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Bayesian Spatiotemporal Model for Life Expectancy Mapping; Changes in Barcelona From 2007 to 2018

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When mapping life expectancy, and investigating its local variation in time, there is a conflict between using large areas and/or mortality data from long periods of time to have low variance life expectancy estimates, and using small areas and single-year mortality data to explore the space–time variation of life expectancy in detail, without bias. Here a Bayesian model is proposed to smooth annual small-area life expectancy estimates and help deal with that trade-off. The specific area effect on life expectancy, together with its spatial and temporal dependencies are modeled through random effects, while the effect of covariates is modeled through a fixed effect component. By smoothing life expectancy estimates directly, instead of smoothing age-specific mortality rates first the way done in the literature, the model used is easier to implement and interpret. The approach is illustrated, by using it to explore how life expectancy at birth of males and of females, and their gap, varied in space and in time in the city of Barcelona between 2007 and 2018, and their relationship with covariates. It is found that, on average, life expectancy has been growing by 0.23 years per year for males and 0.15 years per year for females. The female life expectancy is becoming more spatially homogeneous than the male one, while the rate of life expectancy growth for males turns out to be more homogeneous than for females.

Introduction

Life expectancy is the age that a person in a cohort exposed from birth to death to the mortality rates observed at a given time is expected to live until. Life expectancy can be estimated for a population as a whole, or for subgroups of a population like persons of different sexes, different races, or different ages. Life expectancy is used in many areas, including pension planning, life insurance pricing, and health assessment.

When life expectancy can be estimated at a small-area level, it is very useful to assess health and quality of life inequalities within a region, often through life expectancy maps. The construction of life expectancy maps based on small-area life expectancy estimates is becoming routine, as any cursory search of the internet shows.

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To estimate the life expectancy for the population in a given area and a given period, one needs the age-specific death rates of the population members, which are usually estimated through the mortality rates actually observed at each age among the population in that area during that period. To obtain stable enough life expectancy estimates, one needs to resort to age-specific mortality rates of fairly large populations, and sometimes one also needs to aggregate the mortality data of several years.

When constructing life expectancy maps, one faces the usual bias versus variance trade-off. Unless areas are large enough to have a large enough population, and/or focuses on long enough periods of time, the variability in life expectancy estimates render the maps useless, because they become a patchwork of colors where the largest and the smallest life expectancies correspond to the least populated areas. As a consequence, there is a conflict between using large enough areas and/or mortality data from long enough periods of time to have reliable life expectancy estimates, and using small enough areas and single-year mortality data to be able to explore the space–time variation of life expectancy in detail.

Bayesian models have been proposed to address the problem of mapping disease rates by smoothing small-area disease rate estimates (see, e.g., Clayton and Kaldor 1987; Besag, York, and Mollie 1991; Clayton and Bernardinelli 1992; Mollie 1996). They do that by shrinking small-area rate estimates both toward the global mean as well as toward the local mean estimated through the rates of neighboring areas. The shrinkage toward the local mean accounts for spatial patterns of disease rates that might be explained because of their dependency on unknown risk factors that vary in space. When some of these risk factors are known and can be measured at the small-area level, one can further improve disease mapping by using these specific factors as covariates to further smooth disease rates.

In this paper, we adapt these ideas to build Bayesian models that smooth annual small-area life expectancy estimates for several years, and can be used to map life expectancy and to check the evolution of maps over time. The smoothing is carried out at four different levels, because the shrinking involved acts globally toward the grand mean for each given year, spatially toward the local mean for each year, temporally using past and future values for each given area, as well with the help of covariates associated with life expectancy and measured at the small-area level. The specific area effect, together with the spatial and temporal effects are modeled through a hierarchical (random effects) structure that allows data to dictate the amount of shrinking required at the global, spatial and temporal levels. The effect of covariates is modeled through a fixed effect component.

The approach taken here assumes that one starts with initial annual small-area life expectancy estimates, and the purpose is to smooth them through Bayesian hierarchical models to reduce their variability. That is different from what is proposed in most of the life expectancy mapping literature, that starts by smoothing age-specific mortality rates, and then uses these smoothed estimates to obtain small-area life expectancy estimates, as described in Congdon (2009, 2014a, b), Kulkarni et al. (2011), Jonker et al. (2012, 2013), Stephens et al. (2013), Wang et al. (2013), Bennett et al. (2015), or Alexander, Zagheni, and Barbieri (2017).

When one does not have the small-area age-specific mortality rates for all the areas to start with, maybe because of confidentiality issues, and one only has initial small-area life expectancy estimates, only the approach presented here will be feasible. When small-area age-specific mortality rates are available, which will most often be the case, then one can choose between smoothing them first, as in the mainstream literature, or smoothing life expectancy estimates obtained from non-smoothed age-specific mortality rates, as proposed here. One might also mix

both approaches, and use the models proposed here to further smooth life expectancy estimates obtained from smoothed age-specific mortality rates.

By smoothing small-area life expectancy estimates directly, on top of a series of annual smoothed maps one also obtains small-area life expectancy trend estimates, which are important components of the analysis that are not directly obtainable from models that smooth small-area age-specific mortality rates first. Another strength of modeling directly life expectancy estimates instead of age-specific mortality rates, is that the models are simpler to implement, because they have a smaller number of parameters, and that they are also easier to interpret. By treating the effect of space, time, heterogeneity, and covariates separately, on top of smoothing small-area life expectancy estimates, one also learns about the relative effect of these components on life expectancy.

The use of our method is illustrated by exploring how life expectancy at birth for males and females, and their gap, varied in space and time in the city of Barcelona between 2007 and 2018. The relative effect of covariates, space, heterogeneity, and time on life expectancy in Barcelona is explored. In particular, the evolution of life expectancy inequality among neighborhoods and the gap between female and male life expectancies is also described. This case study is intended as an illustration on ways to present graphically the findings of this type of analysis.

The paper is organized as follows. Section "Initial small-area life expectancy estimates" presents the Barcelona case study, and how the initial small-area life expectancy estimates were obtained. Section "Description of the spatiotemporal model" describes the Bayesian spatiotemporal model proposed, and Section "Life expectancy in Barcelona between 2007 and 2018" uses that model to build annual life expectancy maps and estimate life expectancy trends to help explore the space time evolution of life expectancy in Barcelona. Section "Discussion" discusses extensions of the model.

Initial small-area life expectancy estimates

To illustrate our approach, we use it to construct a time series of annual maps of life expectancy at birth for males and for females in the city of Barcelona between 2007 and 2018, based on nonsmoothed annual life expectancy estimates from its neighborhoods. Here we present how the initial small-area life expectancy estimates were calculated.

The city of Barcelona, with a registered population of 1,616,694 in 2012, is organized in 73 neighborhoods, which are very heterogeneous in size, with the two smallest neighborhoods having only 456 and 1,046 inhabitants in 2012, and the two largest ones having 56,204 and 57,760 inhabitants. The distribution of the population in these neighborhoods is well spread in its range, with the quartiles and the median of this distribution being 10,709, 19,952, and 30,256 on June 30, 2012.

Fig. 1 presents the relationship between the number of males and of females in these neighborhoods. The outlying behavior of neighborhoods 1, 2, and 70, with significantly more males than females, is due to these areas having a significantly larger number of immigrants. The large spread in population sizes leads to neighborhood initial life expectancy estimates having very different variabilities. The fact that about a quarter of all these areas have less than 5,000 males and 5,000 females, means that many of the nonsmoothed small-area life expectancy estimates will have variabilities so large that they will render these estimates useless for mapping purposes.

To obtain the $73 \times 12 \times 2$ initial life expectancy estimates in these 73 neighborhoods, for each one of the 12 years, and for men and women, we rely on the methodology described in

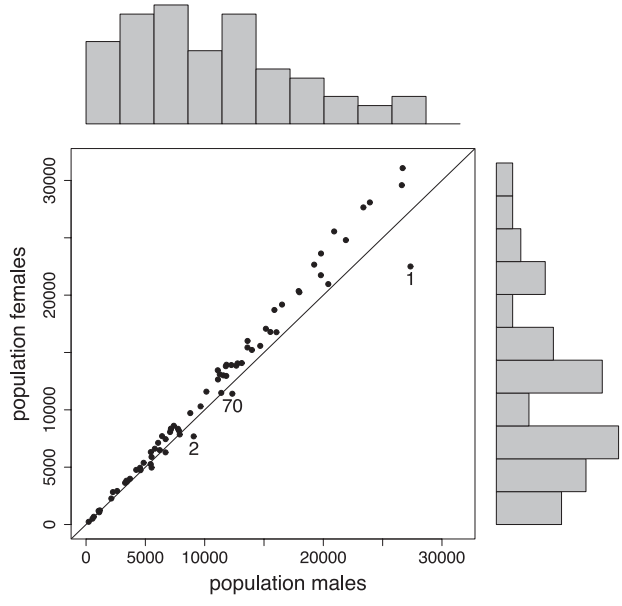

Figure 1. Plot of the number of males and of females in the 73 neighborhoods of Barcelona in June 30, 2012. Neighborhoods 1, 2, and 70 have significantly more immigrants registered than the rest.

Chiang (1968). It uses the annual number of deaths at one-year intervals of age, starting from 0 years all the way up to 89, and it aggregates all deaths at 90 or older into a given category. In a bit over one percent of the instances, involving the smallest areas, we have had to resort to one last category of 85 or older instead, to avoid zero death counts. For an assessment of this life expectancy estimation method, see Toson and Baker (2003), Eayres and Williams (2004), Schervob and Ediev (2011), Jonker et al. (2014b), and Tsimbos, Kalogirou, and Verropoulou (2014). There seems to be an agreement that populations with a minimum of 5,000 people are required to obtain reliable annual life expectancy estimates with this method.

Some of the neighborhoods in Barcelona have such small populations, that it is difficult to obtain life expectancy estimates for them through this method. In particular, there were a few instances of age groups with more annual deaths than their June 30 population. In cases like these, one typically treats life expectancy estimates as missing, and these areas appear as blanks in the map. Instead of that, we proceeded as follows.

For the two smallest neighborhoods, neighborhood 42 with only 220 males and 236 females in 2012 and neighborhood 12 with only 540 males and 506 females, we estimated their life expectancies by merging their annual deaths with the ones for their adjacent neighbors, neighborhoods 41 and 13, respectively, having very similar household income. The neighborhoods 54 and 56, which are adjacent and were the third and fifth smallest ones in 2012, with only 1,110 and 652 males and only 1,068 and 677 females, respectively, were also considered to be a single area for the purpose of estimating their initial life expectancies. Note though that when mapping life expectancies later on, all 73 neighborhoods are considered separate. Hence, the amalgamation of these six neighborhoods into three areas, is made only for the purpose of estimating their initial life expectancies, and not when one smooths these estimates. We preferred this, to treating the

Table 1. Part of the Two 73 × 12 Tables with the Initial Annual Small-Area Life Expectancy Estimates for Men and Women in the 73 Neighborhoods of Barcelona Between 2007 and 2018

Neighb.	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018
Males												
1	73.8	75.9	75.7	75.7	77.1	76.8	78.7	77.5	77.3	79.9	78.3	80.0
2	74.2	75.1	76.8	76.4	79.5	79.2	75.7	75.8	77.4	79.1	76.3	79.7
…	…	…	…	…	…	…	…	…	…	…	…	…	…
73	79.5	79.4	79.8	79.9	81.1	80.5	79.2	80.4	80.3	81.4	80.5	82.0
Females												
1	84.6	84.3	82.1	84.9	86.1	84.4	85.9	85.8	86.5	86.1	84.3	86.4
2	84.9	84.9	83.8	82.9	82.6	88.7	84.3	88.8	82.9	89.0	86.7	86.1
…	…	…	…	…	…	…	…	…	…	…	…	…	…
73	85.8	84.3	87.1	84.0	86.7	85.6	87.0	88.4	86.7	86.1	85.8	87.0

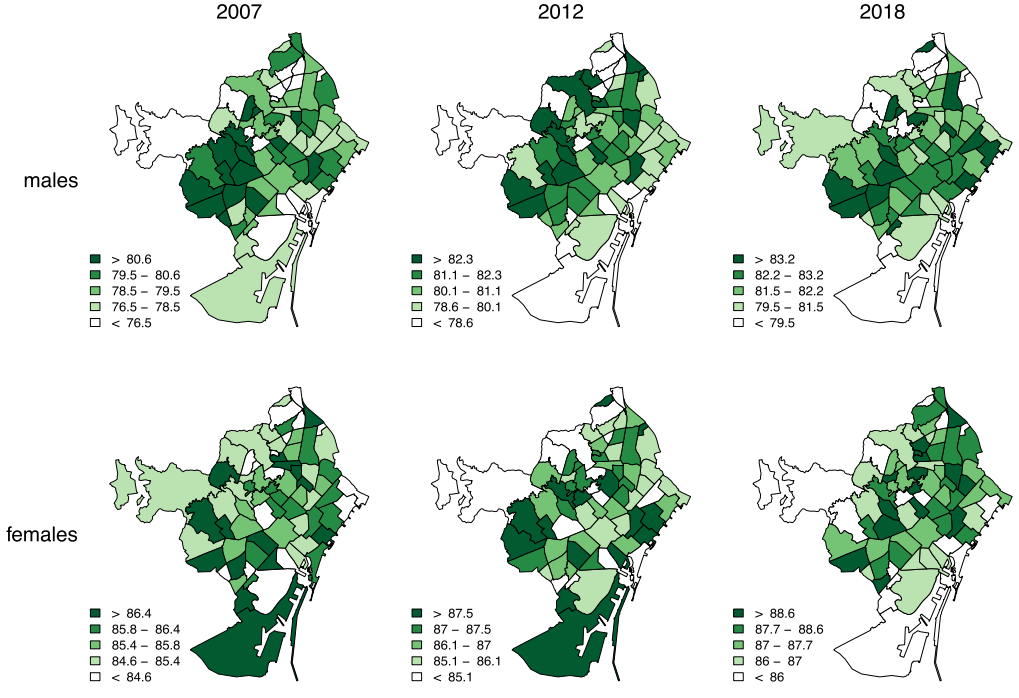

Figure 2. Maps of the initial annual small-area life expectancy estimates, categorized into five classes through their time specific quintiles.

estimates of these smallest areas as missing to start with and let the smoothing model introduced next fill in the gaps.

Table 1 presents part of the initial annual small-area life expectancy estimates for males and for females obtained for each one of the 12 years under consideration. Fig. 2 presents the maps obtained with these un-smoothed life expectancy estimates in 2007, 2012 and 2018, categorized

through their quintiles. In the Appendix, you can find the maps for all the 12 years under study. Note the patchwork appearance of these maps, due to the large variability of most of these annual initial small-area estimates, and the large discontinuities in the values taken by the estimates for a given area in consecutive years.

Many covariates can be used to predict life expectancy, and help smooth initial life expectancy estimates. As covariates relating to the socio-economic level in the area, which has a very well-documented relationship with life expectancy, (see, e.g., Wilkinson 1992; Rogot, Sorlie, and Johnson 1992; Woods et al. 2005; Kulkarni et al. 2011; Chetty et al. 2016; Arias et al. 2018), we have considered the unemployment rate, a household income index, and the educational level measured through the proportion of individuals having a university and/or a high school degree.

Among other covariates not directly related with the socio-economic status, we selected the proportion of people older than 65 living alone, and population density, which in Barcelona turn out to be associated with life expectancy.

The link between living alone and an increase in mortality, and hence with a decrease in life expectancy, is explored, for example, in Koskinen et al. (2007), Pantell et al. (2013) and Ng et al. (2020).

The rationale behind the association between life expectancy and density is less clear cut, but the fact that one investigates life expectancy in a purely urban setting like the city of Barcelona discards it being related to the degree of urbanicity as in Kyte and Wells (2010). In our context, density is capturing the effect of variables not included in the model which are related both with density as well as with life expectancy, like contamination levels, household overcrowding, racial composition or amount of people living in retirement homes.

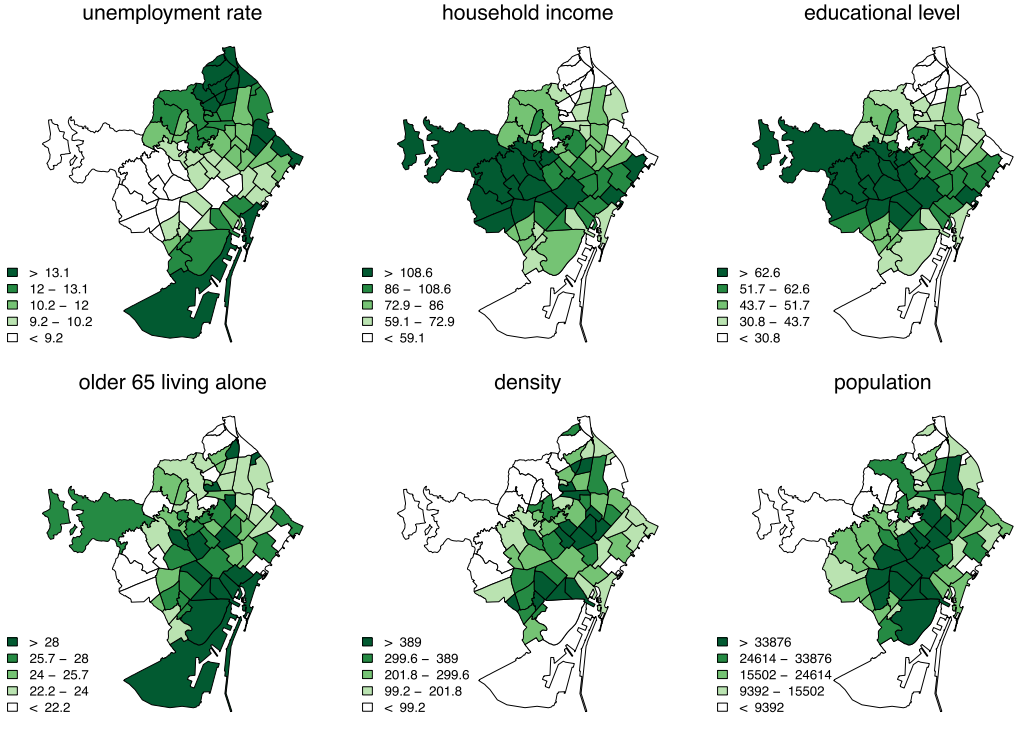

Figure 3. Maps of the value taken by the five covariates considered and of the population in the 73 neighborhoods of Barcelona in 2012.

Fig. 3 maps the value that the five covariates chosen to start with took in 2012 in these neighborhoods of Barcelona, together with the population in them.

Description of the spatiotemporal model

For each area composing the map, i, for $i = 1, \ldots, n$, and each year under study, t, for $t = 1, \ldots, T$, one starts with an initial annual small-area life expectancy estimate, denoted by y_{it}. Our notation will not distinguish between male and female life expectancies, and y_{it} will stand for the initial life expectancy estimate of any subgroup of the population.

For each area, one also has the value taken by p covariates, x_{ji}, for $j = 1, \ldots, p$, evaluated on a baseline year. One could more generally consider models with covariates evaluated every year, but we decided against that because the covariates used do not vary significantly during the periods considered, and their effect on life expectancy has long delays.

Annual initial life expectancy estimates of males (females) of the ith area on the tth year, y_{it}, will be assumed to be normally distributed, which is a sensible assumption given that they are weighted averages of the annual number of deaths at each age, and hence the central limit theorem is in place. That also leads one to assume that the variance of y_{it} is proportional to the inverse of the number of males (females) in the corresponding area at the given time, P_{it}, which is a fact that can also be corroborated empirically.

The expected value of initial life expectancy estimates, y_{it}, will be split into a constant global fixed effect, β_0, and four additive components capturing three different types of dependency, relating to covariates, space, and time, and a fourth component modeling the specific i-th area effect not captured by any of the three dependencies considered.

The first component of the expected value of y_{it}, will be a fixed effect capturing the life expectancy dependence on a set of p covariates, $\sum_{j=1}^{p} \beta_j x_{ji}$.

The second component, γ_i, will be a random effect capturing the spatial dependency of life expectancy. As in conditional autoregressive models used, for example, in Besag, York, and Mollie (1991) and Mollie (1996), γ_i will be assumed to be normally distributed, with expected value:

$$\mathrm{E}(\gamma_i | \gamma_{v(i)}) = \frac{\sum_{k \in v(i)} \gamma_k}{m_i}, \tag{1}$$

and variance:

$$\mathrm{V}(\gamma_i | \sigma_\gamma^2) = \frac{\sigma_\gamma^2}{m_i}, \tag{2}$$

where $v(i)$ is the set of areas that are neighboring with the ith area, $\gamma_{v(i)}$ is the set of all γ_k with $k \in v(i)$, and m_i is the number of areas in $v(i)$.

The third component of the expected value of y_{it}, $(\delta_0 + \delta_i)t$, will be capturing the effect of time on life expectancy. The slope, $(\delta_0 + \delta_i)$, will be the sum of a fixed effect, δ_0, modeling the expected value of the slopes for all areas, and a random effect, δ_i, modeling the i-th area effect on the rate of change in life expectancy. This random slope term, δ_i, will be assumed to have a Normal $(0, \sigma_\delta^2)$ distribution. This linear effect of time provides good fits in developed countries in

recent decades, but a nonlinear component might be needed when the model is intended to cover long periods, or for long term forecasting.

The fourth component of the expected value of y_{it}, α_i, will be a random effect modelling the specific contribution of the i-th area on its life expectancy. This term will be capturing the global unstructured heterogeneity in life expectancy, typically induced by a large set of unobserved covariates, that can neither be captured by the covariates in the model, nor by the spatial dependency term. This heterogeneity component, α_i, will be assumed to have a Normal $(0, \sigma_\alpha^2)$ distribution.

Hence, initial life expectancy estimate of males (females) of the i-th area on the tth year will be assumed to be normally distributed with expected value:

$$\mathrm{E}(y_{it}|\beta, \gamma_i, \delta_0, \delta_i, \alpha_i) = \beta_0 + \sum_{j=1}^{p} \beta_j x_{ji} + \gamma_i + (\delta_0 + \delta_i)t + \alpha_i, \tag{3}$$

where $\beta = (\beta_0, \beta_1, \ldots, \beta_p)$, and with variance

$$Var(y_{it} \mid \beta, \gamma_i, \delta_0, \delta_i, \alpha_i, \sigma^2) = \frac{\sigma^2}{P_{it}}$$

for $i = 1, \ldots, n$ and $t = 1, \ldots, T$, where P_{it} is the number of males (females) of the i-th area on the tth year.

Depending on which ones of the four components of this full model are active and which ones are not, one obtains a set of 16 submodels, ranging from the baseline model with:

$$E(y_{it}|\beta_0, \delta_0) = \beta_0 + \delta_0 t, \tag{4}$$

in place when none of the four components are present in the model, and therefore, there is no difference in life expectancy between areas, and the full model, (3.3). Often, only the eight submodels with the heterogeneity term, α_i, present will be of interest.

We adopt a Bayesian inference approach, requiring one to choose a prior distribution on the parameters of the model to start with, and to compute (or simulate from) the posterior distribution by incorporating the information in the data. The parameters requiring a prior distribution are β, δ_0, σ_γ^2, σ_α^2, σ_δ^2, and σ^2.

As a prior distribution for $\beta_1, \ldots, \beta_p$, we choose independent normal distributions with a prior mean of 0 and a prior variance of 100, which is large because the covariates are standardized and one does not expect the coefficients to be that large. As a prior for β_0 and for δ_0 we also choose independent normal distributions with a prior mean of 80 and 0, respectively, and with a prior variance of 100. The prior mean for β_0 is chosen to be close to the life expectancy in Europe in 2007.

As a prior distribution for σ_γ^2, σ_α^2, σ_δ^2, and σ^2, it will be assumed that their inverses are Gamma distributed with a prior mean of 1 and a prior variance of 100.

In our example, this model is updated based on the initial life expectancy estimates presented in Section 2, using the WinBugs MCMC implementation to simulate from the corresponding posterior distribution (see Lunn et al. 2000). Chain convergence is assessed through visual inspection of the sample traces and by monitoring diagnostic measures, like their sample autocorrelations, described in Gelman and Rubin (1992). Four chains were ran until convergence, discarding the first 10,000 iterations of each chain and keeping one out of ten iterations afterwards. The final analysis is therefore based on 50,000 realization, 12,500 from each chain.

The posterior expected value of $E(y_{it} \mid \beta, \gamma_i, \delta_0, \delta_i, \alpha_i)$ under the full model, or under the model chosen among the fifteen sub-models, is the smoothed estimate of the life expectancy for the i-th area on the tth year, to be used to map life expectancies for the tth year.

Life expectancy in Barcelona between 2007 and 2018

Choice of smoothing sub-model

Here we use the models described above to build the series of life expectancy maps for males and for females in Barcelona between 2007 and 2018, based on the annual initial life expectancy estimates in its neighborhoods partially presented in Table 1. The data used for this study is available upon request from the corresponding author.

The three covariates considered that directly relate to socio-economic status have correlations larger than 0.8, and when all are in the models, educational level becomes the only relevant term of the three. As a consequence, we dropped unemployment and income from the final models, and the covariates are the centered and standardized versions of educational level, proportion of individuals older that 65 living alone, and density.

Table 2 presents the value of the DIC, a model selection criteria proposed by Spiegelhalter et al. (2002), when one uses the initial life expectancy estimates to update the 16 models obtained by including any combination of the four components in the full model, that is, the covariates fixed effect, $\sum_{j=1}^{p} \beta_j x_{ji}$, and the random effects for space, γ_i, for time, $\delta_i t$, and for the heterogeneity not captured by the other components, α_i. Table 2 also provides p_D, the effective number of parameters, which measures the complexity of hierarchical models through the difference

Table 2. DIC and Effective Number of Parameters, p_D, When the Models in Section 3 are Updated with Life Expectancy Estimates in Table 1

Covariates	Spatial, γ_i	Heterog., α_i	Temporal, $\delta_i t$	Male DIC	pD	Female DIC	pD
No	No	No	No	3,999.8	3.0	3,427.4	3.0
Yes	No	No	No	3,511.4	6.0	3,303.4	6.0
No	Yes	No	No	3,404.2	68.2	3,248.4	56.1
No	No	Yes	No	3,403.5	68.9	3,251.5	58.2
No	No	No	Yes	3,656.4	64.5	3,295.0	54.6
Yes	Yes	No	No	3,408.4	52.0	3,244.8	45.2
Yes	No	Yes	No	3,407.4	54.3	3,242.7	46.6
Yes	No	No	Yes	3,446.8	50.4	3,241.7	49.1
No	Yes	Yes	No	3,405.2	69.0	3,249.6	57.4
No	Yes	No	Yes	3,403.5	86.4	3,245.7	73.2
No	No	Yes	Yes	3,403.1	86.0	3,249.2	74.9
Yes	Yes	Yes	No	3,409.0	54.0	3,243.8	47.1
Yes	Yes	No	Yes	3,409.9	66.9	3,240.1	55.1
Yes	**No**	**Yes**	**Yes**	3,407.0	68.7	3,236.0	58.3
No	Yes	Yes	Yes	3,404.1	86.9	3,245.8	74.4
Yes	Yes	Yes	Yes	3,408.6	68.7	3,236.2	59.8

The covariates are the educational level, proportion of individuals older than 65 living alone, and density. In boldface, the model selected to build male and female life expectancy maps.

between the posterior mean of the deviance, and the deviance of the posterior mean of the parameters of interest.

The first model in Table 1, with all four components lacking, is the baseline model (3.5), and the last model in the table, with all four components present, is the full model (3.3). The baseline model has a much larger DIC value than any other model and, in particular, much larger than the four models with a single component, indicating that all four components are meaningful and useful.

The four models that are clearly worse for males, and the three models that are worse for females, are all lacking at once both the spatial as well as the heterogeneity component. Note also that the best two models with a single component are always the third and fourth models, having either the spatial or the heterogeneity component. Hence, either the heterogeneity component or the spatial component should be in the model, but given that they capture a similar type of variability, one might not need to have both of them in there.

For female life expectancy, the model with the smallest DIC is the one with all components present except the spatial one, and it is the model that we will use for mapping. For females, the full model with all components present is the second close best.

For male life expectancy, the smallest DIC is attained by the model without covariates and without the spatial effect, almost tied with simpler models like the ones with only the heterogeneity or only the spatial component. But since the DIC for the model chosen for females is also small, that will be the model used to map life expectancy for males as well.

The submodel picked here, with all components except the spatial one, is a safe pick as a default model when mapping life expectancy. Alternatively one might also use as default models the one with all components except heterogeneity, and the full model with all components present. When implementing this approach in simpler settings though, it might be worth repeating the exercise of updating all sixteen submodels and picking up a simpler model, if the DIC indicates that to be the best option in that case.

Results of the analysis in Barcelona

To illustrate how the selected model smooths initial life expectancy estimates of an area by shrinking them toward a global/local mean, Fig. 4 compares the initial and the model smoothed estimates for two specific neighborhoods. We use neighborhood 11, with 20,416 males and 20,964 females in 2012, to represent large neighborhoods, and neighborhood 49, with only 3,425 males and 3,719 females, to represent small ones. As one expects, the less populated the area, the larger the variability of initial estimates, and the stronger the shrinking effect. To appreciate any spatial or temporal feature in life expectancy time plots or maps, one needs to resort to the smoothed estimates, because the initial ones are far too variable even for the larger areas in this study.

The correlations between male and female initial life expectancy estimates in 2007, 2012, and 2018, which are 0.09, 0.56, and 0.22, are a lot smaller than the correlations between male and female corresponding smoothed life expectancy estimates, 0.94, 0.90, and 0.82. That is another indication that the model improves small-area life expectancy estimates.

Fig. 5 presents the male and female life expectancy maps for 2007, 2012, and 2018 using the estimates smoothed through the model with all components except the spatial one. For the set of maps for all 12 years, see the Appendix. Different from Fig. 2, mapping initial estimates, in Fig. 5 one clearly appreciates the relationship between life expectancy and location. In particular, by comparing Figs. 3 and 5 one checks that there is an association between a neighborhood

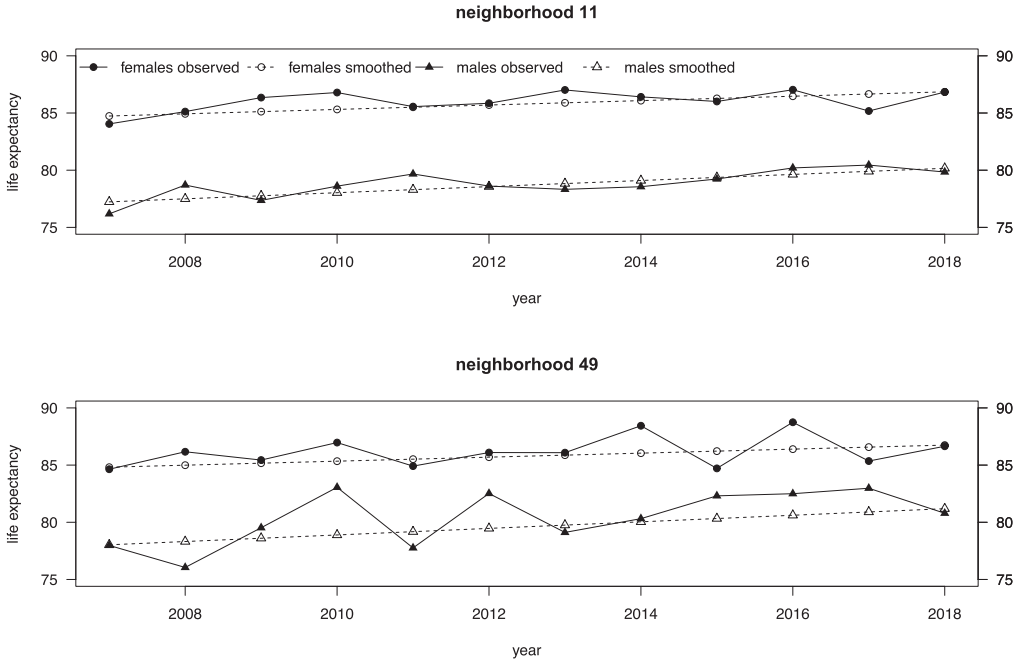

Figure 4. Initial male and female life expectancy estimates, and model smoothed life expectancy estimates for neighborhoods 11 and 49.

having large life expectancy on the one hand, and having large income and education level and small unemployment on the other hand; that is specially so for males.

In Fig. 5, life expectancies are categorized based on time specific quintiles, because the focus is the relative changes of neighborhood life expectancy across time. In the case of male life expectancy very few neighborhoods switch class, and the spatial structure of these five life expectancy classes is very persistent over time. That is in accordance with area linked temporal trend effects, δ_i, for males being of little relevance.

In the case of female life expectancy, the 2007 map shows an almost identical spatial structure as the maps for males, but that spatial dependency associated with income and education washes away with time. The correlation between female life expectancy and education decreases every year starting from 0.72 in 2007 down to 0.52 in 2018, and its correlation with income decreases from 0.57 in 2007 down to 0.40 in 2018. Female life expectancy is becoming a lot less associated with socio-economical level than the male one.

If the focus was the absolute change in life expectancy over time instead of the relative change in different areas, one would use the same class breaks for life expectancy of all years. If one did that in Fig. 5, one would miss the spatial distribution of life expectancy, due to its rapid growth. Note that by checking how class breaks increase from period to period in Fig. 5, one also gets an idea on the overall change over time of life expectancy.

In Fig. 5 one can also appreciate that the variability in male life expectancy across different neighborhoods is a lot larger than the variability in female life expectancy. The difference between the highest and the lowest male life expectancy in a neighborhood was 8.2 years in 2007, and 9.4 years in 2018, with the interquartile ranges being 1.88 years both in 2007 and in 2018.

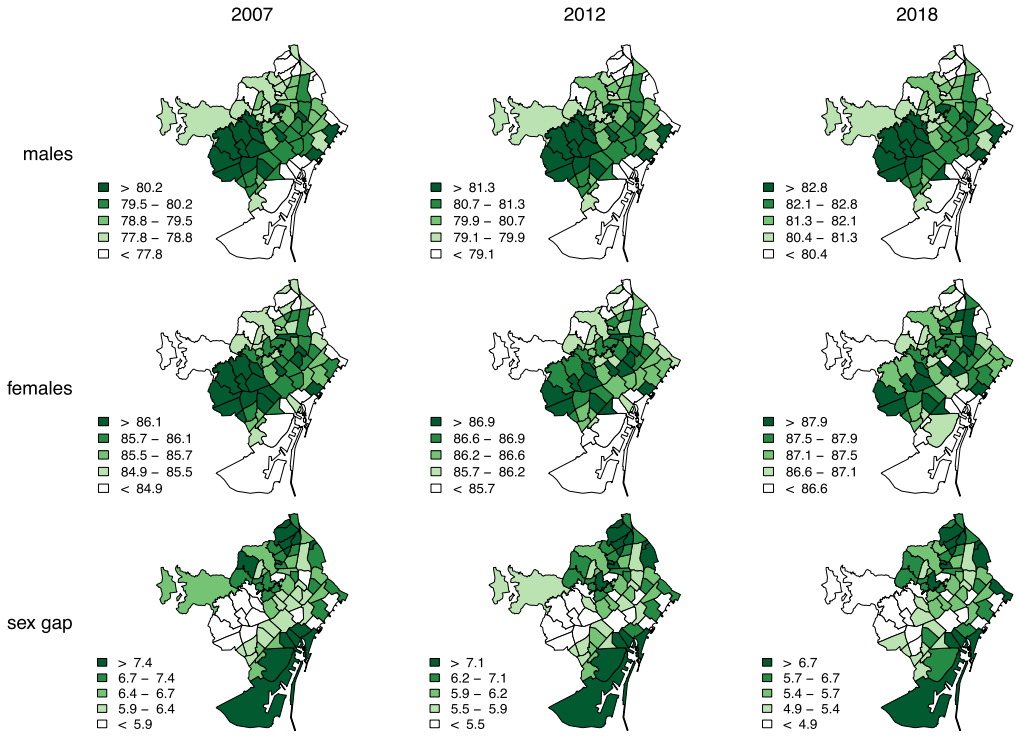

Figure 5. Maps of male and of female life expectancies, and of their gap, estimated with the model that has all terms except the spatial one, categorized in five classes through their time specific quintiles.

Instead, the largest differences in female life expectancies were only 3.5 years in 2007 and 4.6 years in 2018, with an interquartile range of 0.97 years in 2007 and 1.10 years in 2018.

The maps of the estimated gap between female and male life expectancies in 2007, 2012, and 2018, in Fig. 5, show again a spatial dependency pattern similar to the one for life expectancies. That gap tends to be smaller for areas with higher socio-economic status, and it is systematically decreasing along this twelve years period, with a median gap of 6.54 years in 2007, 6.04 years in 2012, and 5.59 years in 2018.

Fig. 6 presents the posterior expected value and the 90% posterior credible interval for the time slopes, $\delta_0 + \delta_i$, estimating the rate at which male and female life expectancies have been growing in the i-th neighborhood. These time slopes are positive for all 73 neighborhoods, and tend to be larger for males than for females, consistent with the fact that the gap between female and male is getting smaller. Fig. 6 indicates that the posterior distribution of the time slopes of all neighborhoods for male life expectancy are very similar, in line with temporal random effects not being that relevant for males. As a consequence, mapping the posterior expected value of $\delta_0 + \delta_i$ would not be that useful in our setting, but it will be useful in cases where temporal random effects are more important.

The posterior distribution of δ_0 is $E(\delta_0 \,|\, y) = 0.23$ years of life expectancy per year for males, and $E(\delta_0 \,|\, y) = 0.15$ years of life expectancy per year for females. This means that between 2007 and 2008 the overall life expectancies at birth for males and for females have been growing on

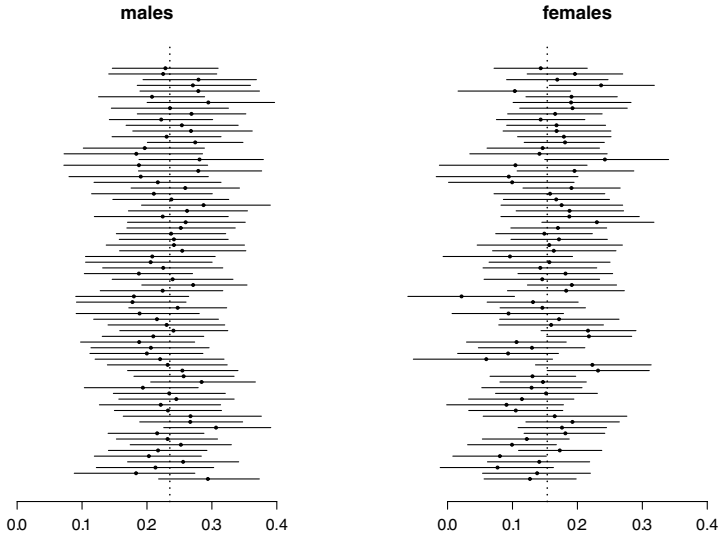

Figure 6. Posterior expected value and 90% credible intervals of $\delta_0 + \delta_i$, the rate at which life expectancies have been growing in each neighborhood. [Correction added on July 21, 2021, after first online publication: Figure 6 was corrected.]

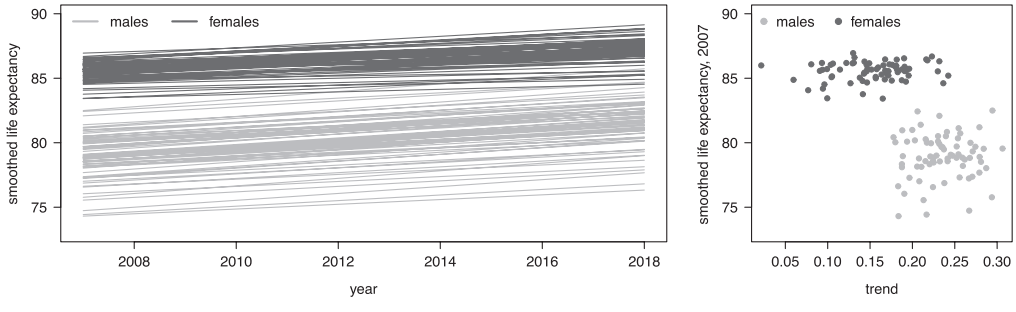

Figure 7. Smoothed estimates of male and female life expectancies as a function of time in the 73 neighborhoods, and plot of the smoothed life expectancy estimate for 2007 against the posterior expected value of $\delta_0 + \delta_i$, which estimates the rate of growth in each neighborhood in years per year.

average at these rates. The smallest estimate of the trend for males, $E(\delta_0 + \delta_i \,|\, y)$, is of 0.18 years per year in neighborhoods 32 and 33, and for females it is of 0.02 years per year in neighborhood 33. The largest trend estimate for males is of 0.31 years per year in neighborhood 10, and for females it is of 0.24 years per year in neighborhood 57.

To further explore the effect of time on life expectancy, and how that time effect varies from area to area, the left panel in Fig. 7 presents how the smoothed estimates of male and female life expectancies in the neighborhoods change with time. On the right panel, one can see that the life expectancy estimate for 2007 is barely related with the temporal rate of growth of life expectancy; It does not hold that the this rate of growth is larger in neighborhoods where life expectancy in 2007 was smaller. In that right panel, one can also observe again that the male life expectancy is more variable than the female one, but the small-area male life expectancy trends are less variable than the female ones.

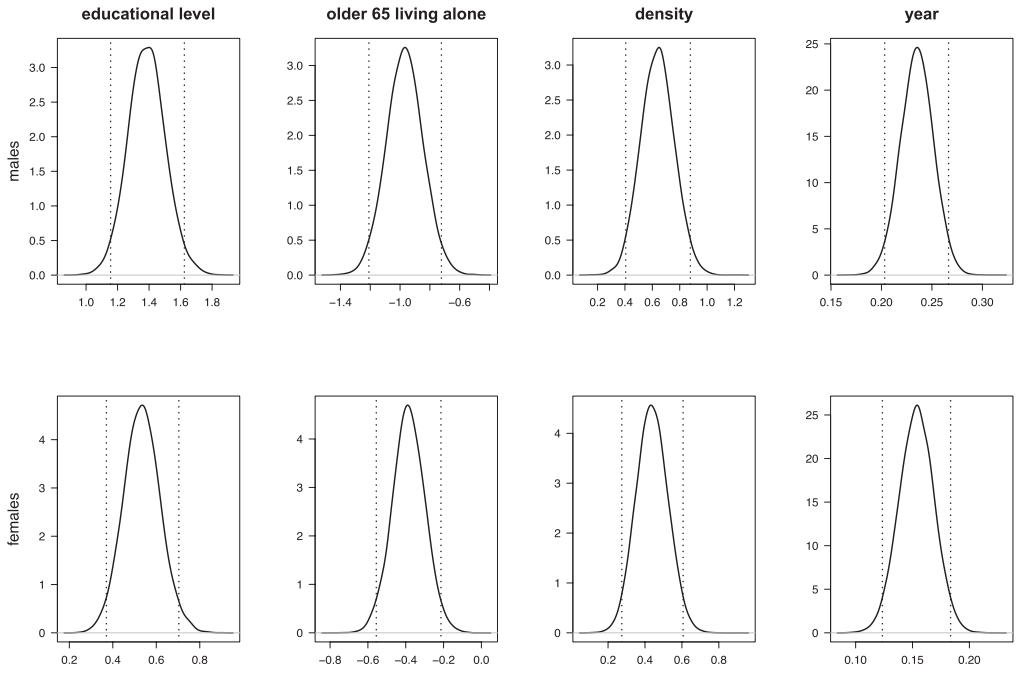

Figure 8. Marginal posterior distributions of the coefficients, β_j, of the covariates and of δ_0 under the model with all terms except the spatial one.

The relevance of the role played by the covariates is backed by the fact that the posterior distributions of their coefficients, β_j, in Fig. 8, all have a mean that is more than two standard deviations away from zero. With everything else being the same, the larger the educational level and the density in the neighborhood, and the smaller the proportion of individuals older than 65 living alone, the larger the life expectancies in that area.

Educational level captures the effect of individuals with higher socio-economic status living longer, which is a feature always found in these studies. The fact that living alone seems to be associated with smaller life expectancy is also documented in the literature.

When the role of density has been explored in regions involving both rural as well as urban areas, one often finds a negative association with life expectancy, due to individuals in rural areas living longer. The case study here involves only urban areas, and hence the positive association found with density is bound to capture the combined effect of factors, other than the degree of urbanicity, that are not in the model but are related both with density and life expectancy. Fig. 3 indicates that density is smallest in areas on the periphery of Barcelona. Factors that might help explain this positive association with density might be the contamination level, the degree of household overcrowding, the racial mix or the percentage of people living in retirement homes in each area.

Discussion

A Bayesian model that smooths annual small-area life expectancy estimates to build life expectancy maps and estimate life expectancy trends has been proposed. Even though it has been used to map life expectancy at birth for males and for females, it can be used to map life expectancy

at any age and for other subsets of a population. Some of the advantages of the model presented are its simplicity, its interpretably thanks to its modularity, and the ease with which it can be extended to match specific requirements.

It is estimated that between 2007 and 2018 life expectancy in Barcelona has been growing between 0.18 and 0.31 years per year for males, and between 0.02 and 0.24 years per year for females, depending on the neighborhood. The median gap between female and male life expectancy estimates in neighborhoods has decreased 0.95 years during these eleven years. And in terms of life expectancy inequality between neighborhoods, life expectancy ranges barely changed, with male range being about twice as large as female range.

The spatial distribution of male and female life expectancies in 2007, together with their gap, is strongly associated with socio-economic status, but female life expectancy is quickly becoming more spatially homogeneous than the male one. In terms of trends, the male ones are more spatially homogeneous than the female ones, that are a lot more variable.

Different settings will allow for different covariates, and the role played by covariates like density will be very different when the model is used to map life expectancy in regions broader than Barcelona, because it will capture differences between rural and urban life expectancies. Also, in our case study two areas were considered either neighbors or not neighbors, but one can use more sophisticated spatial structures incorporating different levels of neighborhoodness depending on the separation between the areas. One could also incorporate a hierarchical structure in the heterogeneity term to account for the fact that areas might be nested into larger units; In Barcelona, for example, one might have used the fact that the 73 neighborhoods are nested into 10 districts.

There is a literature focusing on long term forecasting of life expectancy, (see, e.g., Lee and Carter 1992; Raftery et al. 2013; Kontis et al. 2017). Since they usually deal with large areas that have low variance life expectancy estimates, they do not resort to spatial or covariate smoothing, and focus on modeling the temporal evolution. The appropriateness of the assumption of a linear effect of time on life expectancy is well documented in the literature, (see, e.g., White 2002), but if one intends to explore the evolution of life expectancy maps along longer periods of time, one will need to add a nonlinear temporal component in the model, and maybe let life expectancy variability, σ^2, change with time. The existence of a war, a pandemic or some other large catastrophe during the period of study would also require departing from this linearity assumption.

In life expectancy mapping practice, it is often the case that the initial life expectancy estimates for the smaller areas are missing, because mortality data for them is too sparse to yield reliable estimates. That is the case for example in Arias et al. (2018), where life expectancy is estimated only for areas with more than 5,000 individuals. In our example, we obtained initial life expectancy estimates for all the areas, including some very small ones, at the cost of using some amalgamation at the initial estimation stage. Bijak and Bryant (2016) argues that one advantage of using Bayesian models is that they can be easily adapted to estimate missing values, and hence our approach can help avoid life expectancy maps with blind spots where initial life expectancy estimates are missing.

When the starting point is the set of small-area age-specific annual mortality rates for each area, (instead of initial life expectancy estimates), one can choose between smoothing mortality rates first, and then averaging them to compute small-area life expectancy estimates, as in the mainstream literature, or averaging non-smoothed mortality rates first, to compute initial life expectancy estimates, and then smoothing these estimates, the way considered here. It is open for investigation under which circumstances each one of these two approaches will lead to better

maps. Advantages of smoothing initial life expectancy estimates the way advocated for here are the simplicity and interpretability of the models used, and the fact that the models provide small-area life expectancy trend estimates.

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Appendix A

Maps for all 12 years

References

Alexander, M., E. Zagheni, and M. A. Barbieri (2017). "A Flexible Bayesian Model for Estimating Subnational Mortality." *Demography*, 54, 2025–41.

Arias, E., L. A. Escobedo, J. Kennedy, C. Fu, and J. Cisewski (2018). "US Small-Area Life Expectancy Estimates Project: Methodology and Results Summary." *Vital and Health Statistics*, 2(181), 1–40.

Bennett, J. E., G. Li, K. Foreman, N. Best, V. Kontis, C. Pearson, P. Hambly, and M. Ezzati (2015). "The Future of Life Expectancy and Life Expectancy Inequalities in England and Wales: Bayesian Spatio Temporal Forecasting." *The Lancet*, 386, 163–70.

Besag, J., J. York, and A. Mollie (1991). "Bayesian Image Restoration with Two Applications in Spatial Statistics (with Discussion)." *Annals of the Institute of Statistical Mathematics*, 43, 1–59.

Bijak, J., and J. Bryant (2016). "Bayesian Demography 250 Years After Bayes." *Population Studies*, 70, 1–19.

Chetty, R., M. Stepner, S. Abraham, S. Lin, B. Scuderi, N. Turner, A. Bergeron, and D. Cutler (2016). "The Association Between Income and Life Expectancy in the US, 2001–2014." *JAMA*, 315, 1750–66.

Chiang, C. L. (1968). "The Life Table and its Construction." In Introduction to Stochastic Processes in Biostatistics, 189–214, New York: Wiley.

Clayton, D. G., and J. Kaldor (1987). "Empirical Bayes Estimates of Age-Standardized Relative Risks for Use in Disease Mapping." *Biometrics*, 43, 671–81.

Clayton, D. G., and L. Bernardinelli (1992). "Bayesian Methods for Mapping Disease Risk." In Geographical and Environmental Epidemiology: Methods for Small-area Studies. 201–20, edited by P. Elliot, J. Cuzick, D. English and R. Stern. Oxford: Oxford University Press.

Congdon, P. D. (2009). "Life Expectancies for Small Areas: A Bayesian Random Effects Methodology." *International Statistical Review*, 77, 222–40.

Congdon, P. D. (2014a). "Estimating Life Expectancies for US Small Areas: A Regression Framework." *Journal of Geographical Systems*, 16, 1–18.

Congdon, P. D. (2014b). "Modelling Changes in Small Area Disability Free Life Expectancy: Trends in London Wards Between 2001 and 2011." *Statistics in Medicine*, 33, 5138–50.

Eayres, D., and E. S. Williams (2004). "Evaluation of Methodologies for Small Area Life Expectancy Estimation." *Journal of Epidemiology and Community Health*, 58, 243–49.

Gelman, A., and D. B. Rubin (1992). "Inference from Iterative Simulation Using Multiple Sequences (with Discussion)." *Statistical Science*, 7, 457–511.

Jonker, M. F., F. van Lenthe, P. D. Congdon, B. Donkers, A. Burdort, and J. P. Mackenbach (2012). "Comparison of Bayesian Random-Effects and Traditional Life Expectancy Estimations in Small Area Applications." *American Journal of Epidemiology*, 176, 929–37.

Jonker, M. F., P. D. Congdon, F. J. van Lenthe, B. Donkers, A. Burdorf, and J. P. Mackenbach (2013). "Small Area Health Comparisons Using Health-Adjusted Life Expectancies: A Bayesian Random Effects Approach." *Health & Place*, 23, 70–78.

Kontis, V., J. E. Bennett, C. D. Mathers, G. Li, K. Foreman, and M. Ezzati (2017). "Future Life Expectancy in 35 Industrialised Countries: Projections with a Bayesian Model Ensemble." *The Lancet*, 389, 1323–35.

Koskinen, S., K. Joutsenniemi, T. Martelin, and P. Martikainen (2007). "Mortality Differences According to Living Arrangements." *International Journal of Epidemiology*, 36, 1255–64.

Kulkarni, S. C., A. Levin-Rector, M. Ezzati, and C. J. Murray (2011). "Falling Behind: Life Expectancy in US Counties from 2000 to 2007 in an International Context." *Population Health Metrics*, 9, 16.

Kyte, L., and C. Wells (2010). "Variation in Life Expectancy Between Rural and Urban Areas of England, 2001–07." *Health Statistics Quarterly*, 46, 25–50.

Lee, R. D., and L. R. Carter (1992). "Modeling and Forecasting U.S. Mortality." *Journal of the American Statistical Association*, 87, 659–71.

Lunn, D. J., A. Thomas, N. Best, and D. Spiegelhalter (2000). "WinBUGS - A Bayesian Modelling Framework: Concepts, Structure and Extensibility." *Statistics and Computing*, 10, 325–37.

Mollie, A. (1996). "Bayesian Mapping of Disease." In Markov Chain Monte Carlo in Practice. 359–79, edited by W. R. Gilks, S. Richardson and D. J. Spiegelhalter. London: Chapman and Hall.

Ng, N., A. Santosa, L. Weinehall, and G. Malmberg (2020). "Living Alone and Mortality Among Older People in Vasterbotten County in Sweeden: A Survey and Register-Based Longitudinal Study." *BMC Geriatrics*, 20, 7.

Pantell, M., D. Rehkopf, D. Jutte, S. L. Syme, J. Balmes, and N. Adler (2013). "Social Isolation: A Predictor of Mortality Comparable to Traditional Clinical Risk Factors." *American Journal of Public Health*, 103, 2055–62.

Raftery, A. E., J. L. Chunn, P. Gerland, and H. Sevikova (2013). "Bayesian Probabilistic Projections of Life Expectancy for All Countries." *Demography*, 50, 777–801.

Rogot, E., P. D. Sorlie, and N. J. Johnson (1992). "Life Expectancy by Employment Status, Income, and Education in the National Longitudinal Mortality Study." *Public Health Reports*, 107, 457–61.

Schervob, S., and D. Ediev (2011). "Significance of Life Table Estimates for Small Populations: Simulation-Based Study of Estimation Errors." *Demographic Research*, 22, 527–50.

Spiegelhalter, D., N. Best, B. Carlin, and A. van der Linde (2002). "Bayesian Measures of Model Complexity and Fit." *Journal of the Royal Statistical Society, Ser B*, 64, 583–639.

Stephens, A. S., S. Purdie, B. Yang, and H. Moore (2013). "Life Expectancy Estimation in Small Administrative Areas with Non-Uniform Population Sizes: Application to Australian New South Wales Local Government Areas." *BMJ Open*, 3.

Toson, B., and A. Baker (2003). "Life Expectancy at Birth: Methodological Options for Small Populations." National Statistics Methodological Series, Vol. 33, Norwich: Office for National Statistics.

Tsimbos, C., S. Kalogirou, and G. Verropoulou (2014). "Estimating Spatial Differentials in Life Expectancy in Greece at Local Authority Level." *Population, Space and Place*, 20, 646–63.

Wang, H., A. E. Schumacher, C. E. Levitz, A. H. Mokdad, and C. J. L. Murray (2013). "Left Behind: Widening Disparities for Males and Females in US County Life Expectancy, 1985–2010." *Population Health Metrics*, 11, 8.

White, K. M. (2002). "Longevity Advances in High-Income Countries, 1955–96." *Population and Development Review*, 28, 59–76.

Wilkinson, R. G. (1992). "Income Distribution and Life Expectancy." *The BMJ*, 304, 165–68.

Woods, L. M., B. Rachet, M. Riga, N. Stone, A. Shah, and M. P. Coleman (2005). "Geographical Variation in Life Expectancy at Birth in England and Wales is Largely Explained by Deprivation." *Journal of Epidemiology and Community Health*, 59, 115–20.

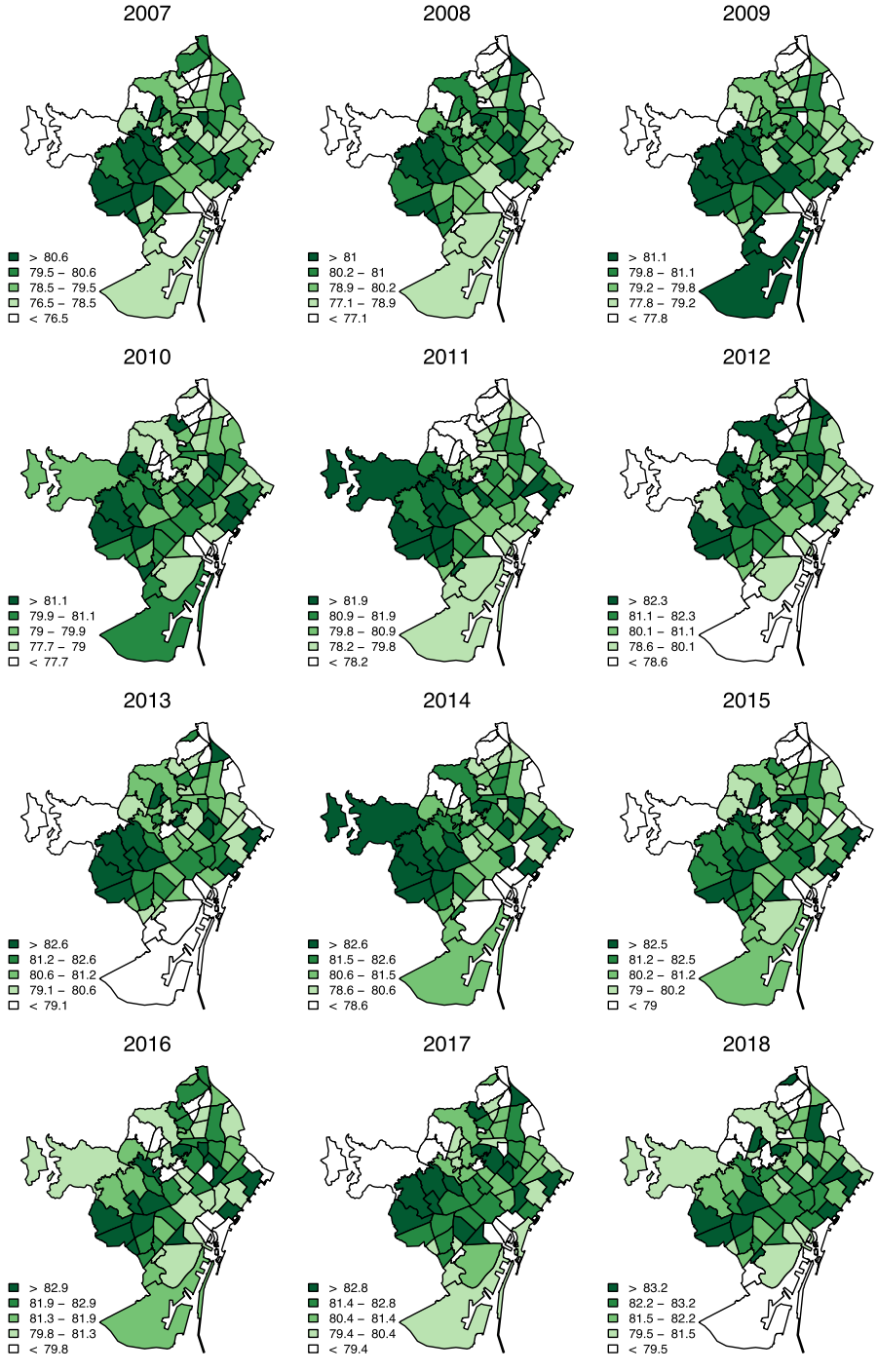

Figure A1. Maps of male initial life expectancy estimates, categorized through their annual specific quintiles.

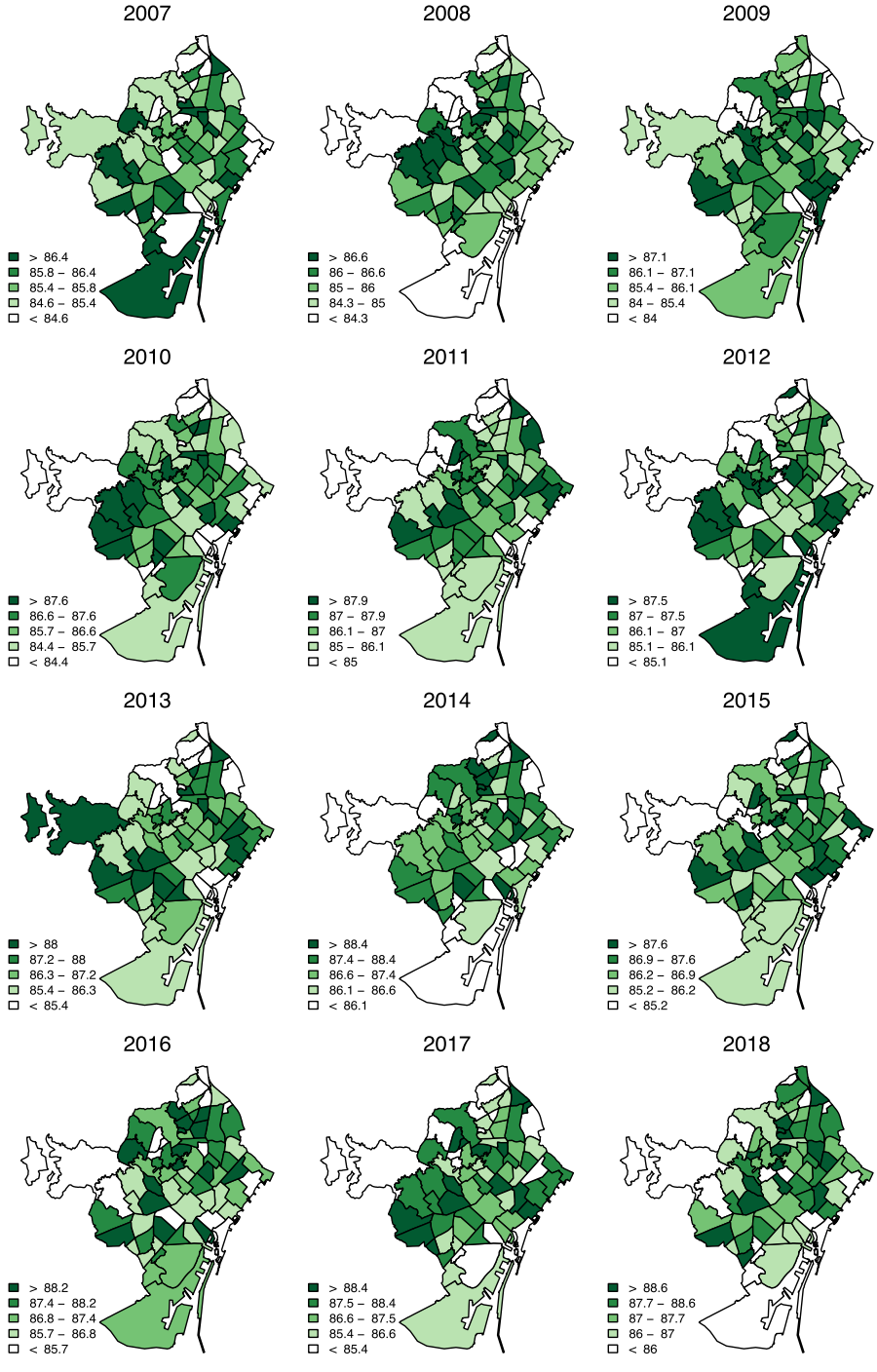

Figure A2. Maps of female initial life expectancy estimates, categorized through their annual specific quintiles.

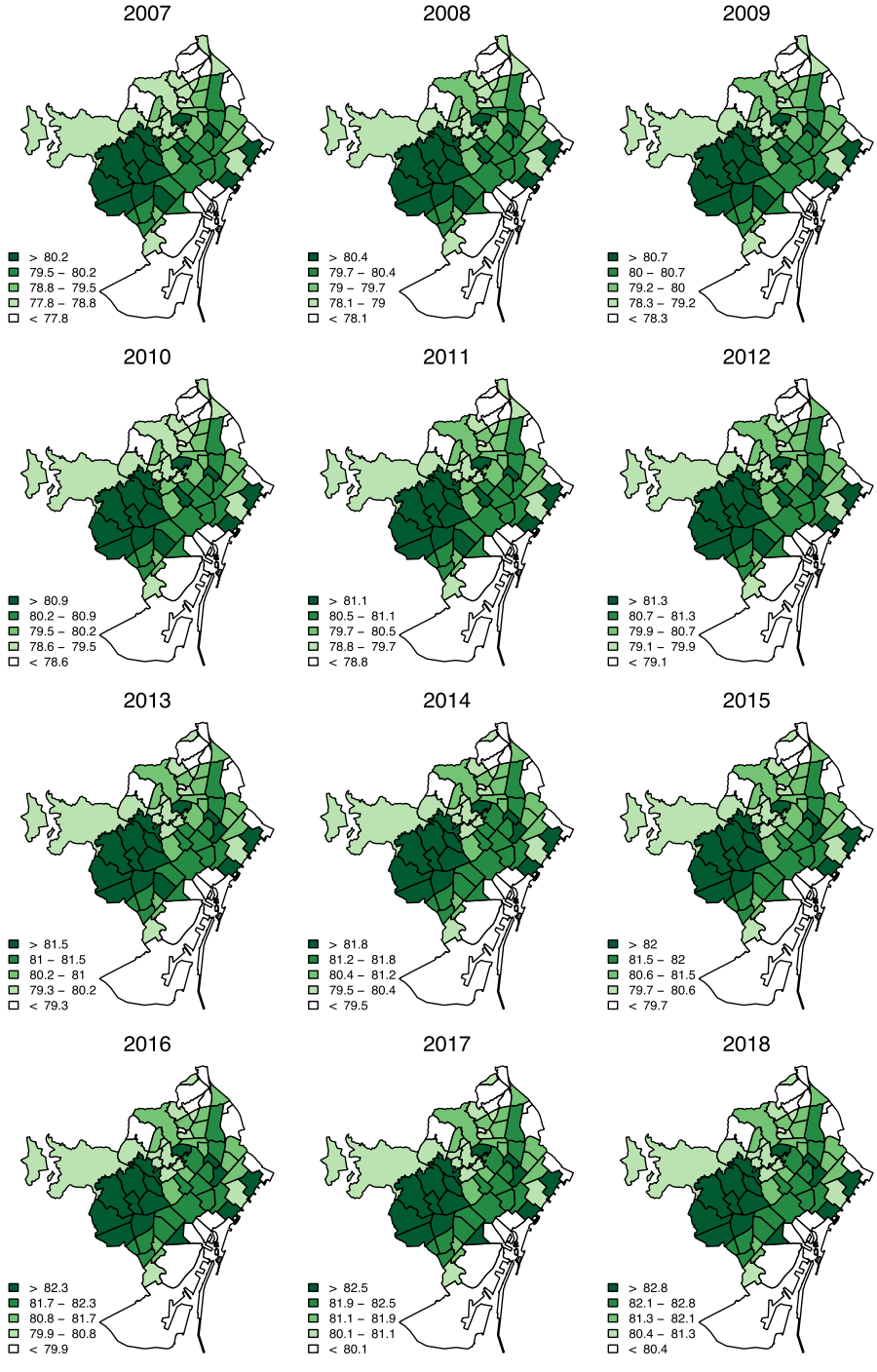

Figure A3. Maps of male life expectancy estimates smoothed using the model with all terms except the spatial one, categorized through their annual specific quintiles.

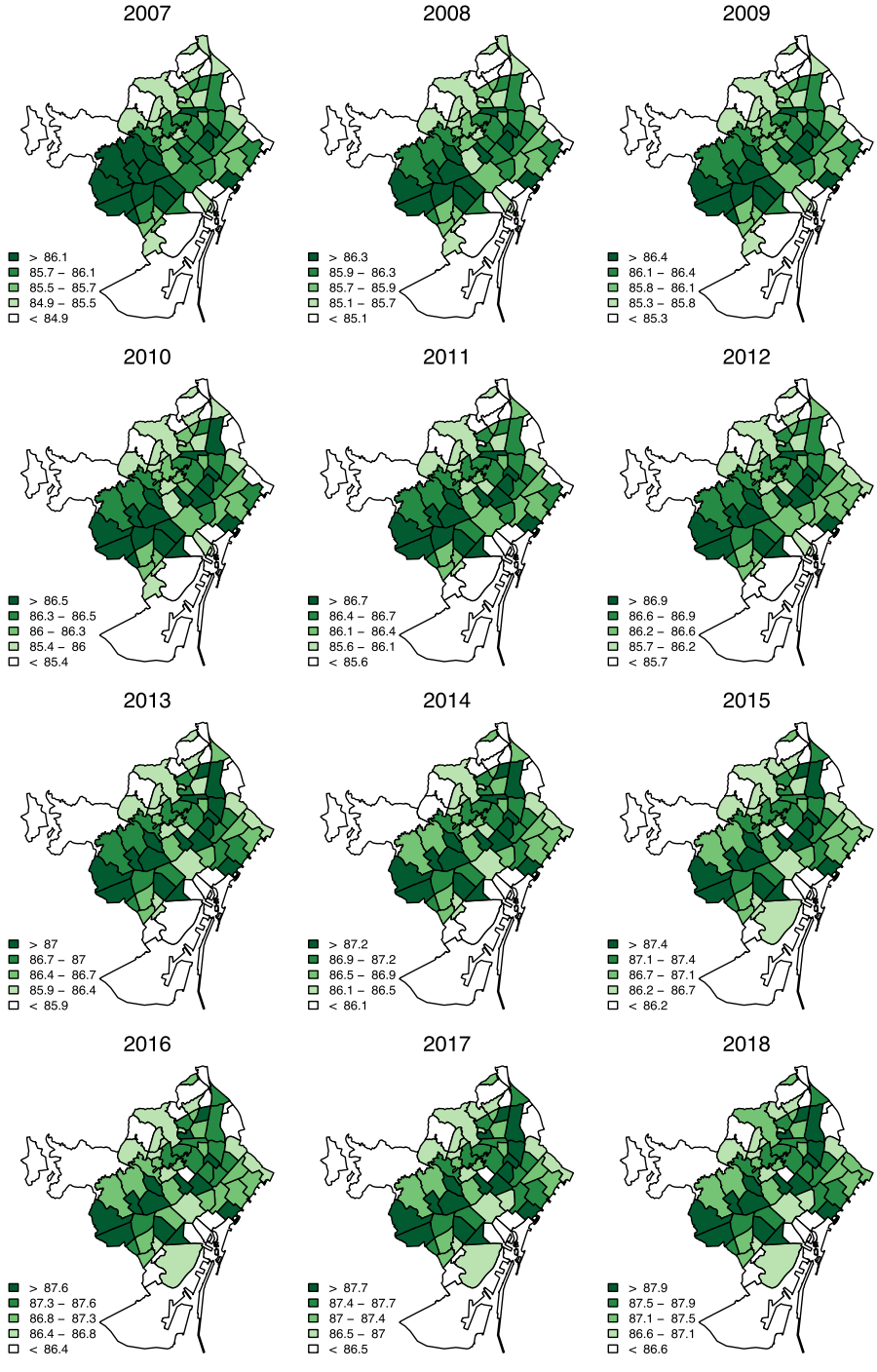

Figure A4. Maps of female life expectancy estimates smoothed using the model with all terms except the spatial one, categorized through their annual specific quintiles.