text{location}_{six}) = \beta_4s + \beta_5sx + \beta_2s + \beta_3sx.$$  

$$\log(\text{dispersion}_{six}) = \beta_7s + \beta_8sx + \beta_9si \times \beta_{10}sx + \beta_{11} \times \log(\text{count}_{H\text{six}}).$$

As can be seen in (6), a shared spatial structure is specified that accommodates potential correlation between the mortality and morbidity part of the HALE model. This allows for a pooling of strength between the mortality and morbidity data for each neighborhood, which are exposed to the same risk-factors and therefore likely to be correlated.

2.1.3. Life table estimations

The third and final component of the HALE model summarizes the estimated age-specific mortality rates and estimated location values into life expectancies and health-adjusted life expectancies. Based on the recommendations made by Tsonis and Baker (2003) and Eayres and Williams (2004), the life expectancies are calculated using the Chiang (1968) life table approach. The health-adjusted life expectancies are subsequently calculated using Sullivan’s (1971) methodology. An excellent introduction to life table calculations using Sullivan’s methodology, including several examples, can be found in the Sullivan’s Guide (www.eurohex.eu).

2.1.4. Bayesian estimation and priors

Bayesian methods are used for the parameter estimations, which involves selecting prior densities for the unknown model parameters and updating those densities via the likelihood of the observed data. In the estimations, the $\beta_0$, $\beta_4$, $\beta_7$, and $\beta_{11}$ parameters are assigned uninformative flat priors from $-\infty$ to $\infty$. The $\beta_1$, $\beta_2$, $\beta_5$, $\beta_6$, and $\beta_{10}$ parameters are assigned multivariate conditional auto-regressive priors with Wishart priors assigned to the precision matrices. The Wishart prior for $\beta_2$ is assigned a 4-by-4 identity scale matrix with 4 degrees of freedom, whereas the other Wishart priors are assigned a 2-by-2 identity scale matrix and 2 degrees of freedom. Finally, the $\beta_3$, $\beta_8$, and $\beta_{10}$ parameters are specified with individual Gamma(1,1) priors.

The model is fitted in OpenBUGS using iterative Markov chain Monte Carlo (MCMC) sampling techniques. The estimations start with 25,000 burn-in MCMC iterations to allow the Markov chains to converge, followed by a total of 75,000 MCMC iterations with a thinning interval of 10 to reliably approximate the posterior distributions. Convergence is evaluated using the Gelman et al. (1995) criteria based on three parallel chains.

2.2. Real-life example

2.2.1. Study setting and small-area level

The proposed Bayesian modeling approach is applied to real-life data of the city of Rotterdam. Rotterdam has a population of approximately half a million people and is the 2nd largest city in the Netherlands. The small-area level used is the official neighborhood-definition as established by Statistics Netherlands. 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, inhabitants, and land use. Neighborhoods are the smallest geographical unit in the Netherlands for which routinely gathered data are available. Several neighborhoods in the city of Rotterdam (together comprising 2.9% of the total population) are excluded from the analysis: either because they have insufficient population for reliable life table estimates (i.e. smaller than 2000 person years at risk in the life tables, cf. Jonker et al., 2012) or because they comprise a public hospital, city park, zoo, airport,
train station, or various industrial and harbor areas and have no population at all.

2.2.2. Population and mortality data
The required population and mortality data for the HALE calculations are obtained from the Dutch population (GDA) and deaths registry (DO). Both databases are maintained by Statistics Netherlands and provide complete and continuous coverage of all Dutch inhabitants. For the life table population data, midyear population counts are extracted from the GDA at the first of July of 2004, 2005, and 2006 and the sum of these counts is taken as the population at risk for the 2004–2006 period. For the life table mortality data, all deaths in the same 3-year period are aggregated. The population and mortality data are both summarized by sex, neighborhood, and age and subsequently converted into standard 5-year abridged life tables with 85+ as the final age group.

2.2.3. Nursing home correction
The selective migration of frail individuals to nursing homes can have a substantial impact on small-area life expectancies and severely distort life expectancy comparisons between areas (Williams et al., 2004). Accordingly, the life table data that constitute the calculations in this paper, with descriptive statistics presented in Table 1, are corrected using previous residential address information (Veugelers and Hornibrook, 2002; Jonker et al., 2012). This approach requires detailed individual information about the nursing home population to re-assign all nursing home inhabitants and nursing home deaths to their last-known residential address. The required individual nursing home address data and previous address information are obtained from Statistics Netherlands.

2.2.4. Health-status data
The required health-status data for the HALE calculations are obtained from the 2005 Health Survey held by the local health authorities of Rotterdam (GGD). The survey contains SF-12 health state measurements of approximately 5700 respondents aged 16 years and older, resulting in an average of 93 respondents per neighborhood. The SF-12 health state instrument is a well-validated and widely used instrument to assess respondents’ health in various health domains. Even though the SF-12 is considerably shorter than the original SF-36 questionnaire, SF-12 summary scores have been found to be good predictors of the original SF-36 summary scores and have reproduced their psychometric performance (Ware et al., 1996; Gandek et al., 1998). Finally, health state preference weights, which are used to aggregate the various SF-12 health state dimensions into a single composite health index as required for the HALE estimations, are obtained from the SF-6D validation study by Brazier and Roberts (2004).

Table 2 presents the descriptive statistics of the SF-12 health status data. In the average SF-6D health status dataset there are 25 boundary observations (all values of exactly 1). These are handled by slightly re-scaling the health-status data, conform the recommendations made by Verkuilen and Smithson (2012). Because the GGD health state survey does not include respondents aged 15 years and younger, perfect health is assumed for the first four age groups in the HALE calculations. Alternatively, HALE at age 15–19 could be reported without making any additional assumptions.

2.3. Simulation study

2.3.1. The benchmark
To substantiate the reliability of the modeling approach and to confirm the validity of the HALE estimates in our real-life example, we have conducted a Monte Carlo simulation study. Similar to other Monte Carlo simulations aimed at validating statistical models (see e.g. Fiebig et al., 2010; Camacho et al., 2011), the benchmark or ‘true’ parameters are based on the estimated model parameters in our reference dataset, which is the dataset of neighborhoods in Rotterdam as described in the previous section. The aim of the simulation study is to verify whether the proposed HALE model is capable of accurately recovering the benchmark HALEs and 95% credibility intervals under the same conditions as encountered in the original dataset.

2.3.2. Creating the simulation datasets
The first step in our Monte Carlo study is to create a large number of new datasets that each represent a single draw from the data generating process that results from the proposed HALE model combined with the posterior means of the estimated model parameters. In total, 2000 different datasets are created. Each of these datasets has the exact same population at risk and the exact same number of survey respondents as in the reference dataset. However, conform the structure of the HALE model, the number of deaths are drawn randomly from a Poisson distribution with means set to the benchmark age-specific mortality rates and the average health-state scores drawn randomly from a beta distribution with shape parameters set equal to the benchmark values. As a result, each simulated dataset has slightly different numbers of deaths and slightly different average health-state scores.

2.3.3. Summarizing the model’s performance
OpenBUGS is used to estimate the model parameters and HALE values for all 2000 simulated datasets. The estimated parameters and HALE values are subsequently summarized in MATLAB. The estimated parameters and HALE values together form distributions from which reliable inferences can be made. Ideally, the HALE model is capable of exactly recovering the benchmark HALE values. This would imply that the bias, which is the average difference between the estimates and the benchmark values, is equal to zero. We also look at the coverage of the reported 95% intervals by counting how often the benchmark HALEs are located.

Table 1

<table>
<thead>
<tr>
<th>Sex</th>
<th>Variable</th>
<th>No. obs.</th>
<th>Mean</th>
<th>Std.dev.</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>Male</td>
<td>Population at risk</td>
<td>61</td>
<td>13,715</td>
<td>7545</td>
<td>2586</td>
<td>36,268</td>
</tr>
<tr>
<td></td>
<td>Number of deaths</td>
<td>61</td>
<td>124</td>
<td>110</td>
<td>597</td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>Population at risk</td>
<td>61</td>
<td>14,294</td>
<td>8532</td>
<td>2515</td>
<td>43,558</td>
</tr>
<tr>
<td></td>
<td>Number of deaths</td>
<td>61</td>
<td>143</td>
<td>148</td>
<td>10</td>
<td>773</td>
</tr>
</tbody>
</table>
within the reported 95% credibility intervals. Values below 95% indicate that the credibility intervals are too optimistic and values greater than 95% that they are too conservative. Ideally, the coverage should be equal to 95%.

3. Results

Table 3 shows the results of the estimations by summarizing the posterior LE and HALE estimates of the HALE model for the individual neighborhoods in Rotterdam. As can be seen, females have an average LE that is 4.8 years higher than that of males. In contrast, the average HALE of females is only 2 years higher. Hence when quality of life is taken into account, the health advantage of women reduces considerably. This is also reflected by the difference between LE and HALE, which represents the number of years spend in poor health. As can be seen, women spend on average 2.8 more years in poor health than men.

Also the range of estimated values differs between LE and HALE: for both males and females the range of LE is 6.2 years, whereas the range of HALE is 9.2 and 9.6 years for males and females, respectively. Health inequalities between neighborhoods are thus more pronounced when health-adjusted life expectancies are taken into account. Another important aspect of the estimations, which is not included in Table 3, is the average size of the standard errors. Compared to the range of 6.2 and 6.1 years in LE, the average standard errors are 0.76 for males and 0.79 for females. The average standard errors of the HALE are 0.96 and 1.06, which is, relative to the range of estimated HALE, slightly smaller.

Fig. 2 visualizes the relationship between LE and HALE. Note that LE in this figure is calculated using only the mortality data (i.e. without taking correlations with morbidity into account), whereas HALE is calculated using the combination of mortality and morbidity data and the borrowing of strength approach as described in the previous section. Accordingly, Fig. 2 nicely illustrates the added value of the HALE compared to LE calculations. As can be seen, LE and HALE are strongly correlated. This holds both for males and females and is to be expected because HALE is partially based on the same data. However, there is also substantial (i.e. up to 3 years) variation in HALE at any given level of LE. The latter implies that LE and HALE are similar but certainly not identical, and that the morbidity data in the HALE calculations are not overwhelmed or clearly dominated by the mortality data.

![Fig. 2](image_url) Life expectancy versus health-adjusted life expectancy, by gender, for neighborhoods in Rotterdam, The Netherlands, 2004–2006.

Fig. 3 contains a map of the estimated HALE in neighborhoods in Rotterdam, separately for males and females. Several neighborhoods are not included in the HALE calculations; as mentioned, these are mostly industrial or harbor areas but also those neighborhoods that contain the public hospital, city park, zoo, airport, and central train station of Rotterdam. As can be seen, the geographic pattern of HALE is very similar for males and females. There are three distinct areas with neighborhoods that have relatively low HALEs, with the most problematic neighborhoods located south of the river (the Maas) and in the older northern neighborhoods of Rotterdam.

Table 4 contains the individual HALE estimates for several neighborhoods in Rotterdam. For both males and females, the 10 neighborhoods with the lowest estimated HALE are selected since these are arguably the most interesting for policy purposes—of course, other selections may be relevant in different situations. Instead of only looking at the means of the posterior HALE distributions, Table 4 also reports the (posterior) probability that each of the selected neighborhoods belongs to the top-5 of neighborhoods with the lowest estimated HALE. This measure takes the full uncertainty of the HALE estimates into account and provides a more reliable means of comparing areas with the worst health performance. As can be seen, the exact ranking of neighborhoods is uncertain and the five worst performing areas cannot be exactly identified. In fact, looking at simple rankings can be misleading; when the standard deviation of the neighborhoods’ posterior HALE estimates are different, the estimated probabilities for neighborhoods with higher HALE estimates can be equally high or even higher than that for neighborhoods with lower HALE estimates. In other words, not only the point estimates but also the relative size of the standard deviations is important when
Comparing HALEs of different neighborhoods and the estimated (posterior) probabilities incorporate both of these aspects into a single measure.

Table 5 contains the main results of the Monte Carlo simulation. The estimated bias of the HALE estimates is close to zero (−0.003) for males and slightly positive (0.067) for females. Compared to the average value and the range of male and female HALE (see Table 3), the bias is negligible. Interestingly, the coverage of the 95% credibility intervals is somewhat higher for females (94.2%) than for males (93.1%). This means that even though the reported HALE are slightly less accurate, the accompanying standard errors and 95% credibility intervals are slightly more accurate for females than for males.

To be able to explain the observed differences in bias between males and females, Table 6 contains a more detailed overview of

<table>
<thead>
<tr>
<th>Measure</th>
<th>Sex</th>
<th>Male</th>
<th>Female</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bias</td>
<td></td>
<td>-0.003</td>
<td>0.067</td>
</tr>
<tr>
<td>Coverage</td>
<td></td>
<td>93.1</td>
<td>94.2</td>
</tr>
</tbody>
</table>

* Results are based on 2000 simulation iterations.
the estimated bias for the age-specific mortality and the age-specific health-adjustment rates (which are the two inputs for the HALE calculations). As can be seen, the bias for the age-specific mortality rates is almost identical for males and females and essentially equal to zero for all age groups. The bias for the health-adjustment rates are slightly larger and also very similar for males and females. The only real difference is the larger bias of the mortality and the age-specific health-adjustment rates for younger age-groups. This pattern is also present in the descriptive statistics (see Table 2) and given the small sample size for this particular age group—only 6 observations in the entire dataset—the observed bias can be easily explained.

### 4. Discussion

The presented HALE modeling approach makes use of a Bayesian random-effects methodology that pools strength over the observed male and female mortality rates and health-adjustment rates for younger age-groups. This pattern is also present in the descriptive statistics (see Table 2) and given the small sample size for this particular age group—only 6 observations in the entire dataset—the observed bias can be easily explained.

Additionally, a particularly attractive feature of the small-area example is that neighborhoods with the lowest HALE can be identified while taking the full uncertainty of the estimates and life table calculations into account. Such information can be valuable for governments and local health-authorities, who increasingly rely on small area-based approaches at reducing health inequalities but thus far have no reliable summary measure of (small-area) population health at their disposal.

The presented Monte Carlo simulation evidence confirms that the results for Rotterdam are almost unbiased and that the coverage of the 95% credibility intervals is close to 95%. Accordingly, the uncertainty of the HALE estimates is accurately reflected in the reported standard errors and credibility intervals. In fact, the Monte Carlo results are very similar to those reported by Jonker et al. (2012), which further supports the validity of the small-area life table approach based on Bayesian random-effects estimations.

It should be noted that the main benefit of the proposed methodology is that it allows for an attractive and reliable summary measure of population health to be calculated at a (much) smaller geographic level than has thus far has been possible. HALE is indeed attractive: it is sensitive to the severity of morbidity within the population, provides balanced attention to fatal as well as non-fatal health outcomes, and can be readily compared between areas with very different population age structures. Especially at the small-area level, where local differences in age structure are not averaged out as much, this is a clear advantage. Moreover, the HALE estimates can be easily corrected for the location of nursing homes and the interpretation of the results is relatively straightforward, which makes HALE well-suited to communicate to a broad audience.

An important issue in the calculation of HALE, both in small and larger area analyses, is the reliance on an external set of health state preference weights to derive average health state values. One issue is that these value weights are treated as fixed coefficients in the HALE estimations, even though they are, in fact, estimates derived from a benchmark study themselves. Consequently, the variability of the HALE estimates is slightly under-predicted if the weights are treated as fixed coefficients (Parkin et al., 2010). A more important issue, however, is that health state value sets vary significantly between countries. In the presented example for Rotterdam, a UK value set for the SF-6D is used because there is no Dutch SF-6D health state tariff yet. This can have a major impact on the estimated HALE; evidence from Heijink et al. (2011) shows that estimated HALE at the national level can differ between 2% and more than 20% depending on the value set used in the calculations. Admittedly, this evidence is based on the EQ-5D, which is an alternative health state instrument to the SF-6D, but it does emphasize the importance of using a health state value set that is as relevant as possible to the areas under investigation.

Finally, even though the proposed methodology already provides a comprehensive and coherent approach to estimating HALE at the small-area level, several improvements and extensions can still be envisaged. First of all, the required historical previous address information for the nursing home correction may not always be available. If so, an attractive alternative is to model the impact of nursing home deaths directly in the life table calculations, which allows for a correction of the age-specific mortality rates of the age groups that are directly affected (i.e. those of 65 years and older). As shown by Jonker et al. (2013), such an alternative correction can provide a close approximation of the ideal previous address correction, with the advantage that it only relies on the aggregate percentage of nursing home deaths in each area. The latter is considerably less detailed and consequently easier to obtain than historical address information for the entire nursing home population.
Secondly, the GGD health status survey that was used to obtain SF-12 health-state measurements was conducted in the non-institutional population. Accordingly, the SF-12 health-state measurements that constitute the HALE calculations are restricted to the healthier non-nursing home population and this is likely to result in an upwards bias in the health-state measurements and in a reduction in the difference between the estimated LE's and HALE's. Alas, it is not possible to correct for this bias without additional data. Based on the results of Jonker et al. (2013), however, we know that the nursing home excluded measurements only affect the level of the life table measurements without invalidating comparisons between areas. And with additional SF-6D health-state measurements within the nursing home population, nursing home corrected HALEs could be calculated using the same approach as described by Jonker et al. (2013).

Thirdly, for public health researchers and health authorities it would be interesting to monitor HALE over time. This can, of course, be accomplished by applying the proposed methodology to several independent cross-sectional datasets. However, it is also relatively straightforward to extend the proposed modeling approach with a time dimension. This has the advantage that it allows for a slightly adapted version of Sullivan's methodology that is also robust to situations in which age-specific health-state prevalences change significantly over time (Imai and Soneji, 2007). Additionally, it allows for a pooling of strength between adjacent years in addition to the correlations between genders, age groups, areas, and mortality/morbidity that are included in the current specification. The latter not only improves the reliability of the estimations, but also allows for explicit and appropriate inferences about measurements of compression vs. expansion of morbidity, the existence of a typical time trends, and the effects of interventions at the small area level.

Fourthly, after having estimated HALE at the small area level, it would also be interesting to further investigate the spatial variation in HALE in terms of associations with area socioeconomic characteristics and direct risk factors such as noise and air pollution. This can be done using follow-up regression that take the precision of the estimated HALE as well as the spatial configuration of the neighborhoods into account, as suggested by Arcaya et al. (2012). Moreover, latent concepts that are important in the explanation of spatial variation in HALE, such as neighborhood deprivation and neighborhood social capital, can be summarized and included in the regressions using Bayesian factor analysis; see e.g. Congdon (2011) and Mari-DellOlmização et al. (2011).

In conclusion, the proposed methodology is versatile and provides a coherent framework for estimating HALE in small-area analyses. Compared to traditional, fixed effects life table estimations that can only be used for populations of at least 5000 person years at risk, the proposed Bayesian life table approach can produce accurate life table estimates for geographical areas with populations as small as 2000 person years at risk. Similarly, by pooling strength over geographical areas, sexes, age groups, and similarities between mortality and morbidity, significantly smaller sample sizes for the required health state surveys are required. This can reduce costs for future HALE surveys and makes HALE calculations using existing surveys increasingly more feasible.

References


