Variation in life expectancy and mortality by cause among neighbourhoods in King County, WA, USA, 1990–2014: a census tract-level analysis for the Global Burden of Disease Study 2015

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Summary

Background Health outcomes are known to vary at both the country and local levels, but trends in mortality across a detailed and comprehensive set of causes have not been previously described at a very local level. Life expectancy in King County, WA, USA, is in the 95th percentile among all counties in the USA. However, little is known about how life expectancy and mortality from different causes of death vary at a local, neighbourhood level within this county. In this analysis, we estimated life expectancy and cause-specific mortality within King County to describe spatial trends, quantify disparities in mortality, and assess the contribution of each cause of death to overall disparities in all-cause mortality.

Methods We applied established so-called garbage code redistribution algorithms and small area estimation methods to death registration data for King County to estimate life expectancy, cause-specific mortality rates, and years of life lost (YLL) rates from 152 causes of death for 397 census tracts from Jan 1, 1990, to Dec 31, 2014. We used the cause list developed for the Global Burden of Disease 2015 study for this analysis. Deaths were tabulated by age group, sex, census tract, and cause of death. We used Bayesian mixed-effects regression models to estimate mortality overall and from each cause.

Findings Between 1990 and 2014, life expectancy in King County increased by 5·4 years (95% uncertainty interval [UI] 5·0–5·7) among men (from 74·0 years [73·7–74·3] to 79·3 years [79·1–79·6]) and by 3·4 years (3·0–3·7) among women (from 80·0 years [79·7–80·2] to 83·3 years [83·1–83·5]). In 2014, life expectancy ranged from 68·4 years (95% UI 66·9–70·1) to 86·7 years (85·0–88·2) for men and from 73·6 years (71·6–75·5) to 88·4 years (86·9–89·9) for women among census tracts within King County. Rates of YLL by cause also varied substantially among census tracts for each cause of death. Geographical areas with relatively high and relatively low YLL rates differed by cause. In general, causes of death responsible for more YLLs overall also contributed more significantly to geographical inequality within King County. However, certain causes contributed more to inequality than to overall YLLs.

Interpretation This census tract-level analysis of life expectancy and cause-specific YLL rates highlights important differences in health among neighbourhoods in King County that are masked by county-level estimates. Efforts to improve population health in King County should focus on reducing geographical inequality, by targeting those health conditions that contribute the most to overall YLLs and to inequality. This analysis should be replicated in other locations to more fully describe fine-grained local-level variation in population health and contribute to efforts to improve health while reducing inequalities.

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Introduction

For the past two decades, the Global Burden of Disease (GBD) studies[1,2]—a systematic and comprehensive effort to measure and compare population health globally—have documented large differences among countries across a wide range of health outcomes. Other research has long shown that certain health outcomes vary, often drastically, subnationally, at the first or second administrative level[3–7] and on a much more local scale.[8–13] There have been efforts to combine these two approaches and describe a comprehensive set of health outcomes at the first or second administrative level in selected countries.[1,14,15] This research has highlighted substantial subnational variation across a wide range of health outcomes. However, this type of comprehensive investigation has not been done at more local levels.

Previous analyses done at very local levels are limited to a relatively small set of health outcomes and locations, primarily because of the scarcity of appropriate data (in particular, the absence of precise geographical

Research in context

Evidence before this study

In the USA, a large and growing body of evidence suggests that population health outcomes vary substantially among counties, even those within the same state or in close geographical proximity. A small number of studies have examined how certain measures of population health vary on a finer geographical scale and revealed further disparities within counties. However, the statistical challenges posed by the small numbers and limited availability of appropriate data with precise geographical information have hindered attempts to comprehensively describe local variation in health outcomes within counties. To our knowledge, no systematic and comprehensive analysis has been done to explore population health outcomes at a census tract level within the USA.

Added value of this study

This study applies recently developed small area estimation methods to mortality data in King County, WA, USA, to estimate life expectancy and rates of death and years of life lost from 152 causes at the census tract level. These estimates make it possible to describe within-county disparities, identify neighbourhoods where the burden of specific causes of death is much higher than in the county as a whole, describe the most significant causes of death in any particular neighbourhood, and evaluate the contributions of different causes of death to overall inequalities in years of life lost within King County.

Implications of all the available evidence

Health outcomes can vary substantially even within relatively small areas. Geographically precise information on a wide range of health outcomes is required to pinpoint the particular health needs of each community and to identify and combat avoidable disparities.

information in otherwise suitable datasets) as well as the statistical challenges posed by the very small numbers at this level of analysis. Death registration systems are an important potential source of data for use in analyses of local trends in health outcomes: death registration data are typically accompanied by very precise geographical information (eg, street addresses, although this level of detail might be difficult to obtain in practice) and include information about a wide array of health outcomes. A new small area estimation approach has been developed for estimation of cause-specific mortality on the basis of death registration data at the county level in the USA.[16] These models have been validated and found to perform well even in populations as small as 1000, and thus could also be used for analyses at more local levels, both in the USA and in other countries with similar high-quality death registration data.

See Online for appendix

To show the feasibility and value of these methods for estimation of a wide range of health outcomes at a very local level, we considered King County, WA, USA. King County—which includes the city of Seattle, surrounding cities and suburbs, and more rural areas in the Cascade mountain range—has a population of more than 2 million and ranks among the top 5% of counties in the USA in terms of both household income and life expectancy.[17–19] Nonetheless, among different regions and neighbourhoods within King County there is considerable variation in levels of education, poverty, and racial and ethnic composition. Previous research by the local health department (Public Health—Seattle & King County) has found almost a 10-year gap between the lowest and highest life expectancies observed in 48 Health Reporting Areas in King County.[20] However, more granular information, particularly related to specific causes of death, has not been produced.

In this analysis, we estimated life expectancy and cause-specific mortality for 152 causes of death from 1990 to 2014 for each of King County's 397 census tracts. We then used these estimates to describe spatial trends and to quantify disparities in mortality within King County. We also assessed the contribution of each cause of death to overall disparities in all-cause mortality in King County.

Methods

Overview

In this census tract-level analysis, we estimated life expectancy at birth, cause-specific mortality rates, and years of life lost (YLL) rates by cause for each of King County's 397 census tracts (appendix p 36) annually from 1990 to 2014. Broadly, there were three steps in this process. First, death registration data were tabulated by cause and redistribution algorithms were applied to account for the presence of so-called garbage codes (codes that are implausible or insufficiently specific) in these data.[1,21] Second, small area models were used to generate estimates of all-cause and cause-specific mortality rates by census tract, year, and age.[16] Third, estimated age-specific mortality rates were used to construct estimates of life expectancy at birth, age-standardised mortality rates by cause, and age-standardised YLL rates by cause in each census tract and year. The sections below describe the set of causes analysed and each step of this process. We also describe how we decomposed variation in the overall (all-cause) YLL rate by cause. This research received institutional review board approval from the University of Washington (Seattle, WA, USA).

Cause list

We used the cause list developed for the GBD 2015 study for this analysis.[1] This cause list is arranged hierarchically

in four levels, and within each level the causes are mutually exclusive and collectively exhaustive. For this analysis, we included all causes of death in the GBD hierarchy for which there were at least 75 deaths in King County between 1990 and 2014 (these causes represent 99·9% of all deaths recorded during this period). The appendix (pp 10–16) lists all fatal causes in the GBD hierarchy and indicates whether each cause was included or excluded from this analysis.

Data

We obtained records of all deaths that occurred among King County residents between Jan 1, 1990, and Dec 31, 2014, from the Center for Health Statistics, Washington State Department of Health. We extracted age, sex, underlying cause of death, and place of residence (ie, census tract) at time of death for each decedent. Underlying cause of death codes were recorded with the International Classification of Diseases, revisions 9 (1990–98) and 10 (1999–2014), and were mapped to the GBD cause list (appendix pp 17–28). For deaths that were found to have been assigned garbage codes, previously described garbage code redistribution algorithms were used to reassign these deaths to likely true underlying causes (further information is available in the appendix).[1,16] Deaths were tabulated by age group (<1 years, 1–4 years, 5–9 years, and with 5-year age bands continuing up to 80–84 years, and ≥85 years), sex, census tract, and cause of death.

Population counts by age group and sex for each census tract were obtained from the Washington State Office of Financial Management (OFM). These estimates are based on census data and information on changes in housing stock, and are updated on an annual basis. We also made use of four covariates: the proportion of the population that is black; the proportion of the population that is Hispanic; the proportion of the adult population that has graduated college; and an indicator for census tracts where more than 25% of the population comprises college or graduate students. The first two covariates were derived from the OFM population files, which included information by race and ethnicity. The last two covariates were derived from data collected in the decennial census and in the American Community Survey (an annual survey series done by the US Census Bureau starting in 2005 to supplement data from the decennial census).

Small area model

Following the method described by Dwyer-Lindgren and colleagues,[16] we applied Bayesian mixed-effects regression models to estimate mortality overall and from each cause. These models were specified as $D_{j,t,a} \sim \text{Poisson}(m_{j,t,a} \cdot P_{j,t,a})$ and $\log(m_{j,t,a}) = \beta_0 + \boldsymbol{\beta}_1 \cdot \mathbf{X}_{j,t} + \gamma_{1,a,t} + \gamma_{2,j} + (\gamma_{3,j} \cdot t + \gamma_{4,j,t}) + (\gamma_{5,j} \cdot a + \gamma_{6,j,a})$, where $D_{j,t,a}$ is the number of deaths, $P_{j,t,a}$ the population, and $m_{j,t,a}$ the underlying mortality rate in census tract j, year t, and age group a; β_0 is a fixed intercept; $\boldsymbol{\beta}_1$ is the vector of fixed covariate effects; $\gamma_{1,a,t}$ are age-level and year-level random effects; $\gamma_{2,j}$ are census tract-level random effects; $\gamma_{3,j}$ and $\gamma_{4,j,t}$ are census tract-level and year-level random effects; and $\gamma_{5,j}$ and $\gamma_{6,j,a}$ are census tract-level and age-level random effects. $\gamma_{1,a,t}$, $\gamma_{2,j}$, $\gamma_{3,j}$, and $\gamma_{5,j}$ were assigned conditional autoregressive priors;[22,23] $\gamma_{4,j,t}$ and $\gamma_{6,j,a}$ were assigned mean-zero Normal priors. Gamma(0, 1000) hyperpriors were assigned for the inverse variance of each random effect and Normal(0, 1·5) hyperpriors were assigned for the logit-transform of the correlation parameters in $\gamma_{1,a,t}$, $\gamma_{2,j}$, $\gamma_{3,j}$, and $\gamma_{5,j}$. Further information about the small area model is available in the appendix.

The models were fitted with the Template Model Builder package[24] in R version 3.2.4.[25] For the purposes of fitting these models at the tract-level, β_0 was fixed at $\sum_a \sum_t \log(m_{t,a}) / (n_a \cdot n_t)$ and $\gamma_{1,a,t}$ was fixed at $\log(m_{t,a}) - \sum_a \sum_t \log(m_{t,a}) / (n_a \cdot n_t)$, where $m_{t,a}$ is the mortality rate for the county as a whole in year t and age group a as previously estimated.[16] Predicted mortality rates were raked (ie, scaled) to ensure consistency between different levels of the cause hierarchy (ie, the sum of all subcauses is equal to the parent cause anywhere in the hierarchy) and between tract-level and county-level estimates (ie, for any given cause, the county-level estimate is equal to the population-weighted average of the tract-level estimates).[26] During raking, causes in the GBD hierarchy that were excluded from this analysis were subtracted from the totals assuming that the fraction of total deaths due to these causes was the same in every tract as in the county as a whole. Age-specific mortality rates were age-standardised by use of the US 2010 Census population as the standard.

Calculation of life expectancy and years of life lost

Life expectancy at birth was calculated on the basis of estimated age-specific all-cause mortality rates. We used the method described by Wang and colleagues[27] to extrapolate mortality rates at older ages and then applied standard demographic techniques to construct period life tables for each census tract and year.[28] Life expectancy at birth was extracted from these life tables for every census tract and year.

Age-standardised YLL rates were constructed on the basis of estimated age-specific all-cause and cause-specific mortality rates. First, age-specific YLL rates were calculated for each cause, tract, and year by multiplying the age-specific mortality rate by life expectancy at the average age of death in each age group from the reference life table from the GBD 2015 study.[1] Age-specific YLL rates were then age-standardised by use of the US 2010 Census population as the standard. Additionally, county-level age-standardised YLL rates were constructed by use of the same procedure based on previously estimated mortality rates.[16]

Uncertainty

To quantify uncertainty around all estimates, we generated 1000 draws from the posterior distribution of

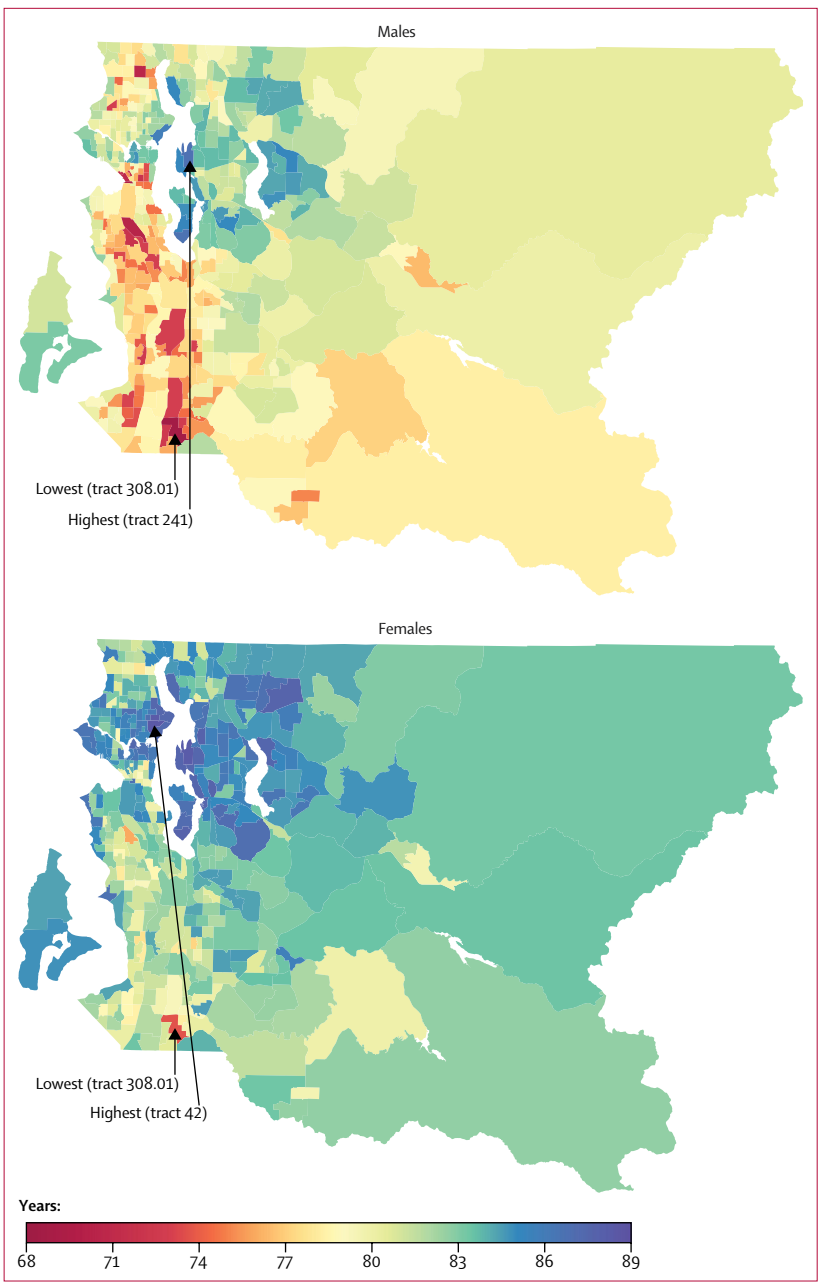

Figure 1: **Life expectancy at birth by census tract in King County, WA, 2014**

the mortality rate for each cause, tract, year, age, and sex, and did all subsequent calculations for each draw. The final point estimates for all quantities (ie, mortality rates, YLL rates, and life expectancy) were derived from the mean of these 1000 draws and the 95% uncertainty intervals (95% UIs) were derived from the 2·5th and 97·5th percentiles. When comparing two time periods or locations, differences were considered to be statistically significant if the posterior probability that the quantity of interest in one time period or location was greater than the other exceeded 95%.

Decomposing variation in the YLL rate by cause

To quantify the contribution of each individual cause to overall disparities among census tracts in the age-standardised YLL rate, we constructed counterfactual scenarios that eliminated disparities in mortality from each cause in turn. Specifically, we considered a scenario where all tracts had the lowest observed YLL rate from the selected cause (by age, sex, and year) and then recalculated the age-standardised all-cause YLL rate in each tract under these new conditions. For each cause, we calculated the percentage reduction in the SD (a measure of absolute disparity) of the all-cause YLL rate in the corresponding counterfactual scenario compared with what was observed. We report percentage reductions to highlight the relative contribution of each cause to overall disparities.

Role of the funding source

The funders of this study had no role in study design, data collection, data analysis, data interpretation, or writing of the report. All authors had full access to all the data in the study and had final responsibility for the decision to submit for publication.

Results

Census tract populations for King County varied from 493 to 12 686 across all years, with a median value of 4376. 289 425 deaths were recorded in King County between 1990 and 2014; the number of deaths per census tract per year varied from 0 to 139, with a median of 25. For a small minority of deaths (1·35%), no information on residence was available beyond the city or county; these deaths were redistributed to all census tracts within the city or county, in proportion to the population in each census tract. 21·2% of all recorded deaths were found to have been assigned garbage codes and were reassigned to likely true underlying causes.

In 2014, life expectancy in King County was 79·3 years (95% UI 79·1–79·6) among men and 83·3 years (83·1–83·5) among women, placing King County in the 95th percentile for men and 93rd percentile for women, among all counties, in terms of life expectancy. Within King County, life expectancy among men ranged from a low of 68·4 years (95% UI 66·9–70·1) in tract 308.01 in Auburn to a high of 86·7 years (85·0–88·2) in tract 241 in Clyde Hill. Life expectancy among women ranged from a low of 73·6 years (95% UI 71·6–75·5), also in tract 308.01 in Auburn, to a high of 88·4 years (86·9–89·9) in tract 42 in the Bryant neighbourhood in northeast Seattle (figure 1).

Despite the relatively high life expectancy in King County overall compared with other US counties, there was substantial overlap between the distribution of tract-level life expectancy in King County and the distribution of county-level life expectancy in the USA (figure 2).[19] For men in 2014, no US county had higher life expectancy than the best-off tract in King County, and only 31 (1%) of 3110 counties had lower life expectancy than the worst-off tract in King County. For women in 2014, only one county

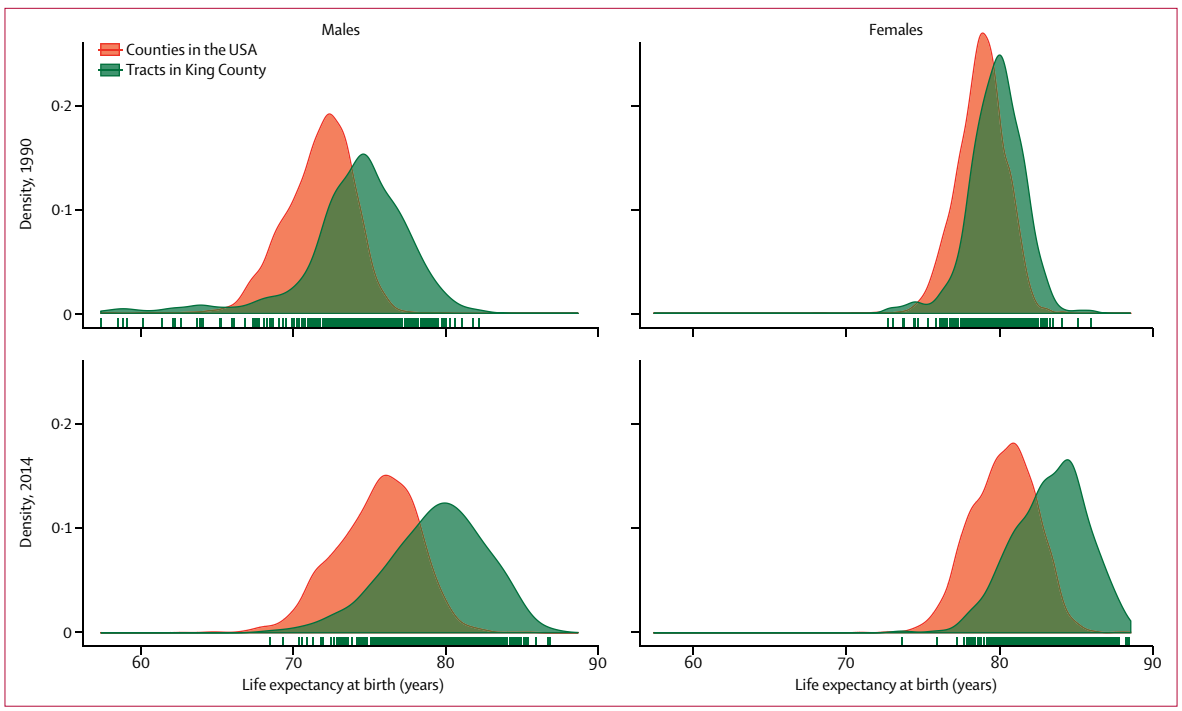

Figure 2: **Distribution of tracts in King County, WA, and counties in the USA by life expectancy at birth in 1990 and 2014**

(Summit, Colorado) had higher life expectancy than the best-off tract in King County, while only four counties (Oglala Lakota, South Dakota; Todd, South Dakota; Sioux, North Dakota; and Buffalo, South Dakota) had lower life expectancy than the worst-off tract in King County.

Between 1990 and 2014, life expectancy in King County increased by 5·4 years (95% UI 5·0–5·7) among men (from 74·0 years [73·7–74·3] to 79·3 years [79·1–79·6]) and by 3·4 years (3·0–3·7) among women (from 80·0 years [79·7–80·2] to 83·3 years [83·1–83·5]). During this same period, we estimated a small decline in life expectancy among men in four tracts and among women in 18 tracts, but in all cases this decline was not statistically significant. We estimated increases in life expectancy in all other tracts (statistically significant in 353 [89%] of 397 tracts for men and in 291 [73%] of 397 tracts for women), but the magnitude of these increases varied widely, from minimal improvement to 16·7 years (95% UI 13·5–20·1) gained for men in tract 75 in the Capitol Hill neighbourhood of Seattle, and 8·1 years (5·2–10·9) years gained for women in tract 82 in the central business district of Seattle (figure 3; appendix p 37).

The gap between the lowest and highest life expectancy among tracts in King County declined by 26·1% for men, from 24·7 years to 18·2 years, but increased by 12·2% for women, from 13·2 years to 14·8 years, between 1990 and 2014. The corresponding IQRs increased by 15·8% (from 3·7 years to 4·3 years) for men and by 60·1% (from 2·1 years to 3·4 years) for women between 1990 and 2014.

In 2014, the ten leading causes of YLL (reflecting the third level of the GBD cause hierarchy) were ischaemic heart disease (12·7%); tracheal, bronchus, and lung cancer (6·3%); self-harm (5·2%); Alzheimer's disease and other dementias (5·2%); drug use disorders (4·5%); cerebrovascular disease (4·4%); cirrhosis and other chronic liver diseases (3·6%); chronic obstructive pulmonary disease (3·3%); diabetes mellitus (2·7%); and colon and rectum cancer (2·7%). For all these causes, the age-standardised YLL rate in King County was below that in the USA as a whole, although this difference was not significant for drug use disorders and for Alzheimer's disease and other dementias. Among all causes responsible for 1% or more of total YLLs, King County had higher age-standardised YLL rates than the USA as a whole only for liver cancer (9·4% [95% UI 0·9–19·4] higher), brain and nervous system cancer (6·9% [0·8–12·8] higher), and falls (4·9% [0·6–9·5] higher). Nonetheless, the highest YLL rates observed among tracts in King County exceeded the highest rates observed among counties in the USA for several causes, including Alzheimer's disease and other dementias, drug use disorders, breast cancer, pancreatic cancer, congenital anomalies, and brain and nervous system cancer.

Spatial patterns in age-standardised YLL rates varied among causes (figure 4; appendix pp 38–190). Many causes followed a similar general pattern to life expectancy, with the highest YLL rates found primarily in tracts in downtown Seattle, south Seattle, and the southern suburbs, and the lowest YLL rates found primarily in Mercer Island and other eastside cities. However, several causes showed markedly different spatial patterns: for example, the highest YLL rates from road injuries were

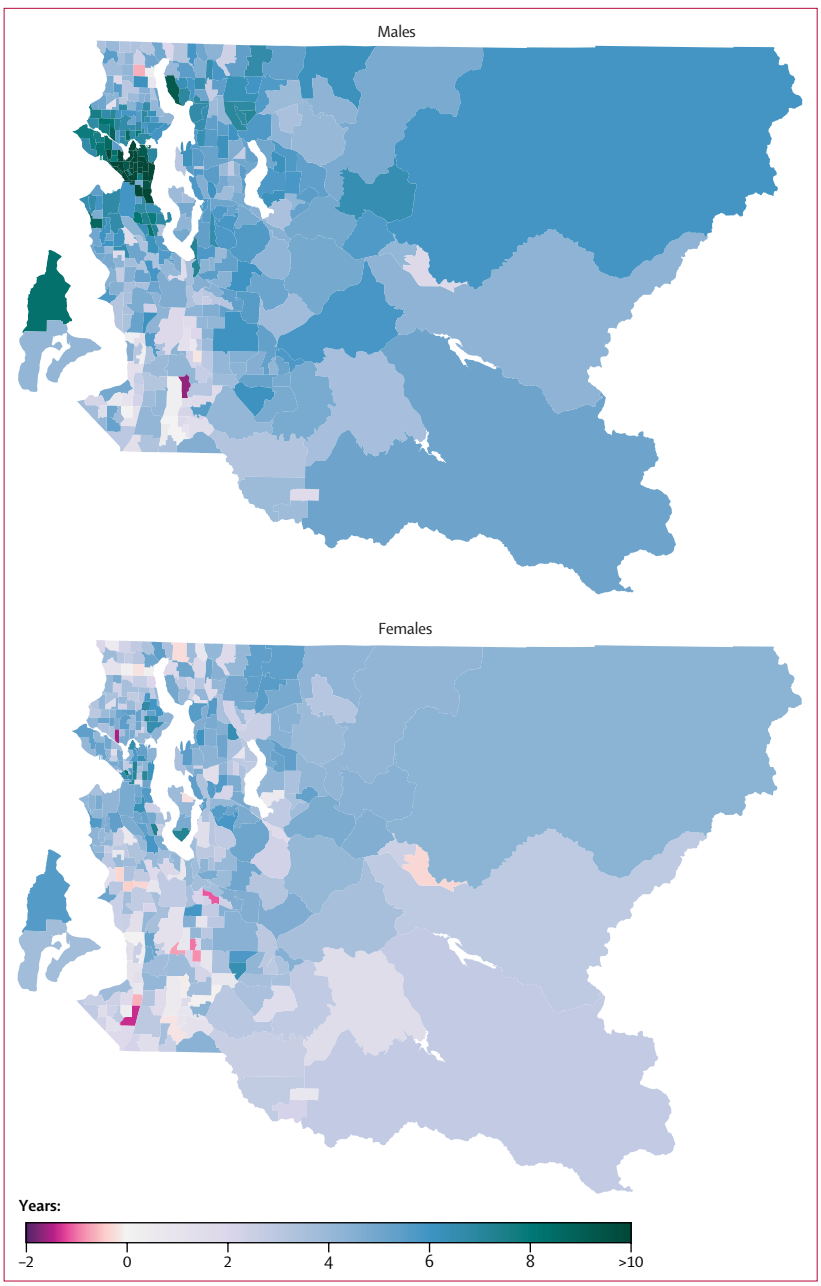

Figure 3: **Change in life expectancy at birth by census tract in King County, WA, 1990–2014**

For the **interactive IHME Viz Hub US Health Map** see https://vizhub.healthdata.org/subnational/usa/wa/king-county

found primarily in southeastern King County, whereas the highest YLL rates from drug use disorders were tightly concentrated in downtown Seattle (figure 4).

Between 1990 and 2014, age-standardised YLL rates decreased for most, but not all, causes. Among causes responsible for 1% or more of total YLLs in 2014, the age-standardised YLL rate increased significantly for drug use disorders (263·7% [95% UI 199·5–347·3]), chronic kidney disease (56·9% [49·0–65·6]), liver cancer (90·3% [65·5–116·4]), endocrine, metabolic, blood, and immune disorders (65·7% [49·7–80·1]), and falls (10·5% [3·6–18·6]; figure 5; appendix pp 66, 133, 140, 149, 173). For several causes, the age-standardised YLL rate decreased in all census tracts (tracheal, bronchus, and lung cancer; road injuries; and cardiomyopathy and myocarditis) or increased in all tracts (drug use disorders). For most causes, however, we identified both tracts that showed increases and tracts that showed decreases. As with spatial patterns in YLL rates, the spatial patterns in changes in YLL rates varied substantially by cause (figure 5; appendix pp 38–190).

Geographical inequality declined between 1990 and 2014 for several prominent causes of death, including ischaemic heart disease (20·9% decline in the IQR for the age-standardised YLL rate; 50·9% decline in the range), self-harm (5·7% decline in the IQR; 44·7% decline in the range), and Alzheimer's disease and other dementias (12·9% decline in the IQR; 20·4% decline in the range; appendix pp 29–31). Over the same period, geographical inequality increased substantially for several other causes, including drug use disorders (226·8% increase in the IQR for the age-standardised YLL rate; 104·2% increase in the range), chronic kidney disease (287·8% increase in the IQR; 6·7% increase in the range), liver cancer (342·5% increase in the IQR; 112·6% increase in the range), and endocrine, metabolic, blood, and immune disorders (178·1% increase in the IQR; 151·7% increase in the range; appendix pp 29–31).

Estimates of life expectancy and cause-specific mortality and YLL rates for all tracts by year and sex are available online in an interactive data visualisation (IHME Viz Hub US Health Map).

In 2014, the largest contributors to absolute disparities in the all-cause YLL rate for men were ischaemic heart disease (18·1%); drug use disorders (8·0%); tracheal, bronchus, and lung cancer (6·7%); cirrhosis and other chronic liver diseases (5·8%); and self-harm (4·5%). For women the largest contributors were ischaemic heart disease (13·8%); tracheal, bronchus, and lung cancer (7·6%); Alzheimer's disease and other dementias (6·6%); cerebrovascular disease (5·7%); and chronic obstructive pulmonary disease (5·1%; figure 6; appendix pp 32–34). In general, causes responsible for a larger percentage of total YLLs also contributed more significantly to disparities in the all-cause YLL rate than did causes responsible for a smaller percentage of total YLLs. However, some causes—most notably, ischaemic heart disease; drug use disorders; cirrhosis and other chronic liver diseases; diabetes mellitus; tracheal, bronchus, and lung cancer; and chronic obstructive pulmonary disease—contributed to disparities substantially more than their share of total YLLs would suggest. Conversely, causes such as self-harm, Alzheimer's disease and other dementias, and breast cancer (for women) contributed substantially less to overall disparities than to total YLLs.

Discussion

At the county level, life expectancy in King County is among the highest in the USA. There are nonetheless substantial

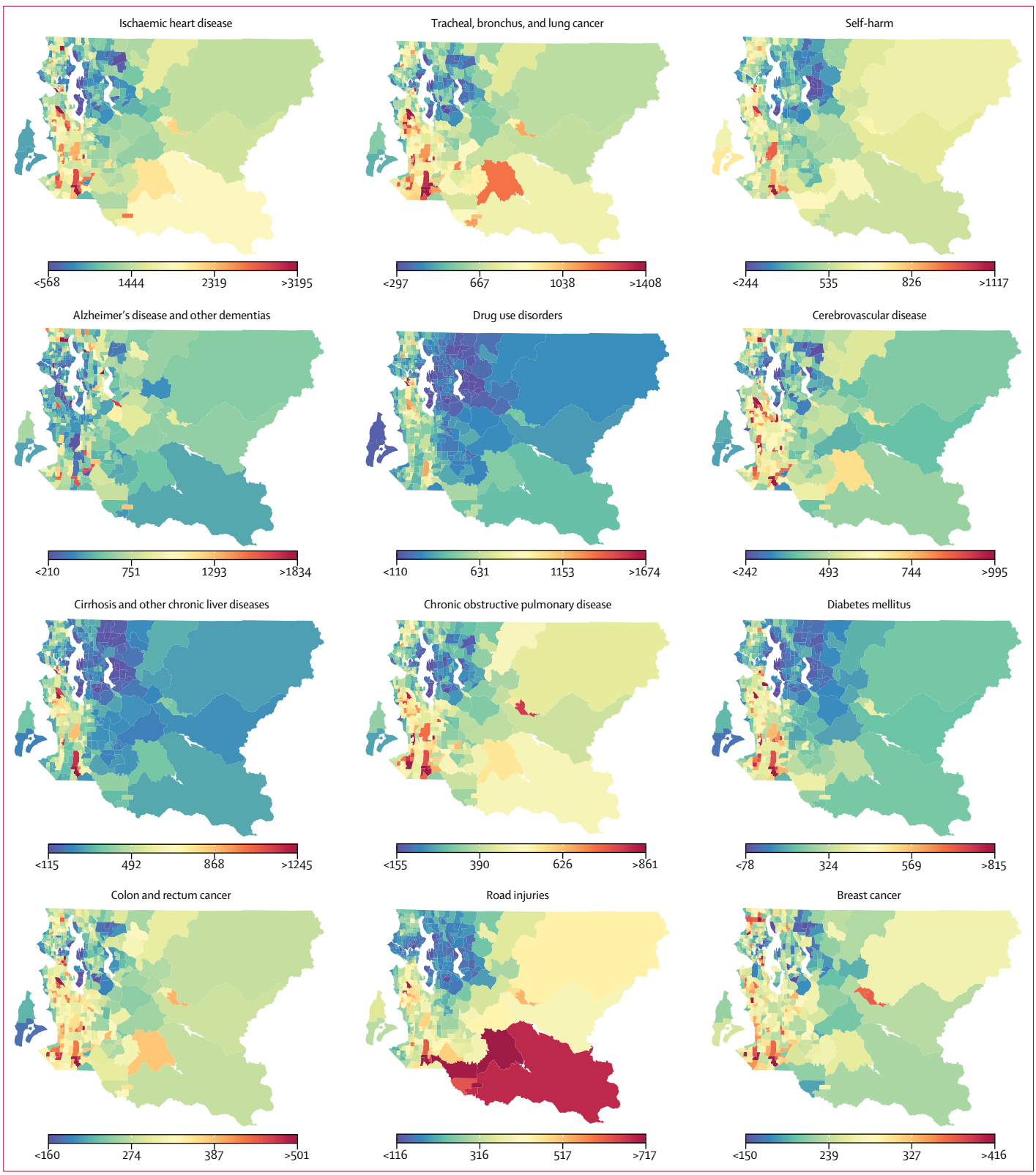

***Figure 4*: Age-standardised YLL rates by census tract and cause in King County, WA, 2014**
YLL=years of life lost. Age-standardised YLL rates by census tract and cause for all 152 causes of death are shown in the appendix (pp 38–190).

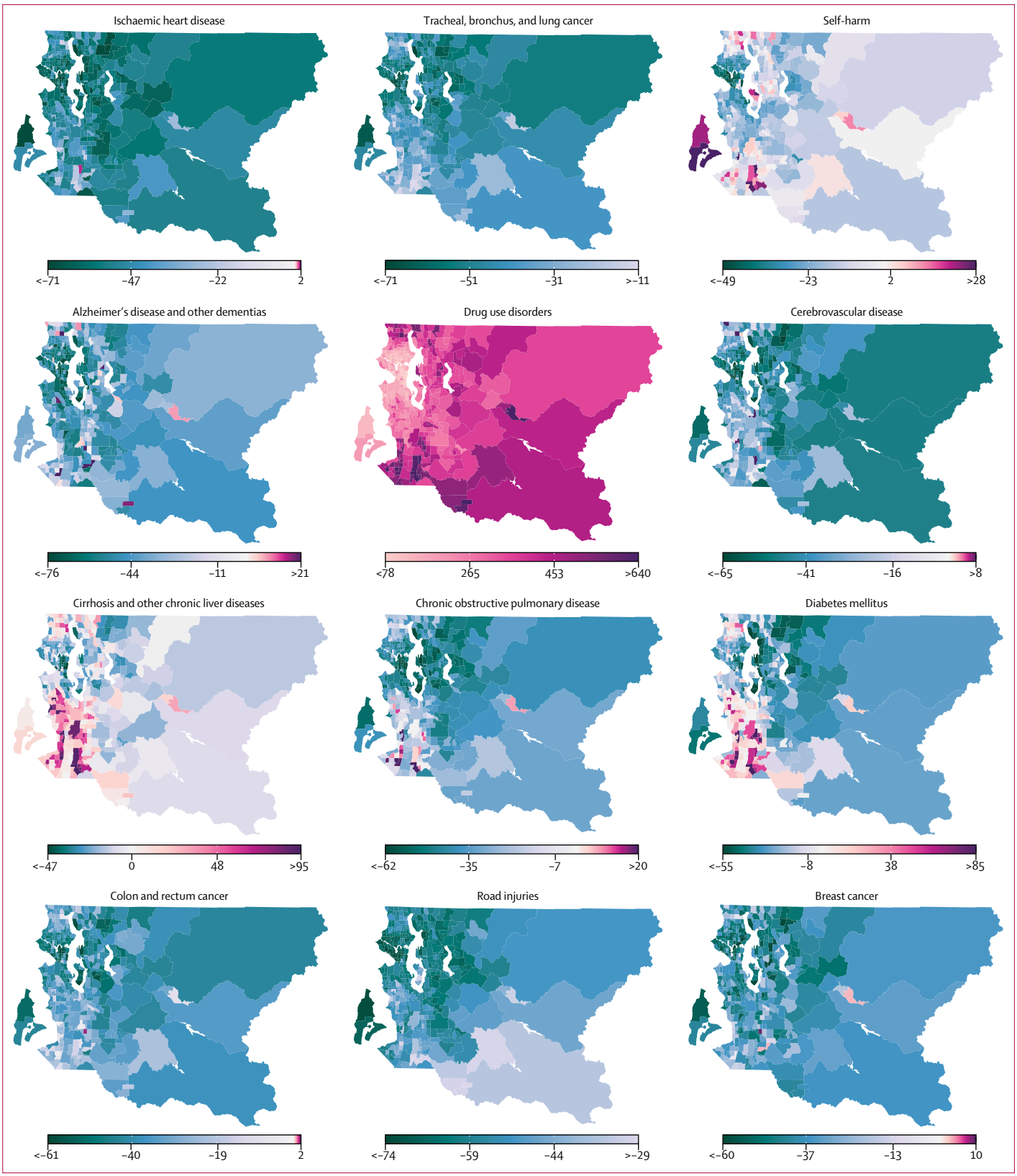

***Figure 5*: Change in age-standardised YLL rates by census tract and cause in King County, WA, 1990–2014**
YLL=years of life lost. Age-standardised YLL rates by census tract and cause for all 152 causes of death are shown in the appendix (pp 38–190).

disparities within this region: in 2014, we found a gap of more than 18 years for men and more than 14 years for women between communities with the lowest and highest life expectancies. County-wide estimates of life expectancy effectively hide communities within the county where life expectancy is much lower, in some cases close to the lowest levels observed anywhere in the USA. Beyond life expectancy, we find that mortality varies substantially within King County for every cause of death. Disparities in overall mortality are not driven by any single cause or small group of causes, but are instead the cumulative effect of disparities across a wide range of health conditions. Although causes that are responsible for larger shares of YLLs are typically also responsible for larger proportions of the overall disparities in mortality within King County, several causes (eg, ischaemic heart disease and drug use disorders) have an outsized influence on these disparities.

With respect to changes during the study period, we identified widely varied, and in some cases divergent, trends in life expectancy among tracts. There was also some evidence of increasing geographical inequalities in life expectancy in recent decades: the range of the observed life expectancy increased for women (although not for men) and the gap between the 25th and 75th percentile increased for both men and women between 1990 and 2014. Rates of change in YLLs for various causes of death were similarly variable and for many causes (eg, cirrhosis and other chronic liver diseases, and diabetes mellitus) we identified both tracts that experienced substantial decreases in mortality and tracts that had substantial increases in mortality between 1990 and 2014. During this period, geographical inequality declined for several prominent causes of death (eg, ischaemic heart disease and self-harm) but increased for other causes (eg, drug use disorders; chronic kidney disease; liver cancer; and endocrine, metabolic, blood, and immune disorders).

This study goes beyond previous analyses of trends in health outcomes within King County[20] in three ways: first, by considering outcomes for each of King County's 397 census tracts, instead of the 48 Health Reporting Areas; second, by considering cause-specific mortality and YLL rates in addition to life expectancy; and third, by considering trends over an extended period of time rather than analysing a single point in time. With respect to geographical granularity, this study confirms earlier findings of substantial variation in life expectancy within King County. In fact, we find much larger geographical disparities at the census tract level than previously reported at the coarser Health Reporting Area level. The disparities observed among census tracts within King County rival those observed among counties in the rest of the USA, underscoring the need to look beyond state-level and county-level measurements and to consider how health varies on a small geographical scale. Beyond

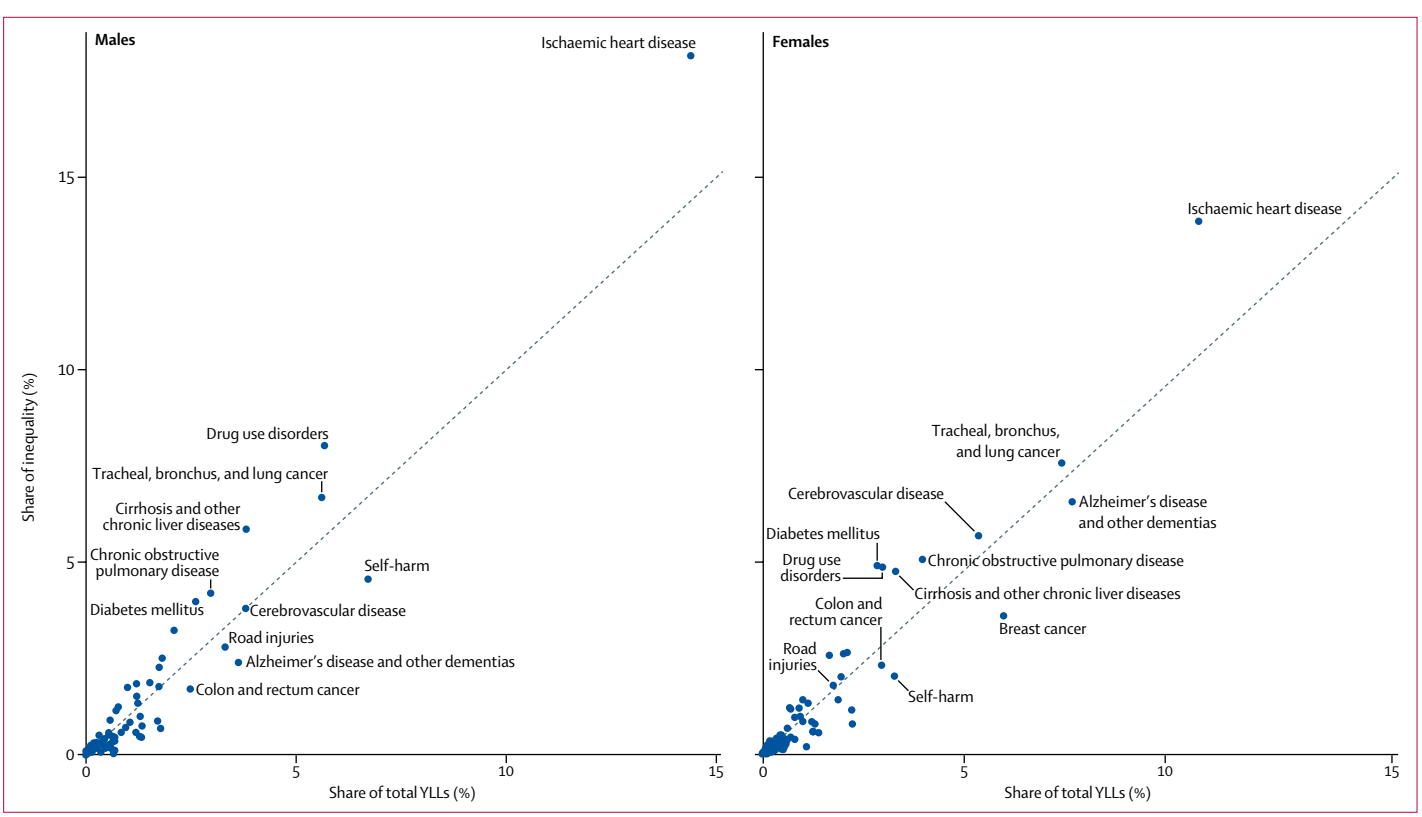

***Figure 6*: Contribution to geographical inequality in age-standardised YLL rates and share of total YLLs by cause, 2014**
YLL=years of life lost. Data on the contribution to inequality in age-standardised YLL rates and share of total YLLs for all 152 causes are shown in the appendix (pp 32–34).

King County, the combination of a very fine level of geographical detail with a comprehensive and detailed cause list is, to our knowledge, unique to this analysis.

The results of this analysis have several implications for King County. First, many causes of death, including several leading causes such as ischaemic heart disease, follow a generally similar pattern that is in turn reflected in maps of life expectancy. This pattern across a number of causes of death suggests common underlying determinants—such as socioeconomic conditions or the prevalence of risk factors such as smoking prevalence—that drive a wide range of health outcomes. Identification and targeting of these underlying determinants is essential for improving health in the most negatively affected neighbourhoods. At the same time, other causes of death (eg, road injuries) have different spatial patterns, suggesting distinct aetiologies that potentially require a different public health response. Second, many causes identified as contributing significantly to lost years of life and geographical inequality in King County have well established risk factors. For example, 18% of all YLLs in the USA, including 19% of YLLs as a result of ischaemic heart disease, 86% of YLLs as a result of tracheal, bronchus, and lung cancer, 17% of YLLs as a result of cerebrovascular disease, and 81% of YLLs as a result of chronic obstructive pulmonary disease, have previously been attributed to tobacco smoke.[29] Other risk factors, such as poor diet, high blood pressure, high body-mass index, high fasting plasma glucose, high cholesterol, low physical activity, and drug and alcohol use, have similarly been linked to causes of death responsible for significant disease burden and geographical inequality in King County.[29] Addressing these risk factors is an important step towards improving health and reducing inequalities in King County. Future research should focus on describing temporal and spatial patterns in these risk factors at a local level within King County to further inform these efforts. Finally, differences in access to or quality of health care might also have a role in explaining differences in health outcomes in King County. Previous research has identified various health conditions (eg, colon and rectum cancer, diabetes mellitus, and maternal disorders) that are highly amenable to treatment and have been proposed (because of their high mortality) as markers of inadequate access to or poor quality of health care.[30] We found substantial variation in mortality from these causes among tracts in King County, suggesting that access to and utilisation of high-quality care is not uniform across all neighbourhoods. This, too, is an important area for further research and attention when considering how to improve health and reduce inequalities in King County.

The results of this analysis also have broader implications. To our knowledge, this study is the first to simultaneously consider such a local level of analysis as well as a detailed and comprehensive set of causes. The significant small-scale geographical variation across multiple health outcomes described in this analysis for King County is likely to be the rule rather than an exception. An efficient and effective policy and public health response requires information about this small-scale variation to appropriately design and target intervention strategies. In particular, this type of information can be used to design strategies that not only improve health overall but also specifically address persistent inequalities. The methodology described here could be replicated in other settings where similar death registration data are available. Moreover, it could be adapted for use with other data sources to describe spatial and temporal trends in key risk factors and the morbidity (not just mortality) caused by various health conditions. At the same time, when producing and using these data it will be important to take care to not further stigmatise already vulnerable populations.[31]

This analysis is subject to various limitations. First, all the data sources used are subject to error: for the death registration data, any of the variables used (eg, age, residence, cause of death) could be subject to misreporting; the population counts and covariates used are themselves estimates and are associated with some uncertainty. Second, the garbage code redistribution algorithms have not been validated against a gold standard such as autopsy because of the absence of such data. Moreover, the garbage code redistribution process is inherently uncertain, but it is not currently possible to quantify this uncertainty and it has consequently not been accounted for in the uncertainty intervals reported in this analysis. Consequently, these uncertainty intervals are likely to be too small for cause-specific quantities. Third, the small area models borrow strength by smoothing over space, time, and age groups, which allows for more precise predictions of the mortality rate but might, in some cases, attenuate unusually low or high mortality rates, causing us to underestimate true variation. Fourth, we report various measures of geographical inequality (ie, ranges, IQRs, and SDs) based on point estimates at the census tract level. This analysis is done for ease of interpretation, but it does not account for the uncertainty in those underlying point estimates. Fifth, we present results in the form of maps, but it is difficult to display uncertainty in this format. Additionally, presenting the data in this way can unintentionally give the impression that rates are constant within areas, when there is almost certainly substantial variation among individuals even within these relatively small populations. Sixth, our estimates for each year represent the population living in a given census tract in that particular year, but these populations might not be stable over time because of migration. We were not able to analyse the effect of migration on changes in life expectancy or cause-specific mortality over time; previous research in other settings has found that this effect can be substantial.[32,33]

In conclusion, the results of this analysis highlight the need to examine neighbourhoods within large counties to assess health needs at a highly local level. Indeed, as the national average masks disparities among states, and state averages mask disparities among counties, our

study shows that county averages can mask considerable disparities at a more local level. Public health is local, and similarly local information is required to increase awareness among residents and policy makers alike of the unique challenges facing communities. We hope that these findings will support action to reduce disparities and improve health.

Contributors

CJLM, AHM, and DF conceived the study. LD-L, RWS, AB-V, CC, and SBF did the statistical analyses. CM and SS provided managerial support. All authors participated in interpretation and summarisation of the results. LD-L wrote the first draft of the manuscript. All other authors (RWS, AB-V, CM, CC, SBF, SS, ADF, AL, EK, JSD, DF, AHM, and CJLM) critically reviewed the manuscript. All authors read and approved the final version submitted. CJLM had full access to all the data in the study and takes responsibility for the integrity of the data and accuracy of the data analysis.

Declaration of interests

AL and EK report grants from the de Beaumont Foundation. All other authors declare no competing interests.

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References

1 GBD 2015 Mortality and Causes of Death Collaborators. Global, regional, and national life expectancy, all-cause mortality, and cause-specific mortality for 249 causes of death, 1980–2015: a systematic analysis for the Global Burden of Disease Study 2015. *Lancet* 2016; **388:** 1459–544.

2 GBD 2015 DALYs and HALE Collaborators. Global, regional, and national disability-adjusted life-years (DALYs) for 315 diseases and injuries and healthy life expectancy (HALE), 1990–2015: a systematic analysis for the Global Burden of Disease Study 2015. *Lancet* 2016; **388:** 1603–58.

3 Pickle LW, Mungiole M, Jones GK, White AA. Atlas of United States mortality. Hyattsville, MD: National Center for Health Statistics, 1996. http://www.cdc.gov/nchs/products/other/atlas/atlas.htm (accessed July 26, 2017).

4 Storeygard A, Balk D, Levy M, Deane G. The global distribution of infant mortality: a subnational spatial view. *Popul Space Place* 2008; **14:** 209–29.

5 Thomas B, Dorling D, Smith GD. Inequalities in premature mortality in Britain: observational study from 1921 to 2007. *BMJ* 2010; **341:** c3639.

6 Chetty R, Stepner M, Abraham S, et al. The association between income and life expectancy in the United States, 2001–2014. *JAMA* 2016; **315:** 1750–66.

7 Wang Y, Li X, Zhou M, et al. Under-5 mortality in 2851 Chinese counties, 1996–2012: a subnational assessment of achieving MDG 4 goals in China. *Lancet* 2016; **387:** 273–83.

8 Asaria P, Fortunato L, Fecht D, et al. Trends and inequalities in cardiovascular disease mortality across 7932 English electoral wards, 1982–2006: Bayesian spatial analysis. *Int J Epidemiol* 2012; **41:** 1737–49.

9 Jonker MF, Congdon PD, van Lenthe FJ, Donkers B, Burdorf A, Mackenbach JP. Small-area health comparisons using health-adjusted life expectancies: a Bayesian random-effects approach. *Health Place* 2013; **23:** 70–78.

10 Zhang X, Holt JB, Lu H, et al. Multilevel regression and poststratification for small-area estimation of population health outcomes: a case study of chronic obstructive pulmonary disease prevalence using the Behavioral Risk Factor Surveillance System. *Am J Epidemiol* 2014; **179:** 1025–33.

11 Hunt BR, Tran G, Whitman S. Life expectancy varies in local communities in Chicago: racial and spatial disparities and correlates. *J Racial Ethn Health Disparities* 2015; **2:** 425–33.

12 National Center for Chronic Disease Prevention and Health Promotion. 500 cities: local data for better health. Atlanta, GA: Centers for Disease Control and Prevention, 2016. http://www.cdc.gov/500cities (accessed July 26, 2017).

13 AIDSVu. City HIV surveillance data. Data methods—ZIP code, census tract, community area/neighborhood/ward. https://aidsvu.org/data-methods/data-methods-zip-code-census-tract/#neighborhood-data (accessed July 26, 2017).

14 Zhou M, Wang H, Zhu J, et al. Cause-specific mortality for 240 causes in China during 1990–2013: a systematic subnational analysis for the Global Burden of Disease Study 2013. *Lancet* 2016; **387:** 251–72.

15 Newton JN, Briggs ADM, Murray CJL, et al. Changes in health in England, with analysis by English regions and areas of deprivation, 1990–2013: a systematic analysis for the Global Burden of Disease Study 2013. *Lancet* 2015; **386:** 2257–74.

16 Dwyer-Lindgren L, Bertozzi-Villa A, Stubbs RW, et al. US county-level trends in mortality rates for major causes of death, 1980–2014. *JAMA* 2016; **316:** 2385–401.

17 National Center for Health Statistics. Vintage 2014 bridged-race postcensal estimates for April 1, 2010, July 1, 2010–July 1, 2014, by year, county, single-year of age (0 to 85+ years), bridged race, Hispanic origin, and sex. June 30, 2015. http://www.cdc.gov/nchs/nvss/bridged_race.htm (accessed Dec 18, 2015).

18 US Census Bureau. Small area income and poverty estimates (SAIPE). State and county data files, 1989–2015. https://www.census.gov/did/www/saipe/data/statecounty/data/index.html (accessed Dec 28, 2015).

19 Dwyer-Lindgren L, Bertozzi-Villa A, Stubbs RW, et al. Inequalities in life expectancy among US counties, 1980 to 2014: temporal trends and key drivers. *JAMA Int Med* 2017; **177:** 1003–11.

20 Public Health Seattle & King County. Life Expectancy at Birth by Health Reporting Area, King County, Washington, 5-Year Average 2010–2014. 2015. http://www.kingcounty.gov/depts/health/data/~/media/depts/health/data/documents/population-maps/life-expectancy-at-birth-HRA.ashx. (accessed July 26, 2017).

21 Naghavi M, Makela S, Foreman K, O'Brien J, Pourmalek F, Lozano R. Algorithms for enhancing public health utility of national causes-of-death data. *Popul Health Metr* 2010; **8:** 9.

22 Leroux BG, Lei X, Breslow N. Estimation of disease rates in small areas: a new mixed model for spatial dependence. In: Statistical models in epidemiology, the environment, and clinical trials, vol 116. New York, NY: Springer-Verlag, 2000: 179–91.

23 Knorr-Held L. Bayesian modelling of inseparable space-time variation in disease risk. *Stat Med* 2000; **19:** 2555–67.

24 Kristensen K, Nielsen A, Berg CW, Skaug H, Bell B. TMB: automatic differentiation and Laplace approximation. *J Stat Softw* 2016; **70:** 1–21.

25 R Development Core Team. R: a language and environment for statistical computing. Vienna: R Foundation for Statistical Computing, 2011.

26 Fienberg SE. An iterative procedure for estimation in contingency tables. *Ann Math Stat* 1970; **41:** 907–17.

27 Wang H, Dwyer-Lindgren L, Lofgren KT, et al. Age-specific and sex-specific mortality in 187 countries, 1970–2010: a systematic analysis for the Global Burden of Disease Study 2010. *Lancet* 2012; **380:** 2071–94.

28 Preston SH, Heuveline P, Guillot M. Demography: measuring and modeling population processes. Malden, MA: Blackwell Publishers, 2001.

29 GBD 2015 Risk Factors Collaborators. Global, regional, and national comparative risk assessment of 79 behavioural, environmental and occupational, and metabolic risks or clusters of risks, 1990–2015: a systematic analysis for the Global Burden of Disease Study 2015. *Lancet* 2016; **388:** 1659–724.

30 GBD 2015 Healthcare Access and Quality Collaborators. Healthcare Access and Quality Index based on mortality from causes amenable to personal health care in 195 countries and territories, 1990–2015: a novel analysis from the Global Burden of Disease 2015 study. *Lancet* 2017; **390:** 231–66.

31 Katikireddi SV, Valles SA. Coupled ethical–epistemic analysis of public health research and practice: categorizing variables to improve population health and equity. *Am J Public Health* 2015; **105:** e36–42.

32 Brimblecombe N, Dorling D, Shaw M. Mortality and migration in Britain, first results from the British Household Panel Survey. *Soc Sci Med* 1999; **49:** 981–88.

33 Boyle P. Population geography: migration and inequalities in mortality and morbidity. *Prog Hum Geogr* 2004; **28:** 767–76.